Geographic Information Systems and Health Applications

Omar Khan

Idea Group Publishing

Geographic Information Systems and Health Applications

Omar A. Khan
Editor

Ric Skinner
Associate Editor

IDEA GROUP PUBLISHING

Hershey • London • Melbourne • Singapore • Beijing

Acquisitions Editor:	Mehdi Khosrow-Pour
Managing Editor:	Jan Travers
Development Editor:	Michele Rossi
Copy Editor:	Maria Boyer
Typesetter:	Amanda Appicello
Cover Design:	Integrated Book Technology
Printed at:	Integrated Book Technology

Published in the United States of America by
Idea Group Publishing (an imprint of Idea Group Inc.)
701 E. Chocolate Avenue
Hershey PA 17033-1240
Tel: 717-533-8845
Fax: 717-533-8661
E-mail: cust@idea-group.com
Web site: http://www.idea-group.com

and in the United Kingdom by
Idea Group Publishing
3 Henrietta Street
Covent Garden
London WC2E 8LU
Tel: 44 20 7240 0856
Fax: 44 20 7379 3313
Web site: http://www.eurospan.co.uk

Library of Congress Cataloging-in-Publication Data

Geographic information systems and health applications / Omar A. Khan [editor].
p. cm.
Includes bibliographical references and index.
ISBN 1-59140-042-2 (cloth)
1. Geographic information systems. 2. Public health--Data processing. 3. Medical care--Data processing. I. Khan, Omar A., 1973-

RA566 .G46 2002
362.1'0285--dc21
2002068750

eISBN 1-59140-076-7

British Cataloguing in Publication Data
A Cataloguing in Publication record for this book is available from the British Library.

Geographic Information Systems and Health Applications

Table of Contents

SECTION I: HEALTH DISPARITIES & COMMUNITY HEALTH ISSUES

SECTION II: GIS & CANCER

SECTION III: INFECTIOUS DISEASE & INTERNATIONAL HEALTH

SECTION IV: HOSPITALS & HEALTHCARE

Foreword

I am very pleased and honored that Omar Khan asked me to assist him in developing this book, *Geographic Information Systems and Health Applications*. Omar and I developed and co-chaired the first two International Health Geographics Conferences in 1998 (Baltimore) and 2000 (Washington, DC). The nearly 500 attendees at those two conferences were exposed to tremendously exciting and informative applications of this relatively "new" technology—new at least in the health. I believe those conferences, as well as several others in recent years, provided many of the contributions to this book, or were the impetus for new work which you will read about here.

"Health Geographics" is a term that came into existence in the mid-1990s when I began to ask if anyone was using GIS technology in the areas of healthcare, health resources, health systems and health science. I was amazed at the number and variety people around the world who were doing truly innovative things, yet thinking they were in a very small minority. In fact, when I explored further and asked if there were any conferences that catered to this group of researchers, I found little happening. When I asked if there should be a 'health geographics' conference, many said yes, but an even surprising number sent me abstracts and asked "When?" and "Where?" I'm saying all this to illustrate that there has been a real need for conferences such as those, and books such as these. There will be many more of both as this powerful GIS technology is woven even deeper into the fabric of healthcare and related health disciplines.

As the first conferences unfolded, we saw many GIS applications focused on problems such as dengue fever, malaria, immunization programs, hospital catchment area mapping, managing habitats for Lyme disease, etc.—all very interesting and excellent uses of this technology. Health Geographics has matured greatly over the past five years—and still has a lot more ground to cover. Now we're seeing applications as mentioned before and in addition, Health Geographics professionals are turning up in cancer research, tracking human pathogens in drinking water supplies, and in some very interesting applications being discussed in hospital GIS circles.

This book presents a very limited overview of some of the ways GIS is being applied in health. I encourage you to read with an open mind, and challenge yourself and your colleagues to think outside the box.

One final comment: I would like to dedicate my efforts on this book especially to Greg and Carrie—they are the absolute pride of my life.

"Think Spatially – Decide Visually – Act Wisely – and Be Satisfied!"

Ric Skinner
Sr. GIS Coordinator
Department of Surgery
Baystate Medical Center
Springfield, MA USA

Preface

The use of Geographic Information Systems (GIS) in the health sector is an idea whose time has come. This is by no means a novel concept; spatial analysis has been around as long as we have thought about spatial associations of disease, whether looking at determinants, distributions, outcomes or utilization. The current applications of GIS in health are diverse and extensive—I have had the privilege of co-chairing two conferences on the topic, and have been impressed with the wide array of geographically enabled projects and processes in the field.

The present GIS environment is heavily driven by technology and such an approach is indeed logical for the most part. However, the needs of less developed countries in utilizing the concepts and technologies of mapping should not be neglected in the continuing evolution of GIS. In the current computing environment, where processors seem to be in need of an upgrade on an annual basis or sooner, it should be realized that there remain barriers to the utilization of GIS, which include the costs associated with training, equipment and personnel as well as with sustainability. It is therefore imperative that the collective health geographics community be an inclusive one and support the use of technologies appropriate to a variety of settings, whether in the developed or the developing world. It is essential that the resources of the technological era be brought to bear on bridging and not expanding the divide between the two.

The technology of health mapping is only as good as the underlying concepts, whether applying to a scientific research question or exploring a new way of planning health delivery. This book is about sharing the results of some of the most innovative and useful ways in which our colleagues are utilizing GIS and spatial analysis to solve health-related issues. I am honored to be associated with the wealth of talent and expertise that lies between these pages. The work you will read about is a small but, I hope, representative sample of the diverse applications in this growing field.

As with our conferences, Ric and I have selected the best of the best in this volume. We have tried to make sure there is a mix of applications from various sub-sectors within the field(s) of health. We have divided the chapters into the following sections:

- *Section 1: Health Disparities & Community Health Issues*
- *Section 2: GIS & Cancer*
- *Section 3: Infectious Disease & International Health*
- *Section 4: Hospitals & Healthcare*

Health disparities have been studied a great deal, but not very much has been done to solve the problems therein using GIS. Health mapping has a great deal to contribute to this area, since much of the discussion is around issues of health and place. Practitioners and academics in the field of community health are well aware of this, and the chapters in the first section of the book address the issue head-on, led off by a conceptual piece co-authored by Dr. Mohammed Akhter, Executive Director of the American Public Health Association, and Dr. Gregory Pappas, one of the country's leading thinkers in this area and former Senior Advisor to the U.S. Surgeon General. The pieces which follow are in-depth analyses of the ways in which geographic methods can be used for community health, health disparities and particular issues affecting communities such as alcohol-related problems. We hope you find *Health Disparities & Community Health Issues* a thought-provoking and informative collection.

Our second section on *GIS & Cancer* reflects the reality that while the global threat of infectious diseases looks to be eradicable (given adequate resources and political will to do so), the scourge of cancer remains a leading cause of morbidity and mortality in the developed world. From Long Island, New York to Galicia, Spain, the authors included in this section provide invaluable insights as to how cancer determinants and outcomes can be mapped and addressed using geographic technology.

Bangladesh, China and West Virginia all have in common the fact that infectious diseases (albeit different ones!) remain a cause for concern. While the so-called epidemiological transition shows a logical progression from infectious to chronic disease, in many regions of the world there remains a dual threat from both. Whether seeing patients in a community health center in Karachi or at a travel clinic in Baltimore, it is readily apparent that the spread of many 'exotic' diseases is a plane flight away—and the world is smaller than it once was. Mapping this world is the task of our authors in the section on infectious disease and international health. While the science of epidemiology is rooted in older, established methods, the authors of this section present innovations on this theme which is apparent in chapters on such as animating rabies patterns, remote sensing in China, spatial modeling in Bangladesh, and an exciting new application of GIS and DNA fingerprinting.

A burgeoning use of GIS in the last few years has been in the hospitals and healthcare sector, and our fourth section is devoted to this emerging field. There are active discussions to expand the application of GIS in this area, discussions which Associate Editor Ric Skinner is actively involved in. This section is a rich collection of theoretical work and case studies from around the world. The applicability of GIS to the scale of individual facilities has not been envisioned previously, but now, a new breed of thinkers is expanding the borders of the use of health mapping both within and beyond the hospital walls. From exploring consumer markets, to mapping patients' access to care, to mapping the human body itself—there is a growing array of interesting and immediately applicable research coming out of this field. We expect to see a lot more in the near future.

This book presents a sampling of the many applications utilizing GIS in the field of health. We hope to hear back from those who will use the book in the classroom, in the workplace and in the field. To the readers of the book, please let us know how you have used it, whether as part of university curricula, as part of your day-to-day applied work or as a resource guide. Your feedback is an invaluable part of this continuing body of work, and is the best way for us to respond to the needs of those who are involved in this dynamic field.

Omar A. Khan
Editor

REFERENCES

Albert, D. P., Gesler, W. M., & Levergood, B. (2000). *Spatial Analysis, GIS, and Remote Sensing Applications in the Health Sciences.* Detroit, MI: Ann Arbor Press.

Campbell, B., Adjei, S., & Heywood, A. (1996). *From Data to Decision Making in Health: The Evolution of a Health Management Information System.* Royal Tropical Institute, Amsterdam, The Netherlands.

Fauveau, V. (Ed.) (1994). *Matlab: Women, Children and Health*. ICDDRB, Dhaka, Bangladesh.

The Institute for the Future. (2000). *Health and Health Care 2010.* San Francisco: Jossey-Bass.

Khan. O. A. (1999). The First International Health Geographics Conference. *American Journal of Public Health*, (April).

Kolb, D. C. (1999). *Team Leadership.* Durango, CO: International Learning Works.

Lang, L. (2000). *GIS for Health Organizations*. Redlands, CA: ESRI.

Mitchell, A. (1997). *Zeroing In: geographic information systems at work in the community*. Redlands, CA: ESRI.

Murray, C. J.L. & Lopez, A. D. (1996). *Global Health Statistics.* Geneva, Switzerland: World Health Organization.

National Research Council. (1996). *Bridge Builders: African experiences with information and communication technology.* Washington, DC: National Academy Press.

Senge, P. M. (1990). *The Fifth Discipline: the art and practice of the learning organization*. New York: Currency Doubleday.

Acknowledgments

Acknowledgments for the most important people somehow seem to wind up in the last lines. I would like to reverse that trend by first thanking my wife and partner, Salwa, for her incredible support through all my endeavors, and turning around the ones seemingly destined for failure. She keeps me grounded and balanced in a world where little else seems to be so. To my son, Zareef, for grinning at me while destroying my past hour's work on the computer, and for making me care more about the former than the latter.

To all the authors who sent in their work, I thank you and apologize for asking for the many revisions I know some of you had to endure. I appreciate your patience. I would also like to acknowledge the invaluable feedback of all those involved in the review process of this book.

To Ric Skinner, my colleague and friend, who initially provided the idea and enthusiasm for our joint work in GIS some years ago (in the last century!), and who agreed to serve as Associate Editor of this book. May we have many more productive collaborations.

To my friends, mentors, colleagues and well-wishers at the institutions I have been or currently am affiliated with: Wilmington Friends School, the University of Pennsylvania, Johns Hopkins University and the University of Vermont.

Thanks are due to my friends and family the world over, whom, I am fortunate to note, are so numerous as to not mention individually. You know who you are; thank you for your love and support.

I appreciate being provided the impetus for this book by Mehdi Khosrow-Pour at Idea Group Publishing, as well as the guidance and timelines provided by Jan Travers and Michele Rossi at the same institution.

This book is dedicated to the health of the least fortunate, the most dispossessed and those whose lives reflect realities that mine cannot begin to comprehend. May our use of the technologies described in this book create positive results for the individuals who most need them.

Omar A. Khan
Fairfax

SECTION I:

HEALTH DISPARITIES & COMMUNITY HEALTH ISSUES

Chapter I

Race, Class and Place: Directions for the Future of Public Health

Gregory Pappas
Macro International, Inc., USA

Mohammed Akhter
American Public Health Association, USA

This chapter is adapted from a presentation made at the plenary session of the 2nd International Health Geographics Conference, March 2000, Washington, DC. At the time, Dr. Pappas served as Senior Policy Advisor to the U.S. Surgeon General. Dr. Akhter is the Executive Director of the American Public Health Association (APHA).

In this chapter we discuss the importance of community in public health science and practice. Community is—first and foremost—place. The science of place and its implication for health has made major strides over the past decade. The first and second international conferences on health geographics marked an achievement in that development. The argument in this chapter draws out the implication of place and community for public health science and practice.

We begin with a review of the well-known facts about racial disparities in health. These disparities have dominated much of public health policy in recent times. Health disparities between social classes help illuminate our understanding of race differences. To understand the ways that race and class determine health, however, we must adopt a more general model—a model for the social determination of health. Review of the literature on the social determinants of health make it clear that future efforts to improve the health of populations must concentrate on modifying the more proximal determinants of health. The study of these proximal determinants requires a shift of focus away from the behavior of individuals onto communities and the processes by which communities take shape. These processes can in turn be represented in graphical and geographical ways, enabling one to examine interconnections between determinants of disparities.

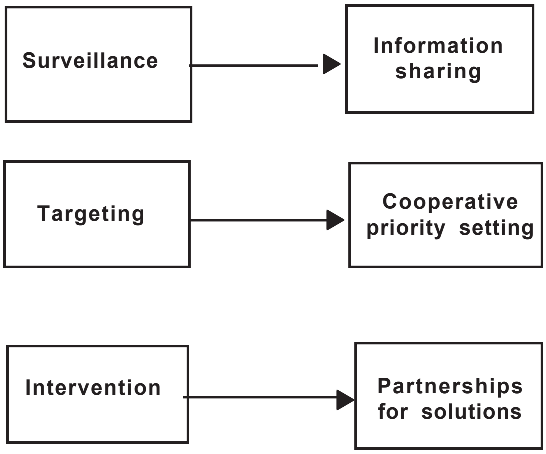
This shift towards the study of 'community' and 'place' also causes us to think differently about our models of public health practice. Current public health practice has been influenced by two distinct traditions, both with historical roots in the 19th century. The dominant model for public health practice—conceptualized as surveillance, targeting and intervention—has its roots in 19th century paramilitary public health institutions. The implications of the military metaphors used in the dominant model are explored in this chapter. Another model for public health, also with antecedents in the 19th century, is the community coalition model. This model, exemplified by the Settlement House movement, gave rise to local public health and social service agencies in American cities that grew up during the last century. Recently, this model has been re-invented or reinvigorated by community responses to the HIV/AIDS epidemic. Communities have resisted surveillance, shunned being targeted, and defied intervention. The future of public health should embrace collaboration with community instead of viewing communities as the object of study and modification (Mays, Miller & Halverson, 2000). Major challenges for public health in the 21st century—behavior change of populations and mobilization of local resources—will require a community-centered approach. The future of public health requires a model that emphasizes sharing of information, collaboratively identifying priorities and finding solutions with partners. A community-based model for public health gives clear direction to future developments of geographic information systems.

RACE, CLASS AND HEALTH IN AMERICA

While the health of the nation as a whole has improved over the past decades, racial and ethnic groups have continued to experience disparities in the burden of illness and death. Our current knowledge of biologic and genetic characteristics of racial and ethnic groups does not explain the health disparities. Differences in health status of African-Americans, Hispanics, Alaskan natives, Pacific-Islanders, Asians and Whites in this country are believed to be the result of the complex interactions among genetic variation, environmental factors, economic variables, health behaviors and discrimination.

Racial and ethnic disparities in health cannot be understood or ameliorated without a clear understanding of the role of social class in the determination of health (Navarro, 1990). The relationship between social class and health is robust and long standing. In European literature this relationship has been known at least since the time of the ancient Romans when Pliny the Elder noted that slaves did not live as long as their masters (Hamilton & Hardy, 1940). Over the past 50 years, a rich literature has demonstrated the complex relationship between social position and health. The disparities between the classes have grown over the past decades in many countries. Pappas et al. demonstrated a growing disparity in death rates between education and income groups, from 1960 to 1986 (Pappas, Queen, Hadden & Fisher, 1993). Subsequent work by Miller et al. demonstrated the same

Figure 1: Evolution of public health practice



trends for occupational classes (Schalick, Hadden, Pamuk, Navarro & Pappas, 1999). Widening mortality-related disparities between classes were observed among whites and among blacks.

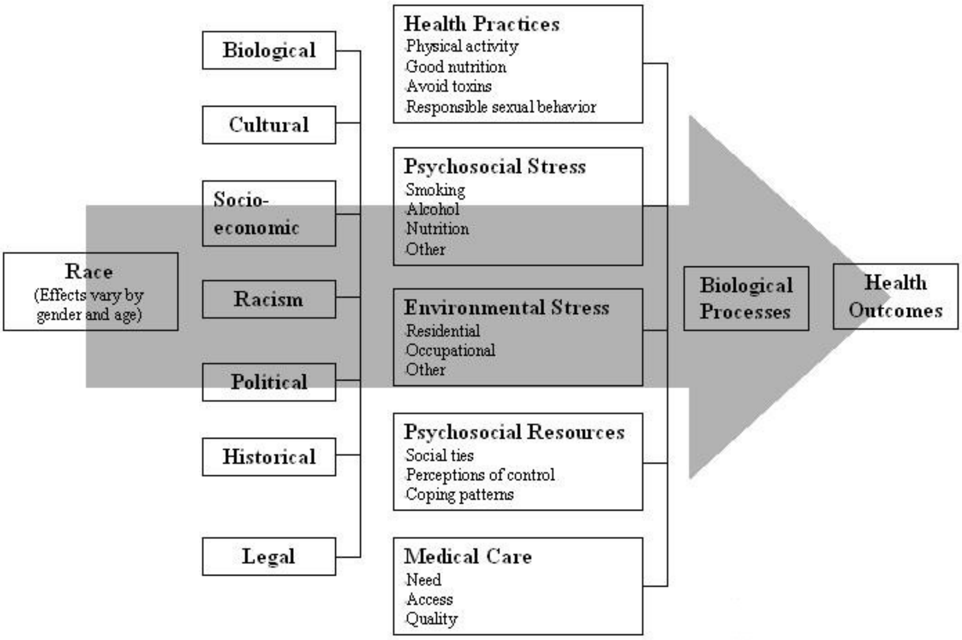
The widening gap in death rates in the United States between classes should come as no surprise. Disparities in life expectancy between blacks and whites increased during the same time period (Kochanek, Maurer & Rosenberg, 1994). For a long time in the United States, race has been used as a proxy for social class in public health A widening gap between the races predicts a widening gap between classes. More recently the complex relationship between race, class and health has been investigated (U.S. Department of Health and Human Services, 1998). Patterns of association with health are similar for race and class. Rogers has demonstrated in a national study of the U.S population that race differences in all-cause mortality can be completely explained by statistically controlling for social and economic variables (Rogers, 1992). The issue of ethnicity enriches the relationships further; while Hispanics in the United State are more commonly of lower income, education status and occupation category, their health status is not uniformly lower than blacks. An explanation for the "Latino health paradox" has not yet been firmly established (Abraido-Lanza, Dohrenwend, Ng-Mak & Turner, 1999), and represents an area for further examination by spatial means, by looking at the community level.

Surgeon General David Satcher has summarized this literature in his words, "Race and class are inextricably linked in the history of America and the health of its people" (Satcher, 2000). While statistical modeling has attempted to tease out the effect of various social determinants of health, for the reality of people's lives, race and class are fused. In American history, race and class have developed interdependently. The health consequences of race and class are part of that history. Newer technologies can and should be part of eliminating these disparities in the future.

MOVING UP STREAM: SOCIAL DETERMINANTS OF HEALTH AND THE ROLE OF PLACE

The relationship between race, class and health has been systematically conceptualized in a literature concerning the social determinants of health. A number of sophisticated conceptual models to explain health disparities, incorporating race and classes, have been developed over the past three decades (Black, Morris, Smith & Townsend, 1982; Susser, Watson & Hopper, 1985; Smedley & Syme, 2000; Williams, 1990; Williams & Collins, 1995). While there are important differences between these models, they draw from a similar literature and differ in emphasis, rather than in major assumptions. David Williams arranges variables in hierarchical fashion from distal (physiological determinants of health) to proximal (broadest historical consideration) (Williams, 1990). The Williams model puts race and class on a par, without giving one preeminence over the other. Most distal, closest to health outcomes, are biological and physiological processes. In the middle level of the model are the policy levers familiar to most public health professionals that emphasize behavior change and access of health care. More proximal variables include market forces, poverty, social class, inequality, racism, bureaucratic structures and policy (Link & Phelan, 1996). Other models, while similar in the broadest sense, give prominence to one variable or another. Polednak, for example, focuses his attention on the consequences of racial discrimination and segregation on health (Polednak, 1989). A comprehensive and comparative analysis of models has not been attempted in the literature. The point being made is that race and class must be understood in terms of a conceptual framework within which broad social forces are proximal determinants of health.

Figure 2: A framework for understanding the relationship between race, class and health



McGinnis and Foege have tried to quantify the magnitude of these proximal factors in their paper on avoidable deaths, and estimate that over half of deaths could be prevented through behavior change and public health measures (McGinnis & Foege, 1993). This study has been methodologically superseded in a paper by Lantz et al. that simultaneously examined the role of poverty alongside other risk factors (Lantz, House, Lepkowski, Williams, Mero & Chen, 1998). In this longitudinal study of mortality, the authors demonstrated that poverty strongly predicts mortality (RR 2.2) even when important risk factors (smoking, body weight, age, race and sex) are simultaneously considered. Put another way, the overall conditions in communities explain more of ill health than individual behavior.[1] The causes (and by extension, the solutions) of diseases and ill health of population are "upstream." *Place*, i.e., the community-level, is where illness arises and where we must work to prevent them. With GIS tools coming into their own, it is therefore time to realize their potential for analysis, beyond mere portrayal and visualization.

The HIV/AIDS epidemic provides a recent example of the importance of community for public health practice. During the early phases of the epidemic, lesbian and gay groups created an effective response when assistance from government and public health professionals was not available. Indeed, critics have charged that government agencies undermined early community strategies that were later adopted widely (Michael, Gagnon, Laumann & Kolata, 1994; Odets, 1995; Signorile, 1993). Traditional models of public health practice were ill-suited to the task of rapid transformation of community norms regarding sexual behavior. Communities created an effective model as a matter of survival; resources were mobilized, at times despite obstacles created by professional practitioners. The lesson for many has been that public health practice needs newer and more adaptable, community-centered models to address behavior change.

TOWARDS A NEW MODEL FOR PUBLIC HEALTH PRACTICE

To improve the health of populations in the 21st century, we must work to improve our understanding of how life in communities patterns health behaviors and how communities themselves are organized. Changing individual behavior requires shifts in community norms, social structures and conditions of everyday lives that determine these behaviors. Despite dramatic innovations in technologies in health care and the pharmaceutical industry, we increasingly appreciate that only broad community participation can ensure the equitable distribution of these technologies.

At the heart of the dilemma is the model of practice taught in most schools of public health and used in public health agencies. The classic model of public health practice has been based on the concepts of surveillance, targeting and intervention, and appears in a number of versions (Institute of Medicine, 1988). The Institute of Medicine in its report "The Future of Public Health," set out three core functions for public health practice: assessment, policy development and assurance (Institute of Medicine, 1988). On reflection, this model is only a slight modification of the classic model, and the professional dominance implicit in the IOM model can be traced to the historical antecedents of our institutions.

The classical model for public health has its roots in 19th century paramilitary public health institutions (Rosen ,1993), and the "public health police" of Kaiser Wilhelm's Germany were a model for early U.S. public health. Military terms, more than vivid metaphors, have provided a template for the culture and guided practices of our public health institutions. The organizational structure of public health is another part of this legacy that needs little mention: starting with a focus on the community leads public health to a very different mode of practice.

The problems with the classical model should by now be clear. Communities have for a long time told us that they do not want to be under surveillance, they do not want to be our targets and that they no longer want to be intervened upon. A community-centered approach to public health practice should emphasize information sharing, collaborative identification of priorities and searching for solutions with our partners. This will require not just effective representation of the issues via health atlases, but deeper and more analytical work to provide insights linking community conditions with public health outcomes. Such work with the aid of geographic technologies cannot only identify negative conditions but also highlight positive ones, which can be optimized for a community's health.

This transformation of the public health practice model is schematically presented in Figure 1. The new approach to public health practice has, in part, come out of the community response to the HIV/AIDS epidemic and the critique that lesbian and gay groups have had regarding traditional public health practices (Butler, 1996). Community public health activists have unfortunately had to struggle against government in their efforts, which have included protection of confidentiality, needle exchange and local control of resources. The task of public health is to listen to communities and understand how professional public health practitioners can work in concert to achieve shared goals. It is promising that government agencies and foundations have been moving to a model of community-based public health practice in recent years.[2]

The community-based model for public health practice has its antecedents in the urban reform movement and relies heavily on building the community coalitions. The community-based model is exemplified by the Settlement House movement (Addams, 1999). The urban reform movement, of which settlement houses were part, improved the health of the urban poor in the United States by changing the conditions in which they lived. Led by women like Jane Adams, Margarett Sanger and Susan B. Anthony, this reform movement worked by organizing communities, working with the political structures and working with all segments of community life—education, work, the physical environment, the status of women and civil society. The movement transformed American life and gave rise to local public health and social service agencies in cities around the United States (Rosen, 1993).

CONCLUSIONS: POLICY, PLACE AND THE FUTURE OF PUBLIC HEALTH

The increasing professionalization of public health during the last century has had a paradoxical effect. While science and institutions have developed, there has been a reliance on the model of practice that separates public health institutions from communities they intend on serving. A full history of the origins of current public health practice and its consequences is yet to be written.[3] Clearly, the major challenges for public health in the 21st century—behavior change and mobilization of local resources—will require a community-centered approach, focusing on the role of place and the attributes that go with it. Movement in this direction is well underway.

The systematic study of place and health, as evidenced by the chapters in this book, will support the evolution of a community-centered public health practice. The future of public health requires a community-centered model that emphasized sharing of information, collaboratively identifying priorities and finding solutions with partners. This is a challenge to both the way we do business and the methods we use. Geographic Information Systems and its evolving iterations possess the right set of tools to meet such a challenge. The community-based model for public health practice gives clear direction, as well as a challenge, to those who will develop such tools in the 21st century.

ENDNOTES

[1] For a more comprehensive treatment of the relationship between poverty and place see: Jargowsky, P.A. (1998). *Poverty and Place: Ghettos, Barrios and the American City.* Russell Sage Foundation.

[2] A footnote to the discussion about the role of the gay community in the HIV/AIDS epidemic is necessary. Critiques have suggested that there are few lessons to be learned from the experience of the gay community because they

are rich, educated and white. Most public health challenges are in communities with few resources. This formulation errs in two ways. First, all gay men and lesbians are not wealthy, well educated and white. Second, while the leadership of that community is privileged, it reached out across class, race and cultural boundaries to create an effective coalition to combat the epidemic. It is the importance of coalition building and the need for leadership that embraces the need for multi-racial, multi-class coalitions that are perhaps the major lessons to be learned. Recent work by William Julius Wilson in his book *Bridging the Racial Divide*, has eloquently made this point: Wilson, W.J. (1999). *The Bridge Over the Racial Divide: Rising Inequality and Coalition politics*. University of California Press.

[3] Laurie Garrett's book, *Betrayal of Trust,* makes a contribution in this direction. Chapter X, which outlines the history of public health in the United States, falls short by focusing solely on infections diseases and because it lacks a conceptual framework: Garrett, L. (2000). *Betrayal of Trust: The Collapse of Global Public Health.* New York: Hyperion.

REFERENCES

Abraido-Lanza, A.F., Dohrenwend, B.P., Ng-Mak, D.S. & Turner, J.B. (1999). The Latino mortality paradox: A test of the "salmon bias" and healthy migrant hypotheses. *American Journal of Public Health,* 89(1543–1548).

Addams, J. (1999). *20 Years at Hull-House.* New York: St. Martin's Press Inc.

Black, D., Morris, J. N., Smith, C. & Townsend, P. (1982). *The Black Report.* London: Pelican.

Butler, J. (1996). *Excitable Speech: A Politics of the Performative.* Routledge.

Hamilton, A. & Hardy, H. L. (1940). *Industrial Toxicology*. New York: Hoeber.

Institute of Medicine. (1988). *The Future of Public Health*. Washington, DC: National Academy Press.

Kochanek, K. D., Maurer, J. D. & Rosenberg, H. M. (1994). Why did black life expectancy decline from 1094 through 1989 in the United States? *American Journal of Public Health,* 84, 938–944.

Lantz, P. M., House, J. S., Lepkowski, J. M., Williams, D. R., Mero, R. P. & Chen, J. (1998). Socioeconomic factors, health behaviors and mortality: Results from a nationally representative prospective study of US adults. *JAMA*, (279),1703.

Link, B. G. & Phelan, J. C. (1996). Understanding sociodemographic differences in health – the role of fundamental social causes. *American Journal of Public*

Health, 86, 471–472.

Mays, G. P., Miller, C. A. & Halverson, P. K. (2000). *Local Public Health Practice: Trends and Models.* American Public Health Association.

McGinnis, J. M. & Foege, W. H. (1993). Actual causes of death in the United States. *JAMA,* 270(18), 2207–2212.

Michael, R. T., Gagnon, J. H., Laumann, E. O. & Kolata, G. (1994). *AIDS, In Sex in America: A Definitive Survey*. (pp. 199–218). Boston: Little, Brown and Company.

Navarro, V. (1990). Race or class versus race and class: Mortality differentials in the United States. *Lancet,* 336, 1238–1240.

Odets, W. (1995). The fatal mistakes of AIDS education. *Harper's Magazine*, (May), 13-17. Taken from *AIDS Education and Harm Reduction for Gay Men: Psychological Approaches for the 21st Century, AIDS & Public Policy: Spring* (1994). Frederick, MD.

Pappas, G., Queen, S., Hadden, W. & Fisher, G. (1993). Socioeconomic disparity in mortality in the U.S. *New England Journal of Medicine,* 329(2), 103–109.

Polednak, A. P. (1989). *Racial and Ethnic Differences in Disease.* New York: Oxford University Press.

Polednak, A. P. (1991). Black-white differences in infant mortality in 38 standard metropolitan statistical areas. *American Journal of Public Health,* 81(11), 1480–1482.

Rogers, R. G. (1992). Living and dying in the USA: Sociodemographic determinants of death among blacks and whites. *Demography,* 29, 287–303.

Rosen, G. (1993). *A History of Public Health.* Johns Hopkins University Press.

Satcher, David, Surgeon General, in a taped speech for the George Washington University broadcast, "Race, Class and Health." May 15, 2000.

Schalick, L. M., Hadden, W. C., Pamuk, E., Navarro, V. & Pappas, G. (1999). The widening gap in death rates among income groups in the United States from 1967–1986. *International Journal of Health Services:*, 30(1), 13–24.

Signorile, M. (1993). *A Queer's Own Story, from Queer in America*. (pp. 18–35). Random House: New York.

Smedley, B. D. & Syme, S. L. (2000). *Promoting Health: Intervention Strategies from Social and Behavioral Research*. Washington, DC: National Academy Press.

Susser, M., Watson, W. & Hopper, K. (1985). *Sociology in Medicine.* New York: Oxford University Press.

U.S. Department of Health and Human Services. (1998). *Health United States.*

Washington, DC.

Williams, D. R. (1990). Socioeconomic differentials in health: A review and redirection. *Social Psychology,* 53, 81–99.

Williams, D.R. & Collins, C. A. (1995). US socioeconomic and racial differences in health: Patterns and explanations. *Annual Review of Sociology,* 21, 349–86.

Chapter II

Understanding Health Disparities Through Geographic Information Systems

Samuel Soret
Loma Linda University, USA

Karl J. McCleary
The Penn State University, USA

Patrick A. Rivers
Arizona State University, USA

Susanne B. Montgomery and Seth A. Wiafe
Loma Linda University, USA

The emerging discipline of health geographics uses the concepts and techniques of medical geography (Meade, Florin & Gesler, 1988) together with modern automated Geographic Information Systems (GIS) methods to investigate health issues (Ricketts, Savitz, Gesler & Osborne, 1994). The main aim of this chapter is to bring the exciting potential contributions inherent in this approach to the attention of health practitioners and researchers.

With the development of powerful, yet affordable geo-technologies, digital maps and visual displays are produced that can be used for research, *practice and/or health policy analysis. One major advantage of this technology is that complex information can be displayed for the consumer in more intuitive, self-explanatory form. This is accomplished by linking and overlaying health data to standard census geographic areas which can be accessed quickly and flexibly from national and state agencies (Devesa, Grauman, Blor, Pennello, Hoover & Fraumeni, 1999; Kim, 1998).*

This chapter will illustrate how a GIS-based, multi-method approach can be applied to the study of health disparities. Using the pressing public health issue of access to kidney transplantation in California as an example, we will explore the notion of health disparities using a geographic conceptual framework for studying and understanding existing gaps in transplantations conducted. Different GIS techniques to addressing this issue are presented with a discussion of the relative advantages of each approach and a final review on how to most effectively use a GIS-based approach in studying health disparities.

PERSISTENCE OF HEALTH DISPARITIES

Public health has been traditionally concerned with disease prevention and health promotion activities directed at populations or communities rather than individuals (Turnock, 2001). Considerable effort has been devoted to the assessment of health needs and disparities in our communities. Health disparities exist both at a global scale and at the national level. Poor countries have fewer resources to invest into developing their public health infrastructure as compared to wealthier nations. In the United States (U.S.), one of the most developed and affluent countries in the world, persistent, and often increasing, health disparities between various racial and ethnic populations have been documented. Minority groups consistently lag behind the majority of Americans in almost all morbidity and mortality rates, as well as access to health care (United States Senate, 2000). Similarly, minorities are documented to receive generally less health care services, including but not limited to appropriate preventive care, intensive hospital care, cardiovascular procedures and organ transplants (Fiscella, Franks, Gold & Clancy, 2000). Health disparities are not limited to minorities, but include the underserved rural areas and areas of low socioeconomic status (United States Senate, 2000). Health indicators for rural areas are similar to those of minority groups. Health disparities have also been cited in relation to type of health insurance coverage, and access to health care by the 'working poor' (Hogue, Hargraves & Collins, 2000). In addition, health disparities exist with regard to gender, with women documented to suffer health disparities more than men (United States Senate, 2000).

Eliminating health disparities in the U.S. will require a national commitment and concerted effort at preventing disease, promoting health and delivering appropriate care. The U.S. Department of Health and Human Services Initiative to Eliminate Racial and Ethnic Disparities in Health, one such effort, has six target areas: infant mortality, cancer management, cardiovascular diseases, diabetes, HIV infection and immunizations.

However, beyond obvious differences in disease and access rates by certain population groups, current health data are inadequate in helping us understand how to best address these existing disparities. Fiscella et al. (2000) suggest that the way current health data are reported does not accurately portray these disparities. They recommend to at least stratify data by socioeconomic status and race/ethnicity, and conclude that there is a need to improve data collection methods and use new tools that are sensitive for displaying such disparities. To better identify health disparities for all potential high-risk populations and monitor the effectiveness of health interventions targeting these groups, new approaches in the use of existing data need to be implemented. We believe that GIS technology and methods are appropriate new tools to meet this challenge.

GIS TECHNOLOGY AND METHODS FOR UNDERSTANDING HEALTH DISPARITIES

GIS Technology

Many questions concerning health and ill-health are related to space (Loslier, 1995). However, the incorporation of geographic analysis into public health science and practice has been slow. A major deterrent has been the lack of adequate tools for the management and analysis of spatially defined data. The use of geo-information technologies is offering new opportunities for research and planning in public health and policy.

GIS has been described as one of the most exciting of the new information technologies (Yasnoff & Sondik, 1999). It has been extensively used in natural resource management, public works, transportation and government but until recently, has been largely ignored in public health and socio-behavioral research (Albert, Gesler & Levergood, 2000). Intuitively, GIS can be defined as an information technology that uses (digital) maps to interpret complex data (Clarke, 2001). GIS allows the user to look at new relationships between variables, as one can bring together many different types of data (i.e., health, resource use/allocation, census, transportation, etc.). This in turn provides the social and physical context necessary for enhancing analysis in health planning and policy to emerge (Maguire, Goodchild & Rhind, 1991). Equally important, GISs permit the generation and investigation of spatial hypotheses that open new vistas for analyzing latent relationships from previously static and cross-sectional data (De Lepper, Scholten & Stern, 1995; Novick, 1999).

Health Disparities Occur in a Geographic Context

Eliminating health disparities requires more than political will and administrative resources; it is equally a matter of timely, accurate and geographically defined information (Stern, 1995). Health problems vary in geographic space, as do the needs of people.

This need for spatially referenced information—and improved analytical methods—is particularly acute in the current climate of changing health needs, risks, health care delivery and public health practice (Roper & Mays, 1999). By capturing the spatial dimensions of this evolving environment and linking them with important attributes aggregated at a variety of geographic levels (e.g., census block, census tract, ZIP code, county or state), GIS and spatial analysis can be powerful tools for better distinguishing and modeling the context within which health disparities occur. A multi-level approach can help alleviate the limitations imposed by the ecologic fallacy (i.e., drawing inferences about individuals from population level data) and by aggregation bias, as we are not restricted any longer to applying large-area statistics (such as county averages) to individuals or small geographic zones.

Also since most traditional research efforts in the study of health disparities have emphasized individual-level factors (e.g., age, gender, race, etc.) (Fiscella et al., 2000; Williams & Rucker, 2000), conclusions may be limited by the atomistic fallacy—failing to consider the context in which individual behavior occurs (Richards, Croner, Rushton & Brown, 1999). Moreover, rarely has the role of geography (place of residence) been examined in the context of health inequalities. Yet recent information indicates that health care patterns in the United States depend more on where individuals live than on their needs or preferences (Dartmouth Medical School, 1996, 1998).

Geographic Variation as a *Marker* of Health Disparities

Currently health disparities are measured uni-dimensionally by racial or socioeconomic groups, without taking into account their geographic context. Once we add the geographic (i.e., two-dimensional) component, the search for spatial patterns of variation in health disparities is possible. Since we expect spatial patterns to arise from geographically defined measures of health status and/or access to care, we expect that health inequalities in populations will be manifested as geographic clustering (i.e., nonrandom spatial variability). Thus mapping techniques and formal methods of statistical spatial analysis could be used to assess the geographic variation of health disparities. Once such spatial patterns are identified, they can be investigated ecologically with respect to factors including socioeconomic characteristics, population behaviors, barriers to access, institutional effects, etc. This additional layer of information would allow us to more effectively target and design interventions and/or policies to address the geographically identified inequalities.

Using GIS and Spatial Analysis for Identifying Health Disparities

The added value of GIS technology and methods can be appreciated when we consider the difficulties associated with an ecologic approach to the issue of health disparities. In contrast to cross-sectional or unidimensional data, patterns are difficult to decipher in two dimensions, especially when the data contain random error (“noise”) from inaccurate records of cases and populations, misallocated cases and similar data quality challenges.

Four important practical problems arise when we want to use spatially defined data (Bailey & Gatrell, 1995). The first of these is the instability of spatial patterns across geographic scales. A second challenge is the lack of any natural ordering or indexing in space—in contrast to time series data, which are evenly spaced and unidimensional. This problem translates into a difficulty to define proximity when we use a set of sites or zones that are distributed irregularly in space. Moreover, autocorrelation or (spatial) dependence extends in general over several directions, not just one. Third, another set of problems occurs in connection to what happens on the edge or boundary of our region of concern (county, state, etc.). The *modifiable areal unit problem* arises when data for pre-defined zones—such as ZIP Codes which are arbitrarily assigned—are used, as the results will be conditional upon the spatial configuration of the utilized zones. Finally, another set of problems arises when we consider the complexity of the geographic “landscape,” where many physical and human features overlap and/or criss-cross.

Elucidating health disparities, or alternatively, demonstrating improvements in the health outcomes or access of a population, requires small-area measurements. This is especially relevant to the tradition of public health where tracking of health status as well as many public health interventions target communities, i.e., small geographic areas. Although difficult, assessing the effectiveness of public health outcomes or interventions and policies is optimally done at the population level, rather than the individual level. Roper and Mays (1999) have pointed out the value of GIS technology and methods for examining population-level processes and effects as expressed in the spatial and geographic distribution of populations and/or communities. GIS-based methods “often provide more accurate and unbiased measures" (p. vi) of health processes than conventional approaches, which do not take into account spatial dependencies in the data.

Finally, if health outcomes or health care access are mapped for small areas, such as ZIP Codes, census tracts or census block groups, the estimated statistics become unstable as they are based on increasingly smaller populations. When they are displayed on a map, readers may incorrectly infer that existence of a geographic pattern identifying locations for targeted interventions (Bithell, 2000; Kulldorff, 1999). Data can be mapped using larger geographic units to alleviate this problem. For example, state-and county-level maps are usually produced to display health statistics. However, these maps have limited value for detecting high-or low-rate areas that are either found within part of a county, or that cross county boundaries. Thus, by using traditional approaches we incur in the loss or dilution of local detail important in identifying at-risk populations.

As an alternative, through advanced techniques of spatial analysis (GIS), we can capture and display small-area statistics while maintaining the stability of the estimated rates. Spatial filtering ("smoothing") is one such technique that can be used to increase statistical power by borrowing strength from space (i.e., neighboring zones) (Rushton, 1997). Other approaches such as density-equalizing methods (Dorling, 1994; Merrill, Selvin, Close & Holmes, 1996) or empirical Bayesian estimation (Yasui, Liu, Benach & Winget, 2000) have been proposed.

Even after data smoothing, since geographic variability can arise by chance, formal testing for spatial randomness is required to identify likely—statistically significant—clustering (Anselin, 1996; Chou, 1997; Odland, 1988). Statistical tests of spatial randomness fall under two main types: focused and global (Kulldorff, 1999). While the former attempts to ascertain the geographic locations of clusters, the latter detects a general tendency toward clustering—without pinpointing the precise location of the clusters.

In addition, health geographics relates to human populations (Cressie, 1993). This fact gives population density a crucial importance. Sometimes apparent geographic patterns may be observed simply due to the spatial variation in the distribution of the population; in other words, population density acts as confounder (Lawson, 2001). Talbot, Kulldorff, Forand and Haley (2000) have recently proposed a method for explicitly incorporating population density into adaptive kernel estimation techniques.

GIS technology and methods enable the exciting convergence of multidisciplinary perspectives to the issue of health disparities. GIS-based approaches can help health researchers, practitioners and policy makers acquire new insights into eliminating health disparities and developing new ways to apply our existing knowledge toward this goal. Next, we will illustrate the benefits of a GIS-based approach by examining kidney transplantation in California.

BACKGROUND ON ORGAN TRANSPLANTATION

Rapid advancements in organ transplant technology, access to transplantation, greater educational awareness and proactive legislation supporting donation and equitable allocation have dramatically increased the demand for organs. Unfortunately, the supply of organs has not kept pace with the burgeoning number of transplant candidates on the waiting list. Despite modest increases in the number of donors, recent projections indicate that the current shortage for solid organs will worsen (Niemcryk, Aronoff, Marconi & Bowen, 1994).

Recently, the Centers for Medicare and Medicaid Services (CMS), formerly the Health Care Financing Administration (HCFA), submitted a final ruling on the organ allocation criteria of the Organ Procurement and Transplantation Network (Final Rule, 42 C.F.R. Part 121, 1998). This ruling is aimed at improving the equitable allocation of organs for transplantation nationally. Under the provisions of this rule, organs will be allocated according to objective standards of medical status and need, irrespective of where the organs are procured or harvested. According to the American Medical Association Council on Ethical and Judicial Affairs, Ethical Opinion E-2.16 on Organ Transplantation Guidelines states: "Organs should be considered a national, rather than a local or regional resource. Geographical priorities in the allocation of organs should be prohibited except when transportation of organs would threaten their suitability for transplantation (Point #6; http://www.ama-assn.org/ama/pub/category/2503.html, under Entering Keywords using Policy Finder)."

The focus of existing organ allocation research has primarily been on medical criteria while making the assumption that donor management practices and allocation methods are similar among organ procurement organizations (OPOs) and transplant centers. Most of this research has been cross-sectional in design and has focused on identifying clinical predictors of allocation, while negating pre-existing "local first" or regional practice constraints existing in the transplant community. While this pattern and its fallacy has been documented by Ozcan et al. (1999), our research is, to our best knowledge, among the first to employ a geographical or GIS approach to health disparities in organ allocation.

TRANSPLANTS AND MEDICAL NEED: DO THEY CORRESPOND?

One of best ways to illustrate the current health disparities in organ procurement and transplantation is to use the data on the underlying illness, such as End Stage Renal Disease (ESRD) as a 'proxy' for demand for new kidneys. Actual renal transplantation is then compared to the "need" and used as a model for the assessment of geographic disparities (Ayanian, Cleary, Weissman & Epstein, 1999; Dartmouth Medical School, 1998). Another plus to using this organ as an example is that unlike other medical procedures, all patients with ESRD are assessed for transplantation. Therefore, all potential candidates for transplantation can be located. Since kidney transplants account for over half of all organ transplants in the United States, this organ reflects many of the existing challenges faced by those on the national organ waiting list. According to the End-Stage Renal Disease Network, Regions 17 (Northern California) and 18 (Southern California), as of June 30, 2000, the number of persons with ESRD waiting on a kidney in California was 8,427. To better grasp the magnitude of these state numbers, consider the prevalence of ESRD nationally. On September 14, 2001, the United Network for Organ Sharing (UNOS) National Patient Waiting List included 49,919 persons waiting for a kidney transplant. Estimating the cost of providing renal replacement therapy to this population gives a clear picture of the health policy consequences of this illness with a cost of $7.3 billion in 1990 for 200,000 patients. By 1997, Medicare spent $11.76 billion a year on ESRD patients, a significant increase in spending from the early nineties (Tell, Hylander, Graven & Burkart, 1996).

The literature on ESRD provides compelling evidence about health disparities among ESRD patients. These disparities include the customary renal replacement therapy as well as the distribution of renal transplants. Disparities are in disfavor of African Americans who unfortunately have a higher incidence and prevalence of ESRD (U.S. Renal Data System, 1999). Although comprising about 15% of the U.S. population, African Americans account for 37% of the ESRD population. Notwithstanding this need, African Americans were found to be less likely than whites to be referred for evaluation for renal transplants. Moreover, of those who are considered appropriate for transplantation, African Americans were significantly less likely to be referred for evaluation. Overall, African Americans receive less than 25% of cadaveric kidneys, and about 14% of kidneys from living donors (Young & Gaston, 2000). Similarly, supporting data are available on renal transplants between the period of 1987 and 1995 (Scantlebury, Gjertson, Eliasziw, Terasaki, Fung, Shapiro, Donner & Starzl, 1998). We believe that such patterns are not accidental or based on medical need issues alone as assumed by Reddan, Szczech, Klassen and Owen (2000), who argue that since renal transplants are provided by a single health care provider (i.e., Medicare), transplantation disparities are eliminated. We believe such an assumption to be erroneous. For example, when comparing the United States experience with ESRD to the United Kingdom, the rate of renal replacement (transplantation) among African-Caribbeans and Asians is three to four times higher than whites (Raleigh, 1997). This high utilization was explained by need rather than by proximity to renal units.

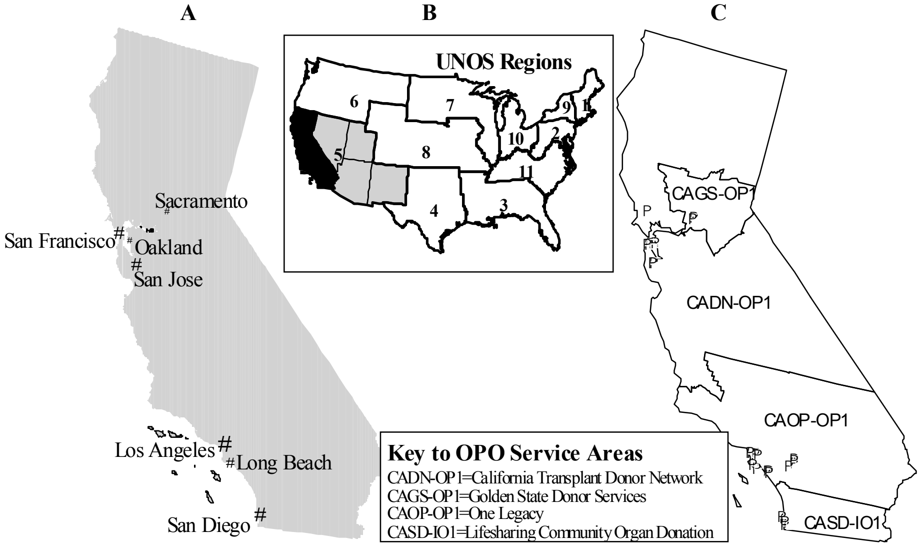
We know that organ transplantation varies by factors related to the health care delivery system, organ acceptance and rejection criteria, proximity to transplantation centers, local organ donation rates, organ assignment policy and the demographics of the donor pool (Reddan et al., 2000). While much of the existing disparity is attributed to the biologic differences of susceptibility to developing ESRD among certain races, this does not however account for all of the disparities. This leads many researchers to conclude there are inherent systemic barriers within the health care system, including the possibility of treatment bias in physician practice patterns. Transplantation inequalities among the African American population may imply subsequent inequalities in optimal care. It is also likely that such disparities are not limited to African Americans, but include other minority racial/ethnic groups as well.

RENAL TRANSPLANTATION AS A MODEL FOR HEALTH DISPARITIES: A GEOGRAPHIC ASSESSMENT OF KIDNEY TRANSPLANTATION

California Organ Procurement and Transplantation Network (OPTN). As a geographic reference, Figure 1a shows the main seven urban areas in California: Los Angeles, San Diego, San Jose, San Francisco, Long Beach, Oakland and Sacramento. California's OPTN is located within Region 5 of the United Network for Organ Sharing along with four other Western states—Arizona, Nevada, Utah and New Mexico (Figure 1b). Four organ procurement organizations (OPOs), located in large metropolitan areas with high population density, cover a remarkable service area of over 32 million people. The two northern OPOs are located in San Francisco, the Bay Area and Sacramento. The two southern OPOs are located in the Greater Los Angeles Area and the San Diego Metropolitan Area. Each OPO serves a CMS-defined service area where potential donors are generated from local hospitals by referrals of cadaveric solid organs (i.e., heart, lung, kidney and pancreas). Interspersed within this vast OPO network are 25 affiliated transplant centers (Figure 1c). It is within this geographically defined area that we will examine the effectiveness of existing organ allocation practices across the transplantation network.

Measures for Assessing Health Disparities. In order to assess kidney transplantation, we used California Office of Statewide Health Planning hospital data (1995–1998) and U.S. Census derived population estimates. Hospital patient discharges were the unit of service used as a reasonable proxy for the prevalence of the disease, ESRD and of access to kidney transplantation, the optimal treatment

Figure 1: Map of California and its major cities (A). California's Organ Procurement and Transplantation Network is located within Region 5 of the United Network for Organ Sharing (UNOS) (B). California's Transplantation Network consists of four OPOs and 25 affiliated transplant centers that serve over 32 million people (C).



for persons with ESRD. Dialysis, although a life-extending therapy, exacts its own toll on persons with renal failure.

ESRD and transplantation cases were identified and extracted by their corresponding ICD-9 CM codes. The following codes were used:

1 ESRD, Not Otherwise Specified—Code 585
2 ESRD with Manifestation of Diabetes—A *two-code* combination of 585 and 250.40-250.43
3 ESRD Due to Hypertension—Codes 403.00, 403.11, 403.91
4 ESRD with Hypertensive Heart and Renal Disease—Codes 402.02, 404.03, 404.12, 404.13, 404.92, 404.93
5 Kidney transplantation—Code 55.69

After excluding out-of-state cases, the retained discharge events were then geocoded to GIS maps of California ZIP Code boundaries made using files from Geographic Data Technologies (GDTs). The processed data set contained 388,443 ESRD discharge events, including 5,161 kidney transplant procedures (1.3 percent of the total). The variable of interest is access to renal transplantation, defined as the proportion of kidney transplant procedures, and whether this proportion varies geographically across California. This measure, which identifies the relationship between utilization and underlying disease, is the most direct, and ultimately, one of the most relevant measures of access (Eggers, 1995).

In general, it is desirable to have the individual locations of cases and underlying population rather than using data aggregated to areas such as ZIP Codes or counties. The results will have better spatial resolution since they are not dependent on the location of the area's centroid point. We applied a technique described by Talbot et al. (2000) to alleviate the problem of arbitrariness in assigning the geographic location of ZIP Code centroids. Population-weighted centroids were calculated for each California ZIP Code using 1990 census data at the census block level. For each ZIP Code, we summed the number of kidney transplants as well as the total number of ESRD occurrences. All ESRD discharge events in a particular ZIP Code polygon were then assigned to the geographic coordinates of the population-weighted ZIP Code centroid.

Spatial Smoothing Techniques. Smoothing or spatial filtering is a descriptive technique to map data collected within small geographic areas and still maintain the stability of the estimated health parameters. The estimated rate or ratio of the variable of interest at a particular location, or grid point, is calculated by incorporating information about the observed data at neighboring areas within a fixed distance from the location in question. Discs centered at specific locations are set to overlap to allow neighboring points to share observations. Contouring or advanced GIS functions to process raster data can then be used to produce smoothed maps where geographic trends are recognizable. In the end, 'smoothed' maps more clearly represent the continuous distribution of the underlying illness as a naturally occurring phenomenon, without the administrative boundary constraints of ZIP Codes.

Building upon the ideas proposed by Rushton and Lolonis (1996), Rushton, Krishnamurthy, Krishnamurthy, Lolonis and Song (1996), Kafadar (1996, 1999) and McCleary, Soret, Rivers and Montgomery (2001), we have adapted the techniques recently presented by Talbot et al. (2000) to implement a GIS-based adaptive kernel estimation method for creating smoothed maps of kidney transplantation access in California (Bailey & Gatrell, 1995; Breiman, Meisel & Purcell, 1997). In these maps, the spatial filter (or kernel) is defined in terms of near constant population sizes rather that constant geographic size. In other words, the discs containing the clusters of data are larger in sparsely populated areas compared to urban areas.

The geographic unevenness of California's population density can be observed in Figure 2a, from the very sparsely populated Sierras and deserts on the eastern half of the state, to the very densely populated metropolitan areas along the

Pacific coast. For example, San Francisco has more than 6,000 people per square kilometer, Los Angeles 5,000, while several rural towns have less than 0.3 persons per square kilometer. This makes California an ideal geographic region for illustrating the application and performance of spatial filtering methods when there is heterogeneity in the population density.

We compared the smoothing technique using a variable window size with the fixed geographic size approach. For both methods we used a 2 km grid for the disc centroids. The grid contained approximately 120,000 points, which covered the state, along with a 2-km buffer around the state line.

Calculation of Standard Risk Ratios. An indirectly standardized relative risk ratio—traditionally, a standardized morbidity/mortality ratio (SMR)—is defined as a function of the "risk" in receiving a kidney transplant incurred by a randomly selected ESRD patient residing at a certain ZIP Code relative to the average "risk" in California as a whole (Bithell, 2000; Lawson, 2001). SMRs with values greater than 1 indicate local transplantation activity above the state average, while SMRs with values less than 1 indicate transplantation activity below the state average.

SMRs were derived from counts of the number of kidney transplant procedures that occurred from 1995-1998 for ESRD discharge events by ZIP Code. For both smoothing techniques applied here, we calculated the standard incidence ratio for each point. The study area was covered by a fixed number of evenly spaced grid points. Let n_i be the number of ESRD events captured at grid point i and let N be the total number of ESRD discharge events in the state. Likewise let c_i be the number of kidney transplantation procedures captured at the same grid point i while C is the total number of kidney transplantation cases in the state. The unadjusted, standardized morbidity risk ratio, SMR, is:

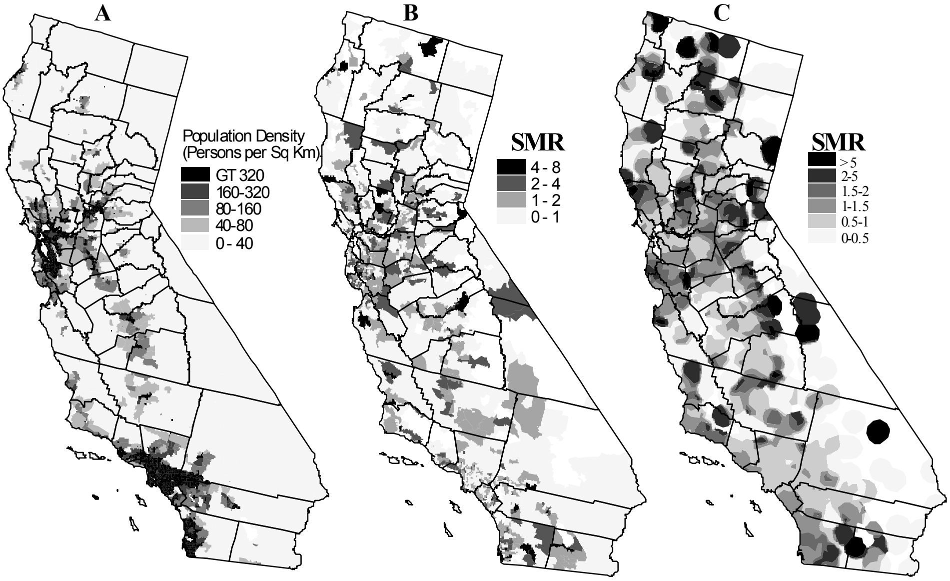
$$\mathrm{SMR}_{\mathrm{i}} = (c_i / n_i)/(C/N)$$

To take into account demographic differences among regions, ratios were adjusted for differences in age, sex and race/ethnicity (Eggers, 1995; Thamer, Henderson, Ray, Rinehart, Greer & Danovitch, 1999). The above equation was modified accordingly to incorporate the three covariates: age, sex and race/ethnicity (Kulldorff, 1999).

Comparing Approaches to Data Handling:

1. Spatial Filters with Constant Diameter. This method captures all transplantation and ESRD discharge events within a fixed geographic radius of the grid point. The kernel size was set to 20, 90 and 205 km, respectively. The latter is the smallest radius that will capture at least 500 ESRD discharge events at each

Figure 2: Map showing population density in California, with county lines added for geographic reference (A); kidney transplantation standard morbidity (relative risk) ratios by ZIP Code, unsmoothed (B), and using a fixed filter size of 20 km at each grid point (C).

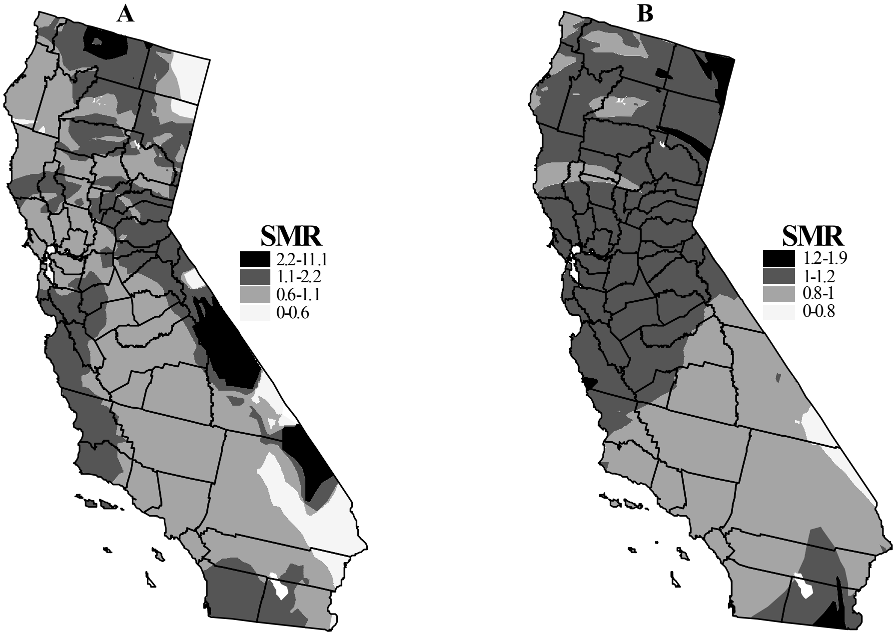


grid point. This is rather large due to the sparsely populated areas of the state's northern and eastern mountainous regions and southeastern deserts (see Figure 2a).

An unsmoothed map is supplied in Figure 2b, showing the SMRs for each individual ZIP Code. There are several areas of high incidence scattered around the state, with no easily interpretable pattern. Since the ratios are unsmoothed, the SMRs are unstable for most areas, except for ZIP Codes with the largest population. If there is any true geographic variation of importance, it is hidden, and nearly impossible to distinguish from what could be described as random spatial noise.

Figure 2c shows the smoothed map using a fixed geographic filter size of 20 km. Areas that appear "blank or clear" represent regions where no ZIP Code centroids were found within 20 km of the grid points. In the most rural areas of the state, this map is similar to the unsmoothed map in Figure 2b, with equally unstable SMRs. Dark patches can be observed in some of the sparsely populated eastern counties, along the border with Nevada. In the urban areas, a considerable level of smoothing has been achieved, furnishing more stable SMRs than in Figure 2b. Please note that in the most densely populated areas such as Los Angeles, the ratios

Figure 3: Kidney transplantation standard morbidity (relative risks) ratios using a fixed filter size of 90 km (A) and 205 km (B) at each grid point.



may be oversmoothed, masking any real differences in SMRs within the city.

To alleviate the problem of unstable ratios in rural areas, we increased the size of the spatial filter. The maps in Figure 3 were generated using fixed filter sizes of 90 km and 205 km in order to reduce random noise for all grid points. The spatial variation in the distribution of the SMRs has been reduced considerably. The highest level of smoothing (see Figure 3b) removed most of the random noise in the rural areas of eastern California. Overall, this map does not convey much useful information in determining the spatial pattern of kidney transplantation SMRs.

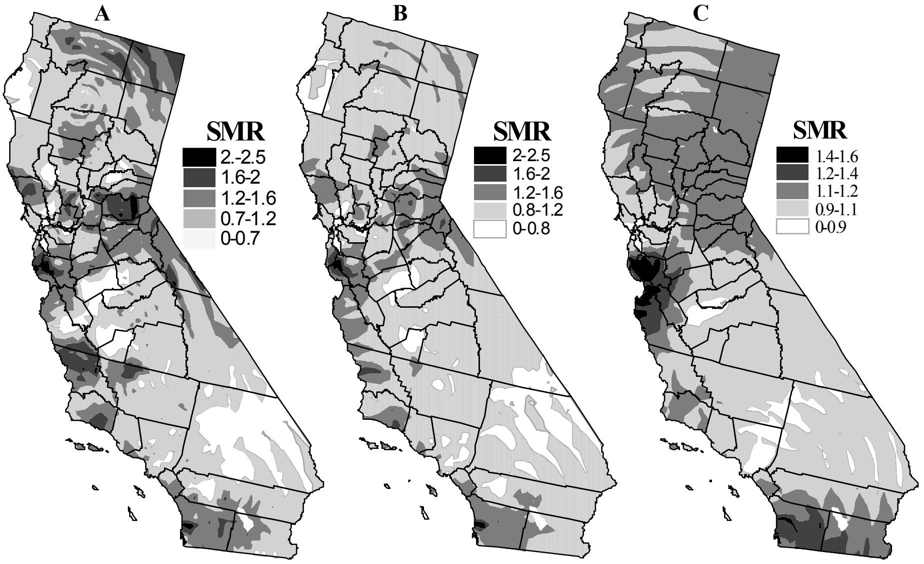
2. A Spatial Filter with Nearly Constant Population Size. This method sets, *a priori*, a minimum number of ESRD discharge events to capture at each grid point. The nearest ZIP Code centroids are successively located and the number of ESRD discharge events added until it reaches a value greater than or equal to the minimum number that has been established. The number of ESRD cases will exceed the predetermined minimum if the last ZIP Code area captured has more events than needed to reach the minimum denominator size.

We tested this method using three population-based kernel sizes, which were set at minimum number of 500, 1,200 and 10,000 ESRD events, respectively. For example, if 500 ESRD discharges were captured, the expected number of kidney transplants is 6.5 at the grid point if the rate within the circle is the same as the overall California rate of 1.3 renal transplants per 100 ESRD discharge events.

The smoothed SMR map using the spatial filter with nearly constant population size of 500 ESRD cases is displayed in Figure 4a. Many of the areas that had a high SMR in the unsmoothed ZIP Code map (Figure 2b) are no longer seen. This suggests that these elevations were likely due to random fluctuations of the ratios because of small numbers of renal patients within a ZIP Code area. Some elevated areas remain though, most prominently in parts of San Diego and San Jose, where kidney transplantation is in some cases more than twice the state average.

To evaluate the effect of changes in filter size, we created maps with different population kernel sizes. Maps produced using nearly equal kernel sizes of 1,200 and 10,000 are shown in Figures 4b and 4c. Unusually high SMRs are tempered as the population kernel increases. This is particularly noticeable in the rural areas where the ZIP Code SMRs were unstable due to the small numbers of renal patients. The high SMRs, which remain as the kernel size increases to 1,200 and 10,000 ESRD discharge events, respectively, indicate that these differences are

Figure 4: Kidney transplantation standard morbidity (relative risk) ratios using a variable kernel size set to capture at least 500 (A), 1200 (B) and 10,000 (C) End-Stage Renal Disease cases at each grid point.



less likely due to chance. Once the population kernel becomes too large, this technique is not useful anymore to detect elevated transplantation ratios in all but in some of the most densely populated regions of San Diego and San Jose/Bay Area. This is apparent in Figure 4c in which the kernel size is set to capture a minimum of 10,000 ESRD cases.

Elucidating Statistical Clusters of Kidney Transplantation. The above described smoothed maps are purely descriptive tools, showing areas with high or low access to kidney transplantation, after "filtering out" some of the random spatial noise. Spatial patterns of kidney transplantation, however, can be deceiving and might represent a spurious relationship that occurs by chance. Additional analytic tests for spatial randomness can eliminate this rivaling hypothesis. Thus, to complement the smoothed maps of ratios, we compared them with the results of analyzing the same transplantation data using the spatial scan statistic, in order to elucidate whether statistically significant geographic clusters were retained or smoothed out.

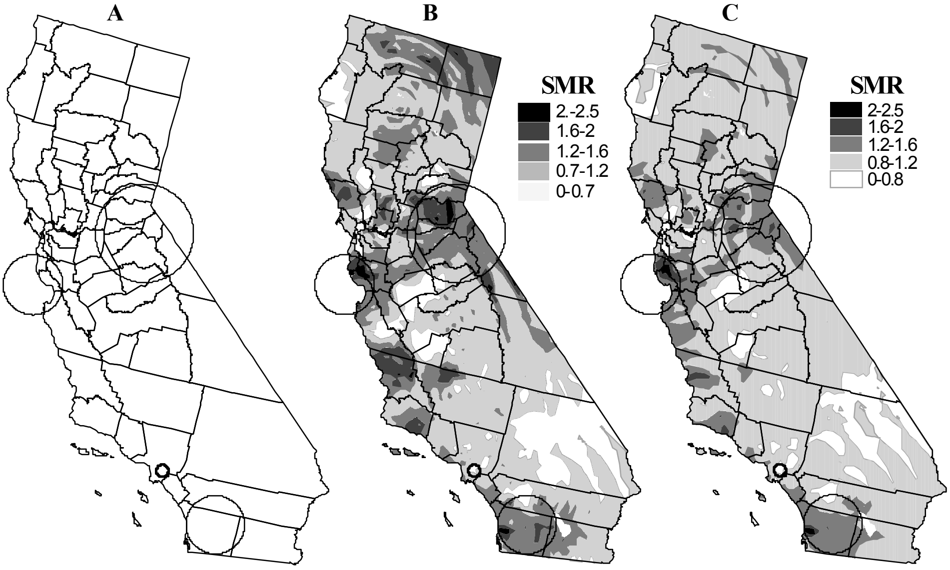
The spatial scan statistic is a robust test for spatial randomness that determines the location of any area of California with greater, or less, access to kidney transplantation, after adjusting for multiple testing inherent in many possible locations and sizes of the area. The maximum size was restricted to 10 percent of all ESRD discharge events in California. Calculations were done using the SaTScan software (Kulldorff, Rand, Gherman, Williams & DeFrancesco, 1998). Discussion and statistical details about this test can be found in Kulldorff and Nagarwalla (1995), and Kulldorff (1997, 1999). Recent health applications are presented in Sheehan, Gershman, MacDougall, Danley, Mroszczyk, Sorensen and Kulldorff (2000), and Talbot et al. (2000).

The most probable areas where transplantation clusters occur, regardless of size, are shown in Table I and Figure 5a. The general areas that have an SMR that is statistically significant, after adjusting for the multiple testing, also show up as high SMR regions on the smoothed maps of kidney transplantation with a kernel of nearly constant population size (see Figures 5b and 5c). Three statistical clusters of

Table 1: Results of spatial scan statistic test for more likely kidney transplant clusters

Geographic area	Kidney transplants	ESRD events	SMR	P-value
Bay Area/San Jose	316	12,054	1.9	< 0.001
San Diego	379	18,452	1.6	< 0.001
Tahoe	149	7,013	1.6	0.01
South East Los Angeles Co.	346	41616	0.7	< 0.001

Figure 5: Likely clusters of access to kidney transplantation using a double-sided spatial scan statistic ($p < 0.05$) (A). The only cluster of diminished-access is in Los Angeles County (restrictions: no cluster can contain more than 10 percent of ESRD cases). Clusters of kidney transplantation overlaid on a map of smoothed kidney transplantation standard morbidity (relative risk) ratios based on a variable kernel size set to capture at least 500 (B) and 1,200 (C) ESRD cases at each grid point. Two areas with apparent high rates of kidney transplantation, along the coast of Santa Barbara and San Luis Obispo counties, are removed by the spatial scan statistic.



greater access to kidney transplantation were identified. One is located in an area roughly corresponding to the Bay Area (SMR = 1.9), south of San Francisco, near San Jose. A second cluster occurs in San Diego County (SMR = 1.6), which also extends into some of the desert resort communities of Riverside County such as Palm Springs. The third and largest cluster (SMR = 1.6) encompasses several semi-rural counties east of Sacramento, around the mountain resort area of Lake Tahoe.

A localized cluster of diminished access to kidney transplantation is in southeast Los Angeles County (SMR = 0.7), including over 20 populous communities adjacent to the city of Los Angeles. This cluster also coincides with a persistent low SMR region in the smoothed maps (Figures 5b and 5c). Therefore, these maps do not smooth over the areas with statistically significant rates except when filters are set too large. We see in Figure 4c that by using a large kernel size of 10,000 ESRD events, the statistically significant areas in the cluster east of Sacramento are smoothed over (Figure 4c). When using a fixed filter size though, areas with a statistically significant SMR are sometimes smoothed out (Figure 3b), and when they are not, there are others with non-significant SMRs that stand out prominently or dominate the map (see Figures 2c and 3a).

Correspondence Between Illness and Treatment

How Are Organs Allocated? Geography vs. Medical Criteria. As discussed earlier, the hotly contested health policy issue in organ transplantation involves the equitable allocation of organs. Notwithstanding the importance of medical criteria, critics have argued about the role of location or geography in allocation decisions. That is, should persons who live in a defined service area be given preference for organs over others who live outside of the OPO's immediate network? Both the government and health professional organizations like the AMA argue in favor of medical necessity as the only criteria for the equitable allocation of organs. Assuming equity in health care access currently exists in the U.S. transplantation network, we now ask the following question: Given natural clustering of disease occurrence, is kidney transplantation randomly distributed to persons with ESRD in California?

By applying a spatial scan statistic to kidney transplantation data (1995-1998), we have demonstrated the existence of statistical clusters as described in the previous section. Therefore, the hypothesis of a geographically random distribution of kidney transplantation is rejected. In other words, the observation of spatial clusters implies that geography (i.e., place of residence) plays a role in determining access to optimal treatment for renal patients in California. What specific local factors influence access to kidney transplantation in the cluster regions remain to be elucidated. Variation in factors such as local health resources, practices or health care market structure has been suggested (Dartmouth Medical School, 1998). The possibility exists though that, simply, local variation in renal disease might account for the observed geographic clustering of kidney transplantation. We explore this question next.

Elucidating Clusters of End-Stage Renal Disease. Once again, the important question is whether or not the distribution and utilization of health care is explained by the underlying illness. In other words, does the pattern of variation in access to kidney transplantation (i.e., treatment) bear a relationship to the distribution of the underlying illness (i.e., ESRD)? Theoretically, treatment should correspond to a higher presence of ESRD in local populations. If after controlling for gender, age and race/ethnicity, clustering of ESRD patients can be demonstrated, the key question of whether illness and access correspond can be investigated by assessing the geographic agreement between ESRD and transplantation clusters.

Using the same techniques already described for the detection of transplantation clusters, we applied the spatial scan statistic to ESRD hospital discharge data in order to assess the spatial clustering of renal disease in California. Denominators corresponding to the underlying "at-risk" population by ZIP Code were based on 1997 updates of U.S. Census statistics for California (Claritas, Inc., Arlington, Virginia). The SaTScan software has built-in functions that adjust for population changes between inter-censual years (Kulldorff et al., 1998). As before, the

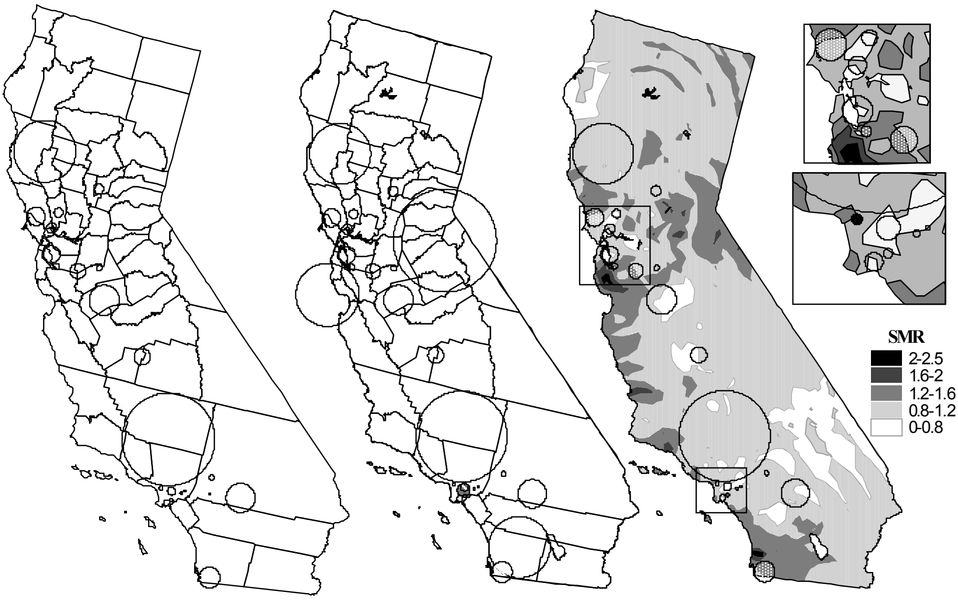
Table 2: Results of spatial scan statistic test for more likely ESRD clusters

Geographic area	ESRD events	Total population	SMR	P-value
Oakland	18369	961828	1.4	< 0.001
Los Angeles/Pasadena/San Fernando	41891	4223720	1.2	< 0.001
Napa	434	6040	8.3	< 0.001
South East Los Angeles Co.	13873	1113343	1.3	< 0.001
San Diego	14527	1204105	1.3	< 0.001
Los Banos/Merced	3016	212074	1.7	< 0.001
Marysville/Yuba City	1501	94898	1.9	< 0.001
Carson/Long Beach	6959	542558	1.3	< 0.001
Hanford/Visalia	2820	224311	1.5	< 0.001
Modesto	2413	202162	1.5	< 0.001
Yucca Valley	1220	68662	1.7	< 0.001
Fremont/Newark	2177	181027	1.4	< 0.001
Glendora	528	32741	2.1	< 0.001
Ukiah	1664	121864	1.5	< 0.001
Eureka	62	562	13.1	< 0.001
Beverly Hills/West Hollywood	3038	237934	1.3	< 0.001
Artesia/Bellflower/Norwalk	2913	263402	1.3	< 0.001
West Covina	2372	207129	1.3	< 0.001
San Bernardino	516	35535	1.7	< 0.001
Tracy	702	62539	1.6	< 0.001
Upland	784	60618	1.5	< 0.001
Vallejo	1804	117644	1.3	< 0.001
Petaluma/Santa Rosa/Rohnert Park	2009	221756	1.2	< 0.001
Victorville	921	75125	1.3	< 0.001

maximum size of the scan window was set again to 10 percent of the underlying population.

The most likely ESRD clusters, irrespective of size, appear in Table II and Figure 6a. Twenty-four clusters are scattered from north to south, largely on the most western portion of the state, corresponding to the more densely populated

Figure 6: Clusters of ESRD using a double-sided spatial scan statistic ($p < 0.001$), indicating medical need (A). Clusters of ESRD, of greater access than the state average, and of less access than the state average, are shown together to assess the spatial correspondence between medical need and access to treatment (B). For the most part, clusters of renal disease do not overlap with clusters of greater access to kidney transplantation. Near Los Angeles, a cluster of poor access to transplantation overlaps with small clusters of renal disease. ESRD clusters are overlaid on a map of smoothed ratios (population kernel size of 1,200) to reveal the underlying cluster-specific transplantation activity (C). Only five renal disease clusters (stippled circles), three in north and two in the south (see bottom inset), occur in areas with greater access to kidney transplantation than the state average.



regions. These clusters are indicative of medical need, identifying areas where renal disease presence is elevated with respect to the state average. The size of the clusters seems to be related to population density, being smaller in urban areas, and larger in less densely populated areas. We compare next how the detected ESRD and transplantation clusters correspond.

Comparison of Results. Figure 6b shows a map overlay of ESRD and kidney transplantation clusters. It can be observed that of the three clusters of greater access to transplantation, only the one in San Diego corresponds with a cluster of renal disease in the greater San Diego metropolitan area. The other two, around the San Jose and Lake Tahoe areas in northern California, occur in regions with no ESRD clusters. The cluster of less access to transplantation identified in southeastern Los Angeles County overlaps with, and is surrounded by, small urban clusters of ESRD. This seems to be a region of concern for public health officials and policy makers, with overlap of higher-than-expected levels of underlying illness and poor access to treatment. Thus one can clearly see how GIS can be used to identify areas of concern for revisiting existing policy and practices.

In addition to spatially comparing both types of statistical clusters, we further explored the correspondence of renal disease and access to treatment by investigating transplantation activity inside the ESRD clusters. Figure 6c shows the ESRD clusters overlaid on a map of smoothed transplantation ratios that are derived by using an adaptive kernel of a nearly constant population size of 1,200. Visual inspection of this map reveals that clusters occur in areas where the smoothed SMRs are below the state average. The results of this technique suggest agreement with the earlier noted lack of general correspondence between illness and treatment.

Some clusters may include more than one SMR range (see Figure 6c), with one zone, for example, representing greater access to transplantation, next to a zone of diminished access. We further characterized ESRD clusters by applying GIS analytical functions for calculating zonal statistics to the 2-km grid from which the smoothed transplantation maps were derived. Thus, we identified ESRD clusters enveloping grid points with maximum SMRs greater than 1, that is, with greater access than the state average. Table III contains the 11 identified ESRD clusters. In addition, with the aid of GIS spatial functions, we calculated cluster-specific transplantation SMRs based on patient discharge data captured inside each of the 11 ESRD clusters. These ratios can be also found in Table III. Out of the 11 clusters, only five have SMRs greater than 1, indicating greater access than the state average. Three of these five ESRD clusters with elevated transplantation SMRs are located in northern California. They can be seen in the top inset of Figure 6c. They correspond to the geographic areas of Freemont-Newark and Tracy-Livermore, north of San Jose, and Petaluma-Santa Rosa-Rohner Park, north of San Francisco.

Table 3: Underlying cluster-specific kidney transplantation ratios, SMRs, for ESRD clusters, which exhibited a maximum SMR greater than the state average.

Geographic area	Max. SMR	SMR
Fremont/Newark	1.5	1.5
San Diego	1.5	1.2
Tracy	1.4	1.1
Beverly Hills/West Hollywood	1.2	1.1
Petaluma/Santa Rosa/Rohnert Park	1.4	1.1
Ukiah	1.3	1.0
Modesto	1.0	1.0
Los Angeles/Pasadena/San Fernando	1.4	0.9
Oakland	1.5	0.8
Los Banos/Merced	1.3	0.6
Hanford/Visalia	1.0	0.5

The remaining two clusters are located in southern California, one in Beverly Hills (see bottom inset in Figure 6c), west of Los Angeles, and the second one in the greater San Diego area. Note that the elevated transplantation SMR in the San Diego area has been also identified as a statistical cluster of greater access paralleling the ESRD cluster. Interestingly, these areas have in common higher-than-average income and general SES levels of the target population.

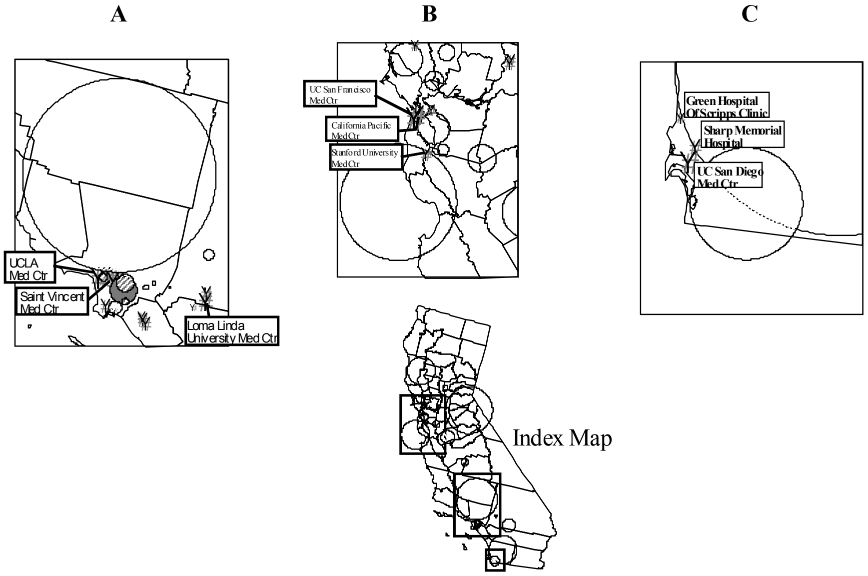
DISCUSSION

The Value of a GIS Model of Health Disparities

Figure 7 shows with greater geographic detail the three main metropolitan areas of the state, combining the locations of both types of clusters, ESRD (medical need) and transplantation (access to treatment), with the transplantation centers (health care resources). The greater Los Angeles metropolitan area shown in Figure 7a illustrates a situation where medical need is apparent. Several ESRD clusters are matched by one cluster of diminished access to transplantation. The greatest concentration of transplantation centers of the state does not ensure adequate access to treatment for the renal patients of the region.

Figure 7b shows the San Francisco and San Jose metropolitan areas. In this region we observe also the presence of several ESRD clusters, indicating medical

Figure 7: The three main metropolitan areas of the state, Los Angeles (A), San Francisco/Bay Area (B) and San Diego (C), are shown in detail combining the locations of both ESRD (medical need) and transplantation (access to treatment) clusters, shown together with the transplantation centers (health care resources). Transplantation centers are displayed as dark circles (with a black dot) of varying diameter according to annual kidney transplantation activity. The three top renal transplantation centers within each region are identified.



need. However, they do not correspond geographically with the location of a cluster of greater access to transplantation approximately encompassing the Silicon Valley. Interestingly, neighboring this transplantation cluster is an ESRD cluster stretching across both shores of the San Francisco Bay, from Oakland to east San Francisco. The two prominent transplantation centers of this region are precisely sitting in this cluster of need. Figure 7c shows the San Diego area, which unlike the two previous regions represents a case where need and access correspond. This is accomplished with fewer health care resources, as only three transplantation centers operate in this region of the state.

In summary, the high/low SMR clusters we identified do not correspond geographically to the underlying illness (ESRD). Our analysis suggests that the likelihood to receive a kidney transplant does not necessary follow the presence of renal disease. Both smoothing techniques and statistical tests of spatial randomness reveal these trends. This suggests that geography seems to play a role in access to kidney transplantation.

The results of our analysis lead us to conclude that geographic health disparities in California suggest local biases. Repeating the popular adage that "all health care is local" bears a surreal truth. We must study the local characteristics of health care delivery and other geographic factors known to affect health. Understanding these clusters of activity may determine our ability to successfully address health disparities on a macro-level. Geographic Information Systems add value to the more accurate and comprehensive treatment of health disparities.

Practical Considerations in Implementing a GIS Model of Health Disparities

There are several recommendations we would make to GIS analysts and health geographers exploring a similar spatial model of health disparities:

One Size Does Not Fit All. Caution: there is no intrinsic size that can be used to smooth all maps in every situation. The choice depends on the nature of the health phenomena being studied, the size of the study area and other considerations. If the filter is too large, it may eliminate true variation, while too little smoothing will leave random noise in the data. Since smoothed maps are primarily descriptive tools, different amounts of smoothing should be tested to see different types of spatial patterns (Figures 4a-c).

Spatial Filtering. Spatial filtering based on windows with a nearly fixed population size are more appropriate for mapping health events in regions, like California, with widely varying population density, than methods based on a fixed geographic kernel size. First, random "noise" in rural, sparsely populated areas, is smoothed to the same level as in urban, densely populated areas, while at the same time enhancing the spatial resolution of urban area estimates. Second, all estimates throughout the study area are approximately equally reliable because the variances of the estimates depend on the population size at risk (Talbot et al., 2000)—which is nearly equalized by this technique.

Population Density. A shortcoming of the population density equalizing method is that the regional map will not have the same resolution throughout, with urban areas based on small windows, and rural areas on much larger ones (see for example, Figure 4a). For example, a map showing a high SMR in a rural area on the northwestern corner of California may give the mistaken impression that the elevation is local in nature, when in fact the rate is based on a much larger territory. Thus, we recommend caution when interpreting these maps. Researchers studying regions with a homogeneous population density, or focus on densely populated urban areas, may want to use fixed geographic filter sizes.

Use Spatial Statistics to Test Observed Geographic Patterns. Geographic approaches to the study of health processes should always be complemented with statistical tests for spatial randomness to determine whether the observed patterns are due to chance or not, and to identify elevated areas (clusters) that are statistically significant. We applied a focused test, the spatial scan statistic, and determined which of the high and/or low areas observed by the smoothing technique were likely random occurrences, and which were statistically significant after adjusting for the multiple testing of many possible cluster locations and sizes.

Smoothed Maps Still Yield Valuable Information. The use of tests for spatial randomness does not mean that the smoothed maps of rates should be discarded altogether, since the general pattern can be useful for generating hypotheses about the cause of the spatial variation. For example, note a persistent area of elevated ratios straddling across Santa Barbara and San Luis Obispo counties, along the coast, between Los Angeles and San Francisco. While this region was not statistically significant, further investigation might be appropriate in order to determine whether or not it shares relevant health care market or sociodemographic characteristics similar to the other areas of greater access to transplantation.

Go Further: Multi-Analytic Methods Are Better. It is important to realize that the smoothed maps do not show the areas with elevated SMR *per se*, but the locations of centroids for which the surrounding circles of a specified size contained an elevated ratio. The precise boundaries of different areas with different SMRs cannot be elucidated from the smoothed maps. These techniques only suggest the general location of areas of higher/lower SMRs. More importantly, these techniques, being descriptive in nature, do not provide the cause underlying geographic variability. The result is an additional tool to alert the researcher to the need for further study and testing of assumptions. Further study is then needed through detailed analysis of socioeconomic, behavioral or health care factors associated with kidney transplantation in these populations.

Advantages of Using a GIS-Based Approach

Why state the obvious? We think this message needs to be explicitly stated. Specifically, we strongly believe that the full potential of GIS is being *underutilized*. There are situations in health services research and practice (e.g., organ transplantation) where some of the more advanced GIS functions can indeed improve our basic understanding and in the end outcomes. GIS are not only useful for mapping and database management activities, but, more importantly, for performing spatial analysis. GIS already is a powerful analytical tool for a wide variety of disciplines that deal with spatial phenomena. Using this example we hope to recruit health care professionals to join other social and behavioral scientists in substantially benefiting from recent advancements in GIS technology.

A GIS-based approach permits the elucidation and understanding of the geographic variability of health differences, making possible the precise identification of under- or over-served regions. The populations residing in those regions can then be characterized demographically and/or socioeconomically using GIS technology. Effective planning of intervention strategies customized to specific populations whose characteristics have been described is thus facilitated.

Geographic differences within groups (e.g., racial/ethnic) or communities can also be investigated. For example, non-geographic studies may reveal adequate access to kidney transplantation for a certain racial/ethnic group as a whole, while negating or omitting how this same group may experience poorer access to treatment in localized areas. In contrast, a whole other group may have poor, but geographically dissimilar access to health care. At localized areas, members of the group may even enjoy adequate access to health services. Thus, GIS can significantly improve the ability to discern such local effects.

Geographic Information Systems enable health researchers and agencies flexible mapping of health-related outcomes as well as of indicators of health care access and resources, in order to investigate their geographic variation. This GIS-based approach may well become an important part of routine assessments of health disparities at the community level, to detect areas with high or low rates of adverse health outcomes, areas where populations are being over-served or receiving inadequate health care.

CONCLUSION

In closing, we have attempted to share with our readers how GIS can inform public health policy and practice. Notwithstanding its powerful exploratory and analytic capabilities, Geographic Information Systems provide the *context for the integration of multidisciplinary approaches and techniques to provide a clearer, more complete picture of health.* In our case, we combined epidemiologic techniques with health services research methods. The power for visualizing data elements as well as analytic results provides a more holistic view of the health disparities problem, suggesting areas or issues that require further elucidation. In addition to answering specific questions about health differences, a GIS approach enables researchers to explore potential geographic policies and practices that may contribute to the existing health disparities. When combined with multi-method approaches, geographic tools and spatial statistics will offer new analytic opportunities for disease assessment and prevention, and will enhance attempts to plan more efficacious interventions.

REFERENCES

Albert, D. P., Gesler, W. M. & Levergood, B. (Eds.). (2000). *Spatial GIS and Remote Sensing Applications in the Health Sciences.* Chelsea, MI: Ann Arbor Press.

Anselin, L. (1996). The Moran scatterplot as an ESDA tool to assess local instability in spatial association. In Fischer, M., Scholten, H. J. & Unwin, D. (Eds.), *Spatial Analytical Perspectives on GIS* (pp. 111-125). London, UK: Taylor and Francis.

Ayanian, J. Z., Cleary, P. D., Weissman, J. S. & Epstein, A. M. (1999). The Effect of Patients' Preferences on racial differences in access to renal transplantation. *The New England Journal of Medicine,* 341(25), 1661-8.

Bailey, T. C. and Gatrell, A. C. (1995). *Interactive Spatial Data Analysis.* Essex, UK: Longman Scientific and Technical.

Bithell, J. F. (2000). A classification of disease mapping methods. *Statistics in Medicine, 19*, 2203-2215.

Breiman, L., Meisel, W. Purcell, E. (1997). Variable kernel estimates of multivariate densities. *Technometrics,* 19, 135-144.

Chou, Y. H. (1997). *Exploring Spatial Analysis in Geographic Information Systems.* Santa Fe, NM: Onword Press.

Clarke, K. C. (2001). *Getting Started with Geographic Information Systems.* Upper Saddle River, NJ : Prentice Hall Inc.

Cressie, N.A.C. (1993). *Statistics for Spatial Data* (Revised ed.). New York: John Wiley & Sons.

Dartmouth Medical School, Center for the Evaluative Clinical Sciences. (1996). *The Dartmouth Atlas of Health Care: The Pacific States.* Chicago, IL: American Hospital Publishing.

Dartmouth Medical School, Center for the Evaluative Clinical Sciences. (1998). *The Dartmouth Atlas of Health Care 1998.* Chicago, IL: American Hospital Publishing.

De Lepper, M. J. C., Scholten, H. J. & Stern, R. (Eds.) (1995). *The Added Value of Geographical Information Systems in Public and Environmental Health.* Dordrecth, The Netherlands: Kluwer Academic Press.

Devesa, S. S., Grauman, D. J., Blor, W. J., Pennello, G. A., Hoover, R. N. & Fraumeni, J. F. (1999). *Atlas of Cancer Mortality in the United States:*

1950-94 (NIH Publication No. 99-4564). Bethesda, MD: National Institutes of Health, National Cancer Institute.

Dorling, D. (1994). Cartograms for visualizing human geography. In Hearnshaw, H. J. & Unwin, D. J. (Eds.), *Visualization in Geographical Information Systems.* Chichester: John Wiley & Sons.

Eggers, P. W. (1995). Racial differences in access to kidney transplantation. *Health Care Financing Review* 17(2), 89-103.

Epstein, A.M., Ayanian, J. Z., Keogh, J. H., Noonan, S. J., Armistead, N., Cleary, P. D., Weissman, J. S., David-Kasdan, J. A., Carlson, D., Fuller, J., March, D. & Conti, R.M. (2000). Racial disparities in access to renal transplantation: Clinically appropriate or due to underuse or overuse? *The New England Journal of Medicine*, 343(21), 1537-1544.

Fiscella, K., Franks, P., Gold, M. R. & Clancy, C. M.. (2000). Inequalities in quality: Addressing socioeconomic, racial, and ethnic disparities in health care. *JAMA*, 293(19), 2579-2584.

Hogue, C. J. R., Hargraves, M. A. & Collins, K. S. (Eds.). (2000). *Minority Health in America: Findings and Policy Implications from the Commonwealth Fund Minority Health Survey*. Baltimore, MD: Johns Hopkins University Press.

Kafadar, K. (1996). Smoothing geographical data, particularly rates of disease. *Statistics in Medicine,* 15, 2539-2560.

Kafadar, K. (1999). Simultaneous smoothing and adjusting mortality rates in U.S. counties: Melanoma in white females and white males. *Statistics in Medicine* 18, 3167-3188.

Kim, J. H. (1998). *Atlas of Respiratory Disease Mortality, United States: 1982-1993* (NIOSH Publication No. 98-157). Cincinnati, OH: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, National Institute for Occupational Safety and Health.

Kulldorff, M. & Nagarwalla, N. (1995). Spatial disease clusters: Detection and inference. *Statistics in Medicine* 14, 799-810.

Kulldorff, M., R R., Gherman, G., Williams, G. & DeFrancesco, D. (1998). *SaTScan v2.1: Software for Calculating the Spatial and Space-Time Scan Statistics*. Bethesda, MD: National Cancer Institute.

Kulldorff, M. (1997). A spatial scan statistic. *Communications in Statistics Theory and Methods,* 26, 1481-1496.

Kulldorff, M. (1999). Geographic Information Systems (GIS) and community health: Some statistical issues. *Journal of Public Health Practice Management*, 5(2), 100-106.

Lawson, A. B. (2001). *Statistical Methods in Spatial Epidemiology*. New York: John Wiley & Sons.

Loslier, L. (1995). Geographical Information Systems (GIS) from a health perspective. In de Savigny, D. & Wijeyaratne, P. (Eds.), *GIS for Health and the Environment, Proceedings of an International Workshop held in Colombo, Sri Lanka, 5-10 September 1994* (pp. 13-20). Ottawa, Canada: International Development Research Centre.

Maguire, D. J., Goodchild, M.F. & Rhind, D. W. (Eds.). (1991). *Geographic Information Systems.* Harlow, UK: Longman Scientific & Technical.

McCleary, K. J., Soret, S., Rivers, P.A. & Montgomery, S. B. (2001). *Assessing Health Access to Organ Transplantation in California: A Geographic Information Systems (GIS) Perspective.* Poster session presented at the annual meeting of the Academy of Health Services Research and Health Policy, Atlanta, GA.

Meade, M., Florin, J. & Gesler, W. (1988). *Medical Geography.* New York: The Guilford Press.

Merrill, D. W., Selvin, S., Close, E. R. & Holmes, H. H. (1996). Use of density equalizing map projections (DEMP) in the analysis of childhood cancer in four California counties. *Statistics in Medicine* 15, 1837-1848

Niemcryk, S., Aronoff, R., Marconi. K. M. & Bowen. G. S. (1994). Projections in solid organ transplantation and wait list activity through the year 2000. *Journal of Transplant Coordination*, 4, 23-30.

Novick, L. F., Richards, T. B. & Croner, C. M. (1999). Issue focus: Geographic information systems in public health, part I. *Journal of Public Health Management Practice,* 5(2).

Odland, J. (1988). *Spatial Autocorrelation*. Newbury Park, CA: Sage Publications.

Organ Procurement and Transplantation Network (1998). Final Rule, 42 C.F.R. Part 121.

Ozcan, Y. A., Begun, J. W. & McKinney, M. M. (1999). Benchmarking organ procurement organizations: A national study. *Health Services Research*, 34(4), 855-878.

Raleigh, V. S. (1997). Diabetes and hypertension in Britain's ethnic minorities: Implications for the future of renal services. *The British Medical Journal,* 314(7075), 209-13.

Reddan, D. N., Szczech, L. A., Klassen, P. S. & Owen, W. F. Jr. (2000). Racial inequity in American's ESRD program. *Seminars In Dialysis,* 13(6), 399-403.

Richards, T. B., Croner, C. M., Rushton, G. & Brown, C. K. (1999). Geographic

Information Systems and public health: Mapping the future. *Public Health Reports,* 114, 359-373.

Ricketts, T. C., Savitz, L. A., Gesler, W. M. & Osborne, D. N. (1994). *Geographic Methods for Health Services Research: A Focus on the Rural-Urban Continuum*. Lanham, MD: University Press of America.

Roper, W. L. & and Mays, G. P. (1999). GIS and public health policy: A new frontier for improving community health. *Journal of Public Health Management and Practice*, 5(2), vi-vii.

Rushton, G. & Lolonis, P. (1996). Exploratory spatial analysis of birth defect rates in an urban population. *Statistics in Medicine* 15, 717-726.

Rushton, G., Krishnamurthy, R., Krishnamurthy, D., Lolonis, P. & Song. H. (1996). The spatial relationship between infant mortality and birth defect rates in a U.S. City. *Statistics in Medicine* 15, 1907-1919.

Rushton, G. (1997). *Improving Public Health Through Geographical Information Systems: An Instructional Guide to Major Concepts and Their Implementation* [CD-ROM] (Version 2.0.). Iowa City: University of Iowa, Department of Geography.

Scantlebury V., Gjertson D., Eliasziw M., Terasaki P., Fung J., Shapiro R., Donner A. & Starzl, TE. (1998). Effect of HLA mismatch in African Americans. *Transplantation*, 65(4), 586-8.

Sheehan, T. J., Gershman, S.T., MacDougall, L.A., Danley, R.A., Mroszczyk, M., Sorensen, A.M. & Kulldorf, M. (2000). Geographic assessment of breast cancer screening by towns, zip codes, and census tracts. *Journal of Public Health Management Practice,* 6(6), 48-57.

Stern, R. M. (1995). Environmental and health data in Europe as a tool for risk management: needs, uses, and strategies. In de Lepper, M. J. C., Scholten, H. J. & Stern, R. M. (Eds.), *The Added Value of Geographical Information Systems in Public and Environmental Health.* Dordrecth, The Netherlands: Kluwer Academic Press.

Talbot, T. O., Kulldorff, M., Forand, S. P. & Haley, V. (2000). Evaluation of spatial filters to create smoothed maps of health data. *Statistics in Medicine,* 19, 2399-2408.

Tell, G.S., Hylander, B., Graven, T.E. & Burkart, J. (1996). Racial differences in the incidence of end-stage renal disease. *Ethnicity and Health*, 1, 21-31.

Thamer, M., Henderson, S.C., Ray, N. F., Rinehart, C. S., Greer, J. W. & Danovitch, G. M. (1999). Unequal access to cadaveric kidney transplantation in California based on insurance status. *Health Services Research, 3*4, 879-899.

Turnock, B.J. (2001). *Public Health: What It Is and How It Works.* Gaithersburg, MD: Aspen Publishers.

United States Senate. (July 26, 2000). *Health Disparities: Bridging the Gap.* Hearing before the Subcommittee on Public Health of the Committee on Health, Education, Labor, and Pensions. 106th Congress, Second Session on examining health care disparities among women, minorities, and rural underserved populations, and the actions of the National Institutes of Health to address these disparities, as well as review a relevant legislation designed to address the issues of health disparities. (S. HRG. 106-695). Washington, DC: U.S. Government Printing Office.

U.S. Renal Data System: USRDS. (1999). *Annual Data Report, 1999.* Bethesda, MD: National Institute of Health, National Institute of Diabetes and Digestive and Kidney Diseases.

Williams, D. R. & Rucker, T. D. (2000). Understanding and addressing racial disparities in health care. *Health Care Finance Review,* 21(4), 75-90

Yasnoff, W. A. & Sondik, E. J. (1999). Geographic Information Systems (GIS) in public health practice in the new millennium. *Journal of Public Health Management and Practice*, 5(4), viii-xi.

Yasui, Y., Liu, H., Benach, J. & Winget, M. (2000). An empirical evaluation of various priors in the empirical Bayes estimation of small area disease risks. *Statistics in Medicine,* 19, 2409-2420.

Young, C. J. & Gaston, R. S. (2000). Renal transplantation in Black Americans. *The New England Journal of Medicine,* 343(21), 1545-1552.

Chapter III

Using a GIS and the American Community Survey to Address Community Health Problems

Jane L. McCall, Amy K. Pasini and Richard B. Wait
Health Geographics and Spatial Analysis Program at
Baystate Medical Center, USA

This chapter describes two case studies that demonstrate how the technology of Geographic Information Systems (GIS) can be combined with community data to address healthcare problems. The purpose is to present a model that can be replicated by other hospitals or those with an interest in promoting the public health.

BACKGROUND

Baystate Medical Center (BMC), located in Springfield, Massachusetts, was contracted by the U.S. Census Bureau to conduct two case studies to demonstrate the utility of annually adjusted data from the American Community Survey (ACS). In addition, BMC is the sponsor of the Injury Prevention Task Force, a city-wide collaboration of community, civic and healthcare organizations formed to address the problem of violence. Stemming from its dual role in both of these entities, BMC has access to medical data from the major area hospitals, geographic data from the City of Springfield Planning Department and community population data from the ACS.

Springfield is a mid-sized city in Hampden County, situated in Western Massachusetts. It has approximately 150,000 people and a surrounding metropolitan area of more than 500,000. Springfield is a major urban center for employment, culture, commerce and government. The city has a diverse mixture of racial, cultural, ethnic and income groups, which characterize different parts of the city. This makes Springfield an ideal climate for investigating the uses of census data.

The American Community Survey is a survey by the U.S. Census Bureau patterned on the decenniel census long-form. Data are collected monthly and used to provide annually adjusted estimates of the population based on a sample of the population. Hampden County is one of 31 pilot sites for the ACS, chosen to demonstrate the utility of yearly data collection. These sites represent diversity in population size, rate of growth, ease of enumeration and region of the country.

The ACS has several advantages over the decennial census. It provides the most current available data on population estimates. Yearly publication of updates allow tracking population shifts over time. This contrasts with census data, which can be as much as 11 years old. This advantage is augmented by the six-month turnaround for the ACS, which contrasts with a two-year turnaround for census data. A further advantage is that additional questions are included in the ACS which are not on the census: these concern school lunch, heating and cooling assistance, food stamps and public housing. This increases the ability of ACS data to address community issues.

There are, however, certain limitations in using ACS data that the reader should keep in mind in reading this chapter. ACS figures are estimates from a sample of the population, not exact counts. These estimates are weighted to give greater representation to areas of greater population size. Weights for the data presented in this chapter are based on 1990 Census population proportions. In 2002 they will be revised with 2000 Census weights, resulting in greater accuracy. These ACS estimates should therefore be used as community profiles with an emphasis on the relative proportions in each population subgroup. ACS is not a count of the population but rather a mechanism for measuring changes and trends in the population in the interval between decenniel Census counts. For example, in interpreting estimates for ethnicity, the focus should be on determining what is the predominant ethnic subgroup in a geographic area rather than on obtaining a count of the number of people in each subgroup.

CASE STUDY: INVESTIGATING LATE-STAGE BREAST CANCER

The first case study for the American Community Survey concerns the utilization of ACS population and housing data in a GIS to improve breast cancer intervention programs. The methodology for this case study can be used as well with decennial census data, when available.

Defining the Problem

In choosing a demonstration project, a relevant problem in the community to be studied had to be defined. To do this, visualization was employed, using data downloaded from the Atlas of Cancer Mortality (Devesa et al., 1999). The Atlas provides the geographic distribution of mortality rates from various cancers in the U.S. according to race, time period and a variety of geographic subdivisions. A type of cancer with high mortality rates over the last 25 years in Massachusetts would represent a particular problem in the state. This was the case with breast cancer in women. The investigators then looked at the magnitude of breast cancer mortality in their own county, Hampden County. While it was not the highest in the state, still the mortality rate of approximately 30 per 100,000 women was of significant concern.

To address the problem of breast cancer mortality, it seemed logical to focus on late-stage disease. Previous research has clearly established that by lowering the rate of late-stage disease with increased mammography screening, breast cancer mortality can be reduced (Feig, 1988; Shapiro, 1994; Tabar, Fagerberg, Duffy & Day, 1989).

Data from the Massachusetts Department of Public Health (MassDPH, 1999) showed that the proportion of breast cancer cases with late-stage disease was higher in Springfield than the rest of the state. From this it was concluded that late-stage breast cancer in Springfield was a significant public health concern and worthy of study. Any findings from this study could be used to plan an approach to improving breast cancer screening intervention.

The purpose of the present study was to create a profile of communities in Springfield in need of increased breast cancer screening. Specifically, the investigators wanted to identify parts of the city with high rates of late-stage disease as well as identify socioeconomic and demographic factors in late-stage disease. This information would aid in resource allocation by focusing intervention efforts on high-risk areas. Furthermore, it would aid in the design of socio-demographically appropriate screening programs.

Study Methods and Results

Data sources for the study are given in Table 1. The City of Springfield Planning Department keeps accurate, up-to-date geographic data in the form of ArcView (ESRI, 1999) shape files that were used for police sector boundaries and for geocoding the locations of cases and mammography facilities. Estimates from the

Table 1: Data sources

Data Type	Description	Data structure	File type	Source
Geographic	Police sector boundaries Springfield streets	Vector (polygons) Vector (arcs)	ESRI shape file “ “ “ “	City of Springfield “ “ “ “
Demographic	ACS population and housing characteristics	Table	ASCII text	U.S. Census Bureau
Clinical	Breast cancer patients	Relational database	Excel/Dbase	Oncology Registries

Table 2: American Community Survey variables

Households	food stamps public assistance income poverty status	*Women > 40*	age race ethnicity educational attainment primary language linguistic isolation marital status employment status place of birth/citizenship status
Families/households	median income income category		
Housing units	occupancy status tenure		
Police sectors	median home value aggregate public assistance income aggregate food stamp benefits	*Youths (10-17)*	linguistic isolation primary language race age sex
Workers	transportation type		

American Community Survey performed in 1999 were obtained on various population and housing characteristics for women over 40. A complete list of ACS variables for both case studies is given in Table 2.

Data on breast cancer patients was obtained from the oncology registries of Baystate Medical Center and Mercy Medical Center. Together these registries capture approximately 95% of the reported cases in the city. A list of data items collected from both registries is given in Table 3.

All cases of breast cancer diagnosed between 1995 and 1999 were included

Table 3: Registry data for late-stage breast cancer study

Geographic Information	street address city zip code	*Clinical/pathologic*	date of diagnosis stage at diagnosis tumor site histology grade side size nodes examined positive nodes
Demographic Information	date of birth age at diagnosis sex race primary language ethnicity marital status		
History	family history smoking status alcohol status parity	*Insurance*	primary

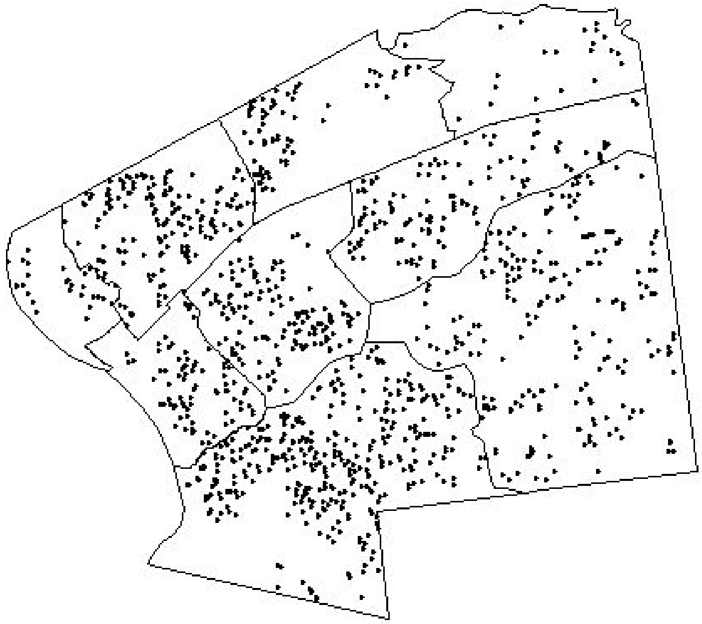
in the study. Late-stage disease was defined as American Joint Cancer Committee (AJCC, 1997) Stage 2 or greater. Case locations were geocoded in the GIS with Arcview (ESRI, 1999), using addresses obtained from the patient data.

For this study, ACS data for 1999 were used. Data were aggregated at the police sector level, as this was the smallest geographic unit giving reasonably precise estimates at the time of the study. There are nine police sectors in Springfield. ACS sampling rates for the sectors ranged between 2% and 4% of the total population.

A dot density map was used to visualize the geographic distribution of cases of late-stage disease to determine where they were concentrated. The spatial scan statistic (Kulldorff, 1997; Kulldorff, Rand, Gherman, Williams & DeFrancesco, 1998) was used to test for geographic clustering of cases. Although data on case locations had to be exported from the GIS into SatScan (Kulldorff et al., 1998), the program output included a geographic file of the most likely cluster locations which could be easily displayed in the GIS. This analysis would reveal where raw numbers of cases were greatest and more resources were needed, e.g., where mobile mammogram units and educational or other intervention programs would likely have the highest yield. Preliminary findings showed no visually or statistically apparent spatial clustering of cases. On this basis, a more global approach to intervention seems warranted.

To account for the size of the underlying population of women over 40 and

Figure 1: Dot density map depicting the case distribution of late stage breast cancer in Springfield



estimate the risk of acquiring late-stage disease, ACS estimates were used as the denominator to calculate the prevalence rate of late-stage disease per thousand women over 40 for the five-year period. These rates were mapped using choropleth maps to look for sectors with unusually high rates. There was one section of the city with an unusually high rate (7.7 cases of late-stage disease per 1,000 women over 40) and one with a particularly low rate (2.1 per thousand). Further investigation was needed to determine those sector characteristics that made residents at particularly high or low risk for late-stage disease.

A spatial regression was conducted using the S-PLUS for ArcView extension (S-Plus for ArcView GIS 1.1) to test for significant socioeconomic and demographic factors in the rate of late-stage disease. It was hoped that this technique would elucidate the effect of various factors not necessarily apparent by mapping and identify characteristics of high-risk population subgroups. The unit of analysis for the regression was police sector. ACS estimates for sector population, and housing characteristics were the independent variables. The dependent variable was the rate of late-stage disease per thousand women over 40. To account for the effect of spatial proximity of the police sectors, we used a first-order neighborhood matrix. After running the spatial regression, residuals were checked for evidence of spatial autocorrelation with the Moran's I statistic (Cliff & Ord, 1981).

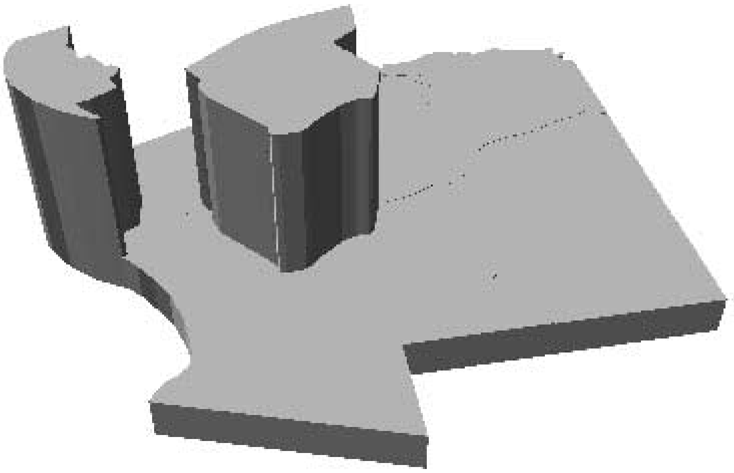
Rates used in this study reflect etiologic factors for overall risk of breast cancer as well as risk of late-stage disease. Since the purpose of the study was to target high-risk areas and population subgroups, it was not necessary to separate out the causes of late-stage disease from those of breast cancer.

Table 4 shows the results of the spatial regression. There were four significant factors in late-stage disease: African-American race, presence of a high school diploma, and foreign-born and married status in women over 40. These factors were all positively related to the rate of late-stage disease — rates of late-stage disease were higher in sectors with high rates of African-American, married or immigrant women over 40, or those with a high school diploma. The number of mammogram facilities in a sector did not affect the rate of late-stage disease in that sector.

Table 4: Results of spatial regression on late-stage breast cancer

Factor	Coefficient	T-test	Significance
African-American race	0.0015	8.54	0.0034
High school graduate	0.0072	19.2406	0.0003
Foreign born	0.0173	31.0393	0.0001
Married	0.0106	19.8701	0.0003

Figure 2: Location of high-risk populations in Springfield



This information is helpful in designing intervention programs. For example, since African-American race and foreign-born status are significant risk factors in late-stage disease, areas of the city with high concentrations of these populations should be targeted for intervention (Figure 2). The fact that rates of late-stage disease were higher in areas with a greater proportion of high school graduates indicates that educational materials should be at a higher educational level so as not to discourage more educated women from participating. The importance of foreign birth suggests potential avenues for reaching high-risk women through various national cultural organizations such as the Greek Cultural Council in Springfield. Finally, the increased risk for African-American women suggests working with African-American organizations, many of which already target specific health problems.

Conclusions

Although the American Community Survey data are only preliminary estimates based on one year of survey data on a relatively small sample of the population, they demonstrate the importance of socioeconomic factors in the geographic distribution of late-stage disease, which is relevant to the design of intervention programs. The data further suggests that the availability of healthcare resources such as mammography does not correlate with predictable trends in breast cancer diagnosis and staging. This study shows how geographic and population data can be used to create a demographic profile of communities by providing denominators for the calculation of risks (incidence or prevalence rates), identifying the size and location of high-risk populations, and providing information on socioeconomic and demographic characteristics which can be used in analysis to identify risk factors in late-stage disease.

CASE STUDY: USING GIS AND THE AMERICAN COMMUNITY SURVEY IN UNDERSTANDING YOUTH VIOLENCE

A similar approach was used to address the problem of youth violence in the city. The aim was to examine factors contributing to youth violence in Springfield with the ultimate goal of designing more effective violence prevention programs. Specifically, investigators wanted to identify police sectors with excessively high rates of youth violence and delineate high-risk population subgroups at which to direct intervention. In addition, they wanted to identify factors that contributed to youth violence.

Analysis was focused on the after-school hours for two reasons. First, previous research had indicated that youth violence was most prevalent during this time period (Snyder, 1997; *Weapons-Related Injury Surveillance Report*, 1998). Second, community-based youth programs would be available during this time period.

Study Methods and Results

Geographic and demographic data sources for the study are the same as those described above. In addition, geographic data from the City of Springfield Planning Department was provided on school locations (points) and school districts (polygons). Data on violent incidents was obtained from the City of Springfield Police Department and a list of variables is given in Table 5. The study population consisted of all violent criminal arrests (which shall be referred to as "incidents")

Table 5: Police data for youth violence study

Incident Characteristics	Offender Characteristics
Location	Home Address
Date/Time	Age
Type of Crime	Race
Arrest made	Sex
	Ethnicity

committed by persons aged 17 and under between the hours of 2 p.m.–7 p.m., Monday–Friday from September 1999–August 2000.

GIS mapping was used for two purposes: to indicate areas of increased crime requiring police vigilance and to help generate hypotheses about factors that might cause violent crime. First, the distribution of incidents throughout the city was visualized with a dot density map, which was overlaid on a map of police sector boundaries (Figure 3a). Next, the location of schools was overlaid onto the dot density map, and a 1,000-foot buffer around the schools was created (Figure 3b).

Figure 3a: Dot density map of violent incident locations overlaid on police sector boundary map

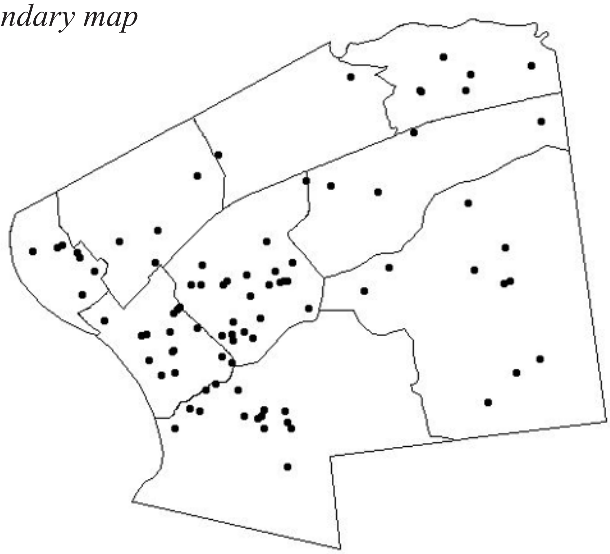
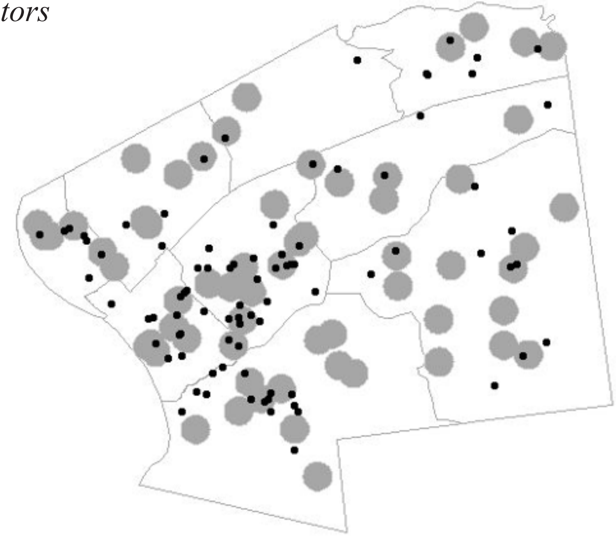


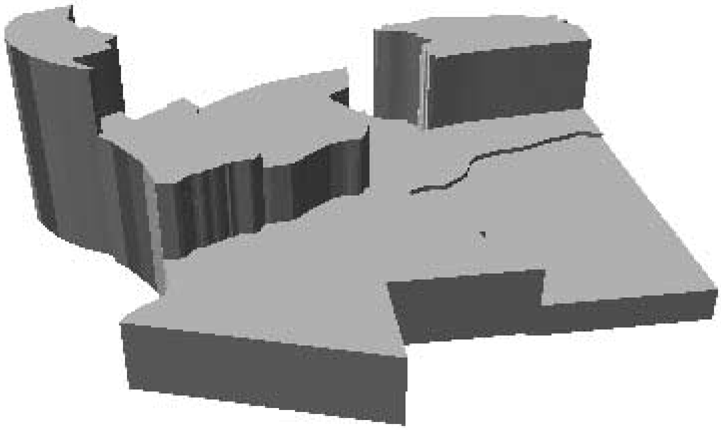
Figure 3b: Addition of 1,000-foot buffers around schools to incident locations and police sectors



The crimes appeared to occur primarily around schools. One hypothesis to test would be that crimes occur near schools, and the number of schools in a police sector was related to the risk of youth crime incidents.

To control for the size of the underlying population-at-risk (10-17-year-olds) and to estimate the risk of violent crime in each sector, the violent incident rate was calculated and displayed on a 3D map (Figure 4). The highest incident rate occurred in Sector A. The spatial scan statistic was again used to evaluate the risk of violent incidents, this time controlling for the underlying total population. The scan statistic verified the higher rate in Sector A (p=0.002). A relative risk of 2.7 indicates that the rate was 2.7 times higher for this sector compared to the others.

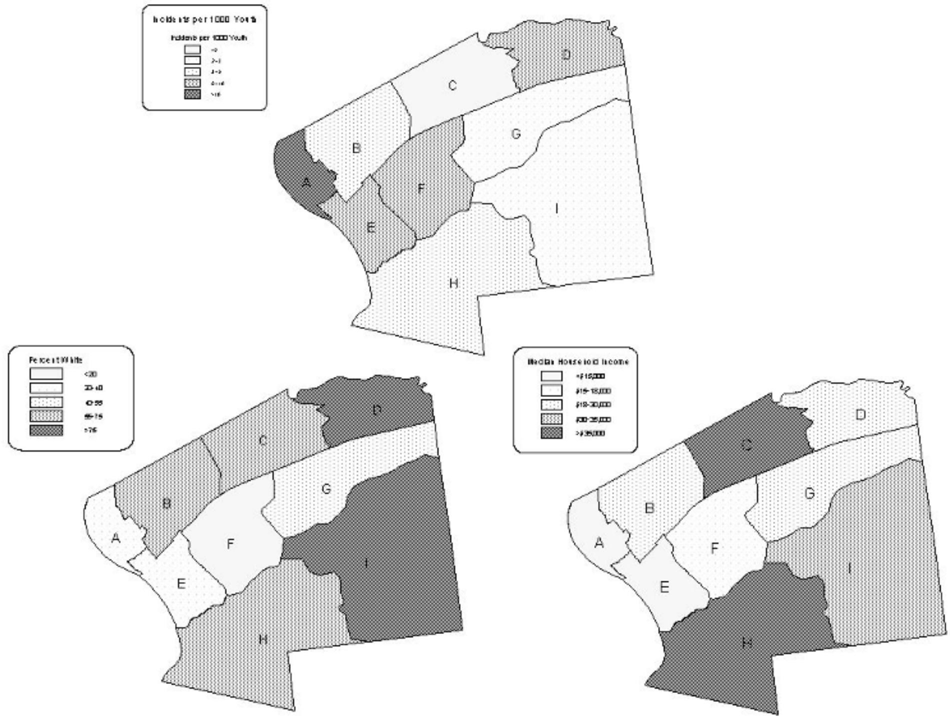
Figure 4: 3D map representing the distribution of violent incident rates per 1,000 total population for the nine police sectors



To generate hypotheses about what socioeconomic factors might be related to the risk of crime in a sector, choropleth maps of the distribution of various socioeconomic factors from the ACS data were constructed and compared to a choropleth map of crime rates (Figure 5). Sectors with the highest incident rates had the lowest proportions of persons of white race and among the lowest median household income. This generated the hypothesis that socioeconomic factors are related to youth crime.

The next step was to test these hypotheses using spatial regression. The unit of analysis was again the police sector. The independent variables were the various demographic and socioeconomic police sector characteristics from Table 2. Two separate spatial regressions were conducted: one where the dependent variable

Figure 5: Comparison of choropleth maps for incident rates and census characteristics



was the violent incident rate based on the incident location, and one with the rate based on the offender's home location. This would address two questions: what factors in the offender's home sector contribute to violence, and what factors contribute to where violence occurs?

Table 6 (above) gives the results of spatial regression on incident location. The total number of schools is included in the model to show that it was not significant. For the significant factors listed, those with a negative coefficient (median household income) were negatively related to the number of incidents — the lower the median household income for a sector, the higher the number of incidents in that sector. Factors with a positive coefficient (total population and black race) were positively related — the higher the total population (all ages) or black rate per thousand, the higher the number of incidents in that sector.

Table 6: Results of spatial regression on violent incidents

Factors in Incident Location	Coefficient	Std. Error	t-statistic	Significance
Intercept	6.7213	1.9483	3.4498	0.0409
Number of schools	-1.1612	0.5513	-2.1061	0.1258
Total population	0.0012	0.0002	5.3579	0.0127
African-American race	0.0187	0.0054	3.4526	0.0409
Median household income	- 0.0003	0.0001	-4.5807	0.0195
Factors in Home Location				
Intercept	-68.2814	7.6747	- 8.8969	0.0030
Median house value	0.0005	0.0001	8.8776	0.0030
Aggregate public assistance dollars	0.0000	0.0000	10.0849	0.0021
10-17-year-olds	- 0.0013	0.0006	- 2.2659	0.1083
White race	0.0349	0.0066	5.2926	0.0132
African-American race	0.0614	0.0072	8.5042	0.0034

Table 6 (above) gives the results of the spatial regression on the youth offender's home location. Factors with a positive coefficient were positively related to the number of criminals residing in a sector—the higher the rate (African-American or white), or total public assistance dollars, the higher the number of offenders. Total youth population was negatively related—offenders tended to live in sectors with lower population rates of 10-17 year olds.

Conclusions

This study gives important information that can be used to address the problem of youth violence in Springfield. Highlighting areas of increased occurrence of violent youth incidents by mapping not only can be used to direct police resource allocation, but can also be used to indicate where intervention programs might be situated. Regression analysis of violent incident rates elucidates the socioeconomic factors contributing to youth violence. If poverty is a contributing factor, then designing youth programs for job training and identifying employment opportunities might be more important than providing after-school activities for youth. Likewise, if violent incidents are more likely to occur in neighborhoods where African-Americans are concentrated, than violence prevention program planners should work with African-American organizations in the community to address the problem together.

SUMMARY: HOW ACS DATA CAN BE USED IN HEALTHCARE

The two case studies described in this chapter demonstrate that ACS data can be used in healthcare in a number of ways. First, ACS population totals provide denominators for the accurate calculation of risks (incidence or prevalence rates) for any healthcare problem on which numerator data exists. Second, ACS demographic and economic data for geographic units, such as the police sectors used in the current studies, can be employed in statistical analysis to identify factors which contribute to increased health risks. The results can be applied to designing demographically and economically relevant intervention and prevention programs. Third, it enables the creation of community demographic profiles by identifying the size and geographic location of high-risk population subgroups. This is a tremendous aid in public health planning and resource allocation.

ACS data can be used in additional ways from the ones described in these case studies. Demographic profiles of geographic areas created with ACS estimates can be compared with profiles of existing patrons of community intervention programs to determine if these programs meet the needs of the populations they serve. ACS population estimates can also be used to calculate projections for the size and location of high-risk demographic subgroups to determine whether, when and where the need for intervention programs will change over time. In addition, they provide timely demographic updates to local community groups as well, to aid in procuring funding. This further stimulates other cooperative community arrangements in research and prevention or intervention planning.

The approach described here can be applied with any census geography (tracts, block groups, etc.) for which ACS estimates are available. This enhances its usefulness for a number of purposes and geographic scales. The broad utility of the American Community Survey in providing accurate and timely data on the population and the economic environment in which it exists make it an essential tool in healthcare. As ACS implementation continues to expand throughout the country, these benefits will become widely available to state and local public health officials, hospitals and others in the community with an interest in healthcare. Hopefully, this chapter will stimulate them to utilize this data in significant ways to improve the health and well being of our population.

REFERENCES

American Joint Committee on Cancer. (1997). *AJCC Cancer Staging Manual* (5th ed., pp. 171-180). Philadelphia, PA: Lippencott-Raven Publishers.

Cliff, A. D. & Ord, J. K. (1981). *Spatial Processes: Models and Applications.* London: Pion, Ltd.

Devesa, S. S., Grauman, D. J., Blot, W. J., Penello, G. A., Hoover, R. N. & Fraumeni, J. F. J. (1999). *Atlas of Cancer Mortality in the United States 1950-94*, Washington, DC: US Govt. Print Off NIH Publ No. (NIH) 99-4564.

ESRI. (1999). ArcView GIS (Version 3.2). Redlands, CA: Environmental Systems Research Institute, Inc.

Feig, S. (1988). Decreased breast cancer mortality through mammographic screening: Results of clinical trials. *Radiology, 167*, 659-665.

Kulldorff, M. (1997). A spatial scan statistic. *Communications in Statistics: Theory and Methods, 26*(6), 1481-1496.

Kulldorff, M., Rand, K., Gherman, G., Williams, G. & DeFrancesco, D. (1998). SaTScan: Software for the spatial and space-time scan statistics. (Version 2.1). Bethesda, MD: National Cancer Institute.

MassDPH. (1999). *MA Screening Mammography Utilization Report*: Massachusetts Department of Public Health.

Shapiro, S. (1994). Screening: Assessment of current studies. *Cancer, 74*(1Suppl), 231-238.

Snyder, H. N. (1997). *National Arrest Statistics: Juvenile Arrests 1996.*

S-Plus for ArcView GIS 1.1(2000). Seattle, WA: MathSoft.

Tabar, L., Fagerberg, G., Duffy, S. W. & Day, N. E. (1989). The Swedish two-county trial of mammographic screening for breast cancer: recent results and calculation of benefit. *Journal of Epidemiol Community Health, 43*, 107-114.

Weapons Related Injury Surveillance Report. (1998). Massachusetts Department of Public Health.

Chapter IV

The Application of Spatial Analysis to the Public Health Understanding of Alcohol and Alcohol-Related Problems

Robert Lipton
Prevention Research Center, USA

D. M. Gorman
The Texas A & M University System Health Science Center, USA

William F. Wieczorek
Buffalo State College-State University of New York, USA

Paul Gruenewald
Prevention Research Center, USA

This chapter describes research that uses spatial modeling to address pressing issues related to a public health understanding of alcohol problems and violence. First, we introduce the language of spatial analysis used in prevention work and discuss the details of spatial research that result in useful public health information, particularly in regard to alcohol-related problems. Issues such as geo-mapping, variable selection, and area definition are discussed in regard to community level occurrence of such problems.

We then discuss the general context for understanding the geographic relationship between alcohol outlet density and violent crime. Finally, we *give a specific example of an analysis focusing on alcohol outlets and violence. This work is related to the major goal of studying the community geography of alcohol problems by mapping the alcohol environment, relating these features of the environment to the spatial distribution of problem events, and analyzing the statistical associations between these measures and drinking behaviors.*

INTRODUCTION

The application of spatial methods to prevention issues in public health is a potentially powerful approach that is quite complex in terms of data demands and implementation. Further, spatial analysis in public health may be considered suspect as a result of the possibility of ecological bias (that is from only having information about total exposure and outcomes while individual exposures and outcomes are unknown). Nevertheless, spatial analysis addresses an often forgotten or misunderstood aspect of public health, the dynamics of people in places. Usually epidemiologists examine individual effects of exposures on illness and only include larger, community-based information as a variable in a multivariate model. The implication of such research is that the individual is the only unit of analysis that is important for helping understand public health problems. At this point in time, however, with advances in computer technology, there are ways to more coherently contextualize the manner in which the individual exists within a larger framework that is composed of both the human community and the physical reality of the environment (streets with intersections, dense vs. sparse neighborhoods, high or low densities of liquor stores or restaurants, etc.).

This broader context of the unit of analysis in public health research is actually an honored part of the history of modern public health and epidemiology. John Snow developed an extensive spatial map delineating water sources for London (Snow, 1855). This clearly displayed a possible testable hypothesis for the characteristic spread of cholera at the time (i.e., the differential use of specific water suppliers). Indeed, at the dawn of modern epidemiological/public health research, spatial analysis was, as a matter of course, naturalistically employed. This promising beginning, however, did not evolve into standard practice in epidemiology, as a more medicalized perspective rose to dominance.

Although it is not difficult to explain why the history of public health in the previous century has mostly concentrated on the medicalized/individualized sense of exposure and disease, the demands of public health can no longer allow us to use such an outmoded approach. The dynamics of human behavior have been treated in a too simple manner; excluding the physical/ecological structure in which individuals exist degrades our abilities as public health professionals to fully characterize both problems and possible solutions. Further, it is not enough to understand the geography of a particular area, or grouping of areas (no matter the detail and complexity of such information). Rather, understanding the dynamic nature of human interactions (i.e., how the environment in one area affects outcomes in another) is a critical part of a more comprehensive approach toward prediction and prevention. Spatial modeling thus not only includes controlling for spatial autocorrelations (adjacent or near-adjacent area similarities for a given measure) but also the possibility of modeling how environmental and socio-demographic exposures may affect outcomes in adjacent areas.

In the following sections we describe research that uses spatial modeling to address pressing issues related to a public health understanding of alcohol problems and violence. First, we introduce the language of spatial analysis used in prevention work and discuss the details of spatial research that result in useful public health information, particularly in regard to alcohol-related problems. Issues such as geo-mapping, variable selection and area definition are discussed in regard to community-based clusters of current alcohol misuse. We then discuss the general context for understanding the geographic relationship between alcohol outlet density and violent crime, and describe the ways in which previous researchers have addressed this issue. Finally, we give a specific example of an analysis focusing on alcohol outlets and violence as a way to make more tangible specific elements of such a project. This work is related to the major goal of studying the community geography of alcohol problems by mapping the alcohol environment, relating these features of the environment to the spatial distribution of problem events, and analyzing the statistical associations between these measures and drinking behaviors. The promise of these areas of research is that they lead to greater understanding of the manifestation of individual problem behaviors in environments that can be regulated and controlled through science-based environmental preventive interventions (Gruenewald, Holder & Treno, 2001).

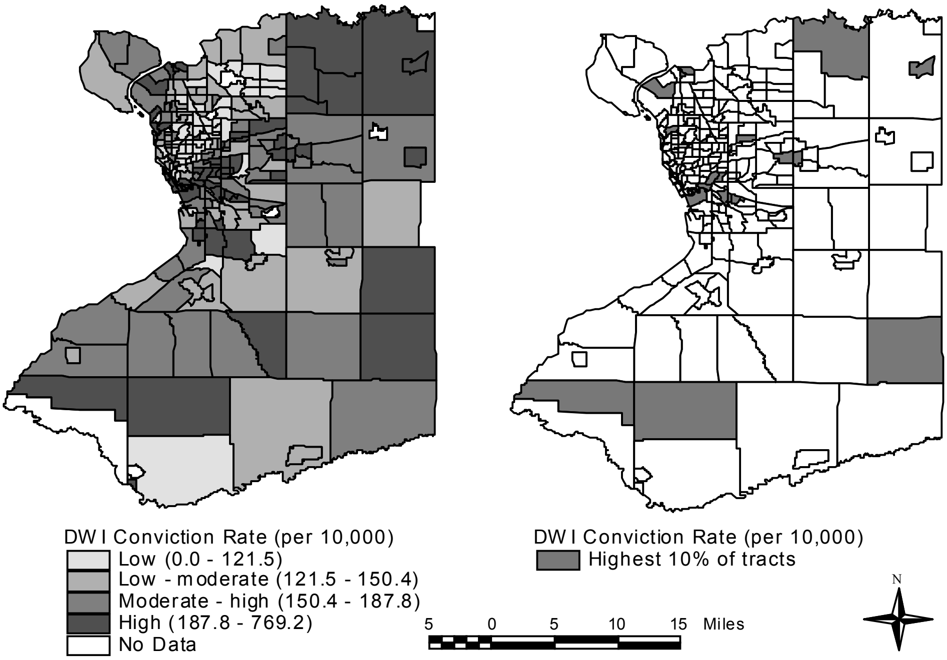
GIS CAPABILITIES AND PREVENTION

A basic understanding of the essential capabilities of geographic information systems (GIS) is critical to the development of prevention activities because alcohol-related problems are not evenly distributed across space. GIS can be defined as a combination of computer hardware, software, spatial data (digital maps) and data with a geographic reference (e.g., alcohol outlets, crime locations) that facilitates spatial analysis. The key functions of GIS are important because they provide access to the broad spectrum of potential spatial analyses that can support the simple targeting of resources as well as the development of more complex models of spatial interactions. Both simple maps of problem rates or clusters and spatial interaction models may be useful for targeting traditional individual-based prevention programs or environmental interventions. Spatial interaction models, however, may be more appropriate for identifying the locations of events (e.g., assaults or crashes) that may be most amenable to environmental or regulatory prevention. In addition, GIS capabilities promote the development of a basic spatial/geographic epidemiology of alcohol use and related consequences, which is critical to the development of prevention programs. A brief overview of GIS functions is presented here (see Wieczorek [2000] and Wieczorek & Hanson [1997] for more details).

The key functions of GIS presented here are: geocoding, data overlays, reclassification function and distance/adjacency measures. Geocoding is a generic term used to describe the GIS function of providing a specific location to descriptive data. Geocoding applies to point data (e.g., alcohol outlet) as well as to areal data (e.g., assaults in a census tract). Sometimes geocoding is known as address matching because the process of matching points to addresses is very common. The advent of the Census Bureau's TIGER system has made geocoding a relatively low-cost and widely available GIS function. However, professional geocoding services have developed to assist persons who are not comfortable in geocoding their own data or because of the high cost of updating digital maps based on TIGER in areas of changing population and new developments. Krieger et al. (2001) compared a number of services and found that it is possible to use these services to accurately geocode data, although there was substantial variation in accuracy between services. Geocoding is the most basic of GIS functions because it transforms descriptive information into a format suitable for spatial analysis.

A GIS-based map may consist of multiple sources of data. The ability to combine multiple layers of information is known as the overlay function. A simple example of an overlay function is to place geographic boundaries (such as for town or census tract) on top of individual points representing DWI offenders. The points within each area can then be automatically counted to create rate-based maps such as those shown in Figure 1. To create rate-based maps from relevant point information, at least three layers of data are necessary (i.e., map of the points, a map with relevant boundaries and Census data on population). The ability to perform an intersection between separate maps, to aggregate data into meaningful geographic areas and to link your data to standard sources such as Census data, highlights some of the processing capabilities of the GIS overlay function that would be nearly impossible to accomplish by non-automated methods (see Wieczorek & Hanson [2000] for an example using regions and mortality data).

Figure 1: Reclassification and targeting prevention



One reason for the high potential of GIS in prevention is the capability of the technology to provide and manipulate visual images. These are a powerful method of conveying information. However, poorly designed images that contain too much or confusing combinations of data may obscure rather that highlight patterns or critical information. The reclassification function of GIS allows the user to easily manipulate the number of categories or the selection of specific information (e.g., crashes by time of day or day of the week). Figure 1 shows how the reclassification function can assist in the targeting of prevention by reclassifying the same data, first as four different categories and then as a single category of the highest rate areas.

To develop models of spatial patterns and interactions requires accurate information on the distance between individual objects (e.g., bars and crashes) and whether areas are adjacent to one another. This is known as the distance and adjacency function of GIS, which allows exact distances to be calculated. Complex spatial models require these types of data, which can be exported from the GIS as a file to be used in spatial modeling software. Adjacency information is often used to examine the possibility of spatial lags which may show that alcohol-related problems (e.g., assaults) are related to the characteristics of nearby areas with specific levels of separation (i.e., spatial lags) (Gruenewald et al., 1996; Lipton &

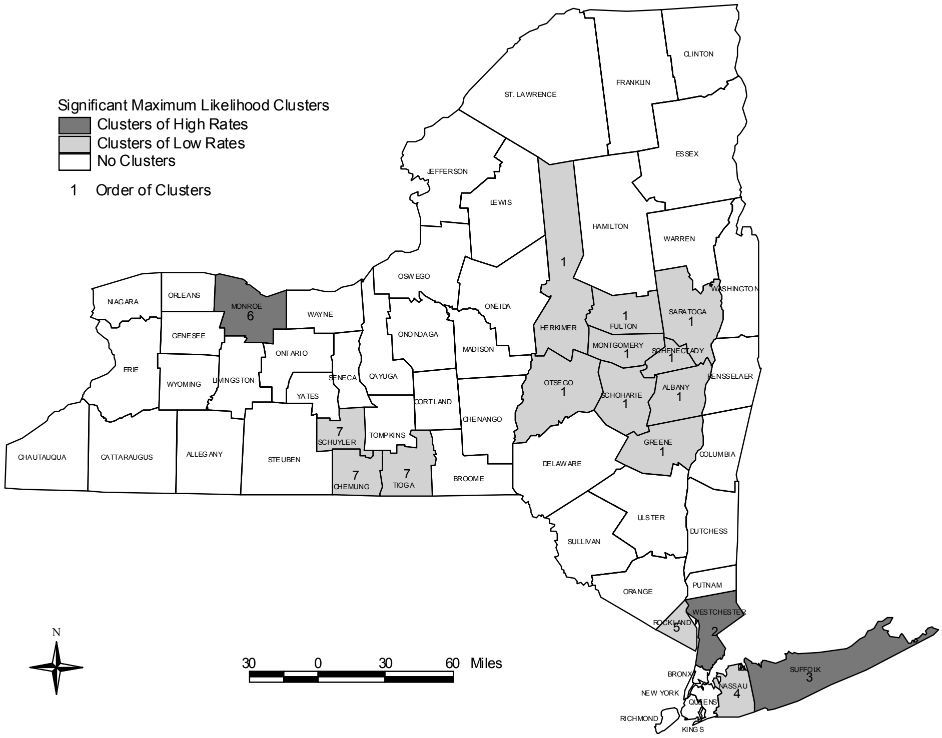
Gruenewald, 2001). Other types of GIS-related functionality (e.g., buffers, neighborhood characteristics) are a subset of the distance functions. The neighborhood function calculates the number of a specific characteristic (e.g., assaults) within a specific radial distance (e.g., 300 yards) of specific point features (e.g., bars). The GIS buffer function uses the distance function on a complex feature such as the road network to identify points within a set distance of the feature (e.g., homes of DWI offenders within 400 yards of a bus line). These relatively simple GIS functions can be used in highly complex ways to provide new insights into the generation of alcohol-related problems and for targeting prevention activities to areas with the greatest need. The work of Harding and Wittman (1995) provides an additional example that utilizes basic GIS functions in support of prevention.

Spatial Clusters

Spatial clusters are a greater than expected geographically close group of occurrences or events (e.g., deaths, crashes, alcohol outlets). Spatial clusters are a natural result of spatial dependencies in the data; by definition, spatially dependent data will have an uneven geographic distribution. The use of spatial cluster analysis was pioneered for finding cancer clusters, especially for rare cancers (Aldrich, 1990; Rickett et al., 1994). Specific spatial clustering techniques can be used with point or geographic area data and may also be used for space-time cluster analysis to examine temporal trends (Jacquez, 1994). Spatial cluster analysis is useful for identifying areas with significantly high or low rates of alcohol problems where services can be targeted, to identify new research questions (e.g., why are rates highest in certain areas), to empirically identify the appropriate scale of analysis in small area studies and to examine the impact of interventions on communities over time (e.g., do the clusters change or disappear in response to interventions).

An example of typical spatial cluster analysis is provided in the Grimson cluster map in Wieczorek (2000). This analysis indicated that significant spatial clusters existed in the DWI offender data, but like most spatial cluster techniques did not identify specific cluster membership. Two recent spatial cluster analytic techniques overcome the limitations of the earlier spatial cluster algorithms. These two methods are Anselin's (1995) local indicators of spatial association (LISA) which is applicable to data on geographic areas, and Kulldorff's (1997) spatial scan statistic which is applicable for both point data and areal data. Anselin's LISA decomposes the standard Moran's I (a general measure of spatial autocorrelation) into local Moran's I for each geographic area and provides a statistical test to identify significant areas. The LISA method identifies both high rate areas and low-rate areas which may be embedded in either high- or low-rate surroundings. Kulldorff's spatial scan statistic is a case-control method that compares the spatial distributions of the cases and controls searching for clusters of cases that significantly differ from

Figure 2: Significant spatial scan clusters of alcohol-explicit mortality



the spatial distribution of the controls. The spatial scan approach is especially flexible in that high-rate or low-rate clusters of any size or shape may be identified. Also, both LISA and spatial scan explicitly identify cluster membership rather than clustering in general.

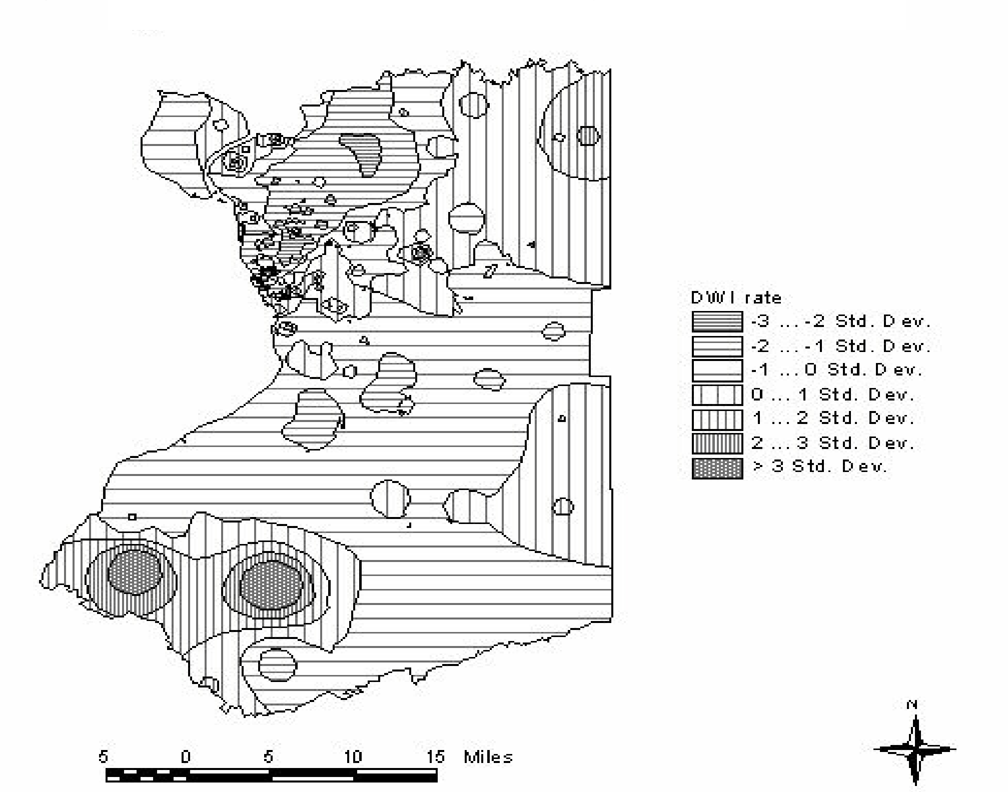
Hanson and Wieczorek (in press) compared the LISA and spatial scan methods to analyze alcohol mortality data. The comparison found that the two methods are largely complementary; the results tended to coincide for both methods. It is important to note that low-rate clusters are as important to identify for prevention purposes as high-rate clusters. High-rate clusters clearly have problems that require prevention/intervention; however, low-rate clusters may be areas at high risk of developing problems, especially if the low-rate area is embedded in surrounding high-rate areas. Characteristics of low-rate areas may also provide important insights into factors important for prevention application in high problem locations. Figure 2 shows a map of spatial scan clusters of alcohol-related mortality in New York. Note that both high- and low-rate clusters are identified. The analysis of county-level data also shows the potential for regional level prevention approaches.

Other Spatial Analytic Techniques

Two additional approaches deserve mention in the context of spatial analysis for prevention. The first technique is a relatively simple method to control spatial autocorrelation in multiple regression analysis. The method is to use a GIS to calculate a generalized spatial potential for the dependent variable used in multiple regression of geographic area data (e.g., Census tracts or Zip Code areas). Wieczorek and Coyle (1998) provide an example of this technique in the context of targeting the neighborhoods of DWI offenders. A generalized spatial potential (GSP) for the DWI rate was calculated for each tract by summing the ratio of DWI rates (V) and distances (D) to every other tract ($GSP_i = V_1/D_1 + V_2/D_2 + \ldots V_n/D_n$). By including the GSP as an independent variable in multiple regression, spatial autocorrelation in the dependent variable is controlled for (allowing the coefficients and statistical tests to be interpreted). This approach is not as statistically elegant or complete as the methods used by Gruenewald et al. (1996), but it is a substantial improvement that may be implemented relatively easily.

The second method with applications for prevention is the development of continuous surface models by using kriging. Kriging can be used to develop contour

Figure 3: DWI conviction rate continuous surface model



maps (e.g., maps that show lines of equal value such as DWI rates) from a limited number of points or areas (which can be given a value at the centroid) (Isaaks & Srivastava, 1989). Continuous surface models overcome the limitations of geographic area such as Zip Code areas because the actual rates within the geographic areas are unlikely to be as uniform as suggested in a map. Kriging creates a continuous surface model by overlaying a grid of cells over the entire areas and calculating a weighted value for each cell based on the distance to surrounding centroids. The values calculated for the grid are then used to create a contour map. An example of kriging is provided in Wieczorek and Hanson (1997). Figure 3 shows a continuous surface model created by applying kriging to the specific tract rates used to generate Figure 1. A continuous surface model may provide a more realistic version of geographic variation that can be used to target prevention and assist in the overall planning of alcohol-related services.

SPATIAL UNDERSTANDING OF ALCOHOL AND VIOLENCE

To better illustrate the application of spatial analysis to public health, we focus on a specific problem that has become of increased concern to researchers and practitioners in the field in recent years—namely, alcohol and alcohol-related problems (specifically, violence).

Theories and Previous Research

Concern with the spatial relationship between alcohol and violence has a fairly long history in the United States, dating back at least to the early temperance movement of the first half of the 19th century (Levine, 1984; Mosher & Jernigan, 2000). Criminology and public health have both understood the importance of this relationship, although it has not necessarily been the central focus of either discipline. However, since the late-1980s, both disciplines have undergone an important shift in their theoretical understanding of the nature of the relationship between alcohol and violence (Mosher & Jernigan, 2000). The public health approach has moved from a focus on the individual and the "disease" of alcoholism to examination of the broad range of socioenvironmental factors that increase the risk of alcohol-related problems (e.g., Holder, 1994; Mosher & Jernigan, 1989). For its part, the criminal justice perspective has shifted from a primary focus on punishment of the individual to show a renewed interest in the ways in which the physical and structural characteristics of neighborhoods encourage and facilitate crime (e.g., Bursik, 1988; Sampson, Raudenbush & Earls, 1997; Stark, 1987). As part of these general trends within criminology and public health, spatial analysis has increasingly been

Table 1: Studies of alcohol outlet density and violent crime using municipalities or smaller units of analysis

Study	Place	Unit of Analysis (n)	Crime[a]	Results
Roncek & Pravatiner (1989)	San Diego	City block (4,598)	Violent	Each additional bar associated with an increment of .4 violent crimes per block per year
Roncek & Maier (1991)	Cleveland	City block (4,396)	Violent	Each additional bar associated with an increment of .9 violent crimes per block per year
Sherman, Gartin & Buerger (1989)	Minneapolis	Address (>115,000)	Predatory	10 of 42 locations with 10 plus predatory crimes over a 1-year period contained bars or liquor stores
Scribner, MacKinnon & Dwyer (1995)	Los Angeles County	City (74)	Violent	Socio-demographics explained 70% of variance in violent crime; alcohol outlet density explained an additional 7%
Scribner et al. (1999)	New Orleans	Census tract (155)	Homicide	Socio-demographics explained 58% of variance in homicide; off-sale alcohol outlet density explained an additional 4%
Alaniz, Cartmill & Parker (1998)	3 northern California cities	Block group (103)	Violent (youth)	2 of 7 socio-demographic variables and alcohol outlet density were predictive of youth violence
Gorman et al. (1998a)	New Jersey	Municipality (223)	Violent	Socio-demographics explained 70% of variance in violent crime; alcohol outlet density explained only an additional .3%
Gorman et al. (1998b)	New Jersey	Municipality (223)	Domestic Violence	Socio-demographics explained 58% of variance in domestic violence; alcohol outlet density explained no additional variance
Speer et al. (1998)	Newark, NJ	Census tact (91) & block group (217)	Violent	Socio-demographics explained 48% (tract) & 27% (block) of variance in violent crime; alcohol outlet density explained an additional 19% & 28% respectively
Gorman et al. (2001)	Camden, NJ	Census block group (98)	Violent	Model comprised of socio-demographics & alcohol outlet density explained 73% of the variance in violent crime; the model was replicated by spatial analysis

[a] The studies include different, but overlapping, types of violence. Violent crime is comprised of murder, aggregated assault, rape and robbery. Predatory crime refers to robbery, rape/criminal sexual conduct, and auto theft. Most cases (>90%) of domestic violence involved assault or harassment, and most victims (80-85%) were female. Youth violent crime is comprised of homicide, robbery, rape, sexual assault, assault, and crime involving weapons, involving either a victim or an offender aged 15-24 years.

used to understand the relationship between the physical availability of alcohol and violence.

Table 1 summarizes small unit analysis studies of alcohol availability and crime that have been conducted by criminologists (Studies 1 to 3) and public health researchers (Studies 4-10). The first group of studies focuses primarily on the role of places—that is, bars—in the generation of crime. The latter group focuses primarily on the role of space—that is Census block groups or tracks containing alcohol outlets—in the generation of crime. The criminological studies are also more overtly theoretically driven than the public health studies. The latter tend to be more descriptive in nature, and for the most part have not offered any explicit theoretical explanations as to why high alcohol outlet density and violence are associated with one another.

The conceptual framework guiding the analysis conducted by Sherman et al. (1989) and Roncek and colleagues (Roncek & Pravatiner, 1989; Roncek & Maier, 1991) was that of routine activities theory. According to this theory, violent crime occurs in places that bring together a motivated offender, a suitable target and the absence of effective guardians (Felson, 1987; Clarke & Felson, 1993). Such places, it is argued, have the potential to become "hot spots" of crime, meaning that criminal activities are likely to concentrate around them. In the early study of Sherman et al. (1989), bars featured prominently among the hot spots of predatory crime identified in Minneapolis using police call data. However, while 10 of their 42 hotspots contained bars, it should be noted that some of these hot spot locations also contained other places (e.g., adult bookstore, park, supermarket) that might also serve to attract potential perpetrators and victims in the context of low guardianship. The work of Roncek and colleagues in San Diego and Cleveland was a more explicit test of routine activities theory. These studies showed that the greater the number of bars on a residential block, the higher the rate of violent crime.

There are a number of features of bars as places that can influence how and why violence occurs within and around them (e.g., age of clientele they attract, amount of crowding and amount of heavy drinking). It is these types of place-specific features of the drinking context, rather than the broader environmental context in which the sale and consumption of alcohol occurs, that routine activities theory leads one to focus on. Moreover, from a spatial perspective, routine activities theory would lead one to expect violent crime to concentrate around the immediate confines of an alcohol outlet, rather than spilling over into surrounding neighborhoods.

In contrast to this focus on place, ecological explanations of violence focus on the features of the broader neighborhood context that relate to crime. These models tend to be multifaceted, incorporating variables drawn from one or more of the following domains: socio-demographic composition (e.g., age, racial and gender composition), social organization (e.g., collective efficacy) and physical structure (e.g., types of land use, disrepair of housing stock). For example, Stark's (1987) ecological model links structural characteristics of neighborhoods to crime and deviance via their effects on elements of the community's "moral order" such as "loss of social control" and "cynicism." The structural characteristics in the model include variables that describe both the socio-demographic composition of neighborhoods (e.g., population density and residential instability) and the physical condition of the environment (e.g., types of property use and physical dilapidation).

For those focused more on the physical or structural characteristics of neighborhoods, violent crime is more likely to occur in communities with obvious evidence of decay and abandonment such as broken windows, wrecked cars, vacant lots, trash, graffiti and certain forms of undesirable commercial establishments such as sex shops (Skogan, 1990; Wilson & Kelling, 1982). As with other ecological variables, the intervening mechanisms linking these "day-to-day aspects" of the neighborhood environment to violent crime are informal social controls and social cohesion. Communities that tolerate physical disorder send the message that no one cares about what is happening or, if they do, that there is not the collective will to do anything about it. This is a more attractive environment in which to commit crime than one in which people take note of what is occurring and act in their collective self-interest. Recently, it has been suggested that alcohol outlets represent an additional form of physical disorder: "broken bottles" and bars send essentially the same message as "broken windows," namely that mechanisms of informal social control have ceased to function (Bennett, DiIulio & Walters, 1996, pp. 64-77).

To the extent that they are compatible with any of these theoretical approaches, the public health studies cited in Table 1 appear more in keeping with the ecological models that focus on space rather than the routine activities focus on place. For the most part, these studies generate models that incorporate the types of variables found in classic ecological studies—that is, age composition, race/ethnicity, residential instability and poverty. They do not incorporate place-level variables such as type of clientele, bar service practices and physical location. The only place variable that tends to be included is outlet classification–specifically, on-sale versus off-sale. Moreover, when public health advocates and researchers speculate on what links high alcohol outlet density to violent crime, they generally do so in terms of the adverse effects that the former has on social integration and order especially in poor urban communities (e.g., Alaniz & Wilkes, 1998; Mosher, 1995). From this perspective, an excess of bars is to the detriment of the local neighborhood ecology—although the exact reasons for this are not entirely clear.

This issue is further complicated by the fact that the effects of greater outlet densities on levels of problems such as violence appear to be context specific (Stockwell & Gruenewald, 2001). This presents both methodological and theoretical challenges. For example, Gorman and Speer (1997) found that even within one mid-sized U.S. city, there was more than one high density neighborhood and that these high cluster neighborhoods were socio-economically and demographically quite diverse. Given this, the problems arising from this concentration of outlets are likely to vary (and in some instances there may in fact be few if any problems). Thus, general theories and principles of intervention are unlikely to be applicable or useful across diverse settings (Stockwell & Gruenewald, 2001).

Rather, theories, methods, data and interventions will need to attend to the contextual features of micro-environments, with GIS and spatial analysis being an integral part of such an approach (Gorman & Speer, 1997; Midford et al., 1998; Stockwell & Gruenewald, 2001).

A Specific Example

An example of how violence and alcohol outlets can be studied spatially is presented below (Lipton & Gruenewald, in press). The spatial characteristics of such an analysis (e.g., control of spatial autocorrelation and modeling the modifying effects of environmental variables on socioeconomic variables) will be highlighted.

This research incorporates perspectives from both the public health and criminological literature in order to examine people in places with regard to alcohol outlets and violence. Similar to the work of Morenoff et al. (2001) and Baller et al. (2001), our analysis includes demographic and socio-economic data so as to capture violence-related to population characteristics (i.e. high unemployment, low rates of high school graduates, etc.). These population characteristics are analyzed in relation to the moderating effects of alcohol outlets on the production of violence. Moderation can simply be thought of as interaction of outlets with people (with a mix of characteristics). This outlet interaction could serve to increase or decrease violence, depending on the composition of population characteristics and outlet presence and type. Further, we examine spatial components of these moderating effects. It is hypothesized, after Gorman et al. (2001), that violence is not only affected by populations and outlets in a target area, but may be affected by population characteristics in adjacent areas.

Our analysis assesses whether such spatial relationships exist and controls for spatial autocorrelations that may obscure the relationship between population characteristics and the production of violence. The primary goal in this example is to test the moderating effects of outlet densities on the production of violence in a given population with a non-zero potential for violence. The sample comprised 766 Zip Codes from four selected areas of California: Los Angeles, the Bay Area, Sacramento and the northern section of the state. The first three areas are heavily urbanized, while the last is quite rural. The three urban areas are heterogeneous in regard to ethnic, age and socio-economic composition, particularly in relation to the rural area that is more homogeneous in most population level measures.

Spatial analysis is quite data intensive and often requires the combining of many disparate data sources. Indeed, the "art" of spatial analysis frequently centers on choices on how variables in different data sets are "knitted" together. Further, the metric and scale of variables must be carefully considered. For example, choosing between Zip Codes or Census blocks not only drastically changes model interpretation, but also involves a series of changes in how variables are aggregated. Additionally, the researcher, more than usual, is placed in a position of having to understand the data, possible sources of error, cleaning issues and variable selection. In this research, data are taken from three different sources: Census data, hospital discharge data and California state data on alcohol outlets.

Alcohol outlets were located by the Zip Code of the premise address obtained from California alcohol beverage control license records and then classified into three types—restaurants, bars and off-premise establishments (largely liquor, grocery and convenience stores). This information was current as of 1991.

The characteristics of local populations were summarized using techniques based on the work of Sampson et al. (1997). In a geographical study of violence and community cohesion, these authors assembled a variety of Census-based indicators into a 10 variable scale, then identified/extracted three sub-categories (using factor analysis) that represented concentrated disadvantage, immigrant concentration and residential stability. We will use census data from 1991 to construct the same three sub-categories.

Hospital discharge data provided information on number of serious assaults per Zip Code. This information was current as of 1991. Hospital discharge "assaults" are hospital admissions labeled as "assaults" by the attending physician. Patient home address is used for each assault case (since the purpose of this research was to understand the dynamics between home environment and the location of alcohol outlets). Distinct from previous studies that have examined violence in terms of capitated measures (e.g., assaults per person), the current analysis used roadway miles per Zip Code as the denominator for the dependent

Figure 4: Conceptual model and outline of Model 3

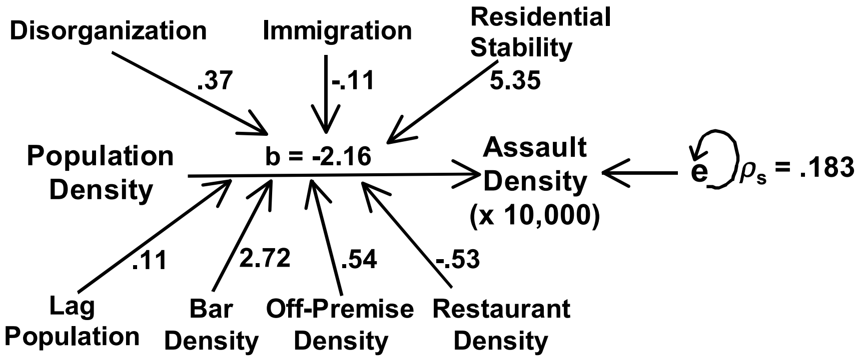
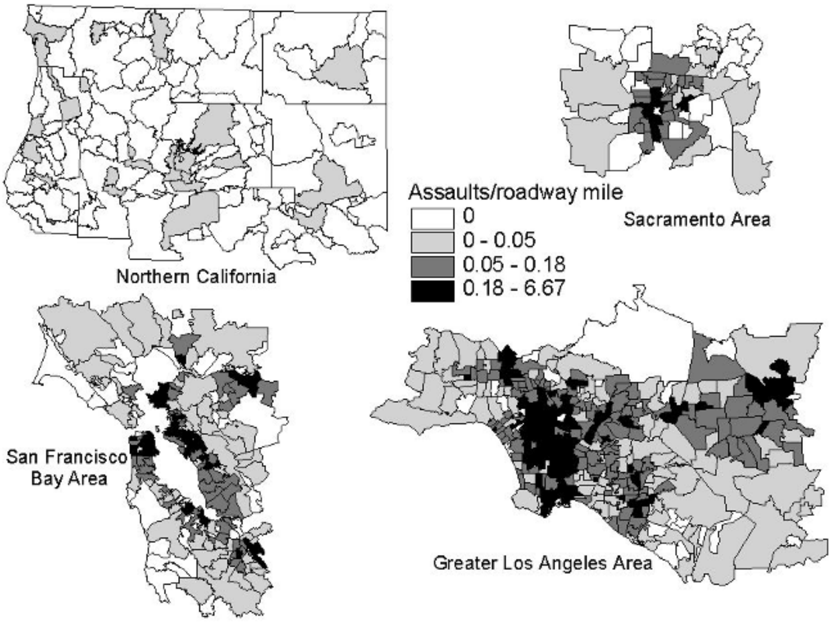


Figure 5: Assaults per mile of roadway



and independent environmental variables. This measure gives a better approximation of area density than does population per area.

Figure 4 (at this point ignore the numbers) shows the general conceptual framework that guides the analysis. We hypothesize that population density has a direct effect on rates of assault, and that the effects of population density on assaults will be modified by population characteristics and the presence of alcohol outlets. The direct effect of population densities on assaults (b) represents the production rate of assaults from the population. This effect is moderated by population characteristics and outlet densities, and may be further modified by the numbers and characteristics of nearby populations (not shown). It is assumed that errors in estimation are not independent, but rather are spatially autocorrelated, r_s.

In Figure 5 assaults per roadway mile are presented for each of the four regions. The difference in concentrations of assaults is apparent in this map, with greater densities occurring where there are greater densities of population. This is not, however, universally the case. For example, the western region of the Los Angeles basin appears to exhibit relatively greater assaults than expected from the population distribution observed. Overlays of Zip Codes are represented on this particular map.

Table 2: Overall model evaluation

Model	ρ_s: *	Z:	p:	ΔG^2 **	Δdf:	p:	R^2p: ***
1. Population Density	.346	7.34	<.001	---	---	---	.570
2. Outlet Density (bars, restaurants and off premise)	.289	5.89	<.001	204.20	3	<.001	.667
3. Population Characteristics (social disadvantage, immigrant presence and resident stability) and adjacent population density	.183	3.51	<.001	798.76	4	<.001	.881

* A measure of spatial autocorrelation for the model

** -2 log likelihood difference referencing successive model comparisons

*** pseudo R-square approximates percentage of variance explained by model

Table 2 shows the overall results of fitting the different models to these cross-sectional data. The table reports the degree of residual spatial autocorrelation, (r_s), its statistical test, (Rao's likelihood ratio C^2 for model [DG^2] comparisons with degrees of freedom and p-values) and a measure of overall model fit in the form of a pseudo R^2 (a measure of the variance explained by each model). For the population density model, (Model 1), absent all other independent measures, population per roadway was significantly related to assaults. Amount of variance approximately explained was .570 and residual spatial autocorrelation was found to be moderate and positive. When outlet densities were added (Model 2), the likelihood ratio statistic and pseudo R^2 indicated a significant improvement in fit to these data concurrent with a reduction in residual spatially autocorrelated error. When the scales representing population characteristics were added (Model 3), the likelihood ratio statistic and pseudo R^2 again indicated a significant improvement in fit to these data, again concurrent with a reduction in residual spatially autocorrelated error.

Table 3 and Figure 4 (note numbers in the figure) present the results of an analysis that includes the direct effects of population variables, alcohol outlets and adjacent population density. Many, but not all, of the estimated coefficients from the model are significant. A direct interpretation of the coefficients of the model suggests that as population density increases, there is a reduction of approximately 2.16 assaults for every 10,000 persons in each Zip Code area. This rate, however, is that expected for an isolated population living in an area with no bars, restaurants

Table 3: Model 3: Associations of outlet densities with rates of assault hospitalizations (x 10,000)

Variable Name	b:	t:	p:*
Population Density	-2.16	02.62	.009
Outlet Densities			
Bars	2.72	4.36	<.001
Off-Premise	.54	1.64	.101
Restaurants	-.53	-3.97	<.001
Population Characteristics			
Social Disadvantage	.37	32.74	<.001
Immigrant presence	-.11	-15.17	<.001
Resident Stability	5.35	2.41	.016
Adjacent (Lag) Population Density (x 10,000)	.11	2.21	.027

Model based estimate for spatial autocorrelation:

$\rho_S = .183$ Z = 3.51 P < .001

*two-tailed

or off-premise alcohol establishments (and rather unrealistically, with values of zero for the measures of population characteristics). This rate is moderated, however, by the presence of large populations in adjacent areas, the densities of restaurants, bars and off-premise establishments, and local population characteristics. This rate is greater in areas where bar densities are greater and restaurant densities are less. This rate is further greater in areas where social disadvantage is greater, immigrant presence less and residential stability greater. Finally, the rate at which local population density produces assaults is greater in areas surrounded by larger populations.

The intrinsic rate of production of assaults at the Zip Code level for this study is the rate observed in a population exhibiting average levels of all exogenous moderating variables. In this case, the intrinsic rate for the production of assaults is .134 per roadway mile, about that observed as the average for the 766 Zip Code areas. The degree to which this rate is moderated by greater or lesser densities of bars and off-premise establishments is presented in Table 4. In this example, the effects of all other exogenous variables are held constant (at their averages) and the

Table 4: Estimated effects of bars on hospital discharge assaults

	Population Density (per Roadway Mile)				
Bar Density (per Roadway Mile)	0:	500:	1000:	1500	2000:
0:	0.00	.20	.41	.61	.81
.5:	0.00	.27	.54	.82	1.08
1.0:	0.00	.34	.68	1.02	1.36
1.5:	0.00	.41	.82	1.22	1.60
2.0:	0.00	.48	.95	1.43	1.90

	Relative Rates (Referred to Average = 0.134)				
Bar Density (per Roadway Mile)					
0:	0.00	1.49	3.05	4.55	6.04
.5:	0.00	2.01	4.03	6.12	8.06
1.0:	0.00	2.53	5.07	7.62	10.15
1.5:	0.00	3.06	6.12	9.10	11.94
2.0:	0.00	3.58	7.09	10.67	14.18

range of effects related to bar densities are given for five levels of population density. The expected range of effects is large. In areas with greater than 1000 population per mile of roadway (n = 15), rates of assaults may range from 3 to over 10 times the level expected on average for the state. At all levels of population density, the presence of greater densities of bars may double the average rate of assaults.

The results of this analysis indicate that it is possible to construct a conceptually well-framed analysis of assault rates that explains to a substantial degree variation in rates of assault between places in California. Shifting from a representation that suggests that outlets on their own create violence to one that presents outlets as providing contexts for violence, the usual pattern of relationships of violence to environmental densities of alcohol outlets continue to be observed. The current analysis suggests, however, that alcohol outlets moderate rates at which violence is produced within areas, and that these effects persist when controlling for spatial effects and other covariates related to the production of violence in local populations (Tables 2 and 3). Notably, positive relationships continues to exist between bar and off-premise outlet densities and assaults, with no relationship to densities found for restaurants (Table 3 and Figure 3). Although the measures of population characteristics are related to rates of assault, the observed relationships are not fully consistent with those observed in studies of urban areas (see Sampson et al., 1997). While, as expected, the measure of concentrated disadvantage is related to greater rates of violence, the measure of immigrant concentration was inversely related to violence rates and the measure of residential stability was directly related to rates of violence. At the geographic scale of the current study (Zip Codes), greater rates of violence are observed in stable, non-immigrant areas with greater concentrated disadvantage. These findings illustrate the context-specific nature of findings in this area of research, as discussed earlier. Bar densities, when controlling for other environmental or socio-demographic measures, are clearly connected to an increase in assaults. Thus, in this example, beyond the obvious finding that denser populations have more assaults, we are able to observe important environmental effects that may be actionable in terms of prevention policy.

SUMMARY AND CONCLUSIONS

In this chapter we have described how spatial methods may be applied in a specific public health area, namely alcohol and alcohol-related problems. Although, an important area of research, it is by no means unique in allowing for spatial/ecological analysis. There are several important factors that should be considered when contemplating public health spatial analysis: 1) Are there specific environmental features (such as the presence of bars or liquor stores) that might help explain an outcome (such as violence)? 2) Is there a dynamic relationship between individual behavior and environmental (area) setting? 3) Do environmental factors, such as alcohol outlets, modify the relationship between socio-demographic factors and the outcome of interest (e.g., violence)? 4) Is there data available to support a spatial analysis? 5) Is the effect of adjacent areas likely to obscure relationships between exposures and outcomes (spatial autocorrelation)?

When studying alcohol-related problems, spatial analysis allows for the integration of disparate types of information into a meaningful story from both a public health and criminological point of view. The ability to put people in places in more than a purely descriptive framework signals a new generation in research that transcends traditional proscriptions against the use of ecological data. Further, measures of community health such as cohesion take on a more fully realized form in a spatial analytical context. Indeed, given that most public health and criminological data are collected at a population level, spatial analysis allows researchers to more clearly observe population-level effects for whatever measures are chosen. In this regard, sometimes it is not as important to understand individual exposures as it is to understand potential environmental ones.

In our discussion of alcohol-related problems, spatial analysis allows us to observe hot spots of greater- or lesser-than-expected problems (such as violence related to alcohol), socio-demographic effects without the bias introduced by spatial autocorrelation (a smearing of effect across geographic areas) and to model how target geographic area rates of violence may be affected by adjacent area alcohol outlet concentration. Further, the mapping capability that is integral to spatial analysis provides a powerful descriptive tool for the display of data (e.g., of crime hot spots in combination with socio-demographic overlays). Such analysis can easily be applied to other issues such as drug use, HIV infection or teen pregnancy rates. Effectively, it is an open field; these techniques can descriptively and analytically be used to better understand a broad range of issues in public health and truly allow for a more rigorous notion of social epidemiology.

REFERENCES

Alaniz, M.A. & Wilkes, C. (1998). Pro-drinking messages and message environments for young adults: The case of alcohol industry advertising in African American, Latino, and Native American communities. *Journal of Public Health Policy*, 19, 447-471.

Alaniz, M.A., Cartmill, R.S. & Parker, R.N. (1998). Immigrants and violence: the importance of neighborhood context. *Hispanic Journal of Behavioral Science*, 20, 155-174.

Aldrich, T.E. (1990). Atlanta, GA: Agency for Toxic Substances and Disease Registries.

Anselin, L. (1995). Local indicators of spatial association—LISA. *Geographical Analysis, 27*(2), 93-115.

Baller, R. D., Anselin, L., Messner, S. F., Deane, G., & Hawkins, D. F. (2001). Structural covariates of U.S. county homicide rates: incorporating spatial effects. Criminology, 39, 561-590.

Bennett, W.J., DiIulio, Jr., J.J. & Walters, J.P. (1996). *Body Count: Moral Poverty...And How to Win America's War Against Crime and Drugs.* New York: Simon and Schuster.

Bursik, Jr., R.J. (1988). Social disorganization and theories of crime and delinquency: Problems and prospects. *Criminology*, 26, 519-551.

Clarke, R.V. & Felson, M. (1993). *Routine Activity and Rational Choice.* New Brunswick, NJ: Transaction.

Felson, M. (1987). Routine activities and crime prevention in the developing metropolis. *Criminology,* 25, 911-931.

Gorman, D.M. & Speer, P.M. (1997). The concentration of liquor outlets in an economically disadvantaged city in the northeastern United States. *Substance Use and Misuse*, 32, 2033-2046.

Gorman, D.M., Labouvie, E.W., Speer, P.W. & Subaiya, A.P. (1998a). Alcohol availability and domestic violence. *American Journal of Drug and Alcohol Abuse*, 24, 661-673.

Gorman, D.M., Speer, P.M. Labouvie, E.W. & Subaiya, A.P. (1998b). Risk of assaultive violence and alcohol availability in New Jersey. *American Journal of Public Health*, 88, 97-100.

Gorman, D.M., Speer, P.W., Gruenewald, P.J. & Labouvie, E.W. (2001). Spatial dynamics of alcohol availability, neighborhood structure and violent crime. *Journal of Studies on Alcohol,* 63, 628-636.

Gruenewald, P.J., Holder, H.D. & Treno, A.J. Environmental approaches to the prevention of alcohol, drug use and related problems. In A.W. Graham (Ed.), *Principles of Addiction Medicine* (3rd ed.), American Society of Addiction Medicine, April 19, 2001 (In press).

Gruenewald, P.J., Millar, A., Treno, A.J., Ponicki, W.R., Yang, Z. & Roeper, P. (1996). The geography of availability and driving after drinking. *Addiction, 91,* 967-983.

Hanson, C.E., & Wieczorek, W.F. (in press). Alcohol mortality: A comparison of spatial clustering methods. *Social Science and Medicine*.

Harding, J.R. & Wittmann, F.D. (1995). GIS enhances alcohol/drug prevention planning. *GIS World, 8*(6), 80-83.

Holder, H.D. (1994). Public health approaches to the reduction of alcohol problems. *Substance Abuse*, 15, 123-138.

Isaaks, E.H. and Srivastava, R.M. (1989). *An Introduction to Applied Geostatistics*. New York: Oxford University Press.

Jacquez, G.M. (1994). *Stat! Statistical software for the clustering of health events*. Ann Arbor, MI: BioMedware.

Krieger, N., Waterman, P., Lemieux, K., Zierler, S. & Hogan, J.W. (2001). On the wrong side of the tracts? Evaluating the accuracy of geocoding in public health research. *American Journal of Public Health, 91*(7), 1114-1116.

Kulldorff, M. (1997). A spatial scan statistic. *Communications in Statistics - Theory and Methods*, 26(6), 1481-1496.

Levine, H.G. (1984). Alcohol problems in America: From temperance to alcoholism. *British Journal of Addiction*, 79, 109-119.

Lipton, R.I. & Gruenewald, P.J. (2001). The Spatial Dynamics of Violence and Alcohol Outlets. Journal of the Study of Alcohol, 63(2), 187-195.

Midford, R., Masters, L., Phillips, M., Daly, A., Stockwell, T., Gahegan, M. & Philp, A. (1998). Alcohol consumption and injury in Western Australia: A spatial correlation analysis using geographic information systems. *Australia and New Zealand Journal of Public Health*, 22, 80-85.

Morenoff, J. D., Sampson, R. J., & Raudenbush, S. W. (2001). Neighborhood inequality, collective efficacy, and the spatial dynamics of urban violence. *Criminology*, 39, 517-560.

Mosher, J.F. (1995). The merchants, not the customers: Resisting the alcohol and tobacco industries' strategy to blame young people for illegal alcohol and tobacco sales. *Journal of Public Health Policy*, 16, 213-30.

Mosher, J.A. & Jernigan, D.H. (1989). New directions in alcohol policy. *Annual Review of Public Health*, 10, 245-279.

Mosher, J.A. & Jernigan, D.H. (2000). A public health approach to preventing alcohol-related violence and crime. *Alcohol and Crime: Research and Practice for Prevention (Alcohol Policy XII Conference Commissioned Papers)*, pp. 1-21. Washington, DC: National Crime Prevention Council.

Ricketts, T.C., Savitz, L.A., Gesler, W.M. & Osborne, D.N., (Eds.). (1994). *Geographic methods for health services research.* New York: University Press of America.

Roncek, D.W. & Bell, R. (1981/82). Bars, blocks, and crimes. *Journal of Environmental Systems*, 11, 35-47.

Roncek, D.W. & Maier, P.A. (1991). Bars, blocks, and crimes revisited: Linking the theory of routine activities to the empiricism of "hot spots." *Criminology*, 29, 725-753.

Roncek, D.W. & Pravatiner, M.A. (1989). Additional evidence that taverns enhance nearby crime. *Sociology and Social Research*, 73, 185-188.

Sampson, R.J., Raudenbush, S.W. & Earls, F. (1997). Neighborhoods and violent crime: A multilevel study of collective efficacy. *Science*, 277, 918-924.

Scribner, R.A., Cohen, D.A., Kaplan, S. & Allen, S.H. (1999). Alcohol availability and homicide in New Orleans: conceptual considerations for small area analysis of the effect of alcohol outlet density. *Journal of Studies on Alcohol*, 60, 310-316.

Scribner, R.A., MacKinnon, D.P. & Dwyer, J.H. (1995). The risk of assaultive violence and alcohol availability in Los Angeles County. *American Journal of Public Health*, 85, 335-340.

Sherman, L.W., Gartin, P.R. & Buerger, M.R. (1989). Hot spots of predatory crime: Routine activities and the criminology of place. *Criminology*, 27, 27-55.

Skogan, W.G. (1990). *Disorder and Decline: Crime and the Spiral of Decay in American Neighborhoods.* Berkeley, CA: University of California Press.

Snow, J. (1855). On the Mode of Communication of Cholera . London: John Churchill.

Speer, P.W., Gorman, D.M., Labouvie, E. W. & Ontkush, M. (1998). Violent crime and alcohol availability: Relationships in an urban community. *Journal of Public Health Policy*, 19, 303-318.

Stark, R. (1987). Deviant places: A theory of the ecology of crime. *Criminology*, 25, 893-909.

Stockwell, T. & Gruenewald, P.J. (2001). Controls on the physical availability of alcohol. In Heather, N., Peters, T.J. & Stockwell, T. (Eds.) *International Handbook of Alcohol Dependence and Problems*, pp. 699-719. New York: John Wiley & Sons, Inc.

Wieczorek, W.F. (2000). Using geographic information systems for small area analysis. In Wilson, R.E. & Dufour, M.C. (Eds.) *The Epidemiology of Alcohol Problems in Small Geographic Areas*, pp.137-162, NIH National Institute on Alcohol Abuse and Alcoholism: Bethesda, MD: (NIH Pub. No. 00-4357)

Wieczorek, W.F. & Coyle, J.J. (1998). Targeting DWI prevention. *Journal of Prevention and Intervention in the Community, 17*(1), 15-30.

Wieczorek, W.F. & Hanson, C.E. (1997). New modeling methods: Geographic information systems and spatial analysis. *Alcohol Health and Research World, 21*(4), 331-339.

Wieczorek, W.F. & Hanson, C.E. (2000). Regional patterns of alcohol-specific mortality in the United States. In Williams, R.C., Howie, M.M., Lee, C.V. & Henriques, W.D. (Eds.) *Geographic Information Systems in Public Health: Proceedings of the Third National Conference*, pp. 669-676, Atlanta, GA: Centers for Disease Control and Prevention.

Wilson, J.Q. & Kelling, G.L. (1982). Broken windows: The police and neighborhood safety. *Atlantic Monthly*, (March), 29-38.

SECTION II:

GIS
&
CANCER

Chapter V

The New Kid on the Block: A Look at How Geographic Information Systems Are Changing the Face of Cancer Research

Jane L. McCall
Health Geographics and Spatial Analysis Program at Baystate Medical Center, USA

In the last 20 years, Geographic Information Systems (GISs) have had an ever-increasing impact on the course of research and planning in many diverse fields, including geography, geology, environmental studies, business and criminal justice. Relatively recently, health care research, including cancer research, has entered this domain. The rapidly increasing use of GIS in health-care research over the past few years is witnessed by the fact that 63% of papers in literature review for this chapter were written in the last five years, and 35% within the last three years.

Epidemiology, the study of disease patterns in human populations according to person, place and time, has been the traditional means of approaching cancer etiology. Combining its tools with those of GIS has enabled researchers to look at the distribution of cancer in new ways and uncover relationships not previously seen with traditional epidemiological methods alone. Through its data integration function, GIS has enabled the use of existing data collected *for other purposes to be applied to cancer research. GIS techniques can enhance the visualization of spatial patterns of cancer, examine the contribution of various risk factors for cancer in new ways and allow hypotheses about cancer etiology to be tested in a spatial framework.*

The purpose of this chapter is to examine the impact of GIS on the direction of cancer research. In doing so, it will consider the application of GIS techniques to research in cancer etiology and compare them to traditional epidemiological methods. Rather than an exhaustive compilation of all the studies in this category, selective examples will be chosen from the literature to illustrate particular applications.

GIS AND ITS SUITABILITY TO CANCER RESEARCH

A Geographic Information System is a set of hardware and software for inputting, storing, managing, displaying and analyzing geographic or spatial data or any information that can be linked to geographic location such as events, people or environmental characteristics. Some of the most common sources of geographic data for a GIS are: printed maps such as those from the U.S. Geological Survey (USGS), areal and satellite images, global positioning systems and U.S. Census TIGER line files, which allow the determination of geographic location (e.g., and y coordinates on a map) from street address. The more widely available sources of non-geographic data for a GIS include worldwide census population tables, satellite remote sensing information and geologic surveys such as those from the USGS. However, any information that can be associated with geographic coordinates, or a geographic identifier such as a street address or geographic region (city, state, county, police precinct, etc.), can be incorporated into a GIS.

The capacity of GIS to integrate data on the three epidemiological components of person, place and time make it particularly suitable as a tool for cancer epidemiological research. With respect to person, it is well established that many cancers are related to demographic factors such as race or sex. Using GIS, the location of cancer cases can be overlaid on maps of population data to visualize relationships between demographic factors and patterns of cancer.

With respect to place, epidemiologists have traditionally examined geographic variation in cancer incidence using maps. Continuing interest in this application is demonstrated by the existence of cancer mortality and morbidity atlases in many countries (*Atlas of Cancer Mortality in Central Europe*, 1996; *Atlas of Cancer Mortality in the European Economic Community*, 1992; Buser, Wolf & Robra, 1984; Cislaghi, Decarli, La Vecchia, Mezzanotte & Smans, 1989; Errezola, Lopez-Abente & Escolar, 1989; Gruger & Schafer, 1989; Lai, 1997; Li, 1989; Li et al., 1981; Luppi, Camnasio, Benedetti, Covezzi & Cislaghi, 1995; Mehnert, Smans, Muir, Mohner & Schon, 1992; Pickle, Mungiole, Jones & White, 1999; Plesko, Obsitnikova & Kramarova, 1996; Semenciw et al., 2000; Wagner, 1989). The ability of a GIS to handle spatial data on a much smaller scale (by pinpointing the exact location of cancer cases) coupled with its ability to handle multiple levels of scale (block group, census tract, city, county, state, etc.) enhance the possibility of uncovering spatial patterns which would be missed by traditional epidemiological methods. In addition, the existence of known environmental risk factors for cancer, which may vary with geographic location, can be investigated with GIS. Data on the levels of many of these risk factors is widely available. Furthermore, new environmental data from field studies can be collected and entered directly into a GIS. Examples of this will be discussed in a later section.

With respect to the third factor (time), information on date of diagnosis, death or recurrence of cancer cases can be entered into a GIS so that temporal and spatio-temporal relationships may be examined.

The visualization and analytic capabilities of GIS enable the user to examine and model the interrelationship between factors on all three epidemiological dimensions of cancer.

THE TRADITIONAL EPIDEMIOLOGICAL APPROACH TO CANCER RESEARCH

To determine cancer incidence rates for different geographic regions without GIS, cancer cases must be manually allocated to appropriate regions based on address. Population-based disease registries supply data on incidence or mortality rates for larger regions such as counties or towns. For smaller regions like census block groups or neighborhoods, or for other non-standard regions, data must be obtained from prospective or retrospective cohort studies, and allocation of cases without the aid of GIS becomes a very time-consuming process. When rates are obtained in this way, the level of aggregation (size of the geographic region) is fixed in advance, unless the user repeats the process again, using a different aggregation level. With GIS, however, the user has the flexibility of easily aggregating data at many different levels and comparing the results.

To examine the geographic distribution of cancer, dot density case maps or choropleth maps of cancer rates are most often used. Dot density maps depict each cancer case as a dot or symbol. Choropleth maps depict the level or intensity of cancer incidence in geographic regions by different colors or patterns. The geographic distribution of socioeconomic, demographic or environmental risk factors is usually mapped in the same way. At best, one dot density map and one choropleth map may be overlaid on each other to compare the distribution of cancer cases with one risk factor, without the ability to overlay or combine several risk factors and cancer cases on the same map.

In traditional epidemiological studies, category-specific or standardized incidence rates are generally relied on to investigate the role of demographic or socioeconomic characteristics in cancer at the aggregate level, without the use of visualization techniques. Regression models may be used to examine several risk factors at a time, but these do not account for the spatial distribution of the cancer or the risk factors.

SPECIFIC GIS FUNCTIONS APPLICABLE TO CANCER RESEARCH

A multitude of functions specific to GIS extends these traditional epidemiological methods of handling disease data. Many of these have been applied to the study of cancer and will be described in the present chapter. According to Bailey and Gattrell (1995), GIS-specific functions can be grouped into four broad categories:

1. data integration and management
2. visualization
3. exploratory spatial analysis
4. mathematical modeling

Data Integration/Management

A key function of GIS is the integration of data from many existing sources. This often eliminates the need to collect primary data for new studies. An excellent example of the diversity of possible data sources is provided by the Cape Cod Breast Cancer and Environment Study. To determine environmental exposure, this study used existing records of land use, pesticide applications, hydrologic data and real estate parcels from universities, federal, state and local agencies, town governments, and fieldwork. It used U.S. Census population counts and real estate land use data to determine denominators for incidence rates. Information on breast cancer cases came from the state cancer registry.

GIS can perform mathematical operations on this integrated data to create new variables or estimate values for existing variables tailored to the purpose of the study. The Cape Cod Breast Cancer and Environment Study used GIS to calculate intercensal population estimates from residential landuse data in order to obtain a better estimate of the population-at-risk for breast cancer. GIS was then used to calculate standardized incidence ratios for different geographic areas.

Another way in which a GIS can create new data is to calculate the degree of environmental exposure to carcinogens. This is exemplified in a case-control study by Lewis-Michl et al. (1996) on the relationship of toxic chemical pollutant exposure and breast cancer on Long Island, New York. The authors used the location history of breast cancer cases, manufacturing facilities and vehicle density estimates for selected highways during a twenty-year time period to compute a weighted-average yearly exposure for each case or control, based on distance of residence from these sources of toxic chemical pollutants.

Smoothing is a mathematical operation often used by GIS to enhance geographic patterns in the phenomenon under study. One application is to smooth out geographic fluctuations in rates that are caused by unstable rates in areas with small underlying populations. A study by Osnes and Aalen (1999) applied a form of Bayesian smoothing to survival rates for breast cancer and malignant melanoma in Norway to look at small-scale survival differences between municipalities.

Another useful function of GIS is to calculate distances to be used in statistical analyses based on spatial contiguity. A study by Athas and Amir-Fazli (2000) used a GIS to calculate patient travel distance to a major population center to examine geographic differences in breast cancer stage at diagnosis. In another study, the authors used a GIS to measure travel distance to radiation treatment facilities to examine the relationship between travel distance and receiving radiotherapy after breast-conserving surgery (Athas, Adams-Cameron, Hunt, Amir-Fazli & Key, 2000). Ward et al. (2000) used remote sensing data in a GIS to reconstruct historical crop patterns and determine zones of probable pesticide exposure to agricultural pesticides. They then measured proximity of residence for non-Hodgkin's lymphoma patients to these zones to determine their degree of exposure.

Another database function of GIS is to establish "topology," i.e., to determine neighbors or establish neighborhoods. A "neighbor" can be defined in numerous ways—areas or entities related by sharing a common geographic border, trade routes or common acquaintances. Kennedy (1988) used a GIS to define different orders of neighbors for counties in 11 Southeast U.S. states (bordering one, two …five counties away) which were then used as variables in a regression model to examine local and increasingly global trends in lung cancer mortality for males and females.

Visualization

The second function of GIS is visualization, consisting primarily of mapping. Using a process called geocoding, dot density maps of cancer cases by exact location can be automatically generated. Using the geocoded data, the total number of cases for a geographic area (e.g., state, county, town, census tract) can be counted and divided by the underlying population of that area to determine prevalence or incidence rates. Choropleth maps can then be generated for different areal configurations. Examples of different configurations of the same geographic region are given in Figures 1-3, which show census block groups, census tracts, and neighborhoods for Springfield, Massachusetts.

This ability to summarize or "aggregate" the data in different ways is a key advantage of GIS. Investigators can define geographic areas (zones) to suit the purposes of their particular study, rather than accepting pre-defined geographic

Figure 1: Census block groups

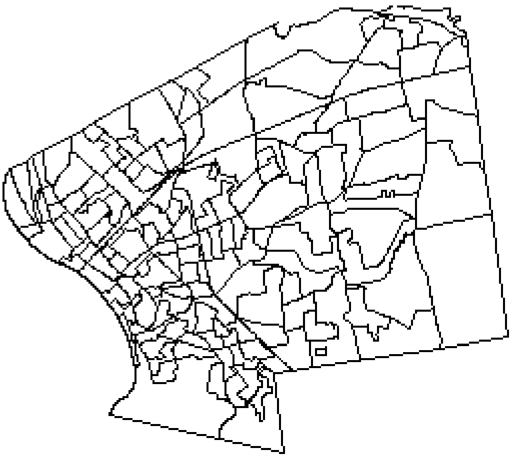


Figure 2: Census tracts

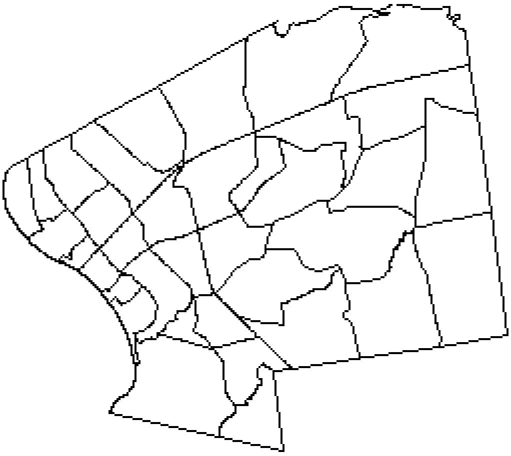
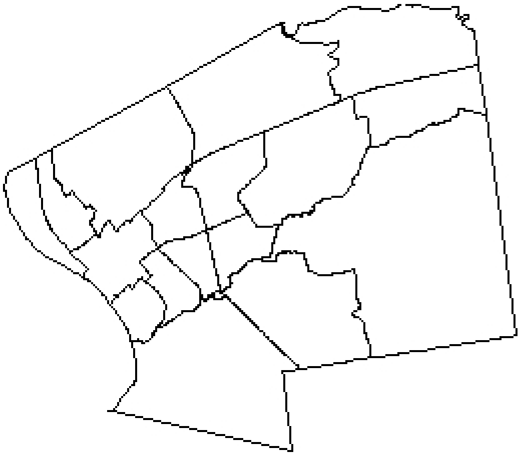


Figure 3: Neighborhoods

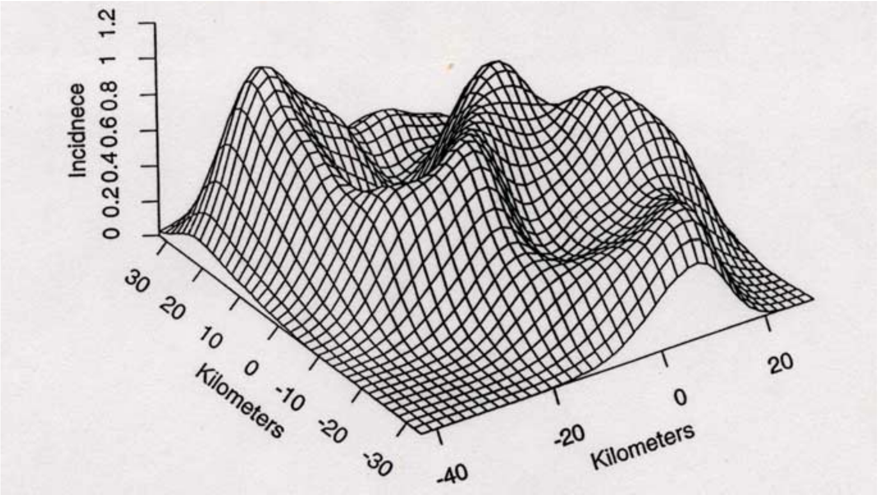


areas that have been established for other purposes. White and Aldrich (1999) provide an example of purposeful aggregation in a study on pediatric cancer. The authors defined zones based on a one-mile buffer around hazardous waste sites, because of their interest in proximity to environmental toxins as a risk factor for pediatric cancer. Another example is provided by the Cape Cod Breast Cancer and Environment Study, where use of environmentally meaningful units such as groundwater zones and public water supply districts (areas served by private wells vs. public water supplies) allowed the investigators to test hypotheses about the contribution of environmental factors to cancer incidence (Brody, Rudel, Maxwell & Swedis, 1996). By defining zones according to different types of environmental exposure, different hypotheses about environmental risk factors could be explored.

Varying the aggregation scheme or intervals by which the attribute to be mapped is classified on a choropleth map can enhance or hide geographic patterns in the data and generate hypotheses. Larger geographic areas or classification intervals result in larger sample sizes and more stable estimates for each area, but can hide patterns in the data due to greater heterogeneity within each area or classification interval. Small areas or classification intervals result in more homogeneity and can enhance meaningful patterns but may result in unstable estimates. The Cape Cod Breast Cancer Environmental Study explored these differences in their data. The authors concluded that examining breast cancer incidence rates at different levels (county, town, census tract and census block group) enabled them to "explore the trade-off between larger sample size and greater statistical power" and "the potentially greater explanatory power of smaller geographic units" (Brody et al., 1996). Cromley and Cromley (1996) explored the use of a classification scheme for choropleth mapping that based the spatial configuration of geographic areas on their attribute similarity. They illustrated the advantages of this method in enhancing patterns in the data compared to traditional classification methods, using data from the German Cancer Atlas.

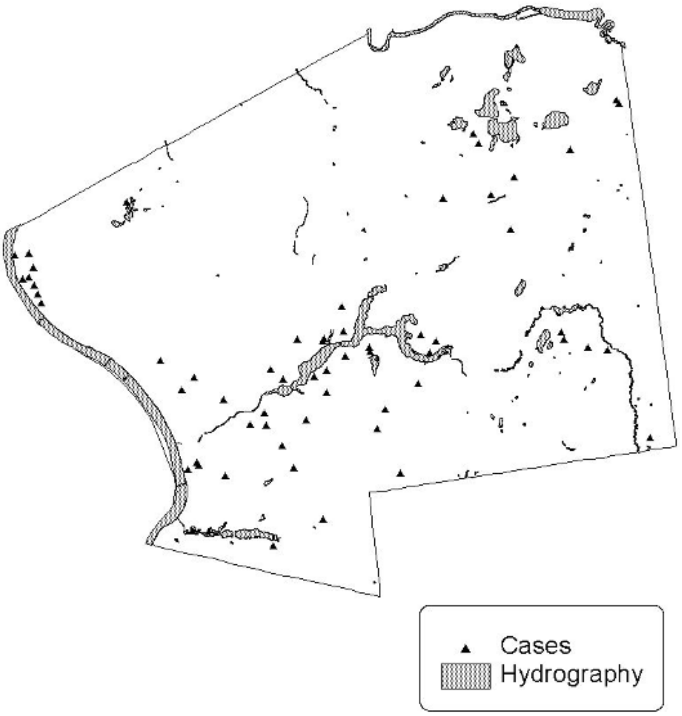
Smoothing techniques like those described in the previous section can be used to eliminate some of the irregularities seen in 2D mapping, and can be particularly useful in mapping cancer incidence rates. Selvin, Merrill, Erdmann, White and Ragland (1998) used kernel smoothing to create a "density equalized map" to depict late-stage breast cancer incidence on a continuous three-dimensional surface with no regional boundaries. This adjusts for the effect of small population denominators in sparsely populated regions, the disproportionate visual impact of large geographic areas on a two-dimensional choropleth map, and the distorted visual impression given by many white areas indicating zero rates.

Figure 4: Density equalized map (Reprinted from Selvin et al., 1998)



The ability of GIS to utilize the many types of new technology for recording and accurately quantifying data on environmental exposure and its capability to map this data has led to more emphasis on environmental factors in cancer research. Point and polygon overlay and buffering are two GIS techniques especially applicable to visualizing the relationship between environmental exposure and cancer. The investigator can overlay the distribution or cases and/or controls (represented by points) with the distribution of environmental features (represented by polygons) to generate hypotheses about risk factors which can then be studied further at the individual level with traditional epidemiological study designs such as cohort or case control (Turnbull, Iwano, Burnett, Howe & Clark, 1990). Figure 5 provides an example of overlay in which area hydrography (water) is overlaid on a map of cancer cases. The proximity of the cases to water generates the hypothesis of carcinogens in the water supply. In the Cape Cod Breast Cancer and Environment Study, investigators overlaid maps of breast cancer cases with maps of the location of cranberry bogs and golf courses indicating areas of presumed pesticide usage, the location of wells with elevated nitrate levels indicating poor water quality, and buffer zones around Massachusetts Military Reservation sites which contained toxic chemicals (Brody et al., 1997; Melly et al., 1997, 1998). Another example of overlay is given by the study of White and Aldrich (1999), in which the authors mapped pediatric cancer cases and overlaid buffer zones around NPL sites.

Figure 5: Example of overlay



Exploratory Spatial Analysis

Exploratory spatial analysis builds on the results of visualization and examines whether visualized patterns or relationships occur by chance. Although many types of exploratory spatial analysis are possible with GIS, its application to cancer has been primarily in testing for clustering of cancer cases. Statistical evidence of clustering in a particular geographic location (point clustering) gives the impetus to look for the presence of possible risk factors in the area and generate hypotheses to be tested to explain the clustering. The ability of GIS to determine the exact location of cancer cases makes it suitable for testing for clustering. Beyond testing for clustering at pre-determined locations, methods such as the spatial scan statistic (Kulldorff, 1997) and the Geographic Analysis Machine (GAM) (Openshaw, Charleton, Wymer & Craft, 1987) and its extension (Besag & Newell, 1991) have been developed to search an area and find locations of clusters. Hjalmars, Kulldorff, Gustafsson & Nagarwalla (1996) used a GIS to search for evidence of clustering of leukemia cases in Sweden, using a spatial scan statistic. Several other studies have applied spatial scan statistics to look for clustering of several different types of cancer over both large and small areas (Hjalmars & Gustafsson, 1999; Hjalmars et al., 1996; Kulldorff, Athas, Feurer, Miller & Key, 1998; Kulldorff, Feuer, Miller & Freedman, 1997; Openshaw, Charleton, Wymer & Craft, 1987; Timander & McLafferty, 1998). Known cancer risk factors that vary geographically in the underlying population can be adjusted for in verifying the presence of clustering (Kulldorff et al., 1997).

In addition to hypothesis generation, tests for clustering have been applied to monitoring cancer incidence from cancer registry data as part of a cancer surveillance program. Turnbull et al. (1990) outline a procedure which they call the "cluster evaluation permutation procedure" for periodic monitoring of cancer clusters as a substitute for reactive testing of cluster alarms after they occur. They applied this to cancer surveillance in upstate New York. White and Aldrich (1999) used a GIS for monitoring leukemia incidence in upstate New York to determine if there was clustering around hazardous waste sites.

Mathematical Modeling

The final function of GIS is mathematical modeling, which can be used to estimate the form of relationship between various factors, or to predict or estimate unknown values. Spatial interpolation is an example of the latter, and is used widely in GIS in other fields. The main application of mathematical modeling in cancer research has been in estimating carcinogen exposure for geographic locations to test causal hypotheses about carcinogen exposure and cancer. An example of this is given by Kennedy (1988), who used spatial regression to examine local and global trends across the United States in lung cancer for males and females.

GIS USED IN CONJUNCTION WITH TRADITIONAL EPIDEMIOLOGICAL METHODS

Perhaps the greatest utility of GIS is its ability to incorporate epidemiological data gathered from traditional studies to perform spatial operations, visualization and analysis. The study by Ward et al. (2000) exemplifies this approach. They used data from a population-based study on leukemia incidence as input for residence location and its relationship to historical crop patterns from remote sensing.

Another way in which GIS can be combined with a traditional approach is to identify excess rates or trends with traditional epidemiological methods (e.g., surveillance, cohort or case control studies) and further investigate these with GIS methods. In their study on breast cancer, Lewis-Michl et al. (1996) identified proximity to industry and traffic as risk factors for breast cancer with a case control study. They then used GIS to estimate and map exposure based on residential history and calculated the odds ratio for past exposure vs. non-exposure. The Cape Cod Breast Cancer and Environment Study resulted from findings by the Massachusetts Cancer Registry of an excess of breast cancer on Cape Cod at the county level which was then investigated at the local level using GIS.

Aside from providing data, traditional studies can generate hypotheses for further study by GIS. In the Cape Cod study, the investigators used a traditional ecological analysis of data from the state cancer registry that did not show any association between breast cancer incidence and elevated nitrate levels in drinking water. They explored this further with GIS using statistical analysis and visualization to generate hypotheses for further study.

Findings from traditional epidemiological methods (cohort, case control) can also be used to corroborate GIS findings or to further study and test hypotheses generated by the GIS. In the Cape Cod study, the GIS identified an elevated number of cases in the area of the Mass Military Reservation (MMR). The investigators corroborated this with a previous case control study that had found a statistically unstable association between breast cancer and gun and mortar positions at the MMR.

LIMITATIONS OF GIS

Despite its tremendous usefulness, GIS has several limitations. One problem inherent in using data from a GIS is the "aggregation problem," which refers to the information loss which occurs when substituting aggregate data for individual-level data. One aspect of this is the "ecological fallacy," the danger in making causal inferences about individuals based on findings from aggregate or group data. Another aspect is the modifiable areal unit problem or "MAUP" which refers to the statistical bias that results from different levels of aggregation (the "scale effect") or different alternative groupings of data at the same level of aggregation (the "zone effect"). Besides the statistical and inferential problems inherent in aggregation, there is the added problem of interpretation — the groupings used with spatial data in a GIS have often been derived for administrative or political purposes. Deductions that can be made from analysis of administrative groupings do not necessarily apply to cancer etiology. Cleek (1979) has discussed the problems introduced by level of aggregation in interpreting complex relationships present in multivariate models of cancer. Although there are several techniques to minimize the effects of the aggregation problem (Wong, 1995), it must still be kept in mind when making inferences from geographic data.

One must also be mindful of another problem with GIS when interpreting studies using this technique. A GIS is only as good as its input data. Inaccuracies in the original sources of geographic data, such as maps or aerial photographs or errors introduced in the process of encoding, must be considered. Many problems in geocoding data from street address can occur, and this problem is magnified in rural areas (White & Aldrich, 1999). In addition to spatial data quality, the quality of non-spatial data obtained from many sources must be verified.

The Federal Geographic Data Committee (FGDC, 1994) has published a set of standards for data sharing and dissemination which includes making information available on the accuracy and quality of data to be used in a GIS. These standards are implemented in the form of "metadata," the documentation that should accompany any GIS data available.

THE PROMISE OF GIS FOR THE FUTURE IN CANCER RESEARCH

Despite the above limitations, GIS is a powerful tool for cancer research that has only begun to be utilized in this arena. One area in which GIS offers the most potential is its application to mathematical modeling. The ability of a GIS to integrate data on complex spatial phenomena, and readily integrate continually updated information, make it ideal for investigating the role of environmental factors and modeling their role in the etiology of various forms of cancer, creating changing and more precise models as new data become available.

Another area where GIS stands to contribute most to cancer research is the study of socio-demographic factors. Considering the strong links shown by previous research between many types of cancer and demographic factors, coupled with the availability of population demographic and socioeconomic data, the utility of using GIS for cancer incidence data seems obvious. This is likely to drive much GIS-related cancer research in the future, because of the increasing emphasis that has been placed on demographic factors in treatment, prevention and resource allocation. Demographic population data can be used to characterize geographic areas with increased cancer incidence to assist in planning intervention programs and allocating resources.

The advent of GIS, its continuing technical growth and its increasing availability make the future of cancer research truly dynamic and exciting.

REFERENCES

Athas, W. F., Adams-Cameron, M., Hunt, W. C., Amir-Fazli, A. & Key, C. R. (2000). Travel distance to radiation therapy and receipt of radiotherapy following breast-conserving surgery. *Journal of the National Cancer Institute, 92*(3), 269-271.

Athas, W. F. & Amir-Fazli, A. (2000). *Geographic Variation in Breast Cancer Stage of Disease at Diagnosis.* Paper presented at the Second International Health Geographics Conference, Chevy Chase, MD, March 17–19.

Atlas of Cancer Mortality in Central Europe (1996). IARC Scientific Publications, 134, 1-175.

Atlas of Cancer Mortality in the European Economic Community (1992). IARC Scientific Publications, 107, 1-213.

Bailey, T. & Gatrell, A. C. (1995). *Interactive Spatial Data Analysis*: Crown Books.

Besag, J. & Newell, J. (1991). The detection of clusters in rare diseases. *Journal of the Royal Statistical Societies, Series A, 154*(1), 143-155.

Brody, J., Foord, K., Maxwell, N., Melly, S., Polk, R., Rudel, R. & Swedis, S. (1997). *Cape Cod Breast Cancer and Environment Study: Results of the First three years of Study*. Boston, MA: Boston University School of Public Health.

Brody, J. G., Rudel, R., Maxwell, N. I. & Swedis, S. R. (1996). Mapping out a search for environmental causes of breast cancer. *Public Health Reports, 111*(6), 494-507.

Buser, K., Wolf, E., & Robra, B. P. (1984). Cancer atlas of Lower Saxony—possibilities and limitations. *Offentl Gesundheitswes, 46*(5), 211-213.

Cislaghi, C., Decarli, A., La Vecchia, C., Mezzanotte, G. & Smans, M. (1989). Italian atlas of cancer mortality. *Recent Results in Cancer Research, 114*, 143-153.

Cleek, P. K. (1979). Cancers and the environment: The effect of scale. *Social Science Medicine, 13D*, 241-247.

Cromley, E. K. & Cromley, R. G. (1996). An analysis of alternative classification schemes for medical atlas mapping. *European Journal of Cancer, 32A*(9), 1551-1559.

Errezola, M., Lopez-Abente, G. & Escolar, A. (1989). Geographical patterns of cancer mortality in Spain. *Recent Results in Cancer Research, 114*, 154-162.

FGDC. (1994). *Content Standards for Digital Geo-Spatial Metadata (June 8)*. Washington, DC: Federal Geographic Data Committee.

Gruger, J., & Schafer, T. (1989). Cancer morbidity atlas of the saarland: An outline of the model project for the analysis of health and environmental data in the Saarland. *Recent Results in Cancer Research, 114*, 34-40.

Hjalmars, U. & Gustafsson, G. (1999). Higher risk for acute childhood lymphoblastic leukaemia in Swedish population centres 1973-94. Swedish Child Leukaemia Group. *British Journal of Cancer, 79*(1), 30-33.

Hjalmars, U., Kulldorff, M. Gustafsson, G. & Nagarwalla, N. (1996). Childhood leukaemia in Sweden: using GIS and a spatial scan statistic for cluster detection. *Statistics in Medicine, 15*(7-9), 707-715.

Kennedy, S. (1988). A geographic regression model for medical statistics. *Social Science and Medicine, 26*(1), 119-129.

Kulldorff, M. (1997). A spatial scan statistic. *Communications in Statistics: Theory and Methods, 26*(6), 1481-1496.

Kulldorff, M., Athas, W. F., Feurer, E. J., Miller, B. A. & Key, C. R. (1998). Evaluating cluster alarms: A space-time scan statistic and brain cancer in Los Alamos, New Mexico. *American Journal of Public Health, 88*(9), 1377-1380.

Kulldorff, M., Feuer, E., Miller, B. & Freedman, L. (1997). Breast cancer clusters in the Northeast United States: A geographic analysis. *American Journal of Epidemiology, 146*(2), 161-170.

Lai, D. (1997). Spatial statistical analysis of Chinese cancer mortality: a comparison study of the D statistic. *Scandinavian Journal of Social Medicine, 25*(4), 258-265.

Lewis-Michl, E. L., Melius, J. M., Kallenbach, L. R., Ju, C. L., Talbot, T. O., Orr, M. F. & Lauridsen, P. E. (1996). Breast cancer risk and residence near industry or traffic in Nassau and Suffolk Counties, Long Island, New York. *Arch Environ Health, 51*(4), 255-265.

Li, J. Y. (1989). Cancer mapping as an epidemiologic research resource in China. *Recent Results in Cancer Research, 114*, 115-136.

Li, J. Y., Liu, B. Q., Li, G. Y., Chen, Z. J., Sun, X. I., & Rong, S. D. (1981). Atlas of cancer mortality in the People's Republic of China. An aid for cancer control and research. *International Journal of Epidemiology, 10*(2), 127-133.

Luppi, G., Camnasio, M., Benedetti, G., Covezzi, I. & Cislaghi, C. (1995). The Italian mortality map at the municipal level. *Epidemiologia E Prevenzione, 19*(63), 132-141.

Mehnert, W. H., Smans, M., Muir, C. S., Mohner, M. & Schon, D. (1992). Atlas of cancer incidence in the former German Democratic Republic 1978- 1982. *IARC Scientific Publications, 106*, 1-384.

Melly, S., Joyce, Y., Maxwell, N. & Brody, J. (1997). *Investigating Breast Cancer and the Environment Using a Geographic Information System.*: Massachusetts Department of Public Health.

Melly, S., Maxwell, N., Joyce, Y., & Brody, J. (1998). *Exploratory Data Analysis in a Study of Breast Cancer and the Environment.* Paper presented at the Public Health Conference, San Diego, CA.

Openshaw, S., Charleton, M., Wymer, C. & Craft, A. (1987). A Mark 1 geographical analysis machine for the automated analysis of point data sets. *Geographical Information Systems, 1*, 335-358.

Osnes, K. & Aalen, O. O. (1999). Spatial smoothing of cancer survival: A Bayesian approach. *Statistics in Medicine, 18*(16), 2087-2099.

Pickle, L. W., Mungiole, M., Jones, G. K. & White, A. A. (1999). Exploring spatial patterns of mortality: the new atlas of United States mortality. *Statistics in Medicine, 18*(23), 3211-3220.

Plesko, I., Obsitnikova, A. & Kramarova, E. (1996). Mapping in epidemiological studies and control of cancer: Experiences from Slovakia. *Journal of Environmental Pathology, Toxicology and Oncology, 15*(2-4), 143-147.

Selvin, S., Merrill, D. W., Erdmann, C., White, M. & Ragland, K. (1998). Breast cancer detection: maps of two San Francisco Bay area counties. *American Journal of Public Health, 88*(8), 1186-1192.

Semenciw, R. M., Le, N. D., Marrett, L. D., Robson, D. L., Turner, D. & Walter, S. D. (2000). Methodological issues in the development of the Canadian Cancer Incidence Atlas. *Statistics in Medicine, 19*(17-18), 2437-2449.

Timander, L. M. & McLafferty, S. (1998). Breast cancer in West Islip, NY: A spatial clustering analysis with covariates. *Social Science and Medicine, 46*(12), 1623-1635.

Turnbull, B. W., Iwano, E. J., Burnett, W. S., Howe, H. L. & Clark, L. C. (1990). Monitoring for clusters of disease: application to leukemia incidence in upstate New York. *American Journal of Epidemiology, 132*(1 Suppl), S136-143.

Wagner, G. (1989). Recent cancer atlas of the Federal Republic of Germany. *Recent Results in Cancer Research, 114*, 103-114.

Ward, M. H., Nuckols, J. R., Weigel, S. J., Maxwell, S. K., Cantor, K. P. & Miller, R. S. (2000). Identifying populations potentially exposed to agricultural pesticides using remote sensing and a Geographic Information System. *Environmental Health Perspectives, 108*(1), 5-12.

White, E. & Aldrich, T. E. (1999). Geographic studies of pediatric cancer near hazardous waste sites. *Archives of Environmental Health, 54*(6), 390-397.

Wong, D. (1995). Aggregation effects in geo- referenced data. In Arlinghaus, S. L. (Ed.), *Practical Handbook of Spatial Statistics* (pp. 83-106). New York: CRC Press.

Chapter VI

Community Breast Cancer Mapping in Huntington, Long Island

Scott Carlin
Southampton College, Long Island University, USA

The Huntington Breast Cancer Action Coalition (HBCAC) recently completed a survey of town residents regarding breast cancer. This chapter reviews how this community group relied upon a network of volunteers and community goodwill to survey local breast cancer patterns and the issues HBCAC confronted in mapping those results. The chapter explains how community-mapping projects differ from mapping projects directed by scientists, private corporations and government agencies. Community organizations often approach maps with different perspectives and goals than these traditional mapping agencies. This chapter emphasizes the significance of the community perspective for understanding and addressing breast cancer. HBCAC is using ESRI's ArcView software to map breast cancer patterns and to overlay various environmental themes, such as local toxic sites, to better understand local breast cancer patterns.

INTRODUCTION

Breast cancer now accounts for almost one out of every three cancer diagnoses among women. It is the most common form of cancer for women, excluding non-melanoma skin cancers (American Cancer Society, 2001). Breast cancer is also the leading cause of death for women between the ages of 35 and 54 (Breast Cancer Action, 2001). While many cancer rates have fallen in recent years, breast cancer rates continue to climb (Associated Press, 2001). Huntington Breast Cancer Action Coalition (HBCAC) was formed in 1993 to educate the residents of Huntington, New York about breast health. A similar coalition on Long Island, in neighboring West Islip, had formed in 1992. Two years later West Islip had developed a "'first of its kind' door-to-door demographic mapping survey" (West Islip BCCLI, no date). HBCAC decided to launch a more detailed and comprehensive survey of Huntington women over the age of 25. Following West Islip's experiences, HBCAC hoped to map its survey data. Maps were proving to be powerful tools for raising public awareness about the prevalence of breast cancer on Long Island. HBCAC's mapping project offers important lessons for both the public health community and organizations involved in community mapping.

Community mapping projects have become an important tool for informing and empowering local citizens. As Common Ground has stated, "Through the process of creating and revising maps, communities are better equipped to proactively address their interests and concerns" (Common Ground, 2001a). Map overlays allow local groups to visualize a wide range of attributes associated with community life, including environmental, health, economic, social welfare, land use, demographic and natural hazards data. Using GIS overlays, community groups can also examine the linkages among these different geographic themes. For example, we can use GIS to look at the way breast cancer patterns correlate with demographic or environmental factors. Health professionals, academics, private corporations and others have already mapped many of these features. If that is true, then what makes community mapping innovative?

First, community maps raise community participation rates by engaging a broad cross-section of the community, most of whom have little or no prior background in mapping projects. In Huntington, HBCAC had no internal mapping resources. HBCAC knew, however, that it wanted to map breast cancer, so HBCAC sought out volunteers and paid interns who could help make that goal a reality. For technical skills, HBCAC sought assistance from Greenman-Pederson, an engineering firm, and researchers at local universities.

Second, community maps are important educational tools. Maps help residents understand local issues by making complex datasets visual. Although the residents of Huntington knew breast cancer was an important issue, the maps helped the community to understand the widespread prevalence of this disease.

Third, community-mapping projects can improve scientific research. HBCAC hopes that scientists will continue to utilize HBCAC's unique database to better understand breast cancer issues in Huntington. This project also gives HBCAC credibility when it comments on scientific research. Many of the scientists that have worked with HBCAC have been impressed with the caliber of HBCAC's projects and have found HBCAC's comments to be valuable. HBCAC has also used its mapping project to push for more scientific research into the environmental factors that contribute to breast cancer on Long Island and elsewhere. As a result of these and other exchanges, the president of HBCAC sits on the oversight committee for the GIS component of the National Cancer Institute's Long Island Breast Cancer Study Project.

Fourth, community-mapping projects are a valuable tool for developing participants' critical thinking skills. They are not simply learning about their communities by reading maps; they are also asking questions of the maps and manipulating the maps to provide answers. Through that process, citizens begin to see their community in a new light. Through its maps and other campaigns, HBCAC wants local residents to question various environmental exposures. Are pest-free lawns worth the risks of potentially higher breast cancer rates? Should residents ignore broad-based usage of toxic substances in their community?

The mapping project also helps local citizens and activists to better understand the complexities involved in map analysis. Residents in high breast cancer areas are continually frustrated by the inconclusive nature of many government studies that try to statistically identify cancer clusters. By gaining a better understanding of mapping technologies and statistical techniques, residents understand why scientific research can often be inconclusive. That knowledge also helps to sharpen advocates' public policy campaigns.

Fifth, community-mapping projects are distinctive because local citizens, often working through non-profit organizations, control the mapping process. They control what is to be mapped, how maps are to be distributed and how they are going to be publicized. This shift can lead to mapping innovations, like breast cancer maps. Citizens often bring new perspectives to mapping, highlighting previously ignored issues and helping to change local public agendas. Maps can strongly influence community perceptions. In Huntington, HBCAC knew they wanted to use maps to explore the relationship between environmental contamination and breast cancer. They wanted to use their maps to heighten public awareness of the usage of toxic substances in Huntington and to explore whether those substances were affecting local breast cancer rates. Local control of the mapping process is particularly important because many community-mapping projects focus on politically sensitive issues. For that and other reasons, relying upon government agencies for these maps can often lead to frustration. Despite that tension, much of the information that community mapping projects draw upon comes from governmental data sources and often requires the cooperation of government officials.

Breast cancer maps provide a good illustration of these tensions. Debates about privacy and data confidentiality have been a frequent source of conflict between government officials and grassroots breast cancer organizations. From the perspective of government, releasing detailed data about breast cancer (or any cancers) can be an invasion of privacy. People's lives can be seriously disrupted by the public release of data describing their health histories. There's a fear that local citizens will be stigmatized or that individuals may lose their jobs. From the perspective of community health advocates, it is essential that the public understand the extent of disease within their community. Detailed community maps provide a powerful visual tool for exposing the ubiquity of breast cancer on Long Island.

Sixth, community-mapping projects improve public policy. Community mapping efforts often begin in a fairly naive way, with local citizens believing that by creating maps and mixing new and old sources of data in compelling ways, they can open a space in public discourse for considering new alternatives. What community groups frequently learn is that the pace of change in government is often much slower than they anticipated or that key elements of their government are hostile to their plans.

Today, a wide chasm has opened in the environmental health field. On the one side are academics and government officials who feel that we must focus on research. These individuals focus primarily on genetic research and, to a lesser extent, environmental research in search of

BENEFITS OF COMMUNITY MAPPING

1. Maps engage the community.
2. Maps are educational.
3. Community involvement can aid scientific research.
4. Participants strengthen their critical thinking skills.
5. Community members control the process.
6. Community maps help sharpen public policy goals.

better answers to the causes of and medical solutions to breast cancer. On the other side are environmental health advocates and some environmental scientists. They believe various cancers are a direct product of industrial-era chemicals. For example, much attention is now focusing upon groups of chemicals that affect the body's hormonal system. In *Our Stolen Future*, Dr. Theo Colburn and her colleagues (1997) argue that synthetic chemicals mimic natural hormones, disrupt the body's endocrine system and trigger hormone-related diseases, like breast cancer.

Therefore in the area of breast cancer, maps have become deeply politicized. At one level, community-based breast cancer maps are about raising public education and awareness. But, at another level, these maps are about changing our understanding of environmental health and changing public policies that affect our health. Rachel Carson (1962) begins her path-breaking book, *Silent Spring*, by noting how intimately we live with modern chemicals—how we eat, drink and breathe pesticides into our bodies without pausing to consider the devastation that these chemicals cause. Dr. Sandra Steingrabber (1997) also emphasized these issues of intimacy. For example, she discussed how mothers pass along PCBs and other chemicals to their newborn children through their breast milk. Both authors emphasized that this knowledge should lead to specific improvements in public policies.

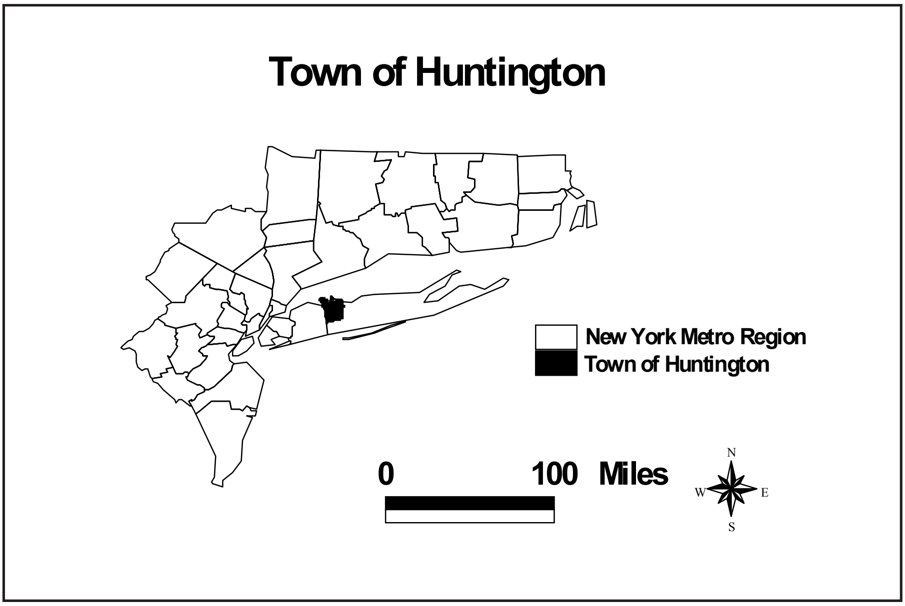
While community-based maps do not create a two-dimensional portrait of these intimate health relationships, they do paint a powerful picture of communities suffering silently, block after block, through devastating illness. Breast cancer maps are a powerful tool for breaking that silence, forcing the public to confront its secrets, and developing new public policies that reduce breast cancer risks and improve the health-care system's effectiveness.

These concerns have prompted HBCAC to promote a new public policy initiative, the precautionary principle: "When an activity raises threats of harm to human health or the environment, precautionary measures should be taken even if some cause-and-effect relationships are not fully established scientifically. In this context the proponent of an activity should bear the burden of proof" (Wingspread, 1998). A diverse array of health and environmental organizations has already adopted this standard.

SURVEYING WOMEN IN HUNTINGTON

In the early 1990's, the Town of Huntington (see Figure 1) had a population of 200,000 (90% white). HBCAC decided to survey the entire town with the goal of mapping and studying breast cancer and reaching a 50% response rate. The

Figure 1: Huntington locator map



survey was written by Roger Grimson, PhD, a biostatistician at the Department of Preventive Medicine at the University Medical Center at Stony Brook; physicians at Huntington Hospital, and local breast health activists. The survey was mailed out to over 68,000 households in September 1993, all known households in the town. The survey was sponsored by Huntington Hospital and supported by Huntington town officials and community volunteers. The survey was written in both English and Spanish, and publicized in community newspapers, radio and television stations; local Parent Teacher Associations (PTAs); and through other civic and religious groups. In response, over 15,500 surveys were filled out and returned (Galgano, 2001).

In June 1994, the Junior League of Long Island and Suffolk County Health Partnership sponsored a second mailing, targeting non-respondent households. HBCAC collected another 9,000 surveys. HBCAC volunteers entered the surveys into a computer. Each survey was reviewed, assigned a record number and supplied with a nine-digit ZIP Code if not provided. (Volunteers manually retrieved the nine-digit ZIP Code from U.S. Postal ZIP Code books.) The surveys were batched in groups of 25. It took 1 to 1.5 hours to enter a batch into the computer database. The initial data entry program was written in 1993 by volunteers in DOS and later revised for Windows.

At a town hall meeting on the evening of March 25, 1995, HBCAC presented preliminary statistics for the 18,955 Breast Health Surveys they had tabulated. Greenman-Pedersen Inc. geocoded and mapped the survey data. Of the respondents, 5,421 indicated that someone in their family had breast cancer (29%); 939 respondents indicated they themselves had breast cancer at some time (5%).

In July 1996, HBCAC completed a third mailing, bringing in another 5,000 surveys. Also, HBCAC utilized Huntington Hospital, town hall, local libraries, doctor offices and beauty parlors to distribute and collect additional surveys. Lastly, volunteers visited specific addresses to urge non-responders to fill out the survey in a "Neighbor-to-Neighbor Campaign." As a result, another 1,300 surveys were collected, bringing the gross total number of surveys up to 30,800.

Errors did occur in the data entry process. Upgrading the data from DOS to Windows proved particularly problematic. The date-of-birth field was lost on thousands of surveys and were re-entered. Again, volunteers spent countless hours making the necessary corrections. The database was also checked for duplicates, which were removed. A more careful verification of the survey was initiated by epidemiologist Erin O'Leary, PhD, and initially consisted of a random selection of 10% of the records, which were compared to the original hard copy of the surveys. When these analyses were complete, 23,777 surveys were deemed acceptable for analysis. The difference between the gross and final count was primarily due to duplicate surveys.

In the fall of 2000, after seven years of work, the survey was completed. HBCAC asked Dr. Erin O'Leary (2001) to analyze the completed survey. Below are some highlights from her findings:

Breast Cancer Survey Findings	
Total number of respondents.	23,777 women
Total female population of Huntington, over age 25.	63,665 women
Survey response rate.	37%
Respondents diagnosed with breast cancer, over age 25.	1,218 women
Breast cancer prevalence rate.	5.1%
Average age of respondents.	51 years
Average age of respondents ever diagnosed with breast cancer.	61 years
Respondents' average number of years living at current residence.	17 years
Average years in residence of women over 25 with breast cancer.	23 years
Average age at breast cancer diagnosis.	53 years

Dr. O'Leary estimated that 37% of the town's female population, over age 25, responded to the survey. Among respondents, 5.1% indicated that they were previously diagnosed with breast cancer. Those respondents were, on average, 10 years older, and had lived at their current residence six years longer than the total survey population.

MAPPING BREAST CANCER IN HUNTINGTON

Breast cancer mapping in Huntington is still in an early phase of development. The mapping process is envisioned as a three-stage process. The first stage, geocoding, is now complete. The second stage of the analysis is to examine the data for possible cancer clusters. The third phase of the research is to correlate breast cancer patterns with known environmental hazards in the region. HBCAC has been collecting environmental data sets and done some very preliminary analysis with those datasets.

Stage One: Geocoding and Mapping Breast Cancer in Huntington

In the spring of 1999, HBCAC, with assistance from Long Island University, was awarded a Conservation Technology Support Grant (CTSP), which provided the organization with computer hardware and software resources to do its own breast cancer mapping. With the assistance of Greenman-Pedersen, Inc., the final surveys were geocoded with data provided by Geographic Data Technology Inc. (GDT) and ESRI's ArcView software. The ZIP+4 geocoded centroids, provided by GDT, enabled HBCAC to successfully geocode over 99% of the survey. Greenman Pedersen, Inc. printed these maps on a large format printer. In January 2001, HBCAC presented their preliminary maps from the completed survey. The maps are now on display in local libraries.

Huntington breast cancer cases were mapped in two ways. First, HBCAC overlaid respondents who ever had breast cancer (see Figure 2) onto respondents who never had breast cancer. Of the 23,777 respondents, 5% had breast cancer in their life. Second, we mapped the percent of respondents who ever had breast cancer at each ZIP+4 (see Figure 3). Many of these percentages were 100%, reflecting the fact that the only respondent from that ZIP+4 had been diagnosed with breast cancer. Those ZIP+4 with no breast cancer cases (0%) were not mapped, to focus upon positive cases.

Response rates (Number of respondents/female population over 25) and prevalence rates (Have breast cancer/total respondents) were mapped by ZIP Code to provide some basic statistics about the distribution of cases (see Figures 4 and 5). Response rates were high in Huntington (11,743) at 51% and Centerport (11,721) at 52%, exceeding the 50% response goal originally set by HBCAC. These were the only two ZIP Codes to meet the original goal. Response rates were

Figure 2: Survey results per ZIP+4

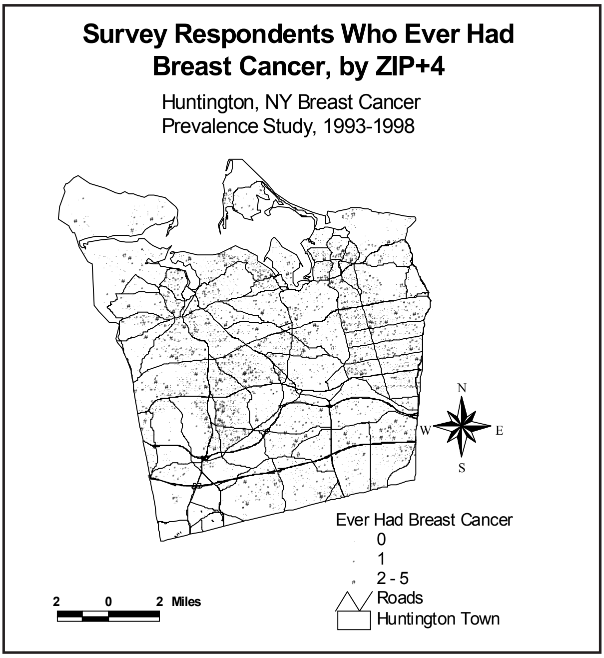


Figure 3: Percent breast cancer cases per ZIP+4

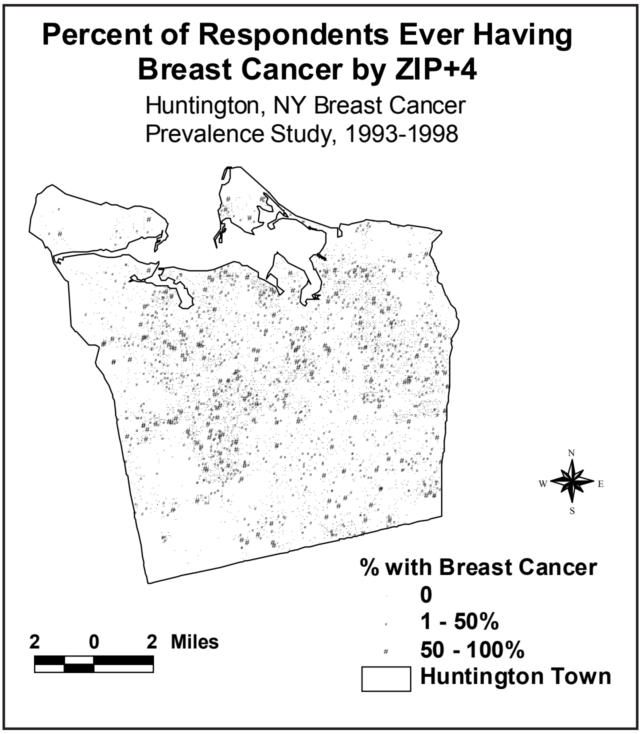
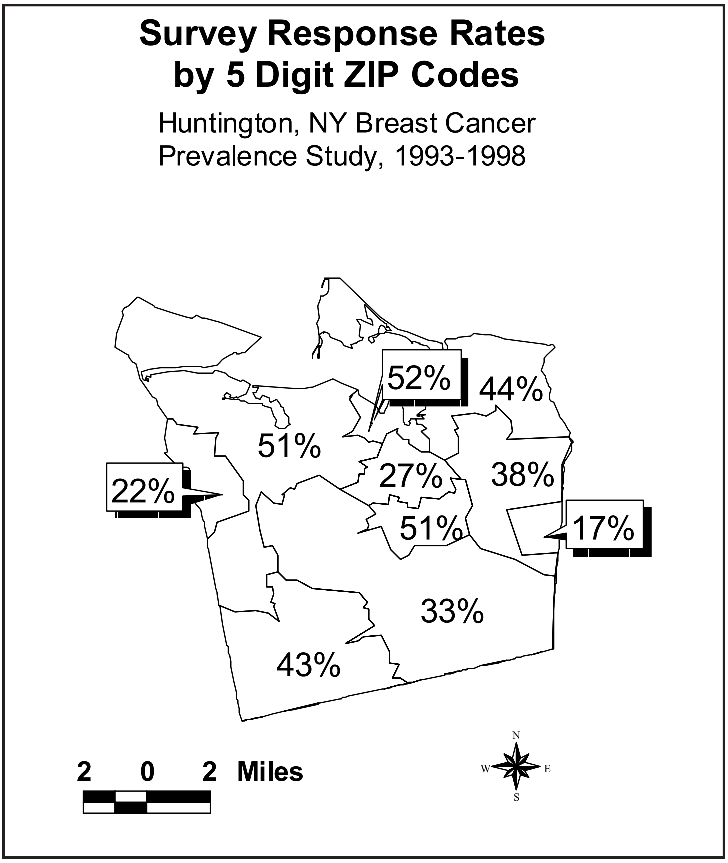


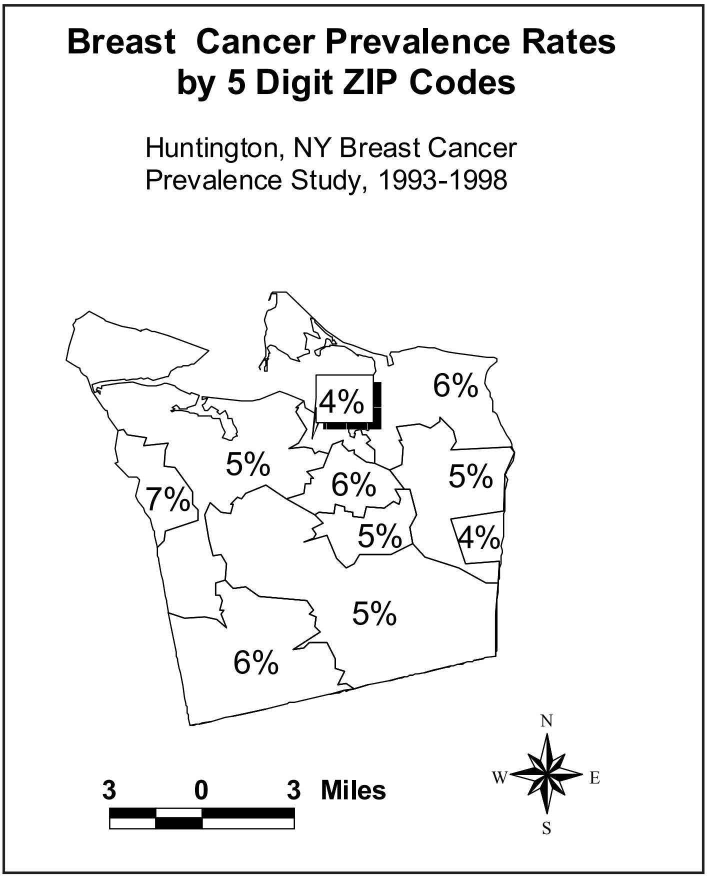
Figure 4: Survey response rates by ZIP Code



surprisingly low in Commack (11,725) at 17%, Cold Spring Harbor (11,724) at 22% and Greenlawn (11,740) at 27%. Prevalence rates were highest in Cold Spring Harbor at 7%, but this may simply be a product of the low response rate in that community.

These basic maps are powerful tools for increasing breast cancer awareness. The maps were first showcased at a community forum in January 2001. The maps will continue to be displayed at local libraries throughout the year. So far, the public's response to these exhibits has been very strong. Local residents are able to carefully examine the maps and reflect upon the information they convey. Many residents find the maps to be shocking; hundreds of color dots on the maps starkly illustrate the prevalence of this disease within their community. This illustrates the educational power that community maps can have. The community has been very

Figure 5: Breast cancer prevalence rates by ZIP Code



appreciative of the ZIP+4 level of detail in these maps, a level of detail that government agencies cannot provide.

In response to the grassroots interest in cancer maps, New York State's Department of Health released county-level breast cancer maps for the state in 1999. Local breast cancer organizations complained that those maps were hardly sufficient for their needs. The next year, the Department's New York State Cancer Surveillance Improvement Initiative (2000) released ZIP Code level maps. Many grassroots organizations, however, were disappointed with these maps as well. These organizations argued that both the county and ZIP Code maps lacked sufficient detail to identify specific cancer clusters.

State officials countered that they could not provide more detailed mapping information without compromising patients' confidentiality. For example, the

Department of Health has stated, "In order to protect patient confidentiality, as is required by state law, some ZIP Codes (those with very few total cancer cases) were combined with a neighboring ZIP Code before being mapped" (New York State Department of Health, 2000). Some local activists were concerned about the use of these averaging techniques. The more data that is averaged together, the less the public can learn about small-area clusters. Also, the choropleth shading techniques used by New York State dulls the sense of crisis felt by grassroots health advocates. On the state's maps there are only a few areas where rates are significantly higher than "expected," and most communities on Long Island are not significantly above the "expected" rates. These expected rates are calculated against state wide averages. Yet, breast cancer rates in New York State, like other northeast states, are significantly higher than national averages. In looking for elevated rates, should Long Island be compared with state rates or national rates? A number of breast cancer activists wanted the state to compare local rates to both rates.

The dot density maps used by HBCAC present a very different picture of breast health in Huntington. Breast cancer rates in most of Huntington's communities are within 15% of the expected rates, according to New York State's maps (New York State Cancer Surveillance Improvement Initiative, 2000). But HBCAC's dot density maps provide a vivid picture that a serious problem exists, a problem that did not exist 40 or 50 years ago. Again, community maps allow us to look at problems from perspectives that government agencies (and private corporations) are reluctant or unable to share.

Stage Two: Cancer Cluster Analysis

In recent years much attention and controversy has emerged around the issue of cancer clusters. Scientific experts are reluctant to label neighborhoods with high incidence of disease a "cluster" when they don't understand the causes of these high rates. In addition to lacking a well-established disease agent, many perceived clusters do not meet standard statistical thresholds for being significantly different from background cancer rates. Cancers are never going to be uniformly distributed across a geographic region. Some clustering is inevitable and can be explained away as due purely to chance. Like marbles dropped from a bag, some cancers "land" closer to other cases. Local residents generally do not like these explanations because many communities live near potentially hazardous land uses. Many residents feel that such explanations are too dismissive of their health fears.

HBCAC, therefore, found itself in a unique position. HBCAC wanted to work with the same tools that scientists were using to investigate their datasets. By undertaking their own analyses, HBCAC did not have to depend upon government agencies for this research and did not need to worry that results were not being honestly provided back to the community. But, HBCAC also learned it had a responsibility to understand and to utilize scientific methodologies if they wanted others to take their results seriously.

New York State's Department of Health, in addition to comparing breast cancer rates in individual ZIP Codes to statewide averages, tested these rates for statistical significance using the SaTScan software. Using probability statistics, SaTScan creates "an infinite number of distinct geographical circles, with different sets of neighboring census areas within them" (Kulldorf, 1998) to identify circular clusters with the highest statistical significance in the dataset. In 2002, HBCAC hopes to complete its own analysis of local breast cancer clusters using this same software. In addition, HBCAC is examining Dr. Gerard Rushton's (1997) spatial filtering software.

Of the 1,250 cases of breast cancer in HBCAC's database (this total includes some cases outside of Huntington), about half of the women had lived in their current homes for 15 or more years prior to their breast cancer diagnosis. If the residency is reduced to 10 years, then the total number of cases rises by 153 to 784 cases. Either way, a significant number of the known breast cancer cases in the dataset cannot be used for cluster analysis because of the need to account for a minimum of 10 years of residency to relate environmental contaminants to spatial patterns of breast cancer. Even this is inadequate, because household exposure may not be the most relevant pathway for understanding these spatial distributions. Nevertheless, this is the best that we can do with the existing survey data. The cluster research will also account for the fact that cancer cases in the town were diagnosed at different time periods. Therefore, it may be useful to control for the timing of diagnosis in looking for cancer clusters in the community.

Stage Three: Mapping Environmental Contaminants

HBCAC, like many other breast health coalitions, has focused a significant amount of resources on trying to reduce the public's exposure to hazardous chemicals. For example, HBCAC distributes "I am fed naturally" signs for local lawns to encourage homeowners not to use potentially harmful pesticides on their lawns. One of the major goals of the mapping project is to raise public awareness about the widespread usage of chemicals in the Huntington community and reduce the public's exposure to harmful chemicals.

A major part of HBCAC's mapping project is to identify toxic sites in Huntington and to map those sites in relation to the breast cancer survey data. HBCAC has been collecting data on a wide range of land uses and toxic emitters for its GIS project. HBCAC now has GIS coverages for: dry cleaning establishments, gas stations, landfills and dumps, golf courses, land use in 1980, land use in 1994, current and archived U.S. E.P.A. Superfund sites and toxic release inventory sites. HBCAC would also like to map the region's water supply distribution system and continues to work with local water supply providers to gain that information.

As part of HBCAC's public presentation last January, we examined sites listed on EPA's online Superfund list, which includes both current Superfund sites and sites that were removed from further consideration for Superfund status. (Most of the Huntington sites on this list are not superfund sites.) We found that women who lived closer to these sites did not have a higher risk of getting breast cancer.

While HBCAC plans to analyze these environmental datasets in more detail, some health organizations are beginning to recognize that industrial sources of contamination, while significant, may not explain the widespread distribution of cancers, like breast cancer. Lifestyle factors may play a larger role in breast cancer than industrial contamination. These lifestyle factors probably stem from multiple sources and could include low levels of contaminants in drinking and bathing water, dairy and meat products, pesticides, health care products, medical radiation, plastics, fossil fuel combustion, etc. While the research is still unclear on exactly which of these products is causing breast cancer, researchers have begun focusing on man-made chemicals that mimic bodily hormones like estrogen to explain rising breast cancer rates. Many of the above substances have these properties.

While HBCAC does not have survey data to understand these subtle lifestyle effects for individuals, we can begin to look at the more concentrated industrial pollution sites.

CONCLUSIONS

When I first began working with HBCAC on its survey, it wasn't clear to me where this project would go. I was skeptical that a grassroots-mapping project could succeed where so many scientists had failed. How could HBCAC help to define the causes of breast cancer or identify new cancer clusters? But HBCAC's mapping project is much broader in focus than those goals.

HBCAC's maps were recently center stage at a Congressional hearing held in Garden City, Long Island. Senators Clinton (NY), Reid (NV) and Chafee (RI), and the Long Island legislative delegation asked a selected panel of scientists and health advocates to discuss "Environmental Contamination and Chronic Diseases" (107th Congress, 2001). HBCAC's President, Karen Miller, was one of those panelists, and three of HBCAC's maps were placed on the stage alongside the elected officials. The maps were filmed by a variety of news outlets covering the event. At that event, Karen Miller asked the elected officials to look at the maps and to understand that each survey respondent, whether they had breast cancer or not, represented a woman who wants better answers and is confident that detailed maps, like HBCAC's, can be developed without compromising her privacy.

The mapping project has already influenced the government's view on health maps. Pressure on New York State from organizations like HBCAC played a role in pushing the state to develop cancer maps for the state and contributed to the state's decision to release ZIP Code-level maps. But New York State must do more. While the government should continue to protect patients' privacy, it's also true that GIS tools can be used to produce maps at a finer spatial scale than ZIP Codes without compromising privacy rights. HBCAC's maps are a powerful reminder of how much momentum exists at the grassroots level for stronger governmental responses to this issue.

While we are just beginning the process of understanding the analytical value of mapping breast cancer in Huntington, the maps have had a powerful effect on local awareness of breast cancer. Hopefully more women and government officials will pay closer attention to breast health issues. By mapping cancer and local sources of contamination, hopefully these maps can also play a role in reducing the toxic burden on our bodies.

HBCAC's mapping project and other initiatives are pushing the organization to expand in new directions. HBCAC recently launched a new campaign "Prevention is the Cure," along with a new web page (http://www.preventionisthecure.org) to promote the precautionary principle. HBCAC is packaging its breast cancer maps and other local campaigns into an innovative toolkit to teach local residents and businesses how they can begin to practice the precautionary principle in their own lives.

In conclusion, community-mapping efforts offer communities a powerful tool for thinking about localities. Maps do indeed influence public perceptions about place, and GIS tools give community organizations greater control over influencing those perceptions of place. Taking control of breast cancer mapping in Huntington has freed the community to ask questions about their community that government officials frequently ignored. The process has also empowered HBCAC to demand more of government. To reluctant officials, HBCAC members have frequently said, "If we can create these maps, then so can you." Specific policy changes have also been made. For example, New York State passed a neighbor notification law for pesticide spraying, which breast cancer groups actively supported. Many more changes, however, still need to be made. The Common Ground Community Mapping Project believes that "community mapping is a way for local citizens to reinhabit their home place" (Common Ground, 2001b). This is precisely the message that HBCAC is trying to create through its maps. For HBCAC, GIS is an important tool for making communities healthier places to inhabit.

ACKNOWLEDGMENTS

I want to thank HBCAC President Karen Miller, HBCAC Survey Director Mimi Galgano and David Mikolaitis of Greenman-Pedersen, who helped prepared several of the maps shown here; Dr. Erin O'Leary of the Silent Spring Institute; John Meglino; Barbara Kearney; and Rocksroy Bailey. A Conservation Technology Support Program Grant, administered by ESRI, Inc. and Hewlett Packard, Inc., also assisted this work.

REFERENCES

American Cancer Society. (2001). *Breast Cancer Facts and Figures 2001-2002.* Atlanta, GA. [On-line]. Available: http://www.cancer.org/downloads/STT/BrCaFF2001.pdf.

Associated Press. (2001). Report: Cancer rates on decline. *Newsday,* June 6, A23.

Breast Cancer Action. (2001). *The Facts and Nothing but the Facts.* [On-line]. Available: http://www.bcaction.org/Pages/GetInformed/Facts.html.

Carson, R. (1962). *Silent Spring.* New York: Fawcett Crest.

Colborn, T., Dumanoski, D. and Myers, J.P. (1997). *Our Stolen Future.* New York: Plume Books.

Common Ground. (2001a). *Why Mapping?* [On-line]. Available: http://www3.telus.net/cground/mapping.html.

Common Ground (2001b). *What is Community Mapping?* [On-line]. Available: http://www3.telus.net/cground/aboutus.html.

Galgano, M. (2001). *Huntington Activists Conduct Large Community Breast Health Survey.* Huntington Breast Cancer Action Coalition. Unpublished Manuscript.

Kulldorff, M. (1998). *SaTScan-Spatial and Space-Time Scan Statistics.* [On-line]. Available: http://www.nci.nih.gov/prevention/bb/satscan.html.

New York State Cancer Surveillance Improvement Initiative. (2000). [On-line]. Available: http://www.health.state.ny.us/nysdoh/cancer/csii/nyscsii.htm.

New York State Department of Health. (2000). First-in-the-Nation Small Area Breast Cancer Maps Issued; ZIP Code-Level Maps also Detail "Areas of Elevated Incidence." [On-line]. Available: http://www.health.state.ny.us/nysdoh/commish/2000/mapissued.htm.

O'Leary, E. (2001). *Breast Cancer Prevalence Study, 1993-1998: Synopsis of Results.* [On-line]. Available: http://www.hbcac.org.

107th Congress. (2001, June 11). *Environmental Contamination and Chronic*

Diseases. [On-line]. Available: http://www.senate.gov/~epw/stm1_107.htm#06-11-01.

Rushton, G. (1998). *Improving Public Health Through Geographical Information Systems.* [On-line]. Available: http://www.uiowa.edu/~geog/health/index.html.

Steingraber, S. (1997) *Living Downstream: An Ecologist Looks at Cancer and the Environment.* Massachuetts: Addison Wesley.

West Islip Breast Cancer Coalition for Long Island, Inc. Mission/History. [On-line]. Available: http://www.wibcc.org/mission.htm

Wingspread. (1998). Wingspread statement on the precautionary principle. Reprinted in *Rachel's Environment & Health Weekly #586*. [On-line]. Available: http://www.monitor.net/rachel/r586.html.

Chapter VII

Application of a GIS-Based Statistical Method to Assess Spatio-Temporal Changes in Breast Cancer Clustering in the Northeastern United States

Daikwon Han and Peter A. Rogerson
University at Buffalo, USA

This chapter examines spatio-temporal changes in breast cancer clustering in the Northeastern United States to assess the statistical significance of clusters using GIS-based kernel methods. It first describes higher-than-average breast cancer mortality rates in the Northeast and introduces statistical methods for detecting geographic clusters of disease. A GIS-based kernel method based upon the theory of Gaussian random fields is applied to the breast cancer mortality data taken from the National Center for Health Statistics' Compressed Mortality File. The method makes use of a map of rates, smoothed using a Gaussian kernel. The maximum smoothed value is compared with the statistic's critical value to identify significant clusters.

Results from the analyses show changes in spatio-temporal clustering patterns in the Northeast during the period 1968-1998. The results reveal not only the existence of statistically significant breast cancer clusters, but also the changing patterns of those clusters over time. Since environmental risk factors may play an important role in explaining the unknown etiology of breast cancer, analyses of spatio-temporal changes of breast cancer clustering may provide important clues to the study of breast cancer and environment relationships.

INTRODUCTION

Breast cancer is the most commonly occurring cancer among women in the United States. It is estimated that one out of every nine women in the United States will develop breast cancer. To explain the causes of breast cancer, epidemiologic investigations have used known risk factors, including demographic and socioeconomic factors, family history factors, and hormonal and reproductive factors, but many other factors remain unknown. Being age 45 or higher for white women, high socioeconomic status, having never married, urban residence, and residence in the Northeastern United States are all considered to be important risk factors (Kelsey and Horn-Ross, 1993; Madigan et al., 1995).

Previous studies of the geographical patterns of breast cancer have found that mortality from breast cancer is highest in the Northeast (Blot et al., 1977; Sturgeon et al., 1995; Kulldorff et al., 1997). Blot et al. (1977) concluded that the location of residence plays an important role in explaining geographic variations in breast cancer risks, especially for post-menopausal women. Sturgeon et al. (1995) evaluated geographic differences in breast cancer mortality rates to explain excess mortality in the Northeast and Midwest relative to the South. The higher rates in the Northeast are in part explained by the regional distribution of risk factors and related lifestyle differences, including late age at first birth, late menopause, early menarche and mammography history. A recent study using a spatial scan statistic found the New York City-Philadelphia Metropolitan area as the most statistically significant cluster (Kulldorff et al., 1997). The study also identified several sub-clusters within the Northeast, including Buffalo, the District of Columbia, Boston and eastern Maine, all with higher-than-average mortality rates.

The purpose of this chapter is to investigate spatio-temporal changes in breast cancer clustering in the Northeastern United States, and to assess statistical significance using GIS-based kernel methods. A newly developed GIS-based kernel method based upon the theory of Gaussian random fields (Rogerson, 2001a) is applied to breast cancer mortality data. The method makes use of a map of rates, smoothed using a Gaussian kernel. The maximum smoothed value is then compared with the statistic's critical value.

In the next section, we begin by reviewing statistical methods for detecting geographic clusters of disease and by discussing uses of kernel-based smoothing in cluster detection. The third section briefly describes the data sets on breast cancer mortality, the study area and the major steps in the analysis. The fourth section introduces the statistical method used in the study, and includes a discussion of the local statistic that is based on the kernel method. The section also provides an appropriate critical value for the maximum local statistic. The fifth section presents results from the analyses of breast cancer mortality, changes in spatio-temporal clustering patterns in the Northeast and the retrospective detection of changes. The final section provides a summary and discussion.

METHODS TO DETECT GEOGRAPHIC CLUSTERS OF DISEASE

Geographers and epidemiologists have long worked to identify spatial patterns and geographic variation in disease data. Many studies concentrate on disease clustering, cluster identification, association with point sources of pollution and space-time disease incidence (see, e.g., Lawson et al., 1999; Elliott et al., 2000). A common question of these studies is: "Is there a disease cluster in an area, and is it significant?" If there is a significant cluster, the next question is: "What are the causes of that particular disease cluster?" Once areas with raised incidence of a particular disease are identified, one may want to pursue the causes of that particular disease cluster by epidemiologic investigations.

Classification of the statistical methods to detect clusters depends upon several factors, including the purpose of the investigation and the methods used (exploratory or confirmatory), the dimension (space or time) and data types (individual or aggregate). Tests are commonly classified as global or local tests, corresponding to tests that focus on the entire area and tests that are confined to particular locations, respectively.

Methods for identifying geographic locations of clusters are often based on scanning methods; such approaches scan a map with windows of varying size, and identify areas of elevated incidence. One of the earliest scanning methods was Openshaw et al. 's (1987) Geographical Analysis Machine (GAM), which is composed of a hypothesis generation and significance testing component, and a GIS component to handle data and display outputs. Besag and Newell (1991) propose a variation on the GAM that searches for clusters only around disease cases. Despite its simplicity, GAM has been criticized for several reasons, even as an exploratory tool (Besag and Newell, 1991). The primary questions concern statistical significance, and modified methods based on the original GAM approach have been suggested (Fotheringham and Zhan, 1996).

Similar methods include the spatial scan statistic (Kulldorff and Nagarwalla, 1995) and the spatial filtering method (Rushton and Lolonis, 1996). The spatial scan statistic considers circles of different sizes at different locations, and considers the likelihood of observing the actual number of cases inside of the circle, under the null hypothesis of no clustering. The likelihood associated with the maximally likely cluster is compared with a critical value established from the $1-\alpha$ percentage point of a ranked list of maximum likelihoods, each associated with a simulation of the null hypothesis. The spatial scan statistic also adjusts for inhomogeneous population density and any confounding variables. The spatial filtering method proposed by Rushton and Lolonis (1996) uses a regular lattice grid and spatial filter areas to assess spatial variation in birth defect rates. They use a grid with cells 0.5 mile apart and a 0.4 mile search radius. The method produces maps showing contours of equal statistical significance associated with the test of the null hypothesis of no spatial pattern. All of these methods use circles and search for clusters across all areas of the study region, so that pre-selection bias can be removed.

Two commonly used methods for mapping spatial variations in disease are maps of relative risk and maps of statistical significance. The former approach is a popular choice and has the advantage of easy interpretation. Maps of the standardized mortality ratio (SMR) fall in this class. However, such maps tend to display the most extreme values in areas of small population. The latter approach, including maps of Poisson probabilities, has the problem of potentially extreme significant levels in areas of large population, due to sample size effects. Alternatively, empirical Bayes estimates or smoothing methods have been suggested as a compromise, and are often used as an alternative approach (Clayton and Kaldor, 1987; Bailey and Gatrell, 1995). Smoothing methods were designed to filter out variability in a data set based on functions of the data in surrounding areas, and kernel-based smoothing methods have received much attention in recent years by investigators.

The GIS-based statistical method used here not only detects the location and size of geographic clusters, but also assesses the statistical significance of clustering. The local statistics are derived based upon smoothed, local kernel estimates which are weighted sums of the observed disease rates in surrounding areas. The maximum local statistic is compared to a fixed critical value. In addition, the approach does not require an additional adjustment for multiple testing, and does not require repetitive simulations or extensive computations since the critical value is derived analytically.

Figure 1: Counties of the Northeastern U.S. as a Study Region Showing the Locations of Major Cities and County Boundaries

DATA AND STUDY AREA

The study area is composed of 217 counties in nine states in the Northeastern United States. A map showing the locations of the 217 counties is given in Figure 1.

Breast cancer mortality data is taken from the National Center for Health Statistics' Compressed Mortality File (CMF). Data on the CMF are based on the National Center for Health Statistics' mortality files that provide statistics on all deaths recorded in the United States. These data are available at the county level for individual years for the period 1968-98, grouped by age, sex, race and all causes of mortality. The data on deaths from breast cancer (International Classification of Diseases-9, code 174) were extracted for the 217 counties in the Northeastern U.S. and aggregated into five-year time periods.

We calculated the expected number of breast cancer deaths using the population estimates provided in the CMF. The population estimates are based on Bureau of the Census estimates of county resident population (National Center for Health Statistics, 2000). The expected number of breast cancer deaths in region i, λ_i, is calculated using the indirect standardization method, by multiplying national age-specific death rates (d_j) by the county population in each age group.

$$\lambda_i = \sum_j p_{ij} d_j$$

where p_{ij} denotes the population at risk in age group j in region i.

The observed and expected numbers of breast cancer deaths for each of the 217 counties in the Northeast were used as input to compute local statistics as described in the next section.

STATISTICAL METHOD

Transformation of the Data

The Freeman-Tukey (1950) transformation, $t = \sqrt{x} + \sqrt{x+1}$, is used to achieve a stable variance, where x is the number of breast cancer cases observed in a county. Though Freeman and Tukey do not give the mean, variance and skewness of the transformed variable, they can be approximated as follows;

$$\begin{aligned} &E[t] \approx \sqrt{4\lambda+1}; \quad V[t] \approx 1; \\ &\text{skewness} \approx (8\lambda+7)\sqrt{\lambda} - (3+4\lambda)\sqrt{4\lambda+1} \end{aligned} \tag{1}$$

where λ = E[x] is the expected number of cases.

The new variable may then be transformed to a standard normal distribution using,

$$y = t - \sqrt{4\lambda+1} = \sqrt{x} + \sqrt{x+1} - \sqrt{4\lambda-1} \tag{2}$$

There are two objectives in transforming the data—one is to achieve a more stable variance, so that regions with small numbers of cases are not inherently more

Table 1: Comparison of skewness associated with transformations

λ	Untransformed	Freeman-Tukey Eq. (1)	Simulation
0.7			.41
1	1	-.65	.07
2	.71	-.47	-.38
3	.58	-.39	-.45
4	.50	-.34	-.40
6	.41	-.28	-.25
10	.32	-.22	-.17
20	.22	.15	-.12

variable than those with large numbers of cases. The other objective is to transform the data to normality to approximate a Gaussian random field.

As the expected number of cases increases from very small values (much less than 1), the Freeman-Tukey transformation stabilizes the variance much more quickly than alternatives, such as Anscombe's (1948) square-root transformation, $t = \sqrt{x + 3/8}$. It is also the case that the Freeman-Tukey transformation leads to a variable that is approximately normally distributed. Table 1 shows that the skewness of the transformed variable is markedly less than the original, untransformed Poisson variable. Simulations were used to evaluate skewness; 10,000 repetitions of Poisson distributed variables with parameter λ were transformed and assessed for skewness. While the original, untransformed data displays positive skewness, the transformed data generally has a slight negative skewness. The table also reveals that, despite its accuracy for higher values of λ, the expression for skewness in (1) is not a reliable guide to the skewness that will be observed for low values of λ (less than about 2). Finally, although the Freeman-Tukey transformation has a desirable empirical skewness of close to zero near λ=1, skewness in this range of λ is very sensitive to the value of λ.

Calculation of Local Statistics and Critical Value

A smoothed local statistic z_i for region i is computed based on the weights w_{ij} associated with a Gaussian kernel (Rogerson, 2001a);

$$z_i = \sum_j w_{ij} y_j$$

$$w_{ij} = (\sqrt{\pi}\sigma)^{-1} e^{-d_{ij}^2/2\sigma^2}$$

where y_j is the normally distributed, standardized variable of interest in region j previously defined, d_{ij} is the distance between the centroids of regions i and j, and σ is the bandwidth (standard deviation) of the Gaussian kernel. It is convenient to scale the weights so that σ may now be interpreted as a multiple of the average length of a spatial unit;

$$w_{ij} = \frac{1}{\sqrt{\pi}\sigma} \exp\{\frac{-d_{ij}^{\ 2}}{2\sigma^2 (A/n)}\}$$

where A is the total area of the study region and n is the number of counties. Hence a choice of σ =1 would imply a kernel width equal to the average distance to an adjacent region.

To help correct for edge effects and irregularly shaped regions, the weights are redefined by dividing the original weights by the square root of the sum of squared original weights.

$$\tilde{z}_i = \frac{\sum_j w_{ij} y_j}{\sqrt{\sum_j w_{ij}^2}} = \sum \tilde{w}_{ij}\, y_j, \tag{3}$$

where the redefined weights are,

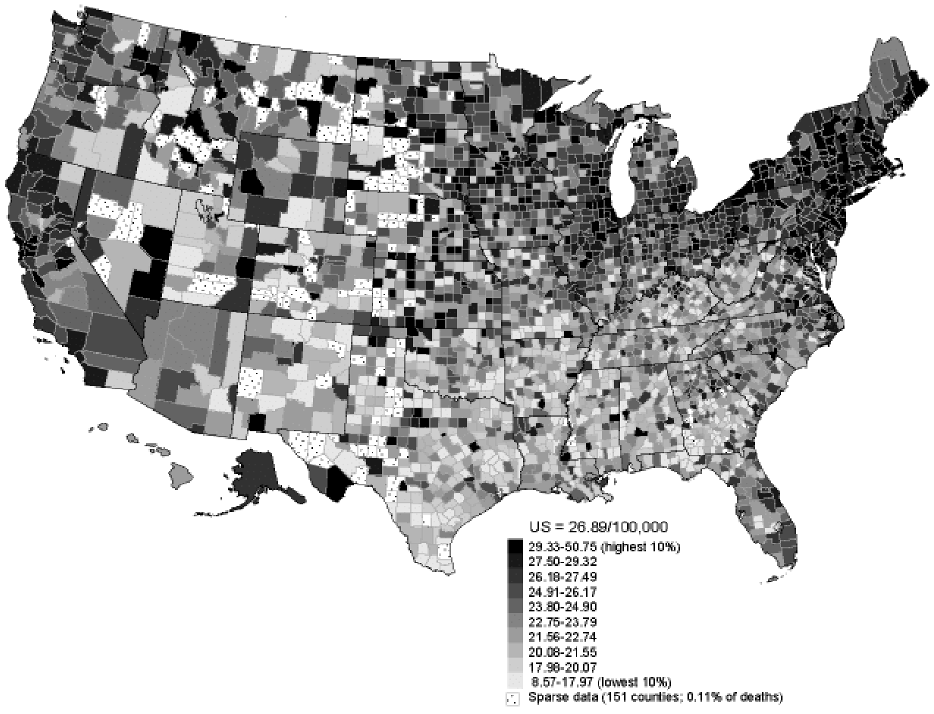
$$\tilde{w}_{ij} = \frac{w_{ij}}{\sqrt{\sum_j w_{ij}^2}}$$

This ensures that the local statistic has mean zero and variance one (see Rogerson, 2001a). Finally, the maximum local statistic, $M = max\ \tilde{z}_i$ is compared with the following critical value:

$$M^* = \sqrt{-\sqrt{\pi}\ \ln(\frac{4\alpha(1+.81\sigma^2)}{n})} \tag{4}$$

The method offers flexibility to control the levels of smoothing through the choice of σ . When cluster size is unknown, different values of σ may be used in an exploratory manner. To illustrate, we produced a map of local statistics, $\tilde{z}_i$, and then used interpolation to produce a continuous surface. After transforming the observed and expected numbers of breast cancer cases to the standardized scores using Equation (2), the local statistics were found using Equation (3). The *x* and *y* coordinates serving as county centroids are given as eastings and northings. They indicate the relative location of each spatial unit from a hypothetical point that is located in the southwestern corner. All distances are given in miles. For the calculation of the scaled weights, the area of an average region is 775.7 square miles, which is the result of dividing the total area (*A*=168,330.3 square miles) by the number of counties (*n*=217). The maximum local statistic was then compared with the critical value, *M**, computed using Equation (4). We used a one-sided test, with α =0.05.

Figure 2: Age-adjusted breast cancer mortality rates by county, white females, 1970-74 (Source: Devesa et al., 1999a)



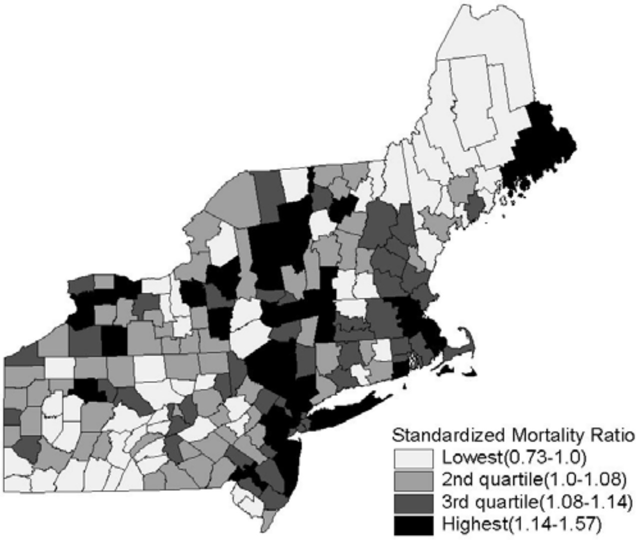
RESULTS

Breast Cancer Clustering in the Northeast

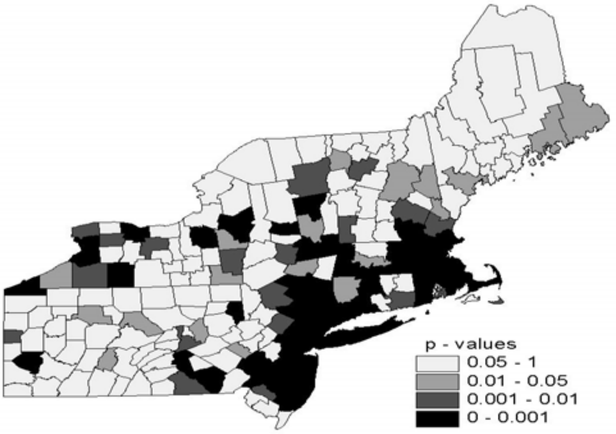
Figure 2, from the *Atlas of Cancer Mortality*, shows age-adjusted breast cancer mortality rates for white females in the US for the period 1970 to 1994. Compared with the average U.S. age-adjusted rate of 26.89 per 100,000, the highest breast cancer mortality rates tend to be in the Northeast and in the northern part of the Midwest. Geographic patterns clearly show that the excess rates in the Northeast have persisted during the time period, although this dominance has diminished over time, compared with the earlier 1950-1969 period (Devesa et al., 1999a).

From the compressed mortality datasets, we identified 306,953 deaths from breast cancer in the Northeast, implying an annual average age-adjusted death rate of 31.87 per 100,000 females during the time period of 1968 to 1998. The average standard mortality ratio in the Northeast relative to the U.S. for the entire time period is 1.13. Figure 3a is a map of the standardized mortality ratio using Equation (5), while Figure 3b shows a map of the *p*-values resulting from individual Poisson tests of randomness in each county using Equation (6).

Figure 3: Spatial variation of breast cancer mortality:
(a) Standardized mortality ratio, 1968-98



*(b) Probability map (*p*-values), 1968-98*



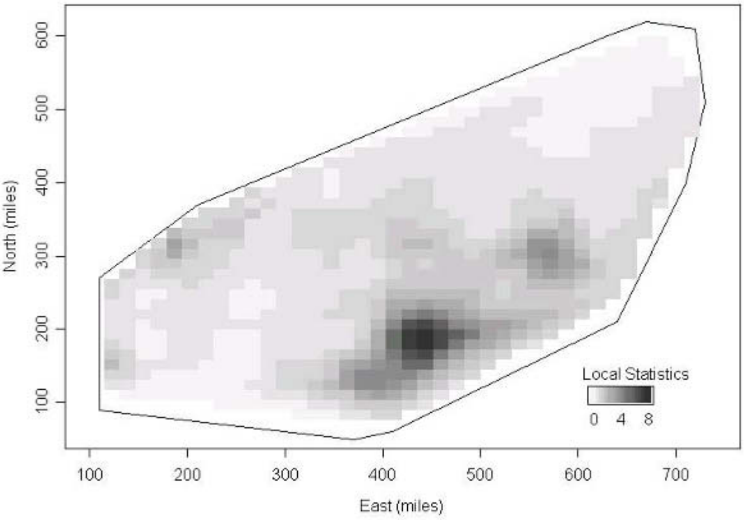
$$SMR_i = \frac{x_i}{\lambda_i} \tag{5}$$

$$p(x_i) = p(X_i \geq x_i) = \sum_{X_i = x_i}^{\infty} \frac{e^{-\lambda_i} \lambda_i^{X_i}}{X_i!} \tag{6}$$

where the SMR in region i is the ratio of the observed number of deaths in region i, x_i, to the age-standardized expected number of deaths, λ_i, and the Poisson probability $p(x_i)$ represents the upper tail of the Poisson distribution with parameter λ_i.

The highest quartiles in Figure 3a are the areas showing a number of deaths from breast cancer that is more than 14% above expected. Figure 3b shows that many counties in the Northeast have an observed number of cases that is statistically significant relative to expectations, especially the darkest areas around New York and Boston. However, interpretation should proceed with caution. The measure of relative risk is likely to have extreme values in areas with small populations. The maps of p-values can also potentially be misleading because regions with large numbers of observed and expected cases are more likely to appear as significant on a map of p-values. This can result from small departures from the underlying assumption of a Poisson model (see, e.g., Cressie, 1993).

Figure 4: Spatial distribution of local statistics in the Northeastern U.S., 1968-1998.
(a) Smoothed map of local statistics based on county centroids



(b) Corresponding choropleth map of local statistics

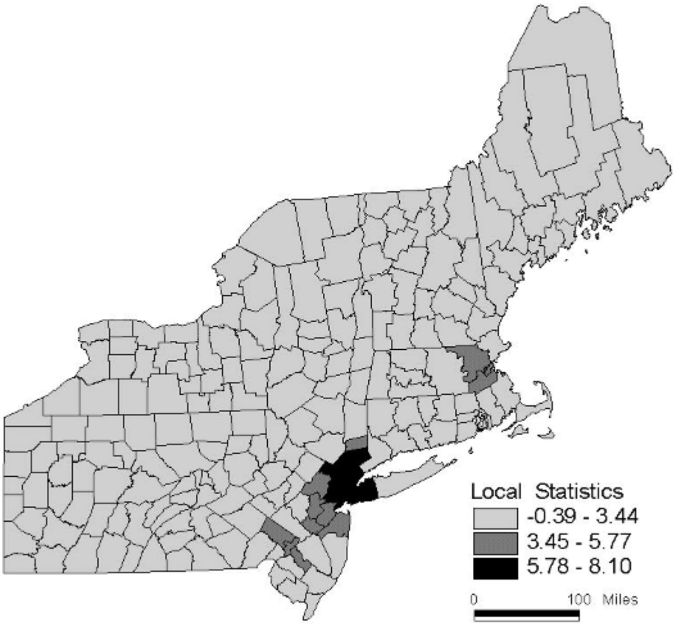


Figure 5: Breast cancer clusters identified using maximum local statistics in the Northeastern U.S., 1968-1998

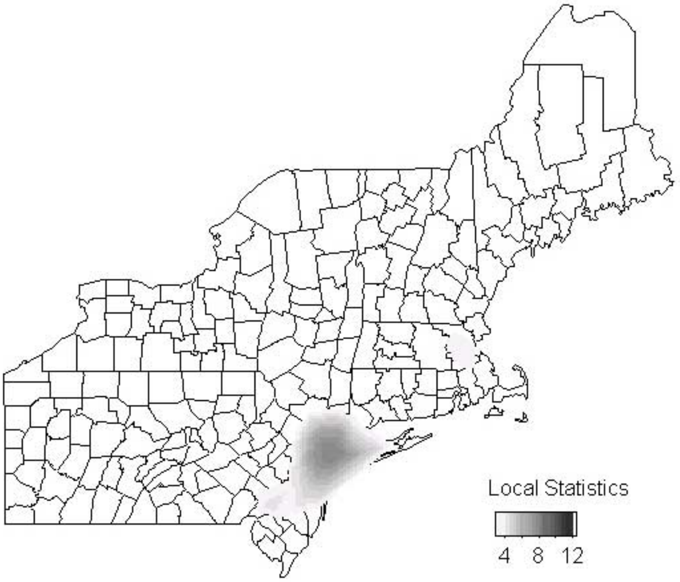


Figure 4 shows the spatial distribution of local statistics for the period 1968 to 1998 in the Northeastern US. Panel (a) is a smoothed map of local statistics calculated at county centroids, and panel (b) is a county-level choropleth map depicting the local statistics. Areas with local statistics greater than 3.45 can be classified as statistically significant clusters. Figure 5 shows the geographic location of two clusters in the study area, exceeding the critical value of 3.45 when σ is 0.6. The maximum local statistic was 8.10, and was obtained in the center of the New York-New Jersey-Philadelphia cluster. The cluster contains 129,778 observed cases and 109,958 expected cases, yielding a relative risk of 1.18. A secondary cluster is identified around Boston. The maximum local statistic for this cluster is 3.95. There are 16,848 cases observed and 14,381 expected in this cluster, with a relative risk of 1.17. The S-Plus program used in the calculation is attached as an appendix.

Because the clusters in Figure 5 are quite close to the border of the study region, we also explored edge correction in the following way. A square grid containing lattice points at intervals equal to 28 miles (which is, approximately, the median distance between county centroids) was overlaid onto the study area. These lattice points were used to assign 14 additional, hypothetical county centroids to the outskirts of the New York-New Jersey-Philadelphia cluster, and six to the outskirts of the Boston area. These new centroids were then assigned values (y_i) randomly chosen from the standard normal distribution, consistent with the hypothesis of no clustering, and local statistics were recomputed. Any edge effects that might exist do not appear to be too severe, since accounting for edge effects leads to a map that is almost identical. Both clusters in New York-New Jersey-Philadelphia and in Boston are only slightly larger, after correcting for edge effects.

Finally, we compared our results with Kulldorff's spatial scan statistic. We performed 9,999 Monte Carlo replications with adjustment for age using the spatial scan statistic and identified the New York-New Jersey-Philadelphia area as a most likely cluster during 1968-1998, with a log-likelihood ratio that is significant at α= 0.01. More than 30 counties in the area are included in the cluster; this is a larger area than the one we identified. In particular, it includes all counties in our analysis plus an additional 13 counties. Although the Boston cluster we identified is not detected when using the spatial scan statistic, the statistic *did* identify the Buffalo area as a secondary cluster, with a significant p-value. Spatio-temporal changes will be further investigated in the next section.

Spatio-Temporal Analysis and Retrospective Detection of Changes

Figure 6 shows temporal trends in the observed and expected numbers of breast cancer deaths in the Northeast. The number of observed and expected

Figure 6: Trends in observed and expected deaths from breast cancer in the Northeastern U.S., 1968-1998

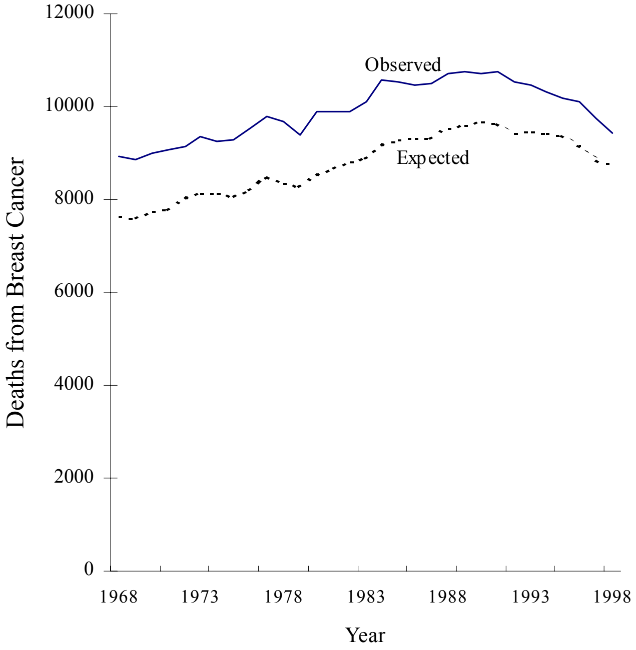


Table 2: Changes in female breast cancer mortality statistics in the Northeast, for three time periods

Periods	No. of Deaths	Age-adjusted Rate*	SMR*	Correlation between Periods	Moran's *I*
1968-1978	101,987	30.75	1.158		.339†
1979-1988	101,981	33.78	1.134	.330†	.274†
1989-1998	102,985	30.96	1.101	.306†	.203‡

* Age-adjusted rates are annual average and per 100,000 female population; SMR= Standardized Mortality Ratio.
† *p*<.01; ‡ *p*<.05, from 1,000 Monte Carlo simulations

deaths increases until the mid-1980s, and then declines during the 1990s. The same trend is apparent for age-adjusted rates (Table 2). However, the standardized mortality ratio displays a different temporal pattern, and has declined over the time period. To identify geographic variations of mortality in space and time, several measures are used to examine the structure of the data. Space-time persistence of the SMR is measured by the correlation coefficient, which shows moderate correlation of 0.33 and 0.306 in the comparison of two time periods (1968-78 to 1979-88 and 1979-88 to 1989-98). Spatial autocorrelation using Moran's *I* was found to be significant at the 99% confidence level. When broken down into 10-year intervals, this measure shows a decline in spatial autocorrelation over time.

Figure 7: Spatio-temporal changes in breast cancer clustering in the Northeastern U.S.

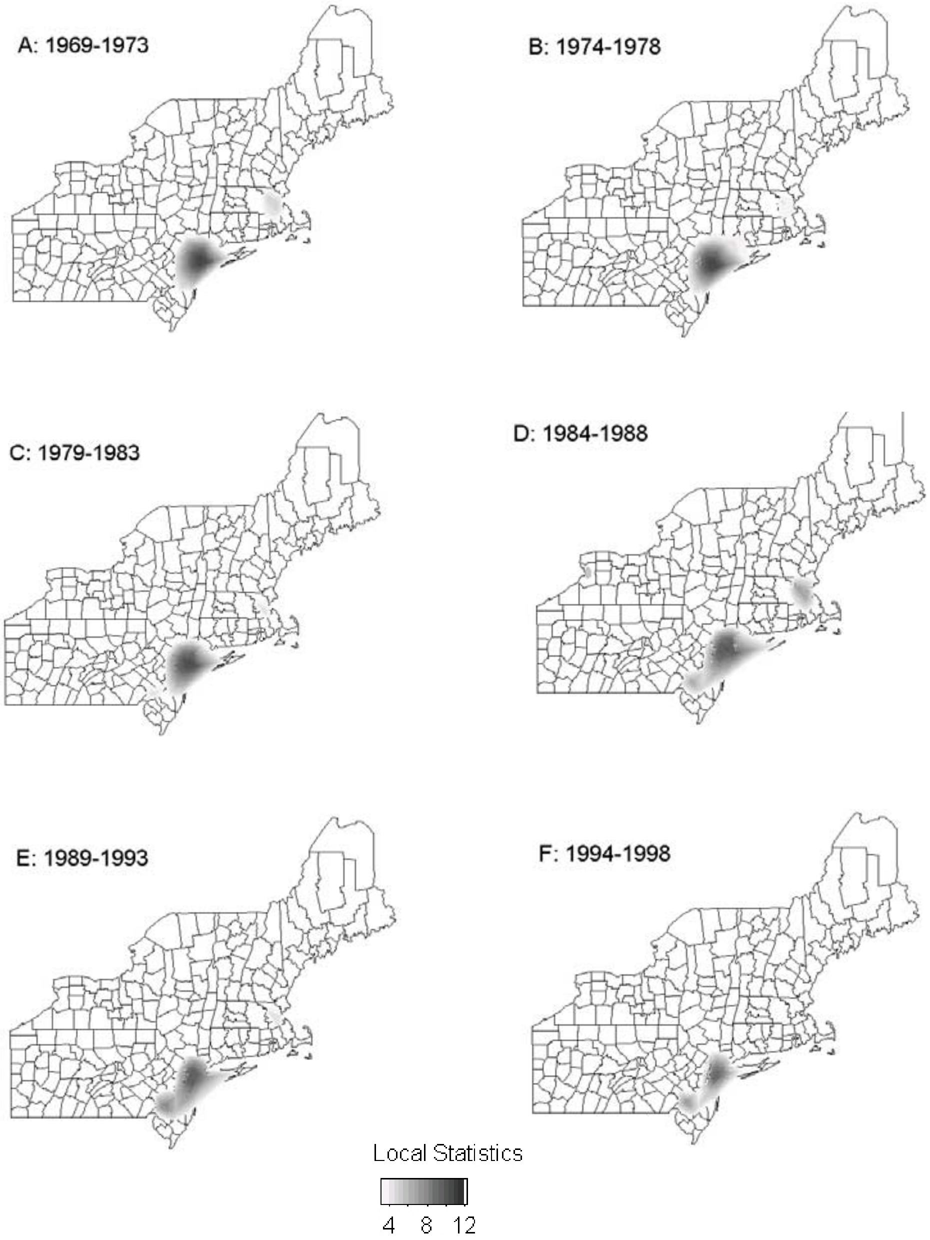


Figure 7 shows spatial-temporal changes in statistically significant clusters in the Northeast. The primary cluster is found in the New York-New Jersey-Philadelphia Metropolitan area. It is big in size and is the only cluster that persists over the entire time period. A secondary cluster is found in Boston and its surrounding area. The Boston cluster declined over time and disappeared for the period 1994 to 1998. A small cluster in the Buffalo area is detected during the period 1984-1989, with a local statistic of 3.83; the values of the average local statistic and relative risk in Buffalo for the entire period are 3.14 and 1.23, respectively. Table 3 shows detailed information for clusters with significant local statistics during the period 1968-1998. Geographic locations, clustering periods,

Table 3: Statistically significant breast cancer clusters identified using maximum local statistics in the Northeast

Geographic Locations		Clustering Periods	RR*	LS*	Counties
NY-NJ -PA	New York City Area	1968-1998	1.18	6.77	Bronx, Kings, Nassau, New York, Queens, Westchester, Rockland, Suffolk, Richmond
	Northern and Central New Jersey	1968-1998	1.18	5.51	Bergen, Burlington, Camden, Monmouth, Essex, Middlesex, Mercer, Hudson, Somerset, Union, Morris, Passaic
	Philadelphia and its surrounding area	1979-1998	1.17	3.85	Delaware, Montgomery, Philadelphia
Boston	Boston and its surrounding area	1968-1993	1.18	3.87	Suffolk, Norfolk, Middlesex
Buffalo	Buffalo	1984-1988	1.27	3.83	Erie

* RR: Relative Risk; LS: Local Statistic

Table 4: Spatio-temporal changes of relative risks and local statistics in the Northeastern breast cancer clusters

Clusters	1969-1973		1974-1978		1979-1983		1984-1988		1989-1993		1994-1998	
	LS	RR	LS	RR	LS	RR	LS	RR	LS	RR	LS	RR
New York City	8.92	1.23	8.47	1.23	7.14	1.18	6.04	1.18	5.39	1.15	4.65	1.13
New Jersey	6.51	1.23	6.06	1.18	5.64	1.19	5.16	1.17	5.32	1.17	4.34	1.13
Philadelphia	2.36	1.09	3.26	1.14	3.87	1.20	4.32	1.18	4.93	1.19	4.36	1.19
Boston	4.68	1.24	3.73	1.17	3.81	1.18	4.93	1.22	3.78	1.17	2.28	1.09
Buffalo	3.03	1.25	3.32	1.22	3.11	1.21	3.83	1.27	2.98	1.25	2.60	1.20

RR: Relative Risk; LS: Local Statistic

and corresponding counties in these clusters are identified and compared. Spatial-temporal changes in these three clusters are further broken down into five smaller clusters, and their changes in relative risk and local statistics over six time periods are summarized in Table 4.

It should be noted that the size of the clusters found by this and similar methods will depend upon the spatial definition of the study area, as well as the temporal aggregation of cases. For instance, it will generally be easier to find clusters if cases are aggregated over a long period of time than if only a single year of data is examined. One might find additional clusters in the Northeast if the study region were redefined to exclude the New York City area (which is characterized by relatively high rates). Similarly, searching over additional spatial scales could lead to clusters of different sizes.

Although the results from the cross-sectional spatio-temporal analysis show significant breast cancer clustering in the Northeast, here we are interested in the retrospective detection of significant changes in spatial patterns. For each year, multinomial probabilities (p_i) may be defined as the likelihoods that a given breast cancer death is located in county i. Of interest is a test of the null hypothesis that these multinomial probabilities do not vary over time. A test of this null hypothesis versus the alternative that there is a single change point dividing the sequence of multinomial observations into two distinct subsets ("before" and "after" the change point) has been suggested by Srivastava and Worsley (1986). They develop the following test for detecting change in a sequence of multinomial observations. Given a n by p+1 contingency table with ordered rows, we wish to test for a change in the row proportions after an unknown row, r. Let Q^2 be the usual Pearson χ^2 statistic for testing association between rows and columns in the full table. Let Q_r^2 be the Pearson χ^2 statistic for testing association between rows and columns in the 2 by p+1 table formed by aggregating the first 1,…,r rows and the remainder of the rows (r+1,…,n). The test statistic is $Q_{\hat{r}}^2 = \max_r Q_r^2$. Extramultinomial variation can be accommodated; such variation may arise in those situations where the multinomial trials are correlated or where the multinomial probabilities are themselves not known with certainty. The variance inflation factor, $\hat{\sigma}^2{}_r$, may be estimated as

$$\hat{\sigma}_r^2 = (Q^2 - Q_r^2)/\{(n-2)p\}.$$

The test statistic, adjusted for this extramultinomial variation, is $K_{\hat{r}}^2 = Q_{\hat{r}}^2 / \sigma_{\hat{r}}^2$, and the quantity $K_{\hat{r}}^2 / p$ has an F distribution with p and (n-2)p degrees of freedom.

Before computing the test statistic, the annual observed vectors of county deaths must be adjusted due to changes in expectations that occur as a result of

Table 5: Retrospective detection of changes, 1968-1998

Sequence	Change Point	K_r^2	F	p
1968-1998	1989	482.4	2.089	<.001
1968-1989	1976	354.0	1.64	<.001
1990-1998	1997	252.2	1.168	.059
1968-1976	1973	249.3	1.154	.075
1977-1989	1980	311.0	1.44	<.001
1977-1981	1976	239.3	1.11	.171
1982-1989	1986	286.7	1.33	.002
1982-1986	1985	217.9	1.01	.46
1987-1989	1987	298.3	1.38	.009

Homogeneous subsets: 1968-1976, 1977-1981, 1982-1986, 1987, 1988-1989, 1990-1998.

population and age structure changes. This is done by multiplying the observed number of county deaths in year *t* by the ratio of the proportion of all expected deaths (for the entire time period) that occur in county *i* to the proportion of all expected deaths that occur in county *i* during year *t*.

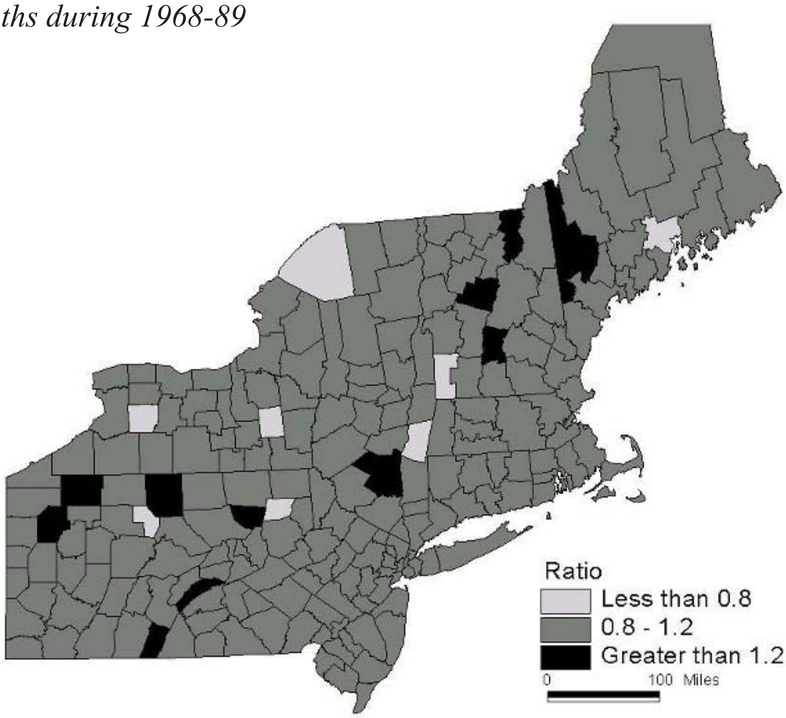
The results are shown in Table 5. The change point statistic is significant, and indicates a change in the spatial pattern of breast cancer following 1989. The data is then divided into two subsets—1968-1989 and 1990-1998. Further tests on these two subsets indicate that the former period may be further subdivided into two distinct subperiods—1968-1976 and 1977-1989. The latter period (1990-1998) does not contain any significant change points. The 1977-1989 period may be further subdivided into 1977-1981, 1982-1986, 1987, and 1988-1989.

It is of interest to ask which counties have contributed most significantly to the changes that have occurred. Table 6 depicts the number of deaths occurring in selected counties for the 1968-1989 and 1990-98 periods. The final column of the table gives the ratio of the county's fractional share of all deaths during 1990-98 to its fractional share of all deaths during 1968-89. Figure 8 shows the spatial distribution of counties, with ratios greater than 1.2, between 0.8 and 1.2, and less than 0.8, while Table 6 shows only those counties with ratios greater than 1.2 or less than 0.8. Counties with ratios less than 0.8 experienced a substantial decline in breast cancer deaths from 1968-1989 to 1990-1998, relative to the rest of the

Table 6: Ratio of county's share of deaths 1990-98 to 1968-89: Counties with Ratios greater than 1.2 or less than 0.8

County	Deaths 1968-89	Deaths 1990-98	Ratio of County's Share of Deaths 1990-98 to 1968-89
Bennington, VT	174	56	0.746
Waldo, ME	115	36	0.725
Columbia, NY	282	96	0.787
Cortland, NY	177	52	0.680
St. Lawrence, NY	411	134	0.758
Wyoming, NY	157	51	0.746
Cameron, PA	33	10	0.676
Wyoming, PA	86	29	0.781
Oxford, ME	154	87	1.309
Ulster, NY	636	345	1.258
Fulton, PA	30	17	1.330
Juniata, PA	64	43	1.577
Potter, PA	56	43	1.770
Sullivan, PA	21	17	1.894
Sullivan, NH	129	81	1.466
Venango, PA	233	126	1.256
Warren, PA	153	87	1.271
Essex, VT	18	12	1.597
Orange, VT	69	43	1.451

Figure 8: Ratio of county's share of deaths during 1990-98 to county's share of deaths during 1968-89



study region. Those counties with ratios greater than 1.2 are generally small counties, with the exception of Ulster, NY.

DISCUSSION

Overall, we found a primary and significant breast cancer cluster in the New York-New Jersey-Philadelphia area that is similar to that found by Kulldorff et al. (1997). The size of the cluster tends to increase until the early 1990s, and has decreased in recent years. We also found a secondary cluster in Boston, where the size of the cluster has decreased over time except during the period of 1984 to 1988. The most notable changes for the time period in our analysis are recent extensions of the New York-New Jersey clusters into the Philadelphia area and declines in the Boston cluster.

Several factors may influence changes in the geographic clustering of breast cancer mortality. The established socioeconomic risk factors of breast cancer might be used to attempt an explanation of the changing patterns of clusters. One of the difficulties in such an ecological analysis is to also obtain other biological or individual risk factors of breast cancer, since geographic variations of disease and changing patterns of clustering are in part explained by the distribution of those risk factors. In our analysis, we found that clusters in Boston and Philadelphia show interesting patterns. The former has disappeared during the 1990s, while the latter has emerged as a new cluster. Further investigations on the risk factors and other factors affecting breast cancer clusters are necessary, since there is no supporting evidence to fully explain these changing patterns.

One approach to explaining the changing patterns of clusters is to look at changes in health-related risk factors. From the SEER (Surveillance, Epidemiology and End Results) statistics available at CDC Wonder (http://wonder.cdc.gov), we note that breast cancer incidence in Boston during the period first increased, and then remained level, while mortality has decreased (Table 4). These patterns of incidence and mortality might in part be explained by changes in health-related behavior, and can be examined using the Behavioral Risk Factor Surveillance System (BRFSS). The BRFSS is widely used by state governments for surveillance purposes and contains information on the breast cancer screening behavior of individuals such as breast exams, mammograms and pap smears. For example, during the 1990s the percentage of women aged 50 or older who had a mammogram within the previous two years was highest in Massachusetts (Center for Disease Control and Prevention, 2001). Although there are time lags between incidence and mortality from breast cancer, we might expect that higher incidence due to early detection of disease will lead to further lowering of breast cancer mortality in the area.

There has been much recent interest in the changing geographic pattern of various cancers stimulated by the National Cancer Institute's *Atlas of Cancer Mortality* (for example, geographic variations in lung cancer; see Devesa et al., 1999b). This interest reflects the importance of geographic perspectives on epidemiologic study. The identification of breast cancer clusters over time may not only provide important clues to the study of cancer and environment relationships, but also may suggest ways of monitoring diseases in a local area by identifying emerging clusters.

This analysis confirms the finding of a previous study that there are significant breast cancer clusters in the Northeast. Application of a GIS-based kernel method to breast cancer data during 1968-1998 shows the changing patterns of those clusters over time. The study adjusts for age and population only, while Kulldorff's study adjusted for race, urbanicity and parity, as well as age. Other factors may also play a role in forming geographic clusters. Further investigation on other confounding variables is required. For example, population density can be used as a proxy of urbanization or environmental exposures, and outcomes may exhibit spatial autocorrelation. For case-control studies, we can assess the effects of known risk factors on disease, and then determine whether clustering exists after controlling for the established risk factors of breast cancer and adjusting for covariates.

The investigation of changes in clustering in space and time could also play a pivotal role in the search for environmental risk factors of breast cancer, since it is also widely recognized that environmental risk factors may play an important role in the development of breast cancer and in explaining geographic variability. Examples of recent studies include the Long Island Breast Cancer Study and the Cape Cod Breast Cancer and Environment Study. These studies attempt to explain elevated risks of breast cancer associated with environmental risk factors from an environmental point of view (Brody et al., 1996; O'Leary, 1999). The excess mortality in the Northeast might be partially explained by the historically higher levels of industrialization of the region. Once significant clusters are identified, it may prove fruitful to search for possible influences of environmental risk factors in the areas characterized by significant clustering. This approach is valuable in uncovering the etiology of breast cancer because exposures at critical times in the past, such as at the time of birth, may cause breast cancer during later, adulthood years.

This study also demonstrates the usefulness of Geographical Information Systems and spatial statistical methods that facilitate the detection of changes in clustering over space and time. Given the advantages of GIS in integrating various sources of data with geo-referenced data, it has been widely adopted in the monitoring of disease and the modeling of exposure to environmental risks. The investigation of spatial-temporal changes of clustering contributes to the development of public health surveillance systems significantly. With the additional development of new statistical methods to monitor and predict space-time clustering (e.g. Rogerson, 2001b), GIS can be effectively used in disease monitoring and surveillance.

ACKNOWLEDGMENTS

The authors are grateful to the National Center for Health Statistics (NCHS) for providing the Compressed Mortality File. The analyses, results and interpretation are the responsibility of the authors and not the NCHS. The support of National Institutes of Health Grant 1R01 ES09816-01, National Science Foundation Award BCS-9905900 and National Cancer Institute Grant R01 CA92693-01 are gratefully acknowledged.

REFERENCES

Anscombe, F.J. (1948). The transformation of Poisson, binomial, and negative-binomial data. *Biometrika,* 35, 246-254.

Bailey, T.C., and Gatrell, A.C. (1995). *Interactive Spatial Data Analysis*. London: Longman.

Besag, J., and Newell, J. (1991). The detection of clusters in rare diseases. *Journal of the Royal Statistical Society Series A,* 154, 143-155.

Blot, W.J., Fraumeni, J.F., and Stone, B.J. (1977). Geographic patterns of breast cancer in the United States. *Journal of the National Cancer Institute,* 59, 1407-1411.

Brody, J.G., Rudel, R.A., Maxwell, N.I., and Swedis, S.R. (1996). Mapping out a search for environmental causes of breast cancer. *Public Health Reports,* 3, 495-507.

Centers for Disease Control and Prevention. (2001). *Tracking Major Health Risks Among Americans: The Behavioral Risk Factor Surveillance System*. Atlanta, GA: U.S. Department of Health and Human Services, Centers for Disease Control and Prevention.

Clayton, D., and Kaldor, J. (1987). Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics,* 43, 671-681.

Cressie, N. (1993). *Statistics for Spatial Data.* New York: John Wiley & Sons, Inc.

Devesa, S.S., Grauman, D.J., Blot, W.J., Pennello, G, Hoover, R.N, & Fraumeni, J.F. Jr. (1999a). *Atlas of Cancer Mortality in the United States, 1950-94*. Washington, DC: U.S. Government Printing Office.

Devesa, S.S., Grauman, D.J., Blot, W.J. & Fraumeni, J.F., Jr. (1999b). Cancer surveillance series: Changing geographic patterns of lung cancer mortality in the United States, 1950 through 1994. *Journal of the National Cancer Institute,* 91, 1040-1050.

Elliott, P., Wakefield, J.C., Best, N.G., and Briggs, D.J. (2000). *Spatial Epidemiology: Methods and Applications.* Oxford: Oxford University Press.

Fotheringham, A.S., and Zhan, F.B. (1996). A comparison of three exploratory methods for cluster detection in spatial point patterns. *Geographical Analysis,* 28, 200-218.

Freeman, M.F., and Tukey, J.W. (1950). Transformations related to the angular and the square root. *Annals of Mathematical Statistics,* 21, 607-11.

Kelsey, J.L., and Horn-Ross, P.L. (1993). Breast Cancer: Magnitude of the Problem and Descriptive Epidemiology. *Epidemiologic Reviews,* 15, 7-16.

Kulldorff, M., and Nagarwalla, N. (1995). Spatial disease clusters: Detection and inference. *Statistics in Medicine,* 14, 799-810.

Kulldorff, M., Feuer, E.J., Miller, B.A. & Freedman, L.S. (1997). Breast cancer clusters in the United States: A geographic analysis. *American Journal of Epidemiology,* 146, 161-70.

Lawson, A., Biggeri, A., Bohning, D., Lesaffre, E., Viel, J.F., and Bertollini, R. (1999). *Disease Mapping and Risk Assessment for Public Health.* New York: John Wiley & Sons, Inc.

Madigan, M.P., Ziegler, R.G., Benichou, J., Byrne, C. & Hoover, R.N. (1995). Proportion of breast cancer cases in the United States explained by well-established risk factors. *Journal of the National Cancer Institute,* 87, 1681-1685.

National Center for Health Statistics. (2000). *Data File Documentation, Compressed Mortality File*, 1968-88. Hyattsville, MD: National Center for Health Statistics.

O'Leary, E. (1999). *Environmental Exposures and Breast Cancer on Long Island.* PhD Dissertation, State University of New York at Buffalo.

Openshaw, S., Charlton, M., Wymer, C., and Craft, A.W. (1987). A mark 1 geographical analysis machine for the automated analysis of point data sets. *International Journal of Geographical Information Systems, 1*, 335-58.

Rogerson, P. (2001a). A statistical method for the detection of geographical clustering. *Geographical Analysis,* 33, 215-227

Rogerson, P. (2001b). Monitoring point patterns for the development of space-time clusters. *Journal of the Royal Statistical Society Series A* 164, 87-96.

Rushton, G., and Lolonis, P. (1996). Exploratory spatial analysis of birth defect rates in an urban population. *Statistics in Medicine,* 15, 717-726.

Srivastava, M.S., and Worsley, K.J. (1986). Likelihood ratio tests for a change in the multivariate normal mean. *Journal of the American Statistical Association,* 81, 199-204.

Sturgeon, S.R., Schairer, C.G., McAdams, M., Brinton, L.A., and Hoover, R.N. (1995). Geographic variation in mortality from breast cancer among white women in the United States. *Journal of the National Cancer Institute,* 87, 1846-53.

APPENDIX

```
**************************************************************************
Title: S-plus program to detect geographic clusters of breast cancer
# compute transformed breast cancer numbers, where nebc is the name of dataset,
# obs6898 and exp6898 are the variable name for the observed number of cases
# and expected number of cases, respectively.
bc1 <- sqrt(nebc$obs6898)+sqrt(nebc$obs6898+1)-sqrt(4*nebc$exp6898+1)

# find distance matrix d6
d2<-dist(c(nebc$east))
d4<-dist(c(nebc$north))
d5<-sqrt(d2^2+d4^2)
 n <- attr(d5, “Size”)
      full <- matrix(0, n, n)
     full[lower.tri(full)] <- d5
      d6<-full + t(full)

# s1 is cluster size (standard deviation of Gaussian kernel)
s1<-0.6

# find weights
w<-1/(sqrt(pi)*s1)*(exp(-d6^2/(2*775.7*s1^2)))
w9<-matrix(w,217,217)
w11<-w9[1,1:217]/sqrt(sum(w9[1:217,1]^2))

i<-2
  while (i<218)
{
w11<-append(w11,w9[1:217,i]/sqrt(sum(w9[1:217,i]^2)))
```

```
i<-i+1
}
w2<-matrix(w11,217,217)

# find local statistics based on weights and transformed values
bc2<-matrix(bc1,217,1)
bc3<-t(bc2) %*% (w2)

# plot the map of areas exceeding the critical value of 3.45
dnorth<-seq(68,607,length=300)
deast<-seq(106,733,length=300)
graphsheet(image.color.scheme= “white on black”, num.image.shades =30,
image.color.table = “255,255,255|0,0,0”)
plot(nebc$east, nebc$north, xlab= “East(miles)”, ylab= “North(miles)”,
xlim=c(100,750), ylim=c(60,620))

i<-(interp(nebc$east, nebc$north, bc3, xo=deast, yo=dnorth, ncp=0, extrap=F))
image(i, zlim=c(3.45,15.42), add=T)
image.legend(c(3.45,15.42),x=650,y=105,size=c(0.9,0.25), hor=T, nint=100)
text.default(x=695,y=120,labels=“Local Statistics”)
title(main= “Breast cancer clusters in the Northeastern US, 1968-1998”)

# print local statistics and find maximum value
bc3
max(bc3)
*************************************************************************
```

Chapter VIII

Geographical Analysis of Disease in Small Areas Using Hierarchical Bayesian Models: Mapping Men's Lung Cancer Mortality in Galicia, Spain

C. L. Vidal-Rodeiro
University of Aberdeen, UK

M. I. Santiago-Pérez and E. Vázquez-Fernández
Public Health Department of Galicia, Santiago de Compostela, Spain

M. E. López-Vizcaíno
Galician Statistical Institute, Santiago de Compostela, Spain

X. Hervada-Vidal
Public Health Department of Galicia, Santiago de Compostela, Spain

The purpose of this chapter is to review and compare two techniques to map the mortality risk of a disease in small geographical areas. The first one is a classical approach consisting of mapping standardized mortality ratios, *which are maximum likelihood estimates of the relative risk under a Poisson model of death counts. In a second step, the authors consider a Bayesian approach that assumes a hierarchical model where the death counts follow a Poisson distribution conditioned by the prior information. These methods have been applied to the study of geographical variation in men's lung cancer mortality from 1978 to 1998 in Galicia, Spain.*

Mapping mortality using the first method has important drawbacks, and there are difficulties to distinguish the mortality pattern. The Bayesian methodology produces smoother maps with a clear mortality pattern and has many advantages over the classical approach.

INTRODUCTION

Disease mapping is an increasing field of interest in the area of public health (Moore & Carpenter, 1999), and the geographical distribution of a disease has an important role in understanding its origin, its causes or its evolution.

In recent years, there have been many efforts to map mortality or incidence from diseases (Lopez-Abente, Pollán, Escolar, Errezola & Abraira, 1996; Pickle, Mungiole, Jones & White, 1996). One of the main problems has been the choice of the appropriate measure to map. The most widely used indicator in geographical representation is the Standardized Mortality Ratio (*SMR*); this offers the advantage of eliminating the confounding effect of the variable by which it is adjusted, usually age, but presents certain drawbacks when the population size varies over the map (Breslow & Day, 1975). In such a case, estimators of different accuracy are obtained in each area; areas having small populations—and thus fewer cases—tend to register very extreme estimations of risk, which then dominate the map and hinder epidemiological interpretation. This is a particular problem for rare diseases where thousands of individuals are needed before a single case is expected to occur. This makes it necessary to utilize information from neighboring areas in order to produce better estimates.

Alternative risk measures may be obtained by applying other modelling techniques that take the sources of spatio-temporal variation into account (Bernardinelli et al., 1995). A simple technique consists in adjusting a Poisson regression model that displays a log-linear relationship between risk and space-time variables. While successful in reducing the variability in risk, this method continues to pose a number of drawbacks. First, in geographical areas having few cases, this model yields unstable estimations due to extra-Poisson variation. Furthermore, if the hypothesis of spatial independence between risks does not hold, the model is not appropriate as it takes no account of a possible correlation between areas.

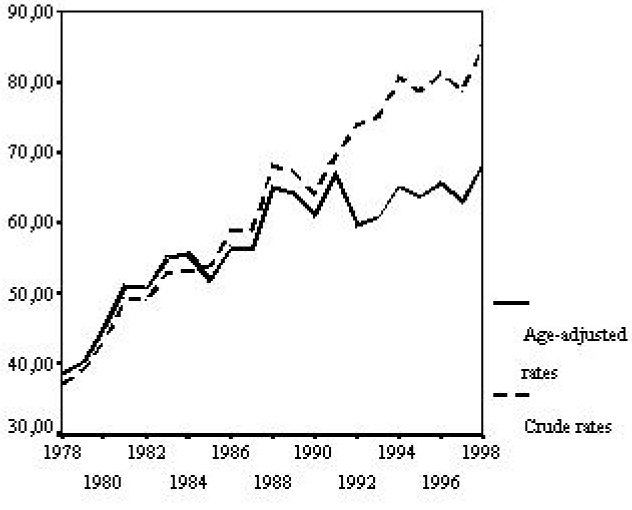
A possible solution to these problems is the Bayesian extension of the model introduced by Clayton and Kaldor (1987) and further developed by Besag, York and Mollié (1991). Basically, this approach provides a way to integrate, in the estimation of the unknown relative risk, local information consisting of the observed and expected number of cases in each area and prior information on the overall variability of the relative risk, their potential similarity in neighboring areas and their connection with geographically defined covariates.

In this work we compare the behavior of the mentioned techniques with the purpose of estimating and mapping relative risks in small geographical areas; this is illustrated by the analysis of the geographical variation in men's lung cancer mortality in Galicia over a 21-year period, taking into account ecological socio-economic factors.

Galicia is a region situated in the northwest of Spain, with a population of around 2,800,000 inhabitants and an extension of 29,575 Km^2; administratively it is divided into 315 municipal areas. In 1998, lung cancer was, in men, the second cause of potential years of life lost, with 5,912 lost years, which supposed the 7.71% among all causes (Dirección Xeral de Saúde Pública, 2000). Lung cancer mortality rates present a clear increasing trend during the study period (Figure 1) due to the strong increment in mortality from lung cancer in people over 65 years.

To study mortality in depth, the following step could be the examination of rates and its trend at the municipality level in order to distinguish areas of high or low risk.

Figure 1: Crude and age-adjusted lung cancer mortality rates in men in Galicia, 1978-1998



A problem would arise: how can we tabulate and deal with 315 estimators with their confidence intervals and their evolution? Hence, geographical analysis emerges as a suitable tool for analyses, synthesis and reporting results.

DATA

The study period, 1978-1998, was divided into three sub-periods of seven years each: 1978-1984, 1985-1991 and 1992-1998.

Age was categorized as under 15 years, 15-24, 25-34, 35-44, 45-54, 55-64, 65-74 and over 74 years. Since very few deaths from lung cancer occur below age 44, we combine the first four categories, which results in five age groups.

Lung cancer mortality data in males, which consist of the numbers of lung cancer deaths in municipality i for time period j, where $i=1, \ldots, 315$ and $j=1,2,3$, were obtained from the National Statistics Institute for the period 1978-1986, and from the Galician Mortality Register for the period 1987-1998. Galician age-specific male population figures were obtained from the 1981 and 1991 Censuses and the 1986 and 1996 Population Registers.

Description of Covariates

It is well known that smoking is a very important risk factor of lung cancer. Because of the fact that there is not direct information on the smoking behavior across Galicia, it should help to include a measure of urbanization in the model, such as urban living or socio-economic status, as a surrogate not only for cigarette consumption but also for other risk factors associated with urban areas. The covariates we have considered here are the total resident population per square kilometer (DEN) as a proxy for urban living, and a socio-economic score (SES), both at the municipality level and referred to 1991. The SES, obtained using the methodology proposed in Silva-Ayçaguer (1997), is a summary of the following variables: infant mortality rate, population density, proportion of people that live in population centers with more than 1,000 inhabitants, proportion of men with high studies, proportion of active people (population above 16 years) in industrial activities and proportion of people in households without running water or electricity.

MODELS

In order to estimate the relative risks (*RR*s), two techniques were used: a classical approach (*SMR*) and a hierarchical Bayesian model. Though described in terms of lung cancer mortality data for Galicia, subject to the pertinent modifications, these models could be used for a more general application.

Classical Approach

Let O_i denote the number of observed cases; E_i the number of expected cases, calculated by using the population broken down by age for each geographical unit, plus the specific mortality rates for the Galician population; and let ξ_i be the *RR*.

The classical approach to disease mapping is based on the assumption that, conditional on the E_is being known, the ξ_is are mutually independent. Moreover, each O_i follows a Poisson distribution with mean $E_i\xi_i$:

$$[O_i \mid E_i, \xi_i] \sim Poisson(E_i\xi_i)$$

Under these assumptions, the maximum likelihood estimate of ξ_i, denoted by $\hat{\xi}_i$, is the *SMR*:

$$\hat{\xi}_i = SMR_i = \frac{O_i}{E_i}$$

Hierarchical Bayesian Model

Bayesian methods estimate the risk of an area by incorporating information from adjacent areas, so as to reduce the effect of random fluctuations unrelated to the risk. Furthermore, on taking account of spatial correlation between adjoining areas, the resulting smoothed maps prove more informative (Bernardinelli & Montomoli, 1992; Knorr-Held & Besag, 1998).

In the Bayesian approximation, Poisson variation is modelled at a first level, and a model for the relative risks is specified at a second level, with area-specific random effects further decomposed into two components: a spatially structured component that takes into account the effects that vary in a structured manner in space (clustering) and a component that models the effects that vary in an unstructured manner between one area and the next (heterogeneity).

The hierarchical model is formulated as follows (Bernardinelli et al., 1995): let O_{ij} be the number of observed cases, E_{ij} the number of expected cases, and ξ_{ij} the RR in municipality i (i=1, …, 315) and period j (j=1, 2, 3).

A likelihood model is specified for the vector of observed cases, given the risk vector,

$$O_{ij} \mid \xi_{ij} \sim \text{Poisson}(E_{ij}\xi_{ij})$$

and the *RR* is modelled as

$$\log \xi_{ij} = \alpha + \phi_i + \theta_i + (\beta+\delta_i)t_j + \gamma X_i + \eta Z_i$$

where α is the mean of the logarithm for *RRs* over all areas, ϕ_i the clustering component, θ_i the heterogeneity component, t_j the time, β the mean of the time trend across all areas, δ_i the space-time interaction effect, and X and Z indicate, respectively, the covariates DEN and SES, with γ and η as their corresponding coefficients.

Estimation of the risk across time in each area is given by $\exp(\beta+\delta_i)$. Following Bernardinelli, Clayton and Montomoli (1995) notation, δ_i is named the differential trend for area i; a value of $\delta_i<0$ indicates that the trend in area i is below the mean, while a value of $\delta_i>0$ implies that the trend in area i is above the mean.

Bayesian modelling requires specification of prior distributions for random effects.

The distribution model for the heterogeneity component is

$$[\theta_i \mid \theta_j, i\neq j, \sigma_\theta^2] \sim \text{Normal}\,(\bar{\theta}_{-i}, \sigma_\theta^2)$$

where

$$\bar{\theta}_{-i} = \frac{1}{I-1}\sum_{j\neq i}\theta_j\ ,\ I = 315.$$

By virtue of this prior distribution, it is assumed that variation in risk between areas is independent and, as a consequence, posterior estimations of the area effect will therefore tend towards an overall mean.

For the clustering component, a spatial correlation structure was used, where estimations of the risk in any area depend on neighboring areas; this was achieved by allocation of weights. Specifically, we take weights equal to 1 in cases where the areas were adjacent (that is, share a common boundary) and 0 in cases where they were not. The conditional autoregressive (CAR) model proposed by Besag et al. (1991) was used:

$$[\phi_i \mid \phi_j, i\neq j, \sigma_\phi^2] \sim \text{Normal}(\bar{\phi}_i, \sigma_i^2)$$

where

$$\bar{\phi}_i = \frac{1}{\sum_j w_{ij}}\sum_j \phi_j w_{ij}$$

$$\sigma_i^2 = \frac{\sigma_\phi^2}{\sum_j w_{ij}}$$

$w_{ij} = 1$ if i,j are adjacent (or 0 if they are not)

Taking the above hypotheses into account, this model tends to shift the estimation of each individual area effect towards a local mean.

Parameters σ_θ^2 and σ_ϕ^2 control the variability of θ and ϕ. Following the recommendations of Bernardinelli, Clayton and Montomoli (1995), Gamma distributions were considered for these parameters.

In order to carry out a full Bayesian analysis, hyperprior distributions for α, β, γ and η must be specified; we assumed (improper) uniform priors for all these parameters.

Estimation of Hierarchical Bayesian Models

For the estimation of the hierarchical model, simulation techniques are required; in this case we used the Gibbs Sampler, which belongs to the Markov Chain Monte Carlo (MCMC) methods and is implemented in the software WinBugs (Spiegelhalter, Thomas, Best & Gilks, 1995). Using the above model and the prior structures mentioned in this section, 12,000 iterations were performed, discarding the first 2,000 to eliminate the effect of the initial values.

A convergence analysis was carried out in order to assess whether the simulated chain converges to the stationary distribution. Several convergence diagnostics have been proposed in the literature (Cowles & Carlin, 1996), the most commonly used monitor the output of relevant parameters. We have used Gelman and Rubin's test, implemented in the Bugs Output Analysis program (BOA) developed by Smith (1999), which consists in running parallel chains with different starting values and testing whether the total variance between the different sequences is no larger than the variance within each sequence. The ratio of these two variance estimates gives a scale reduction factor, which should be close to 1 if the values produced by the algorithm are close to a sample from the stationary distribution.

The MapInfo Professional 6.0 software was used to map the geographic distribution of the *RR*, and quintiles of its distribution to specify cut-points.

Selection of Models

To select the best model of a collection of different Bayesian models, a measure of goodness of fit—usually the deviance—and a measure of complexity—the number of free parameters—can be used. The increase in complexity implies a better fit, though at times the gain in fit is small when compared to the difficulties of interpretation and calculation posed by a more complex model. A criterion that enables simultaneous assessment of fit and model complexity is the Deviance Information Criterion (DIC), a generalization of the Akaike Information Criterion (Akaike, 1973) which was proposed by Spiegelhalter, Best and Carlin (1998)

$$\mathrm{DIC} = D + p_D$$

where D is the deviance based on posterior means of the parameters, and p_D is the effective number of parameters, which is obtained by subtracting a plug-in estimation of the deviance, calculated using posterior means of the parameters, from the posterior deviance.

It must be stressed that DIC should not be used as a strict criterion for the choice of the final model. Other considerations must be taken into account, such as prior knowledge or robustness of the method. Furthermore, DIC is not intended for identification of the correct model, but rather as a method of comparing a collection of alternative formulations.

RESULTS

Before estimating and interpreting any results, the sensitivity of the conclusions to changes in model specifications must be investigated, in this case by using DIC to evaluate goodness of fit and complexity. In Table 1, we present the estimated p_D, deviance and DIC for the full model, described in the previous section, and various simplifications of it.

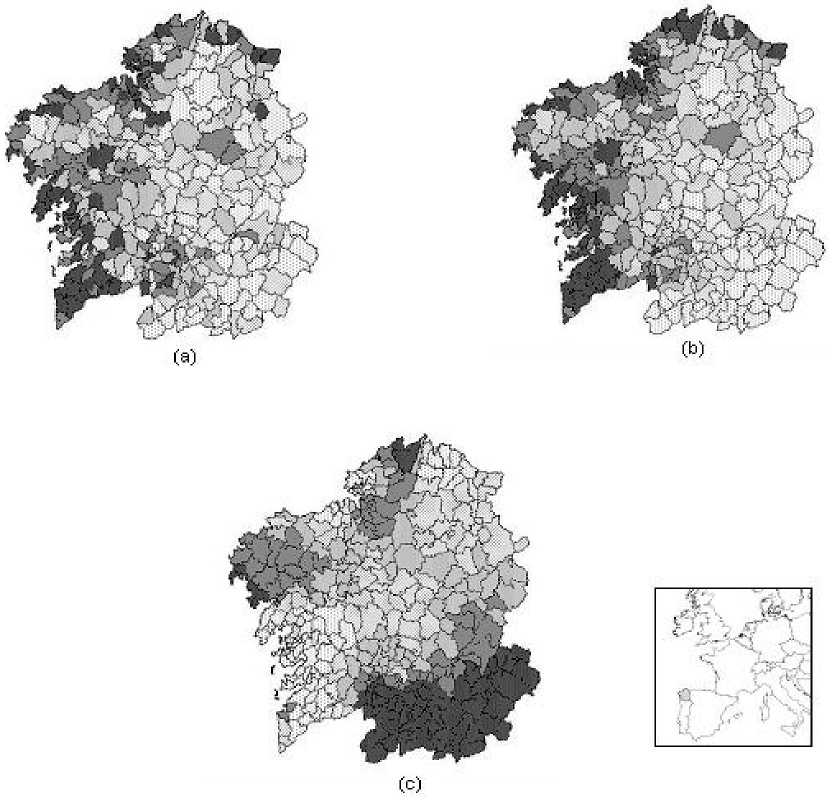
Table 1: DIC, deviance and p_D *for various hierarchical Bayesian models.*

	Model	DIC	Deviance	P_D
I	$\log \xi_{ij} = \alpha + \phi_i + \theta_i + (\beta+\delta_i)t_j$	1228.60	1041.42	187
II	$\log \xi_{ij} = \alpha + \phi_i + (\beta+\delta_i)t_j$	1218.52	1041.42	177
III	$\log \xi_{ij} = \alpha + \phi_i + \theta_i + \beta t_j$	1246.08	1081.42	165
IV	$\log \xi_{ij} = \alpha + \phi_i + \beta t_j$	1241.33	1081.42	160
V	$\log \xi_{ij} = \alpha + \phi_i + \theta_i$	1240.87	1081.42	159
VI	$\log \xi_{ij} = \alpha + \phi_i$	1235.36	1081.42	154
VII	$\log \xi_{ij} = \alpha$	2889.08	2881.42	8

The best two models in terms of DIC are Models I and II, which include the space-time interaction effects. Although both models have the same goodness of fit, the number of effective parameters in Model I, which contain 315 random effect terms (heterogeneity effects) more, is bigger than the effective number of parameters of Model I. This suggests that heterogeneity effects fall far short of random spatial effects in explaining inter-area variability in the *RR*s, to the extent that they may possibly be redundant. As a consequence, the heterogeneity term was eliminated from the model.

It was Model II that was therefore used for subsequent analyses, such as estimation or introduction of covariates.

Figure 2: Lung cancer mortality in men in Galicia, 1978-1998: (a) Raw SMR*; (b) Bayesian smoothed* RR *using Model II; (c) temporal trend using Model II*



Gibbs Sampler convergence was investigated using Gelman and Rubin's test. Scale-reduction factor values of around 1 were achieved, a symptom that convergence was acceptable. Furthermore, the results are not noticeably altered if a larger number of iterations were carried out.

Figure 2 shows the estimated *RR*s for lung cancer, obtained by classic approximation and Bayesian estimation.

The *RR*s are less variable in Figure 2(b) than in Figure 2(a), with the effect of smoothing being in evidence (*SMR*s range from 0.094 to 1.871; the Bayesian estimates of *RR* correct this dispersion, since the pulled estimates range from 0.382 to 1.756). The *SMR*s' variability reflects random fluctuations due to different population size and corresponding small counts.

The maps highlight contrasts in the geographical distribution of risk; the north-west and the south west parts of Galicia appear at higher risk. This pattern is stable in both maps, although, as expected, it emerges more clearly in the map obtained under the Bayesian model.

Figure 3: Spatial distribution of the two covariates: (a) population density; (b) socio-economic score

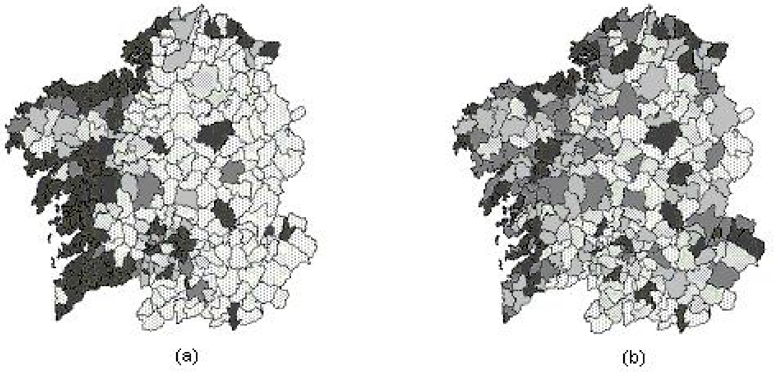

(a) (b)

Figure 2(c) presents the temporal trend for lung cancer in the Galician municipalities and shows that in areas with lower mortality, a rising trend has been in evidence over the course of the last few years.

Figure 3 shows the spatial distribution of the covariates DEN and SES. Urban living and SES show high collineality (they exhibit similar spatial patterns). Lung cancer mortality rates are high in the most populous municipalities, which are also wealthy. In view of the geographical patterns, it would appear that there might be an association between these variables and lung cancer mortality.

Table 2: DIC, deviance and p_D *for the hierarchical Bayesian model with covariates*

	Model	**DIC**	**Deviance**	**P_D**
VIII	$\log \xi_{ij} = \alpha + \phi_i + (\beta+\delta_i)t_j + \gamma X_i$	1222.82	1041.42	181
IX	$\log \xi_{ij} = \alpha + \phi_i + (\beta+\delta_i)t_j + \eta Z_i$	1226.24	1061.42	165
X	$\log \xi_{ij} = \alpha + \phi_i + (\beta+\delta_i)t_j + \gamma X_i + \eta Z_i$	1192.60	1041.42	151

Three different models were estimated with the covariates, and the goodness of fit results are set out in Table 2.

Models VIII and X evince the same goodness of fit, yet the model that incorporates the two covariates has the smallest DIC. The posterior estimations for the coefficients of the covariates using model X are γ=0.0001 (DEN coefficient) with a Bayesian credibility interval of [0.000036, 0.000159], and η=0.0145 (SES coefficient) with a credibility interval of [0.01127, 0.01785], both significant.

Figure 4: Lung cancer mortality in men in Galicia, 1978-1998. Bayesian smoothed RR *using Model II with covariates*

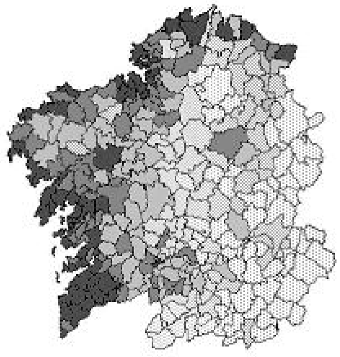


Figure 5: Variability of the RR *estimations in different models*

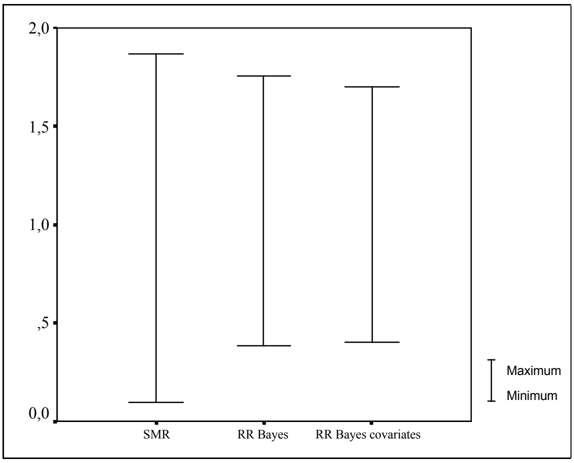


Figure 4 shows the estimations of the *RR*s obtained by adjusting the model with both covariates, and, as expected, the *RR*s shrink further, i.e., they have a smaller variation interval (*RR*s range from 0.403 to 1.702), confirming the relationship between the covariates and the disease. This finding is reflected in Figure 5, which depicts the *SMR* obtained by the classic approximation versus the *RR* yielded by the Bayesian models.

Comparison Between Classical and Bayesian Models in Terms of Mean Square Error.

This section seeks to demonstrate that Bayesian methodology yields better results than the classical method. For comparison purposes, we use the mean square error (*MSE*) of the risk estimations obtained by both methods. To calculate this, we need the true *RR*s, which are unknown. Hence, the solution adopted (Martins, Barreto, Guerra & Sakurai, 1998) consists of treating the *RR*s yielded by the classical method as true, and simulating a series of new observed cases for each area so as to enable estimation of the associated risks. The resulting *MSE*s are as follows: for the Bayesian estimator 5.22, and for the crude *SMR* in the order of 7.61, which means a reduction of around the 31.4%. Accordingly, there is a significant difference in favor of Bayesian methods.

DISCUSSION

This study has addressed various issues in disease mapping: use of classical methods versus Bayesian models, choice of the prior distributions and incorporation of spatio-temporal structures. The emphasis of this study was more on comparing these methods with data than on making theoretical comparisons. Conclusions about comparison of methods have limited validity.

The use of Bayesian models for computing the *SMR* instead of the usual procedures is recommended. Maps of observed *SMR*s may be unstable and are prone to wrong interpretation, as attention is drawn to regions with high or low *SMR*s based on small populations. Smoothing overcomes the problem of overdispersion and enables us to highlight the differences between municipalities. The estimation of the parameters of the hierarchical model can be carried out with algorithms belonging to the class of MCMC methods, which have improved in the last few years and allow us to compute summary statistics for the distribution of *RR*s, which would be extremely hard to obtain with a different computational approach.

The results obtained using Bayesian methods may be sensitive to the choice of priors. Nevertheless, Bernardinelli, Clayton and Montomoli (1995) discuss the insensitivity of Bayesian methods to the choice of priors, but in cases where data are sparse and there is a prevailing conviction of geographical variability, this independence ought to be explored with caution.

From this analysis, interesting results have arisen on the variability of the relative risks. There is indication that a main part of the variability is accounted for by a local clustering structure. Thus, there is some evidence that local risk factors, which might correspond to a complex combination of environmental and socio-demographic local characteristics, relatively stable over time, are influencing the spatial structure of lung cancer mortality.

By including covariate values measured on regions rather than individuals, our analysis is an example of "ecological modelling." As in any ecological study, and due to the "ecologic fallacy" (attributing effects measured in aggregate to individuals), one must interpret results with caution, even when pertinent covariates are included because there are many potential factors of bias which can create discrepancies between the results of a study that analyses data at an aggregate level and the results of those that do so at an individual level. Furthermore, cancer mortality rates rise with age, with the accompanying problem of worse diagnostic quality and ensuing death certification, which may lead to bias in estimation.

In our study we assumed that the covariate measures are error-free. However, this is rather unrealistic. Indeed, Bernardinelli, Pascutto, Montomoli and Komakec (1999) and Xia and Carlin (1998) incorporate covariate measures that are not error-free into the standard hierarchical Bayesian model and demonstrate that, when the underlying error is taken into account, estimations prove more accurate.

Subsequent investigations have led us to assess the extension of the model with the introduction of the age factor and even its interaction with time, because the mortality behavior through the study years is different in the age groups. This necessarily implies a greater number of observations, giving rise to problems in the production of sufficiently accurate posterior estimations.

Another improvement involves the choice of neighbors. A recent study (Vanaclocha et al., 1999) indicates that the option used in this chapter yields better results, but it would nonetheless be interesting to experiment with other alternatives, such as taking all municipalities lying within a given radius of kilometers as neighbors, or taking *k* neighbors lying closest to a given municipality.

REFERENCES

Akaike, H. (1973). Information theory and an extension of the maximum likelihood principle. In Petrov, B. N. & Csáki, F. (Eds.), *2nd International Symposium on Information Theory (pp. 267-281)*. Budapest, Hungary: Akadémiai Kiadó.

Bernardinelli, L., Clayton, D. & Montomoli, C. (1995). Bayesian estimates of disease maps: How important are priors? *Statistics in Medicine, 14,* 2411-2431.

Bernardinelli, L., Clayton, D., Pascutto, C., Montomoli, C., Ghislandi, M. & Songini, M. (1995). Bayesian analysis of space-time variation in disease risk. *Statistics in Medicine, 14,* 2433-2443.

Bernardinelli, L. & Montomoli, C. (1992). Empirical Bayes versus fully Bayesian analysis of geographical variation in disease risk. *Statistics in Medicine, 11,* 983-1007.

Bernardinelli, L., Pascutto, C., Montomoli, C. & Komakec, J. (1999). Ecological regression with errors in covariates: An application. In Lawson, A., Biggeri, A., Böhning, D., Lesaffre, E., Viel, J. F. & Bertollini, R. (Eds.), *Disease Mapping and Risk Assessment for Public Health (pp. 329-348)*. Chichester, England: John Wiley & Sons, Inc.

Besag, J., York, J. & Mollié, A. (1991). Bayesian image restoration, with two applications in spatial statistics (with discussion). *Annals of the Institute of Statistical Mathematics, 43,* 1-59.

Breslow, N.E. & Day, N.E. (1975). Indirect standardization and multiplicative models for rates, with reference to the age adjustment of cancer incidence and relative frequency data. *Journal of Chronic Diseases, 28,* 289-303.

Clayton, D. & Kaldor, J. (1987). Empirical Bayes estimates of age-standardized relative risks for use in disease mapping. *Biometrics, 43,* 671-681.

Cowles, M.K. & Carlin, B.P. (1996). Markov Chain Monte Carlo convergence diagnosis: A comparative review. *Journal of the American Statistical Association*, *91,* 883-904.

Dirección Xeral de Saúde Pública. (2000). *Mortalidade en Galicia 1980-1998*. Santiago de Compostela, Spain: Consellería de Sanidade e Servicios Sociais.

Knorr-Held, L. & Besag, J. (1998). Modelling risk from a disease in time and space. *Statistics in Medicine, 17,* 2045-2060.

Lopez-Abente, G., Pollán, M., Escolar, A., Errezola, M. & Abraira, V. (1996). *Atlas of Cancer Mortality and Other Causes of Death in Spain 1978-1992*. Madrid, Spain: Fundación Científica de la Asociación Española Contra el Cáncer.

Martins, R., Barreto, S., Guerra, H. & Sakurai, E. (1998). Maps of epidemiological rates: A Bayesian approach. *Cadernos de Saude Publica, 14,* 713-723.

Moore, D.A. & Carpenter, T.E. (1999). Spatial analytical methods and geographic information systems: Use in health research and epidemiology. *Epidemiologic Reviews, 21,* 143-161.

Pickle, L.W., Mungiole, M., Jones, G.K. & White, A. (1996). *Atlas of United States Mortality, 1988-1992*. Atlanta, GA: Centers for Disease Control and Prevention.

Silva Ayçaguer, L.C. (1997). *Cultura Estadística e Investigación Científica en el Campo de la Salud: Una Mirada Ccrítica*. Madrid, Spain: Diaz de Santos.

Smith, B. (1999). BOA, BUGS Output Analysis Program. Version 0.4.3. [Computer Software]. Iowa, USA: Author.

Spiegelhalter, D.J., Best, N.G. & Carlin, B.P. (1998). *Bayesian Deviance, the Effective Number of Parameters, and the Comparison of Arbitrarily Complex Models*. (Technical Report). Cambridge, England: MRC Biostatistics Unit.

Spiegelhalter, D.J., Thomas, A., Best, N.G. & Gilks, W.R. (1995). *BUGS:*

Bayesian Inference Using Gibbs Sampling. Version 0.50 [Computer Software]. Cambridge, England: MRC Biostatistics Unit.

Vanaclocha, H., Zurriega, O., Abellán, J.J., Melchor, I., Calabuig, J., Ferrándiz, J., López, A. & Sanmartin, P. (1999). Cartografía de enfermedades en áreas pequeñas: Una aproximación metodológica. *Gaceta Sanitaria*, 13(Supl 2), 33-68.

Xia, H. & Carlin, B.P. (1998). Spatio-temporal models with errors in covariates: Mapping Ohio lung cancer mortality. *Statistics in Medicine, 17,* 2025-2043.

SECTION III:

INFECTIOUS DISEASE & INTERNATIONAL HEALTH

Chapter IX

Using Hierarchical Nearest Neighbor Analysis and Animation to Investigate the Spatial and Temporal Patterns of Raccoon Rabies in West Virginia

Andrew Curtis and Michael Leitner
Louisiana State University, USA

Cathleen Hanlon
U.S. Centers for Disease Control and Prevention, USA

One of the most powerful uses of GIS in the field of public health is as an exploratory data analysis tool. By combining the three post-input defining components of a GIS (data manipulation, data investigation, data analysis), the spatial understanding of a disease can be furthered by identifying patterns of cases, or associations between disease and other spatial phenomena (such as elevation). This chapter sets the groundwork for one such exploratory tool that could be used to identify the spatial and temporal patterns of an infectious disease. The disease in question is raccoon rabies in West Virginia *during 1999-2000. The exploratory tool, animation, has the potential to give insights into an evolving disease pattern that current spatial cluster techniques could miss. The current raccoon rabies epizootic presents a complex spatial surface as multiple disease foci may be present. Added to this could be a residual "background" or enzootic level of rabies. In order to reduce the impact of multiple foci, an appropriate "scale" of animation is needed. This scale has to be of a small enough geographic area that only one disease focus is considered, and is of practical use so that other meaningful spatial information (such as land cover or elevation) can be interpreted. The purpose of this chapter is to decide on an appropriate method of identifying this scale of animation for an infectious disease of this type.*

This chapter will select one commonly used technique, Nearest Neighbor Hierarchical (NNH) spatial clustering, to identify the correct scale and location on which to perform an animation. NNH spatial clustering will be applied to three combinations of Raccoon Rabies data for West Virginia, for 1999, 2000 and both years combined. NNH cluster analysis will also be performed on a four-county area identified as having the highest intensity of rabies cases in the state. These results will then be compared to a preliminary animation of rabies cases in West Virginia from which subjects were asked to identify dynamically evolving disease clusters. An animation was also run for the same area of high disease intensity. Cluster and animation results were compared for similarities. It was found that a spatial cluster technique, such as NNH spatial clustering, provides an adequate means of identifying the scale and location on which a more sophisticated animation can be based. The chapter concludes with a discussion of how, once a scale has been decided, a more sophisticated animation can be constructed and ultimately used to guide the placement of interventions such as oral vaccine barriers.

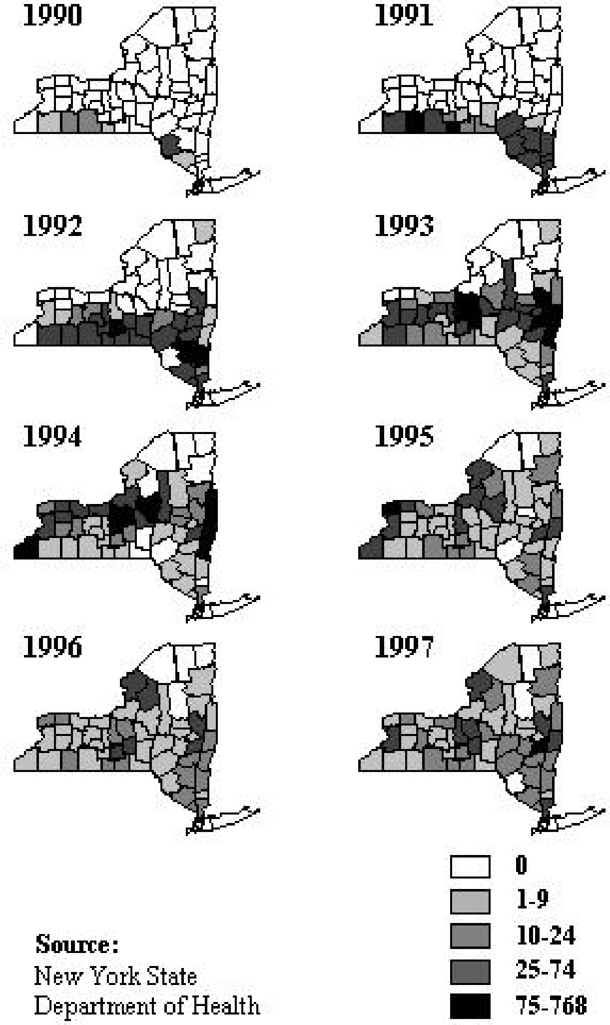
WHY ANIMATE RABIES?

The ultimate origin of the raccoon rabies virus variant remains obscure. The first recorded cases of rabies in raccoons occurred in Florida in the early 1950s. This initial focus slowly expanded over the next four decades throughout Florida, Georgia and South Carolina. In 1977 raccoons infected with rabies were transported into the West Virginia / Virginia border area from Florida by hunting groups (Smith et al., 1984; Jenkins and Winkler, 1987). These translocated animals were the beginning of the most intense rabies epizootic on record in North America. The epizootic burned quickly through the eastern seaboard, spreading at a rate of approximately 10 to 20 miles per year. In 1980, 35 rabid raccoons were identified in West Virginia and Virginia. By 1982, when the disease had spread into

Pennsylvania (Jenkins, 1984) 760 rabid raccoons had been identified in Virginia; 745 are from 1981-82 alone (Hubbard, 1985). Factors that can affect the speed of spread include the geography of the area and habitat conducive to high raccoon densities (Bromley et al., 1979; Kaufmann, 1982) and seasonal conditions, which affect food and shelter resources, general health and disease resistance (Carey et al., 1978). The two epizootics (the first originating from Florida, the second from the West Virginia/Virginia border area), eventually intersected in North Carolina in 1994 (Krebs et al., 1995). At the epizootic front, raccoon populations substantially decline initially, and then gradually recover to a level supporting enzootic levels of rabies.

As an example of how the epizootic could impact a state, Figure 1 shows the

Figure 1: The Spread of Raccoon Rabies in New York State



Source:
New York State
Department of Health

total number of positive raccoon rabies cases as recorded by New York State Health laboratories. Presenting the yearly total in this way clearly shows how the rabies "wave" passed through the state infecting the vast majority of the counties. It should also be remembered that surveillance data of this type will always under-represent the true extent of the disease, largely due to undiagnosed cases among animals that are not submitted for testing. Figure 1, when presented as an animation, provides an excellent example of how an infectious disease spreads. The geographical epizootiology of rabies data investigated at this spatially aggregated level (by county) has previously been presented as a guide to oral vaccine programs (Torrence et al., 1992). In order to gain true insight into both the spatial and temporal interconnections of the disease, a finer spatial resolution is needed.

It is important to understand how both space and time interact in a rabies epizootic. Not only does the disease progress spatially at a temporal rate, but there is also a time frame to the disease in any one static spatial location. Fox rabies has previously been found to exhibit such a temporal "cycle" (Tinline, 1988). Initially disease cases will explode and then rapidly decline as the animal population drops below a level capable of sustaining the disease (Yorke et al., 1979), or alternatively, herd immunity is developed (Coyne et al., 1989). After a two-to-seven year cycle, a second wave of disease will emerge as the population of vulnerable animals (juvenile animals who have not encountered the disease) reaches a level capable of sustaining the disease detectable by the passive system currently in place for public health rabies prevention needs. This cycle could manifest spatially as seemingly unconnected "outbreaks" of disease. The relative densities of rabies reservoir species directly affects disease transmission patterns. Along the eastern seaboard, raccoon populations occur at greater relative densities than foxes, perhaps accounting for the overall sustenance of raccoon rabies for greater than 50 years, whereas rabies among foxes in the Appalachians diminished and ultimately disappeared spontaneously during the late 1970s. Disease control measures such as localized population reduction or vaccine programs may best be focused on "lulls" in the temporal cycle of the disease, as fewer animals are needed to be reached in order to keep the susceptible population below the required disease threshold point. For example, Brown et al. (1990) suggest that vaccine strategies should be targeted during a spring or late winter vaccination, as a maximal level of immunity could be passed on to kits (Rupprecht and Kieny, 1988).

Although raccoon rabies has not yet resulted in any known human cases (the two-to-three human deaths in the U.S. every year are usually the result of bat rabies), it is still an expensive disease to control. Estimates from post-epizootic New York State are that over $2 million are being spent per year trying to control rabies (New York State Department of Health, 1999) as compared to the pre-epizootic expense of $10,000 per year. The money spent includes post-exposure prophylaxis, loss to livestock, vaccination, public education and sometimes a vaccine control program. There is therefore an economic as well as public health need to control the disease. Controls previously enacted for fox rabies included hunting, trapping, poisoning and gassing (Lewis, 1975). It is widely accepted though that these measures are not effective long-term options (Lewis, 1975; MacDonald, 1980), particularly due to higher sustainable raccoon population densities and other differences in the ecology and behavior. Oral vaccine is a publicly acceptable and effective alternative to reduce the at-risk animal population. In order to effectively contain, suppress and possibly eliminate raccoon rabies, it is important to understand when and where the animals are at their most susceptible (Wandeler, 2000).

For this chapter, raccoon rabies in West Virginia, where the originally transplanted epizootic began, is investigated for 1999 – 2000. By using cluster analysis and animation, it will become evident that more than one disease focus exists in the state. Added to this is a background level of rabies that might represent the residual effect of previous disease foci (because of cycling). The surrounding states of Pennsylvania, Maryland and Virginia have all been affected by the epizootic, so spillover infections from these borders is certainly possible. Any vaccine program would have to take into account this complex landscape, while also considering how fast and in which direction the disease appears to be spreading.

PREPARING THE DATA

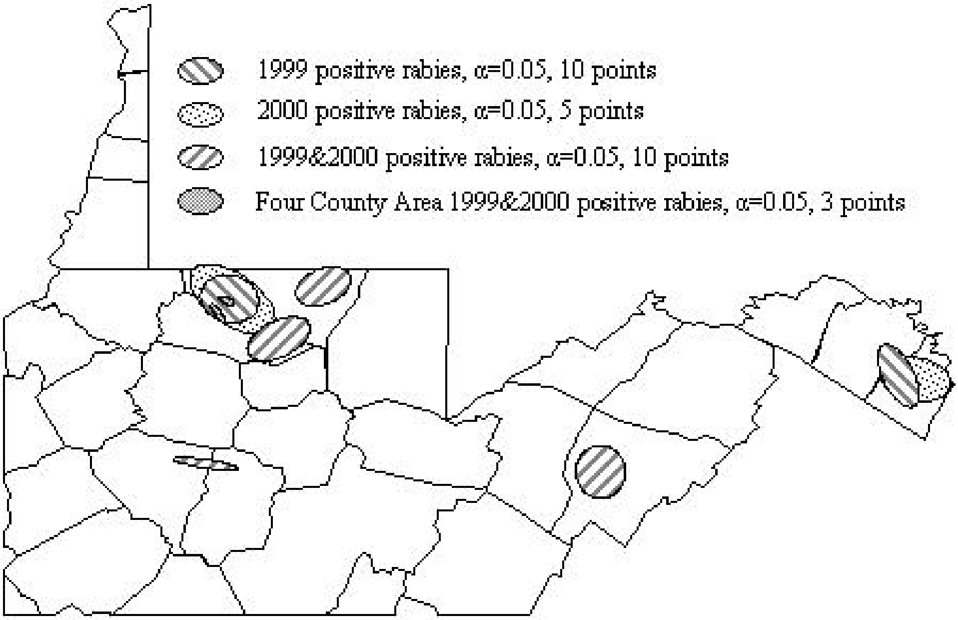
All positive terrestrial animal rabies cases (excluding cases of bat origin) for 1999 and 2000 were compiled by the Centers for Disease Control and Prevention. Local health personnel, predominantly sanitarians, were contacted and asked to provide accurate case location information on detailed maps or decimal latitude and longitude. Decimal latitude and longitude were calculated for cases indicated on maps. The compilation of latitude and longitude is an important component for running an animation or cluster analysis, as aggregate level data could be too coarse to identify multiple foci.

An initial consideration when animating rabies is, which species is to be animated? The current rabies problem on the eastern seaboard is raccoon rabies. Indeed, of the 217 rabid animals found in West Virginia during 1999 and 2000, 152 (70%) were raccoons. Although it is possible that the strain of rabies carried by the raccoons could spillover into other species, the virus has adapted to the degree that these other species are less likely to perpetuate the spread, the most likely outcome being a dead-end mortality. The question then arises, should these other rabid animals be omitted from the animation? Although they might not contribute to the further spread of the disease, they might be passive indicators of the disease movement, especially in areas of relatively few submissions. However, these diseased animals might also result from another rabies virus variant, such as a number of bat virus variants. Without laboratory verification of the strain, animals other than the predominate terrestrial reservoir species should be omitted from the animation. The question still remains even if testing is available, should presumably "dead-end" hosts such as a skunk infected with the raccoon rabies strain be included? Further analysis of the occurrence of theses non-reservoir species cases may illuminate their potential adjunct role in disease sustenance. Nonetheless, for this chapter, only positive raccoon rabies cases were included.

The first step was to just consider the surface spatially, and not incorporate the temporal interactions between the disease cases. For this, the Nearest Neighbor Hierarchical (NNH) Spatial Clustering technique was chosen. This is a commonly utilized technique from a catalogue of methods designed to identify spatial clusters (Everitt, 1974). Spatial cluster techniques aim to group cases together into relatively coherent clusters by optimizing various statistical criteria. The first statistical criterion used in the NNH spatial clustering technique is the distance from each case to its nearest neighbor case and the grouping of two cases into a cluster, if they (the two cases) are spatially closer (have a shorter distance) than would be expected on the basis of chance. This is determined by the probability level (p-value) or level of significance (α). Only cases which fit this criterion are clustered at the first level (first-order clusters). First-order clusters can, in turn, be clustered into second-order clusters, etc., resulting in a cluster hierarchy. The second criterion used in the NNH spatial clustering technique is the minimum number of cases that are required to form a cluster. This criterion is used to eliminate small clusters. The resulting clusters are most commonly visualized as standard deviational ellipses, which not only show the size of each cluster but the distribution of cases within. For this chapter, CrimeStat, a spatial statistics program, was chosen to calculate the clusters in the form of standard deviational ellipses which could be exported as Arc View shape files and overlaid onto the disease surface within the GIS (Levine, 1999).

For each of the cluster runs, the same significance level of 0.05% (or a 5% likelihood that the distance from one case to its nearest neighbor could be due to chance) was used. The number of cases that were required to form a cluster varied according to the number of disease cases present. For positive cases in 1999, a minimum of 10 cases were required to form a cluster. The second cluster run included both 1999 and 2000 level data, and again a minimum of 10 cases were required to form a cluster. The third cluster run included just 2000 data. In this case, no significant clusters were identified at the 10 case level, so the number of cases required for a cluster was dropped to five. The results for these three cluster runs

Figure 2: All significant clusters found with the Hierarchical Nearest Neighbor cluster algorithm

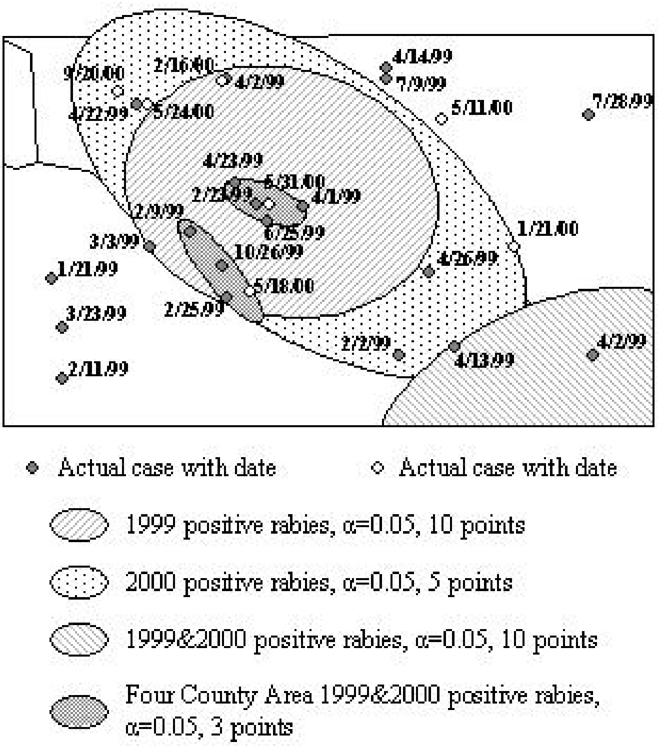


can be seen in Figure 2, with all the one-standard deviational ellipse outputs being overlaid on the same map.

From Figure 2 it appears as though a clustering of cases is evident in the northcentral region. Significant clusters overlap for both 1999 and 2000 data. When 1999 and 2000 data were combined, the significant cluster was drawn further to the southeast. The final cluster run was performed on the four counties of this northcentral region. This changing of scale required the number of positive cases, in order for a cluster to be identified, to be dropped to three.

NNH clustering identifies where significant disease areas occur for any chosen time period (1999, 2000 or a season thereof), but no insight is gained into the temporal progression of the disease. One attempt at visualizing this temporal progression can be seen in Figure 3, which focuses into the northcentral region of the state. On this map the overlapping cluster ellipses are included along with actual disease cases and their dates of submission. Even so, from this graphic it is hard to identify any temporal sequence or pattern to the rabies surface. It is for this reason that animation could provide insight into understanding the spatial/temporal progress of a disease.

Figure 3: The temporal sequence of rabies cases associated where the standard deviational ellipses overlap



ANIMATING RABIES CASES

Cartographic animation requires the addition of a temporal dimension to a series of static maps that include visual variables, such as size, color, shape, etc., and two or three spatial dimensions (DiBiase et al., 1992). The development of cartographic animation from its start in the late fifties (Thrower, 1959) is well documented in Campbell and Egbert (1990). The most obvious application of animation in both the social and physical sciences, and the one adopted for this chapter, is a progression of static surfaces from a common viewpoint. The temporal dimension is ordinarily constructed from scenes sampled at intervals along the range of a series, viewed in chronological order at a constant rate (DiBiase et al., 1992). Animation has also previously been used in the visualization of disease, such as the time-series animation of smoothed monthly incidences of childhood leukemia in England from 1967 to 1987 (Openshaw et al., 1988), and the animation of the diffusion of AIDS in Pennsylvania (Gould, 1989). Both of these studies used aggregated data surfaces rather than the progression of individual disease cases as suggested by this chapter.

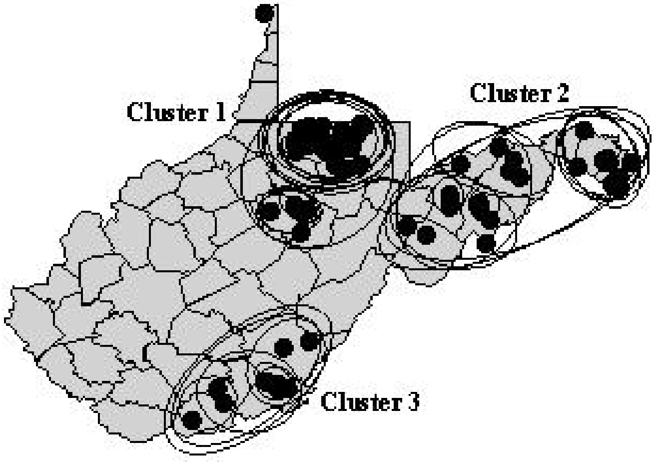
Preliminary Animations

In order to animate rabies for practical use, the scale of the animation has to be sufficient to allow local level land characteristics to be identified on an underlying map. In order to "scale-down" to a suitable area of West Virginia, initial animations were run for 1999 data and subjects were asked to identify what they perceived to be "clusters" of disease. A second animation was constructed for the same four-county area as identified and then investigated by the NNH spatial clustering analysis.

The first animation comprised of each positive raccoon rabies case for 1999 appearing sequentially (by date of reporting) on a county map of West Virginia. Each case appeared on screen as a yellow dot, which then turned to a blue dot one second later as the next reported positive case appeared on screen. All cases remained on screen. Figure 4 shows the last animation slide, including all cases for 1999, and the overlays of areas identified as "clusters" by each of the 10 subjects. Three general cluster areas can be identified on Figure 4. Sub-groups could also be seen within each of these clusters. Cluster 1 was the most consistently identified by the test subjects.

The second animation was performed on the same four-county area as had

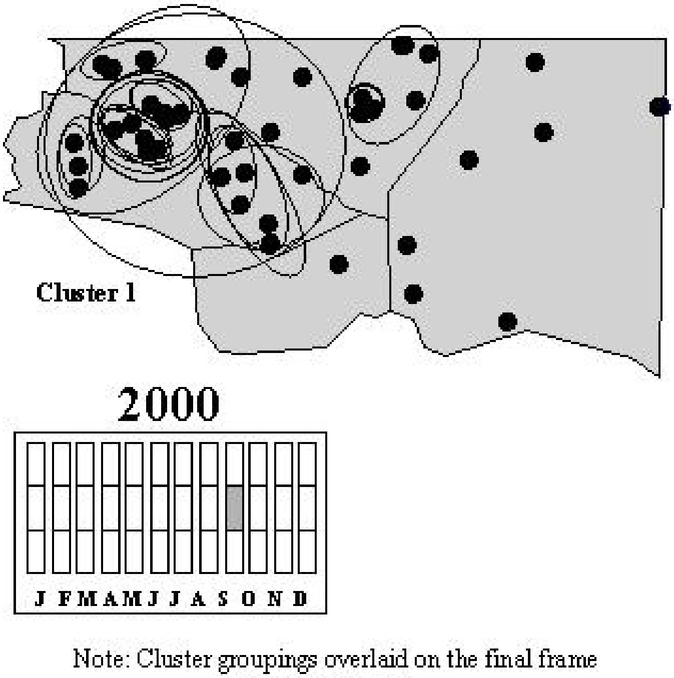
Figure 4: "Perceived" clusters from the 1999 animation



Note: Cluster groupings overlaid on the final frame of the animation been identified by both the NNH spatial clustering analysis and by the test subjects (as Cluster 1). This animation included all cases for 1999–2000, and also included a time chart; as each new case appeared as a yellow dot, so an associated yellow bar, representing the third of the month from which the case was reported, also appeared on screen. This time chart was a crude attempt at increasing the sophistication of the animation by presenting a time frame to the disease. Figure 5 displays subjects' "perceived" clusters.

The "perceived" clusters of both animation runs matched the significant clusters as identified by the NNH spatial clustering approach. This can most clearly be seen in Figures 3 and 5. The two significant clusters found by applying NNH spatial clustering to the four-county area were also regularly identified by the test subjects. What is unclear is how much of an influence the method of animation had on these perceived clusters, with subjects possibly being swayed by the final point distribution irrespective of how the points were dynamically displayed. In effect the subjects could be clustering a similar "static" data surface to the NNH spatial clustering algorithm. The compounding effect of maintaining all cases on screen could be diminished by graduating the color of cases by time. This approach will be discussed in the next section.

Figure 5: "Perceived" clusters from the 1999 & 2000 animation



Note: Cluster groupings overlaid on the final frame of the animation

Improving the Animation

The advantage of animating a disease surface is that an impression of both spatial and temporal pattern (and their interaction) can be gained. In order to construct this animation, a small enough area would have to be investigated that would allow for detail to be included such as land cover and elevation. This chapter has shown that the identification of this scale can be achieved by a common spatial clustering technique such as NNH spatial clustering. Once the "scale" of investigation has been chosen, so more sophisticated animations can be constructed.

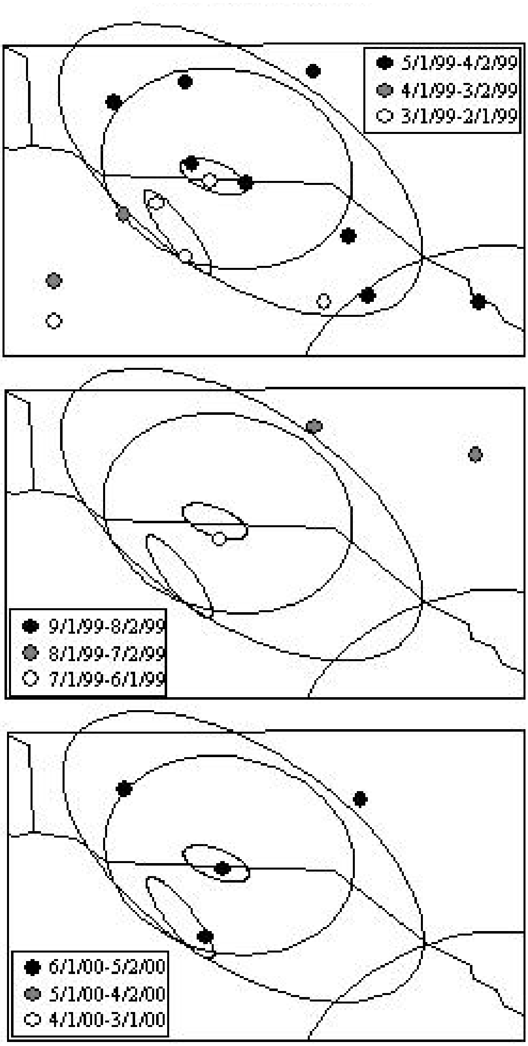
One problem with the animations presented in this chapter was how the temporal dimension was displayed. Two problems occur here, how to separate cases temporally that are not connected, and how to actually represent time. For the first animation, each case was displayed in the sequence of reporting, even though cases could occur from different foci (different sides of the state) and as such have no spatial connection. This problem was reduced once a study area (the four counties) had been identified as the disease cases are more likely to stem from the same foci.

The second problem, how to represent time, was approached by including a time chart which accompanied the animation. A more sophisticated approach would be to have the animation interval scaled to the case reporting interval—a one-day difference in an animal being submitted for testing being represented by a one-second difference in the animation. If done correctly, this would also allow the expert eye to see monthly and seasonal effects of the spread. Again the question of multiple foci affecting this interval would be negated once the correct "scale" of study had been identified.

A related temporal problem is that of case longevity within the animation. If all 1999 and 2000 data are to be included in the animation, should every case remain on-screen even after the passage of a considerable time period, such as one year? One solution to this problem would be to include graduated dots representing time lags. For example, all cases within a 31-day period would remain their original intensity (such as black). After 31 days, and before 62 days, the case would revert from black to gray. Between 62 days and 93 days, the case would revert to white. After 93 days the case would disappear from the animation. Figure 6 shows three variations of Figure 5 where this graduated color approach has been adopted. Notice how different the disease surface appears. Of course more work would need to be done on identifying what would be the correct time interval for each class. This would be further complicated by the possibility of variable incubation periods depending on whether the animal was solitary or part of a communal den (Torrence et al., 1992). Future research could also investigate a possible connection between a rise in the percentage of rabid raccoons (in the surveillance data) to a lagged overall peak in the number of cases (Torrence et al., 1992). This relationship might hold the key to identifying developing spatial clusters.

A further reason to adopt this approach is that an error frame should be placed around each of these rabies submissions. The date used in the animation represents when the animal was submitted, but was the animal found dead, or if it interacted with a human when alive, how advanced was the disease? Because of this fact, the

Figure 6: Incorporating graduated color into the animation



data should be considered as having a uni-directional temporal uncertainty. This means reporting dates should be considered as "fuzzy." A graduated color scheme would help "soften" the temporal sequence.

OTHER DATA CONSIDERATIONS

Rabies surveillance will always be an incomplete data set. Suburban areas have been found to have higher raccoon densities (Bromley et al., 1979), and of course better reporting likelihood (Jenkins and Winkler, 1987). Surveillance data, therefore, is usually significantly positively correlated to the human population of an area (people need to interact with these animals), and significantly negatively correlated to distance from testing facility, representing structural inertia (Curtis, 2000). Techniques have been developed to improve the quality of the data by identifying "holes" in comparison to the surrounding rabies submissions surface (Curtis, 1999). This can lead to improved reporting in areas that do not follow state requirements, or the first step towards an interpolated rabies surface in areas with low human populations. It is also possible to improve these interpolated surfaces by including a classified land cover surface, either through eliminating areas where disease cannot occur (such as a water body), or by introducing a probability surface of where an animal is likely to be found based on previous raccoon population studies (Pedlar et al., 1997).

Similarly, GIS techniques can also be used to improve the quality of the surveillance data. In many cases, either the negative or positive submissions do not include a spatial coordinate. Land cover can again be used as a guide to distribute points across the reporting area (usually a county). An alternative approach could use the positive relationship found between submissions and human population. The total number of submissions could be distributed in proportion to human population across the reporting area. Human population would be mapped at the smallest available spatial area, such as Zip Code, census tract or census block group.

Interpolation methods such as these could be used to calculate a surface of disease rates. Obviously 10 diseased animals from a population of 100 are more indicative of a disease problem than 10 from 1,000. Unfortunately, negative submissions often do not contain spatial coordinates. If the data did contain location, then a clustering technique such as the Spatial Filter (Rushton and Lolonis, 1996) could be used to identify significant disease clusters. By using the same human population-to-submission relationship, small area disease rates could still be used by the Spatial Filter (which assigns the value to the area centroid). However, this technique suffers from the same limitations as NNH spatial clustering in that it is not a spatial-temporal technique, meaning that some judgment again has to be made as to how to break the spatial data into temporal frames (one year, one season, etc.).

Torrence et al. (1992) claim that the percentage of positive raccoons (in effect the rate) is a more accurate measure of the rabies surface and, as such, should be used in determining the placement of an oral vaccine strategy. A further research direction could incorporate this "rate" directly into the animation by dividing the research space into small units and animating (or clustering) the centroid of each unit according to the rate of that cell. In effect a grid is draped over the research space using the GIS and the rates are calculated. This technique is again reliant on negative submissions having X Y coordinates, or alternatively applying one of the interpolation measures mentioned previously. If the grid extent (the space area covered by each cell of the grid) is too large, the power of the animation in understanding the spatial movement of the disease will be compromised.

CONCLUSION

This chapter has taken the first step towards the practical use of animation in disease control. As has previously been discussed, animation offers considerable promise in understanding the spatial and temporal dynamic of a contagious disease. However, practical considerations require the scale of the animation to be based around relatively small geographic areas. This chapter has shown that a traditional spatial cluster technique, such as NNH, can identify these areas for animation. The advantage of using these techniques over the animations presented in this chapter is one of implementation efficiency. Quite simply, it is quicker and easier to perform a spatial cluster analysis than a preliminary animation. The time saved can then be invested in a more sophisticated animation of the small geographic area.

Animation has an important role in future disease analysis. One could imagine an expert watching cases animate over a three-tier surface comprising land cover, elevation and a choropleth surface of interpolated (or recorded) submissions. In this way factors affecting spread, both spatial and seasonal, could be viewed as the disease moves through the area. The next logical step would be to calculate spread rates, and extrapolate them out over areas which are currently disease-free. Current software such as FLY! Software from PCI allow for satellite or photographic images to be draped over digital elevation models resulting in a fly-through, with the "expert" eye seeing the disease in as real a simulation as possible. We can even imagine further into the future when virtual reality landscapes allow us to really "see" the disease spread as it happens, putting us into the disease landscape. From the animation capabilities of the present, or the virtual simulations of tomorrow, visualizing an infectious disease in this manner can provide greater insight into disease spread and control than can be achieved by modeling alone.

REFERENCES

Bromley, P.T., Lochmiller, R.L., & Chapman, D.L. (1979). *Raccoon Biology and Management. Publication 801*. Blacksburg, VA: Virginia Polytechnic Institute and State University.

Brown, C.L., Rupprecht, C.E., & Tzilkowski, W.M. (1990). Adult raccoon survival in an enzootic rabies area of Pennsylvania. *Journal of Wildlife Diseases*, 26(3), 346-350.

Campbell, C.S. & Egbert, S.L. (1990). Animated cartography: Thirty years of scratching the surface. *Cartographica,* 27(2), 24-46.

Carey, A.B., Giles, R.H., Jr., & McLean, R.G. (1978). The landscape epidemiology of rabies in Virginia. *American Journal of Tropical Medicine and Hygiene,* 27, 573-580.

Coyne, M.J., Smith, G., & McAllister, F.E. (1989). Mathematic model for the population biology of rabies in raccoons in the mid-Atlantic states. *American Journal of Veterinary Research,* 50(12), 2148-2154.

Curtis, A. (1999). Using a spatial filter and a geographic information system to improve rabies surveillance data. *Journal of Emerging Infectious Disease*, 5(5), 603-606.

Curtis, A. (2000). Identifying spatial holes in a rabies surveillance surface: comparing results from cartographic visualization to spatial filter analysis. In Flahault, A., Toubiana, L. & Valleron, A. J. (Eds.), *Geography and Medicine* (pp. 40-48). Paris: Editions Scientifiques et Medicales Elsevier SAS.

DiBiase, D., MacEachren, A.M., Krygier, J.B. & Reeves, C. (1992). Animation and the role of map design in scientific visualization. *Cartography and Geographic Information Systems*, 19(4), 201-214, 265-266.

Everitt, B. (1974). *Cluster Analysis*. London: Heinemann Educational Books, Ltd.

Gould, P. (1989). Geographic dimensions of the AIDS epidemic. *The Professional Geographer*, 41(1), 71-78.

Hubbard, D.R. (1985). A descriptive study of raccoon rabies in a rural environment. *Journal of Wildlife Diseases*, 21(2), 105-110.

Jenkins, S. (1984). Mid-Atlantic raccoon rabies outbreak. In Centers for Disease Control and Prevention (Ed.), *Rabies Information Exchange, Public Health Service, U.S. No. 9* (pp. 47-59). Atlanta, GA: CDC.

Jenkins, S.R., & Winkler, W.G. (1987). Descriptive epidemiology from an epizootic of raccoon rabies in the middle Atlantic states, 1982-1983. *American Journal of Epidemiology,* 126, 429-437.

Kaufmann, J.H. (1982). Raccoon and allies. In Chapman, J. A. & Feldhamer, G. A. (Eds.), *Wild Mammals of North America: Biology,Management, and Economics* (pp. 567-585). Baltimore, MD: Johns Hopkins University Press.

Krebs, J.W., Strine, T.W., Smith, J.S., Rupprecht, C.E. & Childs, J.E. (1995). Rabies surveillance in the United States during 1994. *JAMA, 207,* 1562-1575.

Levine, N. (1999). *CrimeStat: A Spatial Statistics Program for the Analysis of Crime Incident Locations.* Annandale, VA: Ned Levine & Associates and Washington, DC: The National Institute of Justice.

Lewis, J.C. (1975). Control of rabies among terrestrial wildlife by population reduction. In G.M. Baer (Ed.), *The Natural History of Rabies, Vol. 2* (pp.53-77). New York, NY: Academic Press.

MacDonald, D.W. (1980). *Rabies and Wildlife, a Biologist's Perspective*. New York, NY: Oxford University Press.

New York State Department of Health, (1999). *The Raccoon Rabies Epidemic*. Albany, NY: Wadsworth Center.

Openshaw, S., Charlton, M., Craft, A.W. & Birch, J.M. (1988). Investigation of Leukemia clusters by the use of a geographical analysis machine. *The Lancet, I*, 272-273.

Pedlar, J.H., Fahrig, L. & Merriam, H.G. (1997). Raccoon habitat use at two spatial scales. *Journal of Wildlife Management,* 61(1), 102-112.

Rupprecht, C.E. & Kieny, M.P. (1988). Development of a vaccinia-rabies glycoprotein recombinant virus vaccine. In Campbell, J. B. & Charlton, K. M. (Eds.), *Rabies: Developments in Veterinary Virology* (pp. 335-364). Boston, MA: Kluwer Academic Publications.

Rushton, G., & Lolonis, P. (1996). Exploratory spatial analysis of birth defect rates in an urban population. *Statistics in Medicine,* 15, 717-726.

Smith, J.S., Sumner, J.W., Roumillat, L.F., Baer, G.M. & Winkler, W.G. (1984). Antigenic characteristics of isolates associated with a new epizootic of raccoon rabies in the United States. *The Journal of Infectious Disease,* 149(5), 769-774.

Thrower, N.J.W. (1959). Animated cartography. *Professional Geographer,* 11(6), 9-12.

Tinline, R.R. (1988). Persistence of rabies in wildlife. In Campbell, J. B. & Charlton, K. M. (Eds.), *Rabies: Developments in Veterinary Virology* (pp. 301-323). Boston, MA: Kluwer Academic Publications.

Torrence, M.E., Jenkins, S.R., & Glickman, T. (1992). Epidemiology of raccoon rabies in Virginia, 1984 to 1989. *Journal of Wildlife Disease*, 28(3), 369-376.

Wandeler, A. (2000). Oral immunization of wildlife. In G.M. Baer (Ed.), *Natural History of Rabies* (pp. 485-503). Boca Raton, FL: CRC Press Inc.

Yorke, J.A., Nathanson, N., Pianigiani, G. & Martin, J. (1979). Seasonality and the requirements for perpetuation and eradication of viruses in populations. *American Journal of Epidemiology,* 109, 103-123.

ACKNOWLEDGMENTS

Mr. Charles Trimarchi, New York State Department of Health, Albany, NY: Wadsworth Center, 1999.

Chapter X

Spatial Cluster Analysis for Etiological Research and Identification of Socio-Environmental Risk Factors

Michael Emch
Portland State University, USA

Mohammad Ali
International Vaccine Institute, Korea

This chapter describes the use of disease clustering methods using diarrheal disease data from a rural area of Bangladesh for which the authors created a household-level GIS database. Understanding distributions of diseases in space and time can be useful for etiologic research and socio-environmental risk factor identification. Disease clustering techniques are not only useful as etiological research tools for chronic diseases but also for infectious diseases. The magnitude of clustering in different areas can assist with the generation of hypotheses about the underlying socio-environmental causes of the clusters. Once clusters are identified, studies can then focus on the socio-environmental characteristics of the areas where clusters are found.

INTRODUCTION

Understanding distributions of diseases in space and time can be useful for etiologic research and socio-environmental risk factor identification. Disease clustering studies can help detect and monitor potential public health hazards. Investigators must adjust for the spatial variation of the population at risk for a disease when identifying disease clusters. If a population distribution is not controlled for, apparent disease clusters might simply reflect the distribution of the population. The goal of spatial clustering techniques is to distinguish between clusters that are due to chance alone and clusters that are associated with some underlying risk factor. Hjalmars et al. (1996), for example, used a geographic information system (GIS) and a spatial clustering algorithm to identify clusters of childhood leukemia in Sweden. In that country, there is public concern that environmental factors, such as high voltage power lines and nuclear power plants, are responsible for the disease. While anecdotal information might suggest that there is a relationship between environmental factors and childhood leukemia, the investigators found no significant spatial clusters associated with nuclear power plants in Sweden.

Disease clustering techniques are not only useful as etiological research tools for chronic diseases but also for infectious diseases. There will usually be more spatial clustering in infectious diseases than in chronic diseases. The magnitude of clustering in different areas can assist with the generation of hypotheses about the underlying socio-environmental causes of the clusters. Once clusters are identified, studies can then focus on the socio-environmental characteristics of the areas where clusters are found. This chapter describes the use of disease clustering methods using diarrheal disease data from a rural area of Bangladesh for which we created a household-level GIS database.

Several different methodologies have been developed for detecting geographical clusters of health events that are represented as points in space. Most methodologies test for global clustering of events (Alt & Vach, 1991; Besag & Newell, 1991; Cuzick & Edwards, 1990; Diggle & Chetwynd, 1991; Grimson, 1991; Moran, 1950; Ranta et al., 1996; Tango, 1995; Walter, 1994; Whittemore et al., 1987). Global cluster analysis is descriptive in nature, i.e., it (a) either detects the location of clusters but cannot be used for inference or (b) can be used inferentially but cannot be used to identify the location of specific clusters (Kulldorff, 1997). This chapter uses the spatial scan statistic proposed by Kulldorff (1997), which can detect spatial clusters of health events and be used inferentially. Clusters of two types of health events, cholera and cholera-like diarrhea, were identified in Matlab, Bangladesh. Once the clusters were identified using several different local cluster analysis techniques, we developed hypotheses concerning whether or not the ecological niches of the two diseases are the same.

STUDY AREA

Matlab has a population of approximately 200,000, and the area is endemic with cholera and other diarrheal diseases. It is 184 square kilometers and comprises 142 villages. The population density is approximately 1,100 persons per square kilometer. The people live in clusters of patrilineally related households called *baris*. Matlab is in south-central Bangladesh, approximately 50 kilometers southeast of Dhaka, adjacent to the Lower Meghna River. The Dhonagoda River flows from north to south bisecting the study area into two approximately equal parts. There are numerous canals in the area that remain dry in the winter and fill with water during the summer monsoon. An embankment adjacent to the Dhonagoda and Meghna Rivers was completed in 1989. The embankment was built primarily to protect the area against monsoon flooding so that three annual rice crops can be grown rather than the previous two. Implementing the embankment has markedly differentiated ecological and economic characteristics between the areas inside and outside the embankment (Emch & Ali, 2001; Myaux et al., 1997; Siddique et al., 1991).

Most people living in Matlab have access to bacteriologically safe tube well water; however, surface water is largely used for cooking, bathing and washing utensils (McCormack et al., 1969; Emch, 1998). Most people use unsafe latrines, which are temporary structures with poor sewage systems (Emch, 1998). Since public sewage systems do not exist, people usually construct latrines near the edge of ponds or on the banks of rivers and canals. In the absence of such water bodies, holes are dug. Most of these holes remain uncovered, and in the rainy season feces overflow and contaminate surface water. Such sanitation conditions are presumed to be the cause of many enteric diseases in the area.

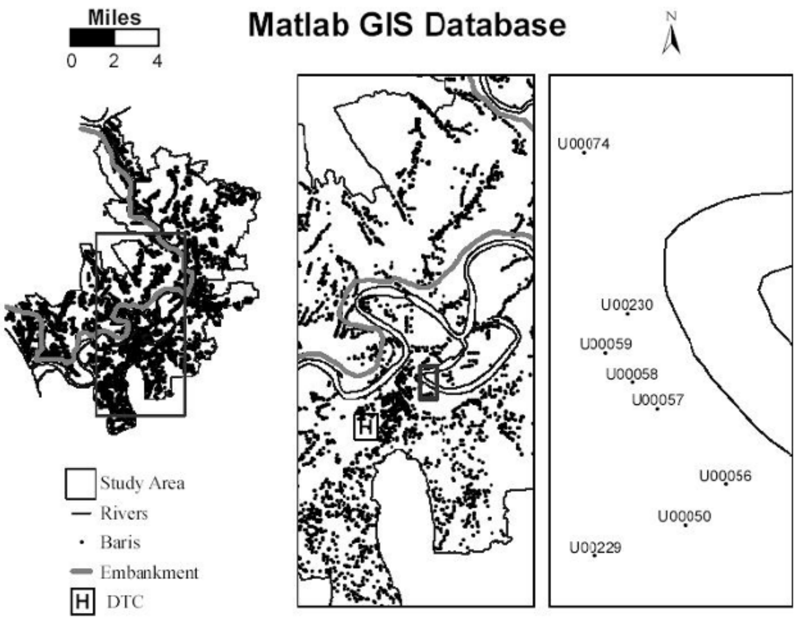
STUDY DATA

This study identifies cholera and cholera-like disease clusters for hospitalized patients from the Matlab study area. Disease clusters are identified for a three-year period, from January 1, 1992, to December 31, 1994. The study data were obtained from demographic surveillance, hospital surveillance, and a spatial database of the study area. The data obtained from the different sources were integrated into the spatial database. Detailed descriptions of the creation of the Matlab GIS are published elsewhere (Ali et al., 2001; Emch, 1998), however, the sources of data and the integration process are briefly described below. Initiated in 1966, the Matlab demographic surveillance system (DSS) has been recording all vital demographic events of the study area population (D'Souza, 1981; Koenig et al., 1988; Phillips et al., 1988). The system assigns all people living in the study area a unique registration number, which identifies their village, *bari,* and household. Community-based demographic data collection is done by 120 community health workers who visit each household every two weeks. The DSS database was used to calculate an annual population during the study period.

The Matlab field research center includes a diarrhea treatment center (DTC), which has in- and out-patient services as well as a laboratory for the identification of pathogens. The Matlab DTC treats about 7,000 to 8,000 diarrhea cases per year at no cost to patients. The DTC maintains motorized boats, which function as a free ambulance service for diarrhea patients, thus ensuring excellent access to the hospital throughout the study area. Approximately 25 percent of the patients admitted to the DTC are from the DSS area. Stool samples are collected for all patients from the DSS area, and the samples are screened for enteric pathogens in the hospital's laboratory. All cases of cholera and cholera-like diarrhea for people living in the study area were identified from the hospital surveillance system. All cholera cases were confirmed by laboratory tests. Cholera-like diarrhea is defined as watery diarrhea without laboratory isolation of cholera-causing bacteria.

A vector GIS database of the study area was created in 1994 to facilitate spatial analysis for health and population studies. The study area data were digitized from 1:10,000 air photographs. The database includes several geographic features of the study area including *baris*, the flood-control embankment, rivers and health facilities (Figure 1). A field survey was conducted to identify all *baris* by their DSS

Figure 1: Study area spatial database



bari code. The Matlab health, demographic and hospital surveillance databases are managed at the individual level. Thus, disease and demographic data were aggregated by *bari*, which are point objects in the Matlab GIS database.

SPATIAL SCAN STATISTIC

The SaTScan software produced by Kulldorff et al. (1998) detects spatial and spatio-temporal clusters of disease. The SaTScan software can (1) evaluate spatial or space-time disease clusters and measure whether they are statistically significant; (2) determine whether a disease is randomly distributed in space or in space and time; and (3) perform geographical surveillance of disease and detect areas of significantly high or low rates. The SaTScan software uses either a Poisson-based model, where the number of events in an area is Poisson distributed under the null hypothesis, or a Bernoulli model, with binary event data for case-control studies. The program adjusts for the underlying distribution of the population. The Poisson model can also adjust for categorical covariates. With the Bernoulli model, cases represent people with the disease being studied and non-cases represent people without the disease or with another disease. The cases and controls can be a sample of the total population or they may constitute the total population. With the Poisson model, the expected number of cases in each part of the study area is proportional to its population size.

All of the models implemented in SaTScan detect clusters in a multidimensional point process and allow variable window sizes to scan for the health events within the study area. The variable window size is important because we usually do not have prior knowledge about the size of the area covered by a cluster. The method also adjusts for the uneven distribution of the population in space while detecting for clusters. The Poisson model is used when the population reflects the underlying risk such as total person years in an area. The method requires case and population counts for a group of points and the geographical coordinates of the points. In the Bernoulli model, the cases and controls are represented by ones and zeros, and the population counts are replaced by the number of controls.

The spatial scan statistic uses a circular scan window, which is moved over the entire study area. The radius of the window varies continuously in size from zero to a user-defined upper limit, which is a percentage of the total population at risk. Clusters indicate areas with lower rates outside a circular scan window compared with higher rates inside a circular scan window. The location and size of the window changes creating an infinite number of distinct geographical circles. There are different sets of neighboring areas within them and each is a possible cluster. The space-time scan statistic is defined by a cylindrical window, with a circular geographic base, for which height corresponds to time. The base is defined the same as for the spatial scan statistic, except that the height reflects the time period of potential clusters. The cylindrical window is then moved in space and time. The result is an infinite number of overlapping cylinders of different sizes and shapes, covering the entire study region, where each cylinder reflects a possible cluster.

Since the scan test uses variable window sizes, computing the number of points at any given time is not possible (Loader, 1991), therefore a likelihood ratio is calculated. Under the Poisson model, the likelihood function for a specific window is:

$$\lambda_p = \left(\frac{n}{\mu}\right)^n \left(\frac{N-n}{N-\mu}\right)^{(N-n)} I(n > \mu)$$

where,
N= number of cases in the whole area,
n=number of cases within the window,
μ is the expected number of cases within the window under the null hypothesis, and
I() is an indicator function.

Since we only scan for clusters with high rates, I() becomes one when the window has more cases than expected under the null hypothesis and in all other cases it is zero. With a set N and m, the likelihood increases with the number of cases in the window.

The likelihood function for the Bernoulli model is:

$$\mathrm{L}(Z, p, q) = \left(\frac{\mathrm{n}}{\mathrm{m}}\right)^{\mathrm{n}} \left(1 - \frac{\mathrm{n}}{\mathrm{m}}\right)^{(\mathrm{m}-\mathrm{n})} \left(\frac{\mathrm{N}-\mathrm{n}}{\mathrm{M}-\mathrm{m}}\right)^{(\mathrm{N}-\mathrm{n})} \left(1 - \frac{\mathrm{N}-\mathrm{n}}{\mathrm{M}-\mathrm{m}}\right)^{(\mathrm{M}-\mathrm{m})-(\mathrm{N}-\mathrm{n})} \mathrm{I}()$$

where,
M=number of controls (or the population) in the whole area and
m=number of controls (or the population) within the window.

The likelihood function is maximized over all windows, identifying the window that constitutes the "most likely" cluster. The "most likely" cluster is the cluster that is least likely to have occurred by chance. The likelihood ratio for the window is noted and constitutes the maximum likelihood ratio test statistic. Its distribution under the null hypothesis and its corresponding p-value are determined by repeating the same procedure on a large number of random replications of the data set generated under the null hypothesis, using a Monte Carlo simulation approach.

The models also detect secondary clusters that have the highest likelihood function for a particular window and do not overlap the "most likely" cluster or other secondary clusters of higher likelihood. The program scans for clusters of geographic sizes between zero and 50 percent of the total population at risk. The methods look for clusters without any predetermined cluster size.

CLUSTERS OF CHOLERA AND CHOLERA-LIKE DIARRHEA

The cholera and cholera-like disease data were aggregated by *bari* for the three study years (1992 to 1994) for the spatial cluster analysis. In order to analyze for space-time clustering, the data were aggregated annually. The *baris* that were further than nine kilometers from the DTC were excluded from the analysis because few cases were found in that part of the study area; this suggested that people might have been less likely to seek medical care further from the hospital. We analyzed approximately 6,000 *baris* within nine kilometers of the DTC. The three-year aggregate population in these *baris* was 456,325. There were 1,200 cases of cholera, which is 2.6 cases of cholera per thousand people per year. The aggregate number of cases of cholera-like diarrhea was 729, which is 1.6 diarrhea cases per thousand people per year. SaTScan analyzes overlapping circles centered on each *bari*, whose radii increase continuously until 50 percent of the total population is covered. In our example the test analyzed 18,000,000 (0.5×6000^2) distinct zones and generated 999 random Monte Carlo replicas of the data set under the null hypothesis, calculating the test statistic for each replica.

The Poisson model is appropriate for these data sets because it controls for the background population. The Poisson model results for cholera are summarized in Table 1. In addition to the "most likely" cluster, the secondary cholera clusters are also reported in the table in the order of their likelihood ratio. The results include only non-overlapping secondary clusters that are significant at the 0.10 level or

Table 1: Spatial Poisson model: Cholera

Zone	Population	No. of cases	Incidence rate/10,000	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	65,981	326	16.47	1.879	65.04	0.001	2856.74
B	428	11	85.65	9.773	15.24	0.001	133.38
C	450	10	74.06	8.450	12.56	0.010	63.45
D	5214	34	21.73	2.480	10.76	0.062	728.32

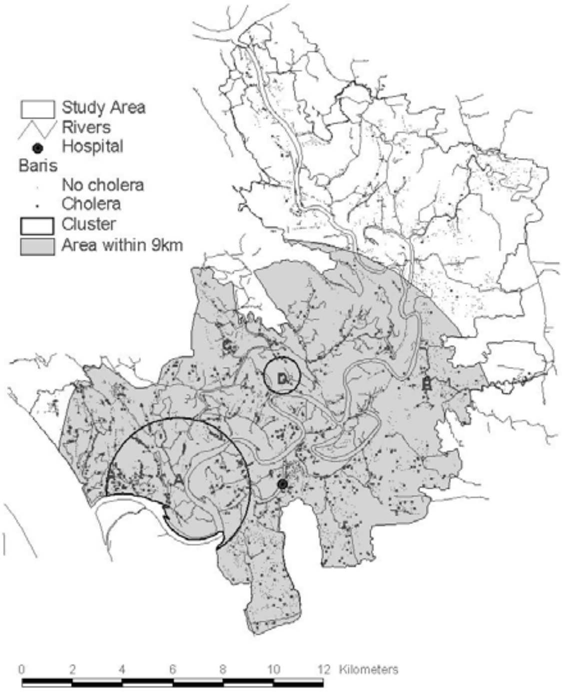
A is the "most likely" cluster, and B, C and D are secondary clusters

Table 2: Spatial Poisson model: Cholera-like diarrhea

Zone	Population	No. of cases	Incidence rate/10,000	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	227,186	485	7.11	1.336	41.63	0.001	9090.92

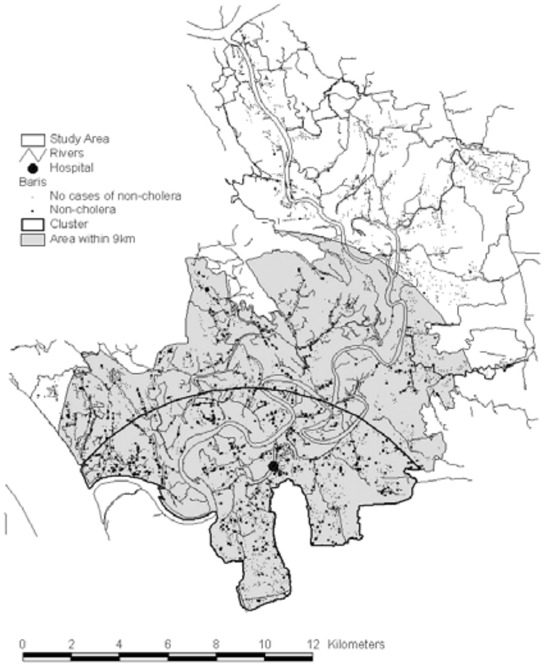
There were no significant secondary clusters

Figure 2: Spatial clusters of cholera derived from Poisson model



better. Clusters comprised of fewer than four *baris* were not included. The results of the cholera-like diarrhea cluster analysis are presented in Table 2. Since no secondary clusters of cholera-like diarrhea were significant, the table is comprised of only the "most likely" cluster of the disease. Figure 2 is a map of the *baris* that formed significant clusters of cholera. The "most likely" cholera cluster (A) is in the southern part of the study area. While the secondary clusters (B, C and D) are more scattered, most secondary cluster *baris* are in the central part of the study area. Figure 3 is a map of the "most likely" cluster of cholera-like diarrhea. There are no

Figure 3: Spatial clusters of cholera-like diarrhea derived from Poisson model



significant secondary clusters. The map shows that the "most likely" cluster is formed by a large number of *baris*.

The Bernoulli model method was used as a comparison for the Poisson model results. In the Bernoulli model, the case file includes *baris* with at least one case, while the control file includes *baris* with no cases. The Bernoulli model was employed using both cholera and cholera-like diarrhea; Tables 3 and 4 summarize the results respectively. Figures 4 and 5 are maps of the Bernoulli cluster *baris*. Comparing Figures 2 and 4, which are maps of cholera clusters using the Poisson and Bernoulli methods respectively, shows that the "most likely" clusters are in the same areas. However, the locations of the secondary clusters obtained using the two methods differ. The map of cholera-like diarrhea obtained using the Bernoulli model (Figure 5) does not completely agree with the map derived from the Poisson model (Figure 3).

Table 3: Bernoulli model: Cholera

Zone	Population	No. of cases	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	860	180	1.751	33.46	0.001	2784.77
B	649	118	1.521	12.02	0.033	3583.16

A is the "most likely" cluster and is the secondary cluster

Table 4: Bernoulli model: Cholera-like diarrhea

Zone	Population	No. of cases	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	2758	366	1.323	29.60	0.001	5006.29
B	116	29	2.492	10.93	.093	741.81

A is the "most likely" cluster and is the secondary cluster

Figure 4: Spatial clusters of cholera derived from Bernoulli model

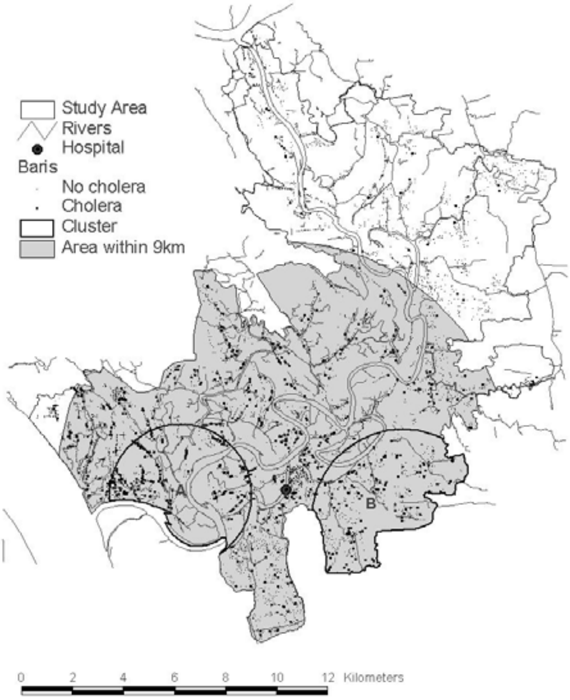
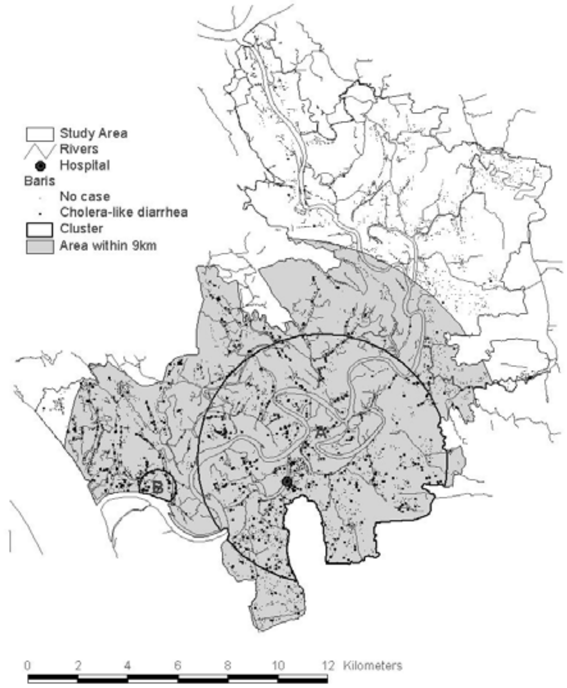


Figure 5: Spatial clusters of cholera-like diarrhea derived from Bernoulli model



The Poisson model was also used to analyze clustering in space and time. The health event and population data were arranged by year so that they could be analyzed in a spatio-temporal framework. The results of the analysis are presented in Tables 5 and 6 for cholera and cholera-like diarrhea respectively. As expected, the results of the space-time analysis yielded fewer clustered *baris* for both diseases. Figures 6 and 7 are maps of the *baris* that form the clusters. The cholera cluster shown in Figure 6 appears to be a subset of the spatial cluster shown in Figure 2. The spatio-temporal cluster of cholera-like diarrhea that is shown in Figure 7 seems to correspond to the spatial cluster identified in Figure 3. This suggests that there was little temporal variation in the cholera-like diarrhea data.

Table 5: Spatio-temporal model: Cholera

Zone	Population	No. of cases	Incidence rate/10,000	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	20078	306	50.79	1.901	61.99	0.001	2760.36
B	291	19	217.58	8.146	23.30	0.001	93.07
C	925	27	97.28	3.642	15.47	0.001	223.54
D	143	11	256.94	9.619	15.08	0.001	133.38
E	150	10	222.20	8.318	12.42	0.011	105.19

A is the "most likely" cluster and B, C, D and E are secondary clusters

Table 6: Spatio-temporal model: Cholera-like diarrhea

Zone	Population	No. of cases	Incidence rate/10,000	Overall relative risk	Log likelihood ratio	P-value	Radius in meters
A	75,807	485	21.32	1.336	41.54	0.001	9090.92

There were no significant secondary clusters

Figure 6: Spatio-temporal clusters of cholera

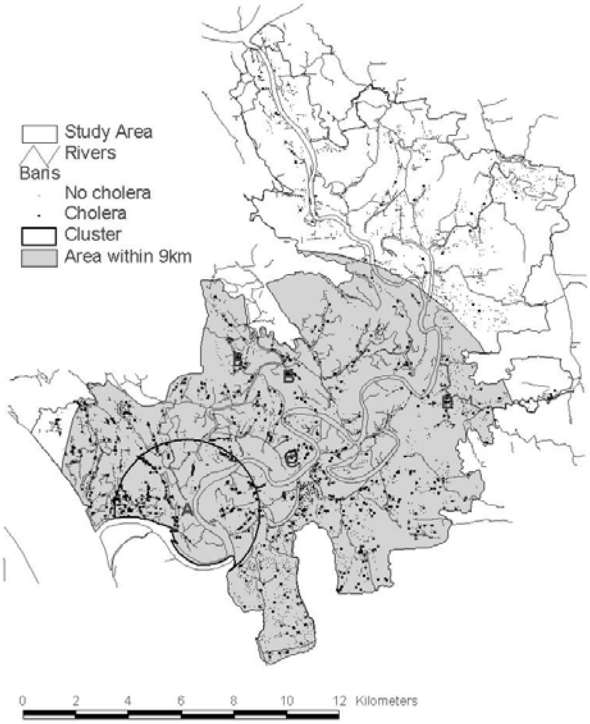
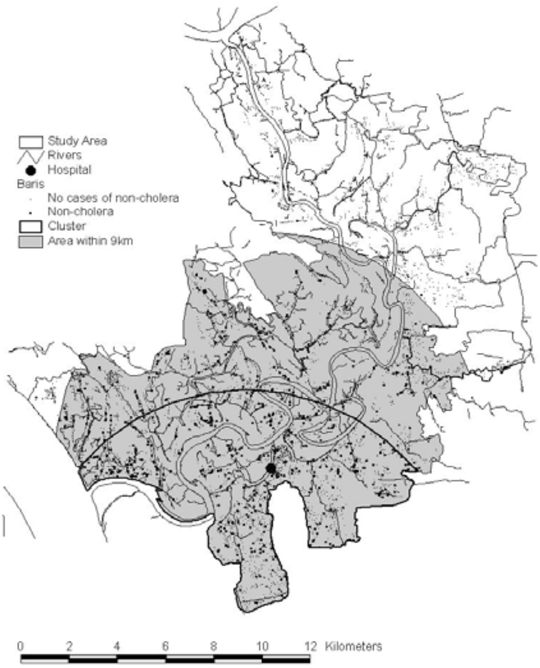


Figure 7: Spatio-temporal clusters of cholera-like diarrhea



DISCUSSION AND CONCLUSIONS

Isolating clusters of disease in space and time identifies places and periods in which people are more likely to contract a disease. Cluster analysis is one method to define outliers in a normal spatio-temporal disease pattern for a particular area. Therefore, clusters represent groups of important disease events for a particular area that public health practitioners might want to investigate further. Maps of spatial clusters (Figure 4) and spatio-temporal clusters (Figure 6) reveal that the disease foci of cholera are in the southern part of the study area. After identifying clusters, knowledge of a study area can lead investigators to develop hypotheses about the socio-environmental characteristics of the areas in which the clusters are found. The southern part of Matlab is near the confluence of the Meghna and the Dhanogoda Rivers. It is also inside the flood-control embankment. Therefore, the disease clusters may be related to flood-control and proximity to these rivers and should be investigated further.

Colwell et al. (1985) theorized that the location of the environmental reservoir of cholera is rivers, canals, brackish ponds and streams. The reservoir contains dormant cholera bacteria, which multiply at certain times of the year because of salinity changes and the number of available attachment sites (plankton) for the bacteria. Rivers, canals, brackish ponds and streams are heterogeneously distributed throughout the study area, thus the environmental reservoir varies spatially. After periods of disease dormancy, people contract cholera from environmental sources; subsequent cases are due to either primary transmission from the environment or due to secondary transmission from other people. We hypothesize that the clusters in the southern corner of the study area are the result of primary cholera outbreaks and then a large number of secondary cases. The people who settled in this area were displaced because of severe erosion of the Meghna River and these people are extremely poor. Characteristics peculiar to this population may have predisposed this group to greater secondary transmission.

The study of spatial and spatio-temporal disease clusters is becoming more widespread in geographical epidemiology and medical geography because of the increasing accessibility of spatial analytical tools. Not only are both local and global clustering software packages easily accessible, but tools for collecting and managing locational information are also becoming less expensive. The SaTScan software used for this project is freeware (http://www.cancer.gov/prevention/bb/satscan.html). The methods are, however, quite processor intensive. In our example we analyzed approximately 6,000 points using a Pentium III with 256 MB RAM and it took 3.5 hours to run. Analyzing 8,348 points took approximately 10 hours. Global positioning system (GPS) receivers that result in spatial accuracies of less than 10 meters are readily available for approximately US $100. Once data are collected using GPS receivers, user-friendly desktop GIS software packages can be used to manage and integrate disease and background population data. The technical and methodological complexities involved in identifying spatial clusters are now relatively easy to overcome. Therefore, spatial cluster analysis can now be used in etiological research and to identify socio-environmental risk factors for diseases.

ACKNOWLEDGMENTS

This research was conducted at the ICDDR,B: Center for Health and Population Research with the support of grants from the Association of American Geographers, the American Institute of Bangladesh Studies, Belgian Technical Cooperation (formerly BADC) and the ICDDR,B. We would like to thank the anonymous reviewers for their helpful comments.

REFERENCES

Ali, M., Emch, M., Ashley, C., & Streatfield, P.K. (2001). Implementation of a medical geographic information system: Concepts and uses. *Journal of Health Population and Nutrition*, 19(2), 100-110.

Alt, K.W. & Vach, W. (1991). The reconstruction of 'genetic kinship' in prehistoric burial complexes—problems and statistics. In Bock, H.H. & Ihm, P. (Eds.), *Classification, Data Analysis, and Knowledge Organization*. Berlin: Springer Verlag.

Besag, J. & Newell, J. (1991) The detection of clusters in rare diseases. *Journal of the Royal Statistical Society, Series A*, 154, 143-155.

Colwell, R.R., Brayton, P.R., Grimes, D.J., Roszak, D.R., Huq, S.A. & Palmer, L.M. (1985). Viable, but non-culturable *Vibrio cholerae* and related pathogens in the environment: Implications for release of genetically engineered micro-organisms. *Bio/Technology*, 3, 817-820.

Cuzick, J. & Edwards, R. (1990). Spatial clustering for inhomogeneous populations. *Journal of the Royal Statistical Society, Series B*, 52, 73-104.

Diggle, P.J. & Chetwynd, A.D. (1991). Second-order analysis of spatial clustering for inhomogeneous populations. *Biometrics*, 47, 1155-1163.

D'Souza, S. (1981) A population laboratory for studying disease processes and mortality–the demographic surveillance system, Matlab, Bangladesh. Special Publication No. 13, ICDDR,B, Dhaka, Bangladesh.

Emch, M.E. (1998). *Spatial and Environmental Risk Factors for Diarrhoeal Disease in Matlab, Bangladesh (PhD Thesis)*. Ann Arbor, MI: UMI Dissertation Services, A Bell & Howell Company.

Emch, M. & Ali, M. (2001). Spatial and temporal patterns of diarrheal disease in Matlab, Bangladesh. *Environment and Planning A*, 33(2), 339-350.

Grimson, R.C. (1991). A versatile test for clustering and a proximity analysis of neurons. *Methods of Information in Medicine*, 30, 299-303.

Hjalmars, U., Kulldorff, M., Gustafsson, G. & Nagarwalla, N. (1996). Childhood leukemia in Sweden: Using GIS and a spatial scan statistic for cluster detection. *Statistics in Medicine*, 15, 707-715.

Koenig, M.A., Fauveau, V., Chowdhury, A.I., Chakraborty, J. & Khan, M.A. (1988). Maternal mortality in Matlab, Bangladesh: 1976-85. *Studies in Family Planning*, 19(2), 69-80.

Kulldorff, M., Rand, K., Gherman, G., Williams, G. & DeFrancesco D. (1998). *SaTScan v2.1: Software for the Spatial and Space-Time Scan Statistics*. Bethesda, MD: National Cancer Institute.

Kulldorff, M. (1997). A spatial scan statistic. *Communications in Statistics: Theory and Methods*, 26, 1481-1496.

Loader, C.R. (1991). Large-deviation approximations to the distribution of scan statistics. *Advances in Applied Probability*, 23, 751-771.

McCormack, W.M., Mosley, W.H., Fahimuddin, M., & Benenson, A.S. (1969). Endemic cholera in rural East Pakistan. *American Journal of Epidemiology*, 89(4), 393-404.

Moran, P.A.P. (1950). Notes on continuous stochastic phenomena. *Biometrika*, 37, 17-23.

Myaux, J.A., Ali, M., Chakraborty, J. & de Francisco, A. (1997). Flood control embankments contribute to the improvement of the health status of children in rural Bangladesh. *Bulletin of the World Health Organization*, 75(6), 533-539.

Phillips, J.F., Simmons, R., Koneig, M.A., & Chakraborty J. (1988). Determinants of reproductive change in a traditional society: Evidence from Matlab, Bangladesh. *Studies in Family Planning*, 19(6), 313-334.

Ranta, J., Pitkaniemi, J. & Karvonen M. (1996). Detection of overall space-time clustering in non-uniformly distributed population. *Statistics in Medicine*, 15, 2561-2572.

Siddique, A.K., Baqui, A.H., Eusof, A., Haider, K., Hossain, M.A., Bashir, I., & Zaman, K. (1991). Survival of classical cholera in Bangladesh. *Lancet*, 337,1125-1127.

Tango, T. (1995). A class of tests for detecting 'general' and 'focused' clustering of rare diseases. *Statistics in Medicine*, 14, 2323-2334.

Walter, S.D. (1994). A simple test for spatial pattern in regional health data. *Statistics in Medicine*, 13, 1037-1044.

Whittemore, A.S., Friend, N., Brown, B.W., & Holly, E.A. (1987). A test to detect clusters of disease. *Biometrika*, 74, 631-635.

Chapter XI

The Use of GIS and Remote Sensing in Schistosomiasis Control in China

Edmund Y. W. Seto and Bing Xu
University of California at Berkeley, USA

Weiping Wu
Shanghai Institute of Parasitic Disease, PC, China

George Davis
George Washington University Medical Center, USA

Dongchuan Qiu and Xueguang Gu
Sichuan Institute of Parasitic Disease, PC, China

Peng Gong and Robert C. Spear
University of California at Berkeley, USA

Despite considerable achievements in the control of schistosomiasis in China, it remains one of the country's most serious public health problems. Geographic information systems and remote sensing provide new tools for better understanding the spatial epidemiology of disease transmission. We present applications of these technologies at both the regional and local scale. At the regional scale, we compare remote sensing approaches for mapping snail intermediate host habitat in the mountainous environment and the flood basins of the upper and lower Yangtze River, respectively. At the local scale, *we present the use of global positioning systems and geocoding of routinely collected field data. High-resolution IKONOS imagery is used to identify landscape characteristics associated with disease transmission at the village level. We conclude with a discussion of the implications of these technologies for improved disease control.*

INTRODUCTION

Schistosomiasis has existed in China for over 2,100 years, and remains one of country's most serious public health problems (Chen & Zheng, 1999). Nearly one million Chinese are infected with schistosomiasis. Despite great success in eradicating the disease in some areas, schistosomiasis remains endemic in 118 counties in seven provinces, placing an estimated 40 million at risk of infection.

The disease is caused by infection by the *Schistosoma japonicum* parasite (Webbe, Sturrock & Jordan, 1993). Humans and other animals become infected via contact with contaminated water. In rural China, such water contact for humans is inevitable for those involved in irrigated agriculture, fishing, cattle grazing, and domestic duties, such as washing. Children who often play in water are also at risk of infection.

The lifecycle of *S. japonicum* begins with the maturation of the parasite into adult worms in the blood vessels of the animal host. These worms, called schistosomes, sexually pair and lay eggs, which are excreted from the host in feces. This is different from *S. haematobium*, in which eggs are excreted in the urine of the infected host. In the absence of waste treatment, these eggs are released back into the environment. The problem is compounded by the use of human and animal excrement as fertilizer in agricultural areas. A new form of the parasite, miracidia hatch from the eggs when they become exposed to freshwater. These free-swimming miracidia must infect an appropriate snail in which to develop. In China, the amphibious *Oncomelania hupensis* snail serves as the intermediate host for the parasite. After a period of asexual reproduction, free-swimming larvae called cercariae leave the snail and are transported in water where they come into contact with animal hosts. Cercaria can penetrate the intact skin of the host, thus infecting them and continuing the lifecycle.

Spatial relationships between the parasite, snail and human (and other animal hosts) habitats are strong determinants of disease risk. For humans, two processes are driven by spatial factors: the infection process, which is determined in part by where contact with contaminated water occurs, and the process of egg dispersion, in which the spread of parasitic eggs is related to human activity such as the geographic distribution of land-use and stool fertilizer use. Snails are also affected by spatial factors: the location of suitable snail habitat, such as appropriate soil conditions, moisture and temperature, and the influence of snail transport, which is related to rainfall, terrain and hydrologic events such as flooding.

Spatial scale should be acknowledged when discussing the aforementioned spatial relationships. At the large, global scale, differences exist in the distribution of intermediate snail host species and associated *Schistosoma* species, which have been mapped by the World Health Organization (WHO, 1993). At this scale, ecological change such as global warming may affect the distribution of schistosomiasis (Martens, Jetten & Focks, 1997). Our focus is on spatial factors that operate at the regional (province and county) and local (village) scale within China. We discuss regional differences in the biology, ecology and epidemiology between different schistosomiasis-endemic areas, the relationship between ecological change and emerging schistosomiasis, and the use of remote sensing as a way to monitor regional changes and perform disease surveillance. In addition, we present our recent work based in Sichuan Province, which illustrates practical uses of geographic information systems (GIS) and remote sensing to better understand schistosomiasis transmission at the local scale.

REGIONAL METHODOLOGIES

Based on work published by Mao (1990), Chinese researchers generally categorize schistosomiasis transmission into one of three different types based on differences in the geography of endemic areas and the ecology of the intermediate host snail. These categories are: 1) plain regions with waterway networks, 2) swamp and lake regions, and 3) hilly and mountainous regions. Similarly, Davis et al. (1999) describe four modes of schistosome transmission in China, which are primarily characterized by the relationships between ecology and the establishment of genetically different subspecies of snail that live in these ecologies.

One mode of transmission relates to Poyang Lake in Jiangxi Province, where the *O. h. hupensis* subspecies of snail serves as the intermediate host. The lake is actually a flood plain completely enclosed by dikes, which resemble a lake during the rainy season and grasslands during the dry season. Because of this unique environment, fishermen and other boatmen are primarily infected during the rainy season, and cattle herders who take their cattle into the grasslands to graze are primarily infected during the dry season. It is hypothesized that more than 85% of transmission is due to cattle, which serve as reservoir hosts for the parasite. Because of annual flooding, most adult snails drown, making the life expectancy of snails in this environment only one year.

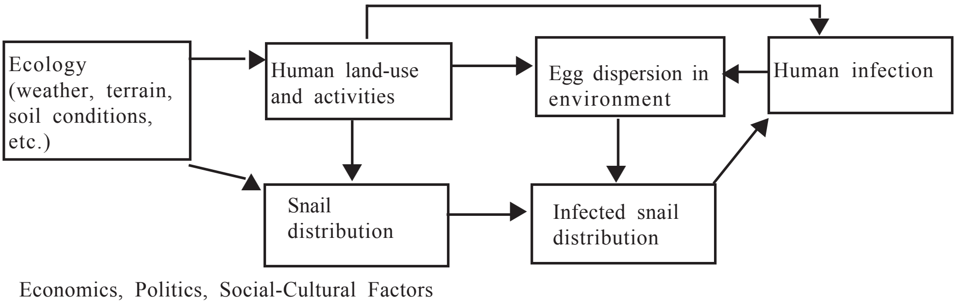
A second mode of transmission is the Yangtze River islands and flood plains such as those in Jiangsu Province. As in Poyang Lake, *O. h. hupensis* subspecies of snail serves as the intermediate host in this environment, where the islands resemble flat, marshy, grazing land, and the flood plains are moderately forested grassland. A major difference from Poyang Lake is the effect of the annual floods, which in this environment sweeps and mixes snails, leaving aggregates of snails of varying ages after the flood.

A third mode of transmission is the canals of Hubei Province, where *O. h. hupensis* subspecies live at the end branches of canal systems in this province. The canal does not flood, as it is protected from the Yangtze River by dikes and water gates that are closed during flooding. As such, snail populations are probably stable in this environment.

The last mode of transmission is the hills and low mountains above the Three Gorges region of the Yangtze River, in Sichuan and Yunnan Provinces. Here, *O. h. robertsoni* subspecies are the intermediate host. These snails are relatively isolated from the effects of the flooding Yangtze, living primarily in small irrigation ditches feeding mixed agricultural fields. The snails, hence, have longer life expectancies, with relatively stable populations, except when perturbed by changes in farming practices. Also since snails are most associated with agricultural fields rather than grazing land, animals play a much smaller role in this mode of transmission.

The underlying theme for both Mao and Davis' classification of schistosomiasis transmission is that differences in geography are associated with differences in ecology, which ultimately affect the nature of disease transmission. We can model this as a complex linkage (Figure 1) starting with natural ecology (weather, terrain and soil conditions), which influences how humans use and interact with the land. For example, ecology can determine to a large extent whether villagers primarily farm, fish or raise cattle. If, for example, villagers are primarily farmers, ecology can dictate what crops they grow, which puts restrictions on how they farm (fertilizer

Figure 1: Linkage of spatial factors influencing human schistosomiasis infection



usage and irrigation system design). In turn, both natural ecology as well as human land-use can affect snail distributions (natural habitat and man-made habitats). Whether a snail becomes infected is primarily a function of overall snail abundance in an area, and whether humans or animals spread eggs into that area. Human infection depends on whether their activity patterns put them at risk of exposure to cercaria released from infected snails. Wrapping around this entire linkage are economic and political factors, as well as social-cultural factors that affect disease transmission.

As this model illustrates, changes in ecological conditions can cascade along the linkages, and have the potential to profoundly change one's risk of schistosomiasis infection. At the regional level, one such change may be the construction of the Three Gorges Dam along the Yangtze River (Gleick, 1998). Currently, two subspecies of snail—*O. h. robertsoni* and *O. h. hupensis*—are separated, each occupying their own ecological niches, upstream and downstream of the gorges, respectively. This may change after the completion of the dam. For example, below the dam, the annual effects of flooding are expected to be minimized. Correspondingly, there is the potential for great change in the established modes of transmission, with unstable snail populations below the dam becoming stable due to greater control of water, the lack of annual flooding and new resulting land-use patterns (Hotez et al., 1997). In contrast, above the new dam will be a huge reservoir, filling the gorges. Ensuing sedimentation may result in the development of marshland-like environments, similar to the Yangtze island mode of transmission that supports the *O. h. hupensis* subspecies. These environmental changes may result in changes in the geographic distribution of both snail subspecies.

Remote Sensing Identification of Snail Habitat

The construction of the Three Gorges Dam presents a challenge for traditional snail habitat surveillance. Current methods rely heavily on field surveys, and as such, are inadequate even for existing environments like Poyang Lake, where an estimated 4,600 km^2 of marshland is potential snail habitat. Post-dam, environmental changes will probably occur not only in Poyang Lake, but also in other areas upstream and downstream of the dam. Moreover, such changes may occur rather rapidly, making it nearly impossible for field surveys to accurately keep track of evolving ecology and land-use.

Because of the Three Gorges Dam, there is strong motivation for the use of remote sensing for regional snail habitat surveillance. Remote sensing provides a means for detecting environmental change over large areas in a relatively economical fashion. Appropriate regional approaches to identifying snail habitat involve methods that account for the aforementioned differences in snail habitat between provinces and modes of transmission. The approach we take here is not to attempt to create a generic classification of snail habitat that applies for all of China, but rather, explicitly acknowledge that there are regional differences in snail habitat, and develop unique remote sensing methodologies that attempt to identify characteristic snail habitat in each region. We present two case studies of this approach: *O. h. robertsoni* habitats in Sichuan Province upstream of the Three Gorges, and *O. h. hupensis* habitats in Poyang Lake of Jiangxi Province.

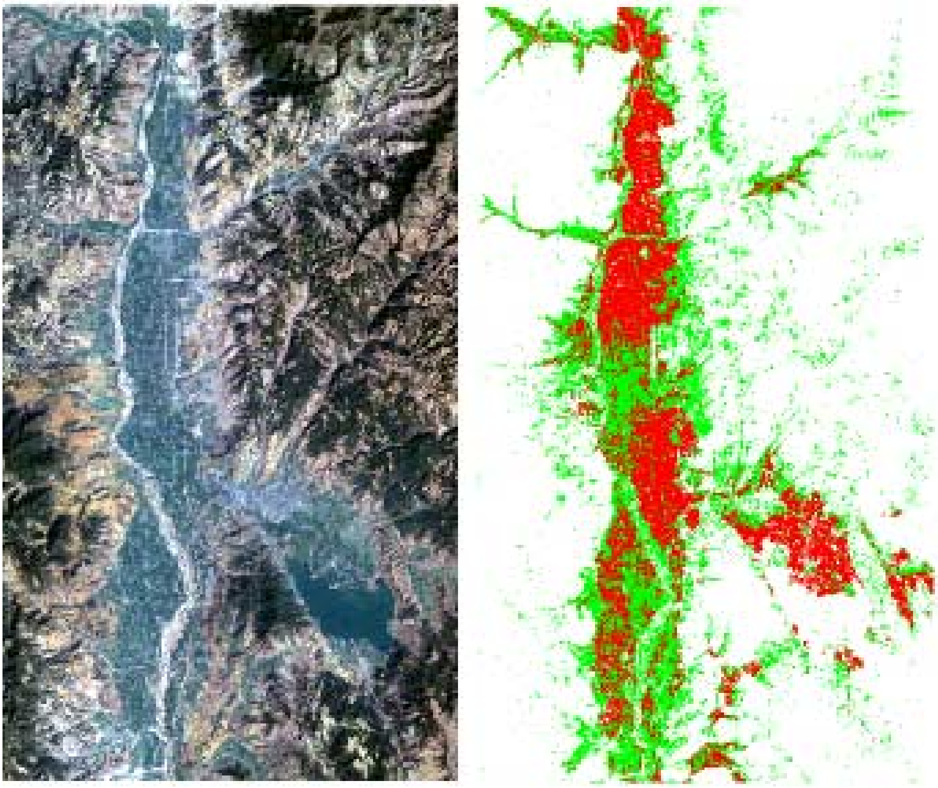
Landsat TM Classification of *O. h. robertsoni* Habitat in Sichuan Province

Seto et al. (2002) present a classification of snail habitat in the Anning River Valley in southwest Sichuan Province from Landsat TM satellite imagery. The Anning River Valley is an endemic schistosomiasis region that characterizes the mountainous type of transmission in China. The valley is approximately 48 km from north to south, and approximately 24 km at its widest point. The predominant snail habitat in this environment is along the walls, just above the waterline of irrigation ditches that feed agricultural fields. As snails prefer the shaded vegetation and slower moving water of smaller tertiary ditch systems, which typically are less then one meter in width, the direct identification of habitat using remote sensing is difficult. However, larger scale phenomena associated with snail habitat, such as soil conditions, crop type and farming practices that vary from area to area within the valley, are discernible through remote sensing. However, since these phenomena vary both geographically, as well as from season to season, the Anning River Valley is a complex environment in which to identify snail habitat.

The availability of year-round soil moisture is an important factor in determining snail habitat, and is one of the main reasons snails live in irrigation ditches. Irrigation ditches line agricultural fields that can be remotely sensed. Hence, the presence of agricultural fields within an area is a simple indicator of potential snail habitat. However, not all irrigation ditches have continual water, as certain crops only occasionally need water, such as corn, which is a major crop within the valley. Also, two growing seasons exist in the Anning River Valley. Seasonal changes from wetter crops to drier crops result in ditches that may have water in one season but are dry in another.

The classification produced by Seto et al. (2002) discriminates between areas that are snail habitat from non-habitat by correlating ground survey data with both spring and fall Landsat TM data. The relatively low cost, sufficient spectral and spatial resolution, and regional coverage of Landsat TM make it ideal for such a study. Non-habitat areas were defined as areas that did not have snails, however, were still within agricultural fields, and to some extent still represented potential habitat that might become snail habitat if seasonal farming practices change. As

Figure 2: Two panels showing Lansat TM of Anning River Valley (left) and classification of habitat using isodata and maximum likelihood algorithms (right)



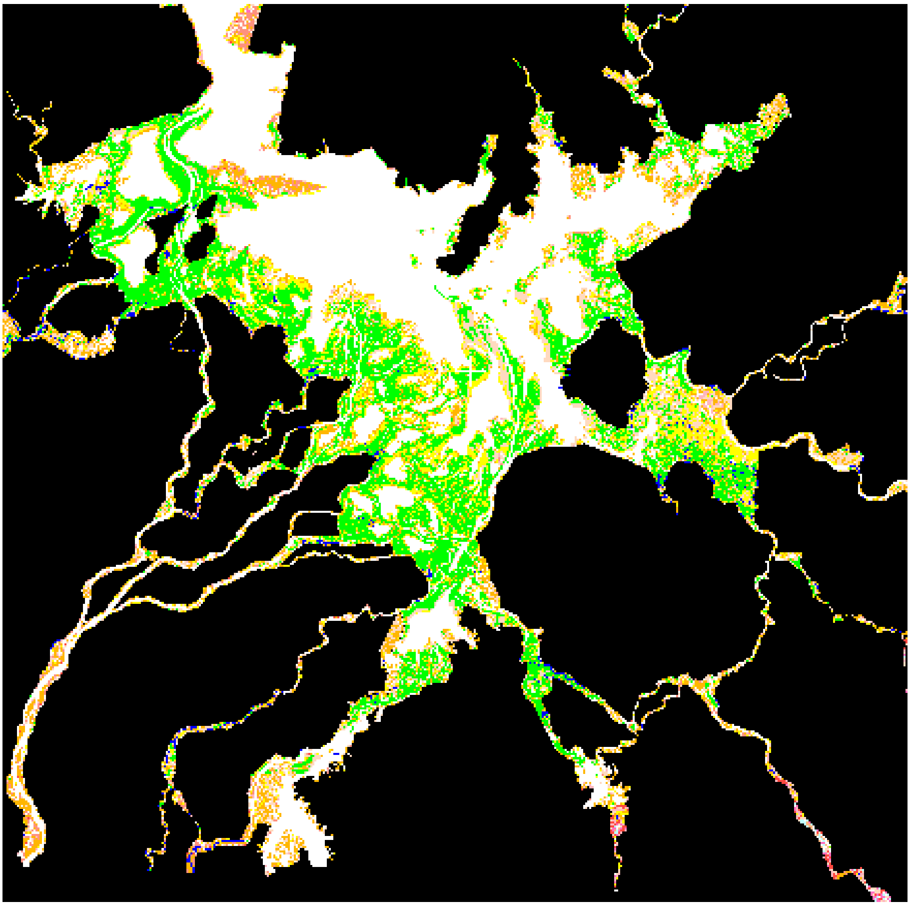
such, both habitat and non-habitat areas identify agricultural land. The resulting classification (Figure 2) clearly shows that land-cover such as city and residential areas, mountain forests, lake and river are excluded as being potential snail habitat. Within potential habitat, areas that are more likely to be snail habitat are identified based on correct spectral properties of the vegetation in both spring and fall. This rather fine-tuned discrimination of spectral properties required a rather complex classification method using clustering algorithms as well as maximum likelihood classification (Duda & Hart, 1973; Foody, Campbell, Trodd & Wood, 1992; Schowengerdt, 1983; Swain & Davis, 1978; Tou & Gonzalez, 1977). A separate validation study revealed that snail habitat could be identified in this environment with greater than 70% accuracy from remote sensing data alone, but could be potentially improved by incorporating information from soil maps.

Landsat TM Classification of *O. h. hupensis* Habitat in Jiangxi Province

In contrast to the relatively complex snail habitat of the Sichuan Anning River Valley environment, which is influenced by human interactions with the land such as mixed land-use and seasonal changes in crops, the Poyang Lake environment of Jiangxi Province may at first seem somewhat simple. A recent study comparing snail habitat soil conditions of the Anning River Valley with that of Poyang Lake suggests that, at the microenvironment level, the habitats are quite different (Seto et al., in press). The lack of particular soil chemicals and silt can serve to exclude snails from areas of the Anning River Valley. However, snails from Poyang Lake exhibit much less dependence upon soil composition and chemistry since soils and snails are most likely spread within the environment during flooding. Recall that the lake is actually a flood basin, which during the low water season is grassland upon which cattle graze and become infected. These grasslands comprise the potential snail habitat in this environment, and are easily recognized from remote sensing. However, the ability for any particular area of grassland to support snails at any given time depends upon soil moisture and the effect of seasonal flooding. Grassland areas that are submerged for too long, or not submerged long enough, will not be suitable for snails. These areas can change over the course of the season as well as from year to year. Hence, just as seasonality plays an important role in Sichuan, it also complicates the use of remote sensing in the Poyang Lake environment.

Landsat TM is a good data source for identifying snail habitat in this region. The large size of the lake and large Landsat TM scenes complement one another. Moreover, the relatively simple grassland snail habitat allows simple unsupervised classification methods to identify land-cover types that are largely correlated with such habitat. Using images from five different dates, spanning April 1998 to January 2001 and both wet and dry seasons, and corresponding field validation data, unsupervised classification methods can produce maps that identify snail habitat with over 80% sensitivity (Figure 3) (Wu et al., 2001). Specificity is not better than 70% though. This is because the ability for identified areas to support snails is highly conditioned on the existence of correct water level and soil moisture at the site, which can fluctuate over time. To account for the effects of flooding and changes in soil moisture, we employ a more complicated approach for this region, which is described in Seto et al. (2002). We first determine the maximum extent of potential snail habitat (grasslands) from the lowest water seasonal image using unsupervised classification. We then determine, from different images over the course of the rainy season, how these grasslands become covered with water. Grassland areas that are under water for too long or too short a period of time are too wet and too dry, respectively, to support snails. Those areas that spend just the right amount of time under and above water are optimal snail habitats.

Figure 3: Unsupervised classification of November 1999 Landsat TM Data for the Poyang Lake Region, with potential snail habitat contained with dikes and shown in grey, water shown in white, and areas outside the dikes shown in black.

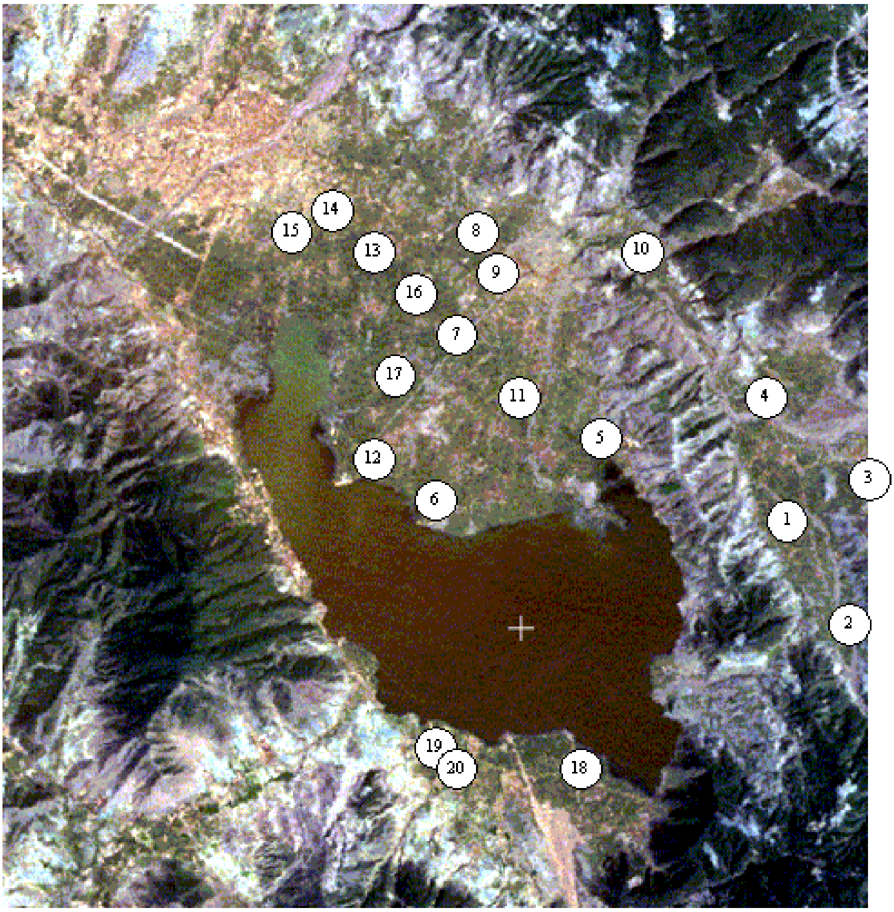


LOCAL METHODOLOGIES

In contrast to the regional methodologies useful in exploring larger-scale evolutions in land-use and snail habitat, smaller-scale applications of GIS and remote sensing are useful in understanding disease transmission at the local village level. Identification of snail habitat at the regional level is important since presence of the intermediate host is a necessary component to transmission. Snail presence indicates that there is the potential for disease transmission; however, it does not indicate the extent of disease transmission. As illustrated above, human infection is not only linked to the distribution of snails, but also to human activity. The amount, density and degree of overlap between the spatial distributions of snails, cercaria and human water contact ultimately determine the extent of disease transmission within a village. Hence, local methods focus first on understanding the density and spatial distributions of snails and cercaria within a village setting, and second on understanding how land-use and water contact activity coincide with those distributions.

Figure 4: Locations of 20 study sites in the Anning River Valley.
Residence groups are:

1. Daxing Xinming Group 3
2. Daxing Xinming Group 7
3. Daxing Shian Group 5
4. Daxing Jianxing Group 6
5. Chuanxing Jiaojia Group 4
6. Chuanxing Zhaojia Group 9
7. Chuanxing Hexing Group 1
8. Chuanxing Minhe Group 1
9. Chuanxing Minhe Group 3
10. Chuanxing Xinlong Group 7
11. Chuanxing Xinqiao Group 4
12. Chuanxing Haifeng Group 5
13. Gaojian Chensuo Group 2
14. Gaojian Zhongsuo Group 8
15. Gaojian Tuanjie Group 2
16. Gaojian Wangjia Group 1
17. Gaojian Wangjia Group 5
18. Hainan Hetao Group 6
19. Hainan Gangyao Group 5
20. Hainan Gucheng Group 6



Our methodologies were developed for 20 residence groups (natural villages) near the city of Xichang, in the Sichuan Anning River Valley region. The villages are typical of the environment of about 90% of the population in the Daliang Mountainous Region. Here, the climate is subtropical with an annual average temperature of 17°C and annual rainfall of about 1000 mm, over 90% of which falls between the beginning of June and the end of October. The residence groups lie within a 12 x 12km area surrounding Qionghai Lake in the valley (Figure 4), and represent approximately 3,900 individuals in four townships: Gaojian, Chuanxing, Daxing and Hainan. The landscape is largely irrigated agricultural land, with two growing seasons. The living and working style of people in a residential group are usually very similar, and the fields that they farm are usually adjacent to their housing areas. Crops and farming practices can differ between townships, which is largely related to differences in natural terrain, soil conditions and socioeconomic factors. In the lowland (elevations 1500 to 1600m) residence groups near the lake, the predominant crops are rice paddy and wheat, whereas in residence groups in the terraced foothills (elevations 1650 to 1850m), tobacco, garlic and corn are more common. In general, the agriculture typical of the river valley plains does not rely heavily on animal husbandry. Preliminary analysis of animal data collected in the fall of 2000 suggest that animals play a small role in disease transmission with small numbers of buffalo and horses, and low infection in each group. In contrast, historical evidence suggests that in some villages over half the human population can be infected. Human infection prevalence is generally thought to be highest for the Daxing groups in the terraced foothills away from the lake, medium for Chuanxing groups, and low for Gaojian and Hainan groups that are near the lake. The dramatic difference in infection over such a small geographic area is most likely related to differences in the aforementioned terrain, soil conditions and economic considerations, as these factors influence land-use and choice of crops within residence groups and townships. Different crops, in turn, require different farming practices, and affect water contact, and human and animal fertilizer usage, two important factors that drive disease transmission.

Ditch Mapping and Georeferenced Snail Surveys and Mouse Bioassays

The risk of infection to humans from water contact is directly related to the concentration of cercaria in that water. Unfortunately, it is difficult to accurately measure cercarial concentration in water in the field. Methods with which we are familiar involve the capture of cercaria on a film, or by filtration, which has limited accuracy, is difficult to setup and impractical for routine use. Instead, two methods are relied upon as surrogates for cercarial concentration. The first method is to use mouse bioassays to estimate cercaria levels. The second method is even more indirect, in which snail surveys are used to estimate the level of snail infection, which are to some extent an indicator of cercarial loading on the environment.

In the traditional snail survey, small areas of irrigation ditch (potential habitat for snails) are sampled for snails. The protocol involves sampling a *kuang* (a 0.11m^2 square frame) at fixed intervals roughly 10m apart (Gu, 1990). Snails are collected, crushed and examined under microscope for the presence of the parasite. This results in estimates of the number of total snails positive (infected) snails, and frames without any snails within a village.

One of the problems with the traditional protocol is that it does not characterize the spatial distribution of the snails within a village. Seto et al. (2001) describe a new protocol in which ditches are first mapped with the Global Positioning System (GPS). The resulting map is then used to geocode snail survey results. There is considerable practical value to these maps, as field researchers can clearly see clusters of high snail density, and perhaps more importantly, positive snail density within the village (Figure 5).

Figure 5: An example GPS ditch map from one of our 20 villages illustrating the spatial distribution of snail survey and mouse bioassay data

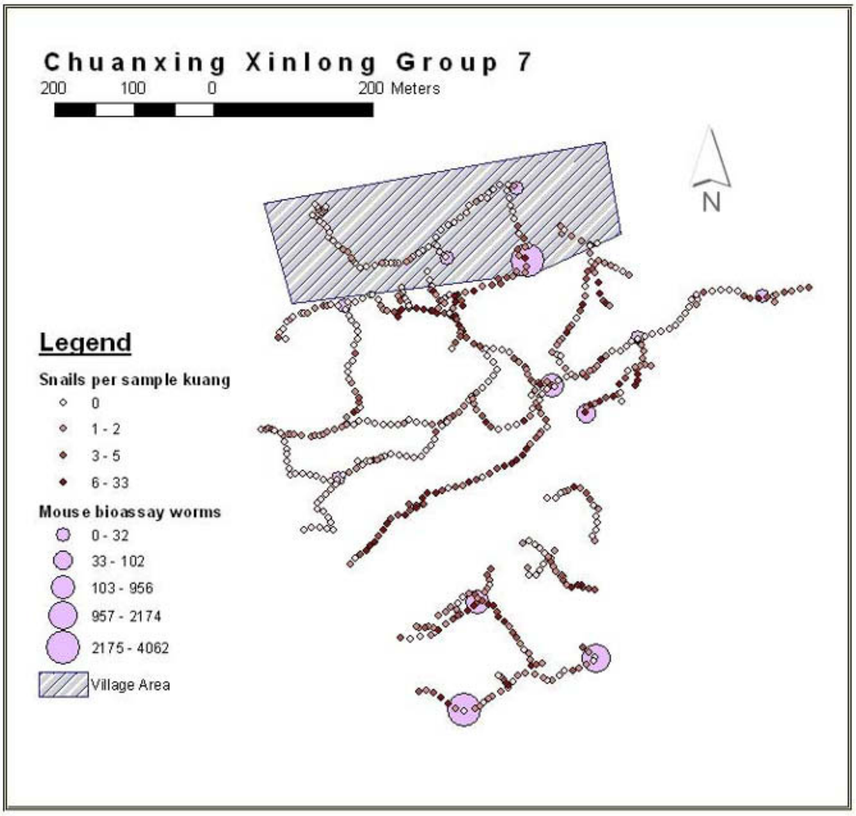


Table 1: Relationship between snail survey data and human prevalence

	Ave # Snails	Ave # Positive Snails	Human Prevalence
Daxing villages	1,496	19	High
Chuanxing villages	820	7	Medium
Gaojian villages	461	0	Low
Hainan villages	652	0	Lowest

Snail surveys were conducted for the 20 Anning River Valley villages using the GPS protocol in the summer of 2000. Snails within *kuang* were sampled at fixed 10m intervals. This interval was determined from an assessment of the spatial aggregation of snail populations along several representative ditch segments, and corresponds to the same distance used in the traditional survey approach. Snail survey results for the four townships suggest a positive correlation between number of snails and disease prevalence (Table 1).

There is an inherent problem with using snail survey results to estimate disease risk. This is due to the relatively low proportion of snails that are infected within a village, which can at times be as low as 0.1%. A few infected snails in an area might conceivably release tens of thousands of cercaria, which drives the infection within the village. There is a chance that infected snails might be missed as a result of the snail sampling process. Hence, in addition to snail surveys, mouse bioassays can be set up at key locations in the village to estimate cercarial concentrations. In a mouse bioassay, a cage of mice is dipped into the surface water of the ditch location for a fixed number of hours each day for a few days, usually totaling 10 hours of exposure. After a month, the mice are sacrificed, and the worms within them are counted.

Mouse bioassays were performed in each of the 20 villages. The GPS ditch map played an important role in designing the mouse bioassay study. Locations were chosen at key water contact locations close to residential areas, and also at inputs to the village to determine what proportion of the cercarial load was attributed to influx from adjacent villages. A GIS database consisting of the ditch map, and snail survey and mouse bioassay results was implemented. The GIS can be used to first identify the locations of positive mouse bioassay, and second to trace upstream from these locations to identify potentially problematic snail populations. The spatial relationship between snail populations and positive mouse bioassays can present opportunities for disease control.

Remote Sensing Identification of Factors Related to Disease Transmission

Remote sensing played an important role in identifying snail habitat at the regional scale. Here we revisit the use of remote sensing, now focused on defining more clearly the spatial relationships between disease prevalence and snail habitat, natural landscape, land-use and human activity at the village level. These within-village relationships are best studied with high-resolution imagery. IKONOS data from Space Imaging, Inc. was acquired for an area that covered 19 of our 20 villages in December 2000. The IKONOS scene covers an 11km x 11km area, and includes four multispectral bands at 4m resolution and one panchromatic band at 1m resolution. At these resolutions, the ability to identify landcover such as residential units, roads, field plots, terraced land and potential crop type is greatly improved.

The goal of our preliminary analysis of the IKONOS data was to correlate different landcover types with disease prevalence by village. The analysis began with a supervised classification of the 4m multispectral IKONOS data using maximum likelihood classification to identify 13 landcover types. Subsequently, circular buffers centered at each village were created. These buffers represent the area of influence, within which landcover, such as the number of residences and amount of agricultural fields, for instance, might affect disease transmission. The buffers were allowed to extend beyond the political boundaries of the village since previous experience with GPS ditch mapping suggested that cercarial transport extends beyond village boundaries. Two buffer radiuses were used for each village: a 500m radius to capture near-field effects, and a 1000m radius to capture far-field effects.

Classification and Regression Trees (CART) (Breiman, 1984; Steinberg & Colla, 1997) was used to correlate landcover types with high, medium and low human prevalence villages. The result of this preliminary analysis was that the majority (five out of six) of the high prevalence villages most notably lacked landcover corresponding to large roads. These villages are predominantly in Daxing County to the east of the lake and separated from the city of Xichang and more prosperous areas by a mountain ridge. Daxing is not only more remote, as evidenced by the lack of large roads, but is also more agricultural, with farming that is quite different from the other villages in the study area. Located in the foothills of the mountains, the villages are largely terraced fields, growing less rice paddies, but more tobacco, which requires more fertilization. Increased fertilization results in more parasite eggs in the environment and higher disease transmission. Also, being farther from the lake and city, it is hypothesized that more Daxing villagers work in the fields, than in other relatively safer occupations.

Villages that do have large roads are predominantly low and medium prevalence villages. Medium prevalence villages have a higher proportion of land devoted to crop fields, as opposed to rice paddies, than low prevalence villages. Crop fields accounted for more than 34.8% of the landcover in seven of the eight medium prevalence villages, whereas all five low prevalence villages had less than or equal to 34.8% crop fields. This is consistent with experience from snail surveys, which suggest that ditches lining paddy fields have fewer snails than those lining crop fields. Furthermore, rice paddies are usually fertilized with chemical fertilizer, reducing the risk associated with widespread parasite egg distribution with stool fertilizer. The larger 1000m radius buffer had a greater impact on prevalence than the smaller 500m radius buffer, illustrating the influence of landcover from neighboring villages.

Snail habitat was also correlated with landcover derived from IKONOS data. The GPS ditch maps and geocoded snail survey results were registered to the classified IKONOS image. Buffers were created by smoothing the snail survey data using an inverse distance weighted interpolation over a 20m radius from each snail sample location. In a comparison of low snail areas (one-to-five snails per kuang) and high snail areas (>20 snails per kuang), we found little difference between landcover. However, the differences that existed suggest that snails prefer areas that are less sandy and consist of crop or bare fields. Moreover, the results of a comparison of the landcover for all snail habitat (>=1 snail per kuang) versus the landcover for the entire villages (500m radius circular buffer centered on village) suggest a slight snail preference towards ditches that line crop fields rather than sandy land or residences.

Thus far our work with IKONOS has been limited to rather crude classifications of the 4m multispectral data. Given the importance of the crop landcover type, an eventual goal is to be able to finely tune a classification to particular crop types for the Anning River Valley villages. The ability to pinpoint different crops through remote sensing will allow us to determine the location of high stool fertilizer usage, snail populations, and different types of harvesting and water contact exposure. A crop type classification would ultimately require new fieldwork and the development of new classification algorithms, which we anticipate will be based on the higher resolution 1m resolution panchromatic IKONOS data. From visual interpretation of the panchromatic data, it is possible to identify rows of crops, which look different from paddies. Furthermore, the structure of terraced fields associated with high disease transmission villages can be identified. A problem with such high-resolution imagery is actually too much information, as automated classification algorithms will need to be developed to perform pattern recognition, identifying landscape features from the reflectance values of clusters of adjacent pixels. We have begun development of such contextual classifiers based on

IKONOS data (Franklin, Wulder & Gerylo, 2001), and hope to be able to apply them to schistosomiasis. Furthermore, given the importance of elevation as a discriminator between high and low prevalence areas, we hope in the future to generate digital elevation models using IKONOS, which will allow for a better understanding of the relationship between elevation, agricultural practices and disease transmission.

IMPLICATIONS FOR CONTROL

Understanding the spatial distribution of disease and the intermediate host at both the regional and local scales, and how such distributions may change over time, are necessary for public health planning and resource allocation. This is especially true for a large, populous and rapidly developing country such as China, where limited funds, ever-changing land-use and modernization through water resource projects require such methods. In China, the available control measures are health education, chemotherapy, snail control and environmental modification. We assess the implications of our methodologies on each of these control measures.

At the regional level, remote sensing provides protection against the threat of disease emergence via broad surveillance of changes in the distribution of the intermediate host. The emergence of snail habitat should initiate the allocation of resources for field studies, and the establishment of county-level resources for health education and chemotherapy administration.

The methods we have presented here explicitly account for regional differences in snail subspecies. Snail subspecies should be treated differently, not only because of their adaptations to different environmental niches, but also because of their potential co-evolution with the schistosome parasite. The efficacy of future schistosomiasis vaccines may exhibit regional variation corresponding to the geographic distribution of snail and schistosome subspecies. In the absence of a vaccine, current strategies employing snail control either through the application of focal molluscicides or environmental modification rely heavily on the ability to understand regional differences in snail subspecies and their spatial distributions.

At the local level, within a region with snail habitat, the spatial relationships between landscape features can differentiate low and high transmission villages. Our GPS ditch maps illustrate the spatial distributions of snails, cercaria and potential water contact zones. If high-risk sites can be identified on such maps, strategies employing focal molluscicding, small-scale environmental modifications, such as reengineering troublesome segments of ditch, are more likely to be effective.

Remote sensing at the small-scale village level using IKONOS imagery is not intended as a means for performing disease surveillance. High-resolution imagery is too expensive to obtain for large areas. Instead, we view high-resolution remote sensing as a way to develop a generic understanding of the linkage between landcover and epidemiology, and quantifying the relationships illustrated in Figure 1 within a particular region. If, through the analysis of remote sensing data, we understand the relationship between snail habitat, water contact and particular crops, it will be possible to determine risk within a village based on simply how much of a risky crop type is grown within and around the village of interest. For control, socioeconomic factors make it difficult for villages to change what they grow. However, some areas in Sichuan have effectively controlled schistosomiasis through environmental modification, by radically changing from high-risk crop fields to low-risk orchards.

Chemotherapy is widely administered in endemic areas as the strategy of choice for controlling morbidity and reducing transmission. There are generally two options for administering Praziquantal, the chemotherapy drug. One option is to provide mass treatment to all villagers. Another option is targeted treatment, providing Praziquantal only to those at highest risk. Local methodologies such as GPS ditch mapping and geocoded snail surveys and mouse bioassays should be considered as tools for potentially determining whether the risk in the village is large or small, widespread or narrowly focused, and how it relates to age groups and occupations within the village that can be targeted for treatment.

New chemoprophylaxis drugs such as Artemether, work to prevent the maturation of worms in humans and hence reduce the spread of eggs (Xiao, Booth, & Tanner, 2000; Xiao et al., 1996). The problem with artemether is that single doses are only effective for a short period of time. For villages where water contact and the risk of transmission spans the agricultural season, artemether will need to be constantly readministered to control transmission. However, in some circumstances, we have found villages that primarily grow tobacco, a crop that is only fertilized two times during the season. In these locations there is the potential to interrupt the transmission cycle by chemoprophylaxis during just the period of fertilization. If this strategy is effective, then GIS and remote sensing become important tools for the administration of this promising drug.

Although we have focused on schistosomiasis in China, the topics discussed in this chapter are generally useful for infectious disease control research within and outside of China. Remote sensing has been applied to a variety of infectious diseases in many different countries (Hay, Packer & Rogers, 1997). Our experience in China has shown the importance in recognizing regional differences in ecology and understanding the spatial scale at which disease transmission factors operate in the development of remote sensing-based surveillance. A similar approach is applicable for comparing and contrasting the geographic distributions and ecologies of the various *Biomphalaria* and *Bulinus* species of snails that serve as intermediate hosts for *Schistosoma mansoni* and *Schistosoma haematobium* in sub-Saharan Africa (Brooker & Michael, 2000). Geographical differences in disease transmission exist for other diseases, some of which have been studied using GIS (Mott, Nuttall, Desjeux & Cattand, 1995). Methods such as GPS ditch mapping presented in this chapter illustrate the power of GIS and GPS technologies that make the collection, management and analysis of spatial data easier, and provide a means for better understanding the relationship between humans and the vectors that carry disease.

ACKNOWLEDGMENTS

We thank the Sichuan Provincial Office of Endemic Disease Control and the Xichang County Anti-Schistosomiasis Station for their field support. This work was supported in part by grants from NIH-NIAID (1 RO1-AI43961-01A1), the Shanghai NIH-TMRC (I P50 AI3946), NSF of China (49825511), NASA (NCC2-5102), NIEHS Mutagenesis Center at the University of California, Berkeley (5 P30 ES 01896-20 ZES1) and the University of California Pacific Rim Research Program.

REFERENCES

Breiman, L. (1984). *Classification and Regression Trees*. Belmont, CA: Wadsworth International Group.

Brooker, S. & Michael, E. (2000). The potential of geographical information systems and remote sensing in the epidemiology and control of human helminth infections. *Advances in Parasitology, 47*, 245-288.

Chen, M. & Zheng, F. (1999). Schistosomiasis control in China. *Parasitology International, 48*(1), 11-19.

Davis, G. M., Wilke, T., Zhang, Y., Xu, X. J., Qiu, C. P., Spolsky, C., Qiu, D. C., Li, Y. S., Xia, M. Y. & Feng, Z. (1999). Snail-schistosoma, paragonimus interactions in China: Population ecology, genetic diversity, coevolution and emerging diseases. *Malacologia, 41*(2), 355-377.

Duda, R. O. & Hart, P. E. (1973). *Pattern Classification and Scene Analysis*. New York: John Wiley & Sons, Inc.

Foody, G. M., Campbell, N. A., Trodd, N. M. & Wood, T. F. (1992). Derivation and applications of probabilistic measures of class membership from the maximum-likelihood classification. *Photogrammetric Engineering and Remote Sensing, 58*(9), 1335-1341.

Franklin, S. E., Wulder, M. A. & Gerylo, G. R. (2001). Texture analysis of

IKONOS panchromatic data for Douglas-fir forest age class separability in British Columbia. *International Journal of Remote Sensing, 22*(13), 2627-2632.

Gleick, P. H. (1998). *The World's Water, 1998-1999 : The Biennial Report on Freshwater Resources*. Washington, DC: Island Press.

Gu, X. G. (1990). *Epidemiological investigation of schistosomiasis in Minhe and Hexing villages, Xichang, Sichuan Province* (Research Report.). Sichuan Institute of Antiparasite Diseases.

Hay, S. I., Packer, M. J. & Rogers, D. J. (1997). The impact of remote sensing on the study and control of invertebrate intermediate hosts and vectors for disease. *International Journal of Remote Sensing, 18*(14), 2899-2930.

Hotez, P. J., Zheng, F., Long-qi, X., Ming-gang, C., Shu-hua, X., Shu-xian, L., Blair, D., McManus, D. P. & Davis, G. M. (1997). Emerging and reemerging helminthiases and the public health of China. *Emerging Infectious Diseases, 3*(3), 303-310.

Mao, S. B. (1990). *Schistosomiasis—Biology, Prevention, and Treatment*. Beijing, PRC: People's Health Press.

Martens, W. J. M., Jetten, T. H. & Focks, D. A. (1997). Sensitivity of malaria, schistosomiasis and dengue to global warming. *Climatic Change, 35*(2), 145-156.

Mott, K. E., Nuttall, I., Desjeux, P. & Cattand, P. (1995). New geographical approaches to control of some parasitic zoonoses. *Bulletin of the World Health Organization, 73*(2), 247-257.

Schowengerdt, R. A. (1983). *Techniques for Image Processing and Classification in Remote Sensing*. New York: Academic Press.

Seto, E., Liang, S., Qiu, D., Gu, X. & Spear, R. C. (2001). A protocol for geographically randomized snail surveys in schistosomiasis fieldwork using the global positioning system. *American Journal of Tropical Medicine and Hygiene, 64*(1-2), 98-99.

Seto, E., Wu, W., Qiu, D., Gu, X., Spear, R. & Davis, G. (in press). Impact of soil chemistry on the distribution of Oncomelania hupensis (Gastropoda: Pomatiopsidae) in China. *Malacologia*.

Seto, E., Xu, B., Liang, S., Gong, P., Wu, W., Davis, G., Qiu, D., Gu, X. & Spear, R. (2002). The use of remote sensing for predictive modeling of schistosomiasis in China. *Photogrammetric Engineering and Remote Sensing, 68*(2), 167-174.

Steinberg, D. & Colla, P. (1997). *CART for Windows 3.6.3 (Version 3.6.3)*. San Diego, CA: Salford Systems.

Swain, P. H. & Davis, S. M. (1978). *Remote Sensing : The Quantitative*

Approach. London ; New York: McGraw-Hill International Book Co.

Tou, J. T. & Gonzalez, R. C. (1977). *Pattern Recognition Principles* (2d printing, with corrections. ed.). Reading, MA: Addison-Wesley Pub. Co.

Webbe, G., Sturrock, R. F. & Jordan, P. (1993). *Human Schistosomiasis*. Wallingford, Oxon, UK: CAB International.

WHO Expert Committee on the Control of Schistosomiasis. (1993). *The Control of Schistosomiasis: Second Report of the WHO Expert Committee*. Geneva: World Health Organization.

Wu, W., Davis, G., Spear, R., Feng, Z., Seto, E., Chen, H., Liu, H., Lu, S., Hua, Z., Zhang, J., Guo, J., Zhu, H. & Lin, D. (2001). *Application of GIS/RS Technology to Studies of Snail Habitat and Distribution in Poyang Lake.* Paper presented at the International Syposium on Schistosomiasis, Shanghai, China.

Xiao, S. H., Booth, M. & Tanner, M. (2000). The prophylactic effects of artemether against Schistosoma japonicum infections. *Parasitology Today, 16*(3), 122-126.

Xiao, S. H., Shi, Z. G., Zhuo, S. J., Wang, C. Z., Zhang, Z. G., Chu, B., Zhen, J. & Chen, M. G. (1996). Field studies on the preventive effect of oral artemether against schistosomal infection. *Chinese Medical Journal, 109*(4), 272-275.

Chapter XII

Bacterial Source Tracking of Nonpoint Source Pollution Using GIS and DNA Fingerprinting Technologies

M. E. Folkoff, E. A. Venso, D. W. Harris, M. F. Frana and M. S. Scott
Salisbury University, USA

This study is only the second to use DNA fingerprinting technology in Maryland to identify fecal coliform sources in order to guide the implementation of water pollution control practices in a watershed with bacterial impairment. By combining the use of digital air photos and GPS with GIS, fieldwork is planned and conducted more efficiently because sample sites can be selected that accurately represent the physical environment of the study area. We can also return to the field and find our sample sites or locate new ones, even in the remotest part of the study area. It is also possible to more accurately map the data directly in the context of its physical environment, greatly increasing the quality of analysis. The integration of DNA fingerprinting techniques with GIS shows great promise for extending our capabilities to identify the controls on water quality and point sources of waterborne health hazards.

INTRODUCTION

Fecal coliform contamination has closed public beaches, reduced shellfish harvesting and threatened recreational areas across the United States, including the

Chesapeake Bay watershed. As in most watersheds, water quality testing currently performed in Chesapeake Bay waterways does not identify the sources of contamination (National Shellfish Sanitation Program, 1997; "Water Quality," 1997a; "Water Quality," 1997b). Therefore, no pollution control or mitigation efforts have been undertaken, despite the large adverse economic and social impact that accompanies this contamination. However, if a specific pollution source could be identified, it may be possible to isolate or remove that source.

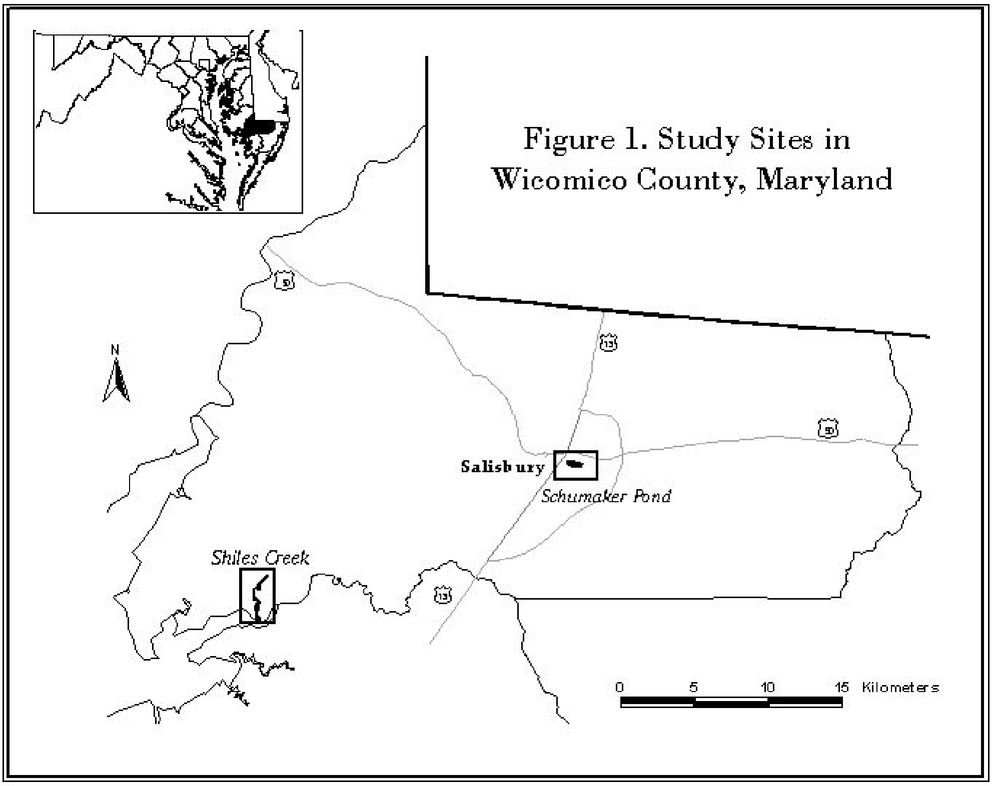
In this study, we describe the role of Geographic Information Systems (GIS) in identifying the sources of beach, river and shellfish bed contamination (and potentially drinking water contamination) by fecal coliform bacteria, specifically *Escherichia coli (E. coli).* The use of GIS to investigate surface water hydrology and water quality has become commonplace in environmental analysis (Engel, Srinivasan & Rewerts, 1993; Fedra, 1993; Hunsaker et al., 1993; Maidment, 1993; Roth & Cyffka, 1999). This project differs from others because it combines GIS capabilities in environmental analysis with the new application of DNA fingerprinting technology to identify the fate, source and transport of fecal coliforms. This integration of techniques shows great promise for extending our capabilities to identify the controls on water quality and nonpoint sources of waterborne health hazards.

Our current research is built upon an earlier successful study using DNA fingerprinting in Granary Creek, a tributary of the Wye River in Maryland. The Wye River project is the first effort in Maryland to use DNA fingerprints to identify coliform sources (Brohawn et al., 2000; Frana et al., 2000). The study described in this chapter is only the second to use DNA fingerprinting technology in Maryland to identify fecal coliform sources in order to guide the implementation of water pollution control practices in a watershed with bacterial impairment. The Salisbury University DNA Fingerprinting Laboratory was the analytical facility for the Wye investigation, and its personnel participated in the development of field and laboratory techniques and interpretation of the data.

The project described here expanded the scope of the Wye Project and is one of the first bacterial source tracking studies to incorporate the use of GIS methods. Rarely have the powerful capabilities of both GIS and DNA fingerprinting been combined to study large-scale environmental pollution problems. DNA fingerprinting for *E. coli* source identification has been used successfully in a few U.S. locations over the past several years with an effective pollution control outcome (Brohawn et al., 2000; Simmons, Herbein & James, 1995; Simmons & Herbein, 1998). The technique is similar to the Pulsed-Field Gel Electrophoresis (PFGE) protocol utilized by the U.S. Centers for Disease Control and Prevention to identify hemorrhagic strains of *E. coli* in human disease outbreaks (Swaminathan et al., 2001). The DNA fingerprints of *E. coli* found in water sampled in the field was compared with DNA that was derived from known *E. coli* sources (animal and human) in order to identify the specific pollution source. GIS was used to store and manage the data collected in the field and laboratory so that the spatial patterns of *E. coli* can be determined.

The results of this research will provide stakeholders with information and guidance for regulatory actions and control measures to improve water quality in the Wicomico River watersheds. Two contrasting study sites that typify the Wicomico drainage were chosen: 1) a suburban pond with an important public beach, Schumaker Pond; and 2) an agricultural/forest basin waterway, Shiles Creek, with a productive shellfish harvesting area located at its mouth (Figure 1).

Figure 1: Location of study sites in Maryland



STUDY CONTEXT

E. coli and DNA Fingerprinting

The mode of transmission for several pathogenic organisms is the fecal-oral route, which includes ingestion of contaminated water. Testing water for the existence of all possible pathogens is a lengthy process and highly impractical. The intestine is the natural habitat of *E. coli*, which is a fecal coliform bacterium. This organism is found in the feces of all warm-blooded animals, so the presence of *E. coli* in water is an indication of fecal contamination and the possible presence of other organisms, which may be harmful. Contamination from fecal material deposited by wildlife and human activity near the shoreline, as well as runoff from nearby fields, roads and developed properties, is flushed into the water body on the falling tide or during rain events.

Most strains of *E. coli* do not cause illness in humans, so this organism is used mainly as a possible indicator of other pathogenic organisms. The absence or low levels of *E. coli* has been used for decades as a superior biological indicator of water safety for drinking water, bathing beaches and shellfish harvesting areas (World Health Organization, 1999; National Shellfish Sanitation Program, 1997).

Different "strains" of *E. coli* inhabit the intestinal tract of different animals. Furthermore, many, if not most, animal species may carry several distinct strains of the bacteria in their gut. Through the use of DNA fingerprinting, it is now possible to identify the probable source of individual strains of *E. coli* based on differences in DNA banding patterns (fingerprints). There is a significant difference between the fingerprints of human and nonhuman strains of *E. coli* (Simmons et al., 1995). The probable sources of nonhuman *E. coli* strains can also be identified (at an 80% confidence level or better) by comparing the DNA banding pattern of an unknown source from a water sample with the pattern of a known source in the Salisbury University library of banding patterns.

The Human Impact of *E. coli* Contamination

Within the Chesapeake Bay watershed, the Lower Wicomico River and the Wicomico River Headwaters Watersheds of Maryland's Eastern Shore have been classified as watersheds in need of restoration under the Maryland Clean Water Action Plan that was set in motion in 1998 by the Federal Clean Water Action Plan (Clean Water Action Plan Technical Workgroup, 1998). Shellfish beds in the Wicomico are monitored by the Maryland Department of the Environment and have been contaminated for the past several years due to fecal coliform bacteria. A few growers still lease oyster beds in the river but must relocate the oysters, at some expense, to other uncontaminated areas prior to harvest to undergo complete purging of bacterial contamination. As importantly, low-income families use fish and shellfish from the river as a food supplement.

In addition, more than a half-dozen boat launches on the river are an indication of the large number of recreational fishermen. For public health considerations, formal swimming waters in the river are tested on a regular basis. These beaches have been closed for several years due to fecal coliform bacteria levels. Several more informal (but very real) swimming areas are not tested, but can be assumed to experience bacterial contamination as well. Again, the source(s) of the coliform bacteria polluting the river is unknown.

STUDY AREAS

The majority of the Wicomico sub-watersheds are almost entirely rural consisting mainly of agricultural land, forest and tidal marsh. A few streams have experienced outbreaks of the toxic organism, *Pfiesteria piscicida*, suggesting that there is already potential ecological disturbance (Burkholder, Mallin, & Glasgow, 1999; Kane et al., 2000). To compound the problem, there is tremendous development pressure in these watersheds. Population increased by more than 15% from 1980 to 1990, and growth is continuing. These new residents expand the need for parks and swimming areas. The city of Salisbury, the largest urban center in the region, has a plan to link together streams along the Wicomico River and its major tributaries to form green-belts. Many tributaries, such as Beaver Dam Creek, include several colonial-era millponds. Suburban development pressure around these ponds is intense. Many developments also have small lots with on-site sewer disposal. Without identification and control of the bacterial contamination, residents will be limited in or excluded from use of waters in the Wicomico River watersheds.

The first study area, Shiles Creek, represents the typical rural land use/land cover in the Wicomico region. Shiles Creek is at the southern end of the Wicomico watershed near the mouth of the river (Figure 2). It is a tidal creek that empties directly into the river near several shellfish beds that have tested positive for elevated levels of *E. coli*. Our sampling area stretches along two miles of the creek near its headwaters including the major tributaries forming its source. The land cover is dominated by agricultural lands with poultry growing operations and large tracts of riparian forest interspersed with extensive tidal marsh. Most major streams have some tidal marsh along their edges.

Our second study area, Schumaker Pond, represents the effect of urbanization on *E. coli* pollution (Figure 3). The pond is a 50-acre impoundment of Beaver Dam Creek, which is part of a major recreation greenbelt stretching through the city of

Figure 2: Sample sites on Shiles Creek: An agricultural/forested watershed

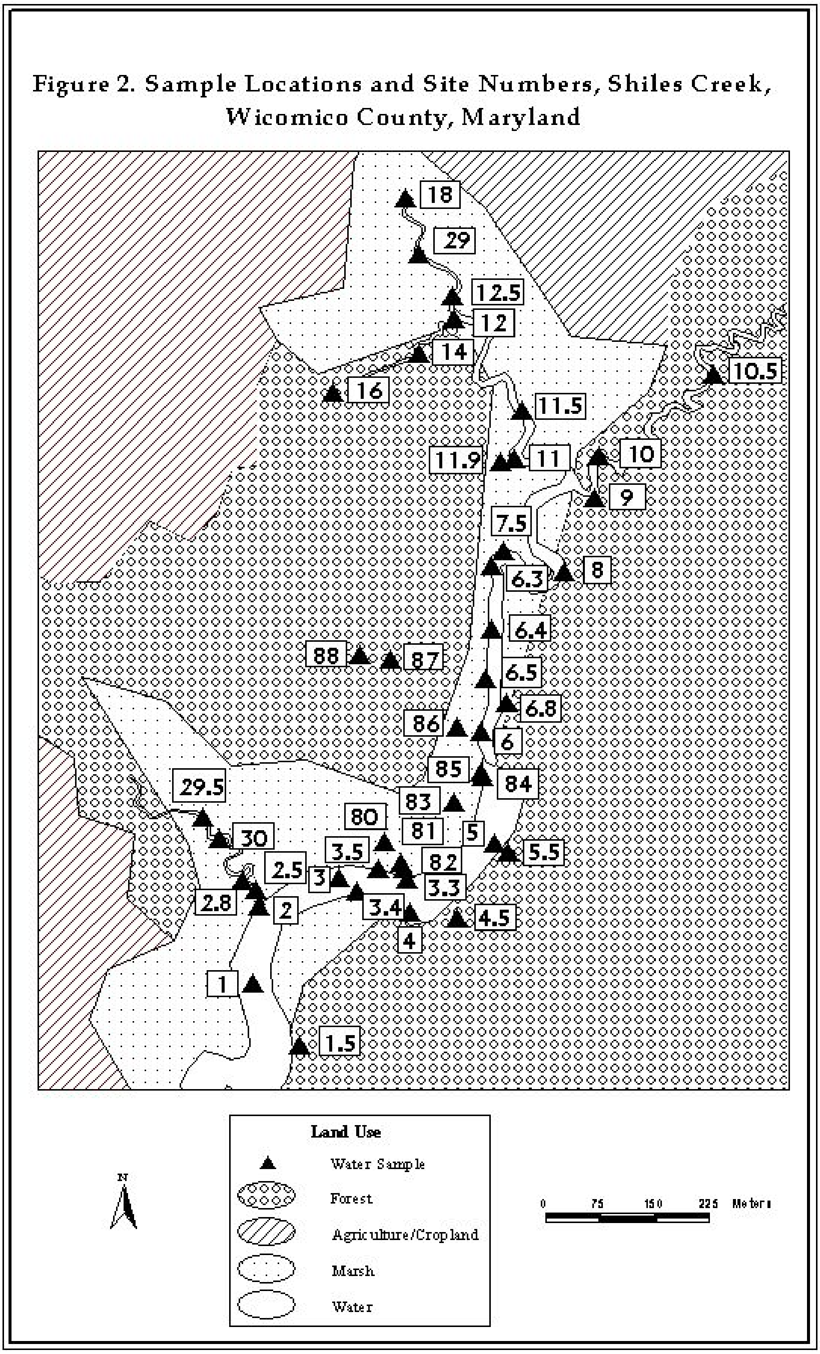
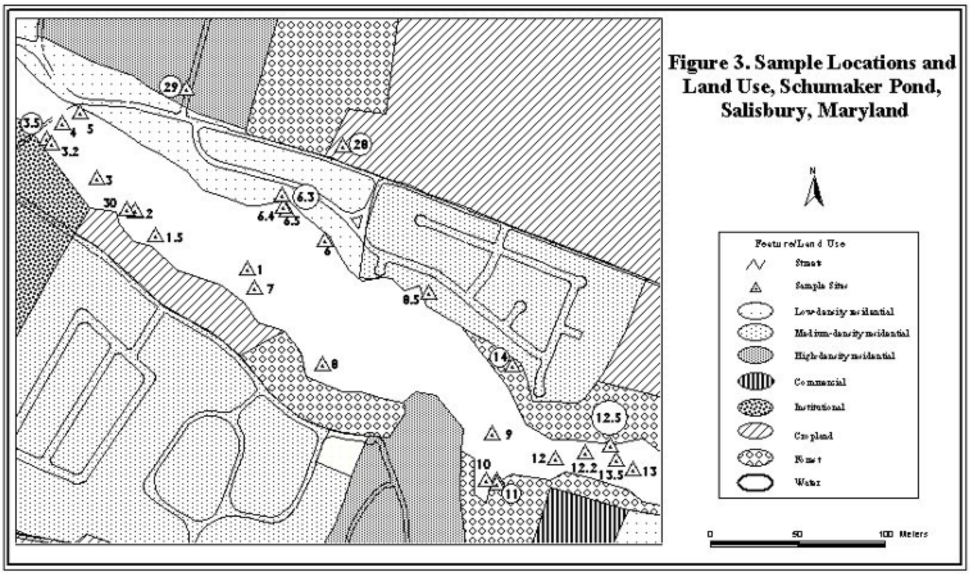


Figure 3: Sample sites on Shumaker Pond: A suburbanizing pond



Salisbury. Surrounding the pond is a mix of new and old residential uses; some have on-site effluent disposal and some are on the sanitary sewer line. There is also intensive institutional development, including a high school and a museum. Along the western shore, there was a popular swimming area that had been a favorite of the county children. Unfortunately, the area has been closed for approximately six years due to high levels of *E. coli*. At first, the pond was closed only for part of the summer, but in the last few years the closure has been made permanent, indicating that over time *E. coli* levels are increasing. The pond is also heavily fished. Residential lots continue to be developed in the watershed as well as on the pond because of the popularity of living on the water.

METHODS

In The Field

Water samples were collected from tributaries of Shiles Creek and from rivulets and culverts draining into Schumaker Pond. Each sample, consisting of one hundred milliliters (ml) of water, was collected and transferred to a sterile collection bottle. Each water sample was analyzed for five environmental variables in the field: temperature, salinity, dissolved oxygen, pH, and conductivity. Additionally, the location coordinates (latitude and longitude) for each sample were obtained using a mapping-grade Global Positioning System (GPS) receiver that has a resolution of 1 meter or less (Trimble Pro XRS). At the same time, the wind, sky conditions and precipitation timing were noted. All of this information, together with position locations, were recorded and stored in the GPS data logger. The water samples were then transported to the Salisbury University DNA Laboratory for analysis. In the GIS lab, these data were downloaded from the GPS in a format compatible for use with the desktop GIS, ArcView.

Samples of fecal matter were also collected and transported in sterile collection containers to the laboratory for analysis (Murie, 1974; Rezendes, 1999). For each identifiable scat sample, the GPS location and the name of the animal species were recorded as well. Water samples were collected routinely. Scat samples were collected throughout the study period and especially while conducting intensive fieldwork on selected sites within each study area.

In the Laboratory

The presence and intensity of *E. coli* contamination in water were measured by counting the density of bacteria in a sample using a modification of the Most Probable Number of colony-forming units (MPN) analysis, "Fecal Coliform Procedure (A-1 Medium), Method 9221 E. 2," from *Standard Methods for the Examination of Water and Wastewater* (APHA; AWWA; WPCF, 1995). DNA fingerprint analysis was conducted on both water samples and scat samples. The laboratory protocol for conducting DNA fingerprinting is lengthy and is beyond the scope of this chapter.

After processing, DNA banding patterns are checked against a library of known banding patterns. Each new scat DNA banding pattern is added to the SU Fingerprint Library. Expanding the DNA library is an important goal because the results of this and future studies of *E. coli* pollution are highly dependent on library size. The DNA library is the standard used for matching DNA patterns from water samples with the DNA patterns for specific sources. The SU Library currently contains over 900 banding patterns of *E. coli* strains known to have come from specific animal species (e.g., deer, cattle, goose, raccoon), including humans. A successful match means a positive identification of the source of *E. coli* in the water. By increasing the size of the library, the ability to match DNA from water samples and identify the sources of *E. coli* will be greatly expanded.

GIS METHODS

The GIS was essential to this investigation because this software is specifically designed to integrate database operations with geographic analysis (Burrough &

McDonnell, 1998). A fundamental use of GIS in this study was to record, store, manage and analyze field data for both the Shiles and Schumaker study areas. GIS served as the primary data control center. Data recorded in the field and laboratory were stored in the GIS as a relational database, making them available for both statistical analysis and geographic analysis. Along with standard querying of this database to determine the nature of the data, a suite of descriptive statistics was run on the MPN data and associated variables. It was possible to run statistical analyses by exporting these data to spread-sheets and a statistical package. The water chemistry variables were analyzed using parametric statistics (Minitab, 2000), but have not yet been analyzed using GIS.

Geographic analysis focused on mapping MPN data and water quality measurements on base maps consisting of air photo images of the study areas. The air photos used are digital orthophoto quarter quadrangles (DOQQs), which are high quality, infrared images with a scale of one inch equals 1,000 feet. At this scale, the resolution of land use/land cover is fairly detailed, making it possible not only to interpret major features such as forest type, wetlands, etc., but also minor features such as individual chicken houses and drainage ditches, even in wooded areas. Successive runs of data analyses on the MPN were mapped on the DOQQ, allowing us to relate patterns of *E. coli* levels to the physical environment in which the sample was located. The ability to iteratively test data while examining and comparing the resulting spatial patterns is unique to GIS.

Sampling

Perhaps most importantly, GIS was critical in mapping and evaluating field and lab results, permitting us to better manage our field-sampling scheme. Although the study areas appear small in area, there are an overwhelming number of potential sites to sample once in the field. The GIS allowed us to more precisely define the physical environment that we needed to study in depth. GIS permits us to make the selections that yield meaningful information about the main sources of nonpoint source pollution in these waters, allowing us to focus sampling on specific source areas of *E. coli*.

Our initial sampling plan for *E. coli* MPN counts involved selecting sites that represent the physical geography of the study areas. We could identify these sites because the DOQQs provided a detailed picture of the study area from which to choose sample sites that reflect the variations in ecology and land use of the source regions for *E. coli*-laden water. In both study areas, these sites were sampled on a monthly basis. This routine sampling was important in determining the temporal and spatial pattern of *E. coli* concentrations as they change throughout the year. Also, by mapping the locations of the raw MPN counts on the DOQQ, we were able to evaluate which physical environments contained streams whose source areas were major contributors to MPN levels.

Determining the sources of *E. coli* required an additional sampling strategy, which was also very much supported by GIS. While most water sampling was routine, given the amount of fieldwork and especially laboratory work involved in obtaining even a single DNA result, we were forced to be very careful in selecting which areas to sample for DNA fingerprinting. Almost all streams in the Chesapeake Bay watershed contain at least a low level of bacterial contamination. Thus, we directed water sampling for DNA fingerprint analysis to streams and rivulets from source areas that were the greatest contributors of contamination to the pond or tributary.

Using the GIS mapping capabilities, we were able to determine which of the initial sample sites consistently had the greatest concentrations of *E. coli*. The streams and rivulets in these source regions were singled out for more intensive water sampling because they are major contributors of *E. coli* and may reflect the major animal sources of bacterial pollution in the study area. Most of the scat samples were also collected from these source areas to determine which animals were contributing to contamination in that locale. By continually refining the analyses of MPN values, the area of sampling was gradually decreased and more individual rivulets sampled in that area. A source region was more precisely delimited in this way, increasing the potential for identifying the specific sources of pollution in that particular physical setting.

In Shiles Creek, the use of GPS in conjunction with GIS was critical to obtaining location positions for making repeated observations at specific sites. Some of these sites consisted of tiny rivulets in a fairly extensive area of marsh that has few distinguishing physical features to use as landmarks. Sampling in densely wooded areas created a similar problem of locating sites and obtaining mapping positions. Using the GPS helped solve this problem by continually giving range and bearing instructions to the sampling team, allowing them to navigate directly to previous sample locations.

To test the accuracy of our GPS observations, the sample sites were mapped and overlaid on the DOQQ. Each sample site location was then compared to its previously recorded location on the map to insure that the same sites had been sampled and that their positions were correctly recorded. Often, it was necessary to zoom or enlarge portions of the photo to make these comparisons. The magnification of a digital computer image of an air photo, compared to using an optical device and a hard copy air photo, results in much greater control of the image and greatly increases the ability to interpret details of the physical environment that the image represents. Some error tolerance in location position was accepted to account for the fact that the GPS was in the aft of a 16 foot canoe whose angle in relation to the shoreline could vary. Any major discrepancies in position were resolved by further GPS field observations. The locations of new sample sites were established by GPS and verified by additional GPS observations on later field collection trips.

GIS ANALYSIS

To determine which sites and their source regions were major contributors of *E. coli*, we made use of the database analysis capabilities of the GIS. Not surprisingly, the results of MPN data analysis revealed that MPN values varied widely between sites, as well as from one field collection trip to another. MPN values fluctuate with the weather, the chemistry of the water, and the movement and habits of animals, both temporally and seasonally. The temporal variations in MPN values in some smaller source regions were particularly high and data variance large. Therefore, we analyzed *E. coli* by ranking each site by MPN values for each field collection trip. Moreover, in an effort to insure consistency, sites were ranked using different criteria, including ranking all sites by mean MPN, highest MPN, MPN > 200 and MPN > 500. MPN counts over 200 result in beach closings.

The results of each rank order analysis were mapped; each site was mapped by their rank for each set of ranking criteria. The results of the ranking analysis were then overlaid on the DOQQ, using different map symbolization to represent the different rank analysis. This technique allowed us to compare results of the different rank order analyses. The sites that were consistently most highly ranked in two or more ranking procedures were considered candidates for further field investigation, including additional scat and water sampling.

The results of the MPN ranking of sites in Shiles Creek suggest that small streams flowing from wooded area are more important contributors of *E. coli* (e.g., Figure 2 sample site 7.5). Field observations in these areas reveal that there is significant evidence of wildlife, including widespread occurrences of animal scat. In Schumaker Pond, the results are more difficult to interpret, but they seem to suggest that runoff carried across large paved surfaces and into storm water culverts to the pond may be an important source of *E. coli.* Although sometimes the relationship between *E. coli* counts and animal activity is evident; for example--we have seen animal tracks (e.g., raccoon) right next to sample sites that had fairly high *E. coli* counts--it may be that in Schumaker Pond, *E. coli* levels are a function of both runoff from paved areas and direct input by animals. However, there is still several more months of sampling to be completed. Additional sampling in the remaining months of the field investigation phase of this study is necessary to verify these findings.

GIS AND DNA MATCHING

Another important use of GIS was the mapping of results of DNA fingerprinting. Some of the more highly ranked sample sites were further investigated by sampling for water and scat to develop DNA matches. However, our research is still in its early stages, as far as DNA fingerprinting analysis of the collected water and scat are concerned. While we have had some successful matches of *E. coli* in water samples to specific animal species, too few samples collected have been through the complete analytical process to make any firm conclusions as to the major or dominant sources in each of the study areas.

No single match of DNA from water to a specific animal source is sufficient to draw conclusions as to the major pollution sources, but our past experience indicates that continued fieldwork and laboratory analysis over the study period should yield a sufficient number of matches to allow the probable sources of the *E. coli* pollution to be identified. GIS analysis will help to explain the location and areas that are the source of the *E. coli.* Furthermore, this research will continue to track the seasonal and temporal factors that help control the spatial pattern of *E. coli* concentrations. From such an effort, it is hoped that an effective policy can be formed to help mitigate the pollution problem.

CONCLUSIONS

This investigation is one of the first to apply PFGE technology and GIS methods to identify the sources of nonpoint source *E. coli* water contamination prior to a disease outbreak. GIS is an extremely valuable tool in managing the field component of the project. By combining the use of digital air photos and GPS with GIS, fieldwork is planned and conducted much more efficiently because it is possible to choose sample sites that better represent the physical environment of the study area. We can also return to the field and find our sample sites or locate new ones, even in the remotest part of the study area. It is also possible to more accurately map the data directly in the context of its physical environment, greatly increasing the quality of analysis. The researcher is no longer limited to field observations of the small area that can be seen surrounding the site or to approximating site locations of data on a map produced for some other purposes. We can directly locate the site and determine physical features characterizing the surrounding area.

Our preliminary work also suggests that the GIS is necessary to conduct spatial analysis because it is possible to iteratively map and explore spatial data in varying ways. Because of the variance in MPN data, we used this capability to determine the sites and physical environments that are the major contributors of *E. coli*.

Comparing maps to determine spatial patterns is certainly not a new technique, but GIS greatly facilitates its operation. While statistical packages and spreadsheets are commonly used for analysis, they are not directly designed to map the output of analysis. GIS integrates both capabilities, such as making maps of the rank ordering of the MPN levels. Just as it is common in a spreadsheet to recalculate data to examine patterns in many different ways, GIS was designed to analyze data iteratively. Unlike spreadsheets, GIS can also map the results of these efforts.

We have just begun to analyze the MPN data in order to determine the spatial pattern of its sources. It does seem, however, that on rural tidal creeks, forested areas are major sources of *E. coli* pollution of water. Forests are, of course, natural places for wildlife to concentrate. However, other physical environments need to be more fully examined to understand their role in bacterial contamination, if any. It does appear that in urban environments there are other sets of controls on *E. coli* concentrations. By combining GIS and DNA fingerprinting, our method of bacterial source tracking may offer significant public health benefits in areas of wildlife contamination control or where human and wildlife *E. coli* strains need to be differentiated.

ACKNOWLEDGMENTS

This project was funded in part by the U.S. Environmental Protection Agency section 319 Nonpoint Source Program through the Maryland Department of Natural Resources. We also wish to recognize the support of Salisbury University, Richard A. Henson School of Science; the Maryland Department of the Environment, Technical and Regulatory Services Administration; and the Wicomico County Environmental Health Department.

REFERENCES

APHA (American Public Health Association), AWWA (American Water Works Association), & WPCF (Water Pollution Control Federation). (1995). *Standard Methods for Examination of Water and Waste Water* (19th ed.). Washington, DC: American Public Health Association.

Brohawn, K., Beatty, W., McKay, R., Ellwanger, M., Evans, B., Frana, M. F., Venso, E. A., & Phipps-Dickerson, M. (2000). *Pilot Study–Fecal Coliform Fingerprints from Nonpoint Source Pollution in Two Eastern Shore Watersheds.* [Final Report for FFY99 CWAP Incremental Section 319(h) Grant 14.00.483.EPA.035.]

Burkholder, J. M., Mallin. M. A., & Glasgow, H. B., Jr. (1999). Fish kills, bottom-water hypoxia, and the toxic Pfiesteria complex in the Neuse River and Estuary. *Marine Ecology Progress Series, 179*, 301-310.

Burrough, P. A. & McDonnell, R. A. (1998). *Principles of Geographical Information Systems.* New York: Oxford University Press.

Clean Water Action Plan Technical Workgroup. (1998, August 28). *Maryland Clean Water Action Plan. Watershed Prioritization and Plans for Restoration Action Strategies.* [Final 1998 Report on Unified Watershed Assessment.] Available: http://www.dnr.state.md.us/cwap.

Engel, B. A., Srinivasan, R. & Rewerts, C. (1993). A spatial decision support system for modeling and managing agricultural non-point source pollution. In M. F. Goodchild, B. O. Parks, & L. T. Steyaert (Eds.), *Environmental Modeling with GIS* (pp. 231-237). New York: Oxford University Press.

Fedra, K. (1993). GIS and environmental modeling. In M. F. Goodchild, B. O. Parks, & L. T. Steyaert (Eds.), *Environmental Modeling with GIS* (pp. 33-50). New York: Oxford University Press.

Frana, M. F., Venso, E. A., Brohawn, K., Beatty, W., McKay, R., Ellwanger, M., Evans, B. & Phipps-Dickerson, M. (2000). *DNA Fingerprinting of Nonpoint Source Escherichia Coli Contamination in the Chesapeake Bay* [CD-ROM]. Proceedings of the Fifth International Symposium and Exhibition on Environmental Contamination in Central and Eastern Europe, Prague, Czech Republic, September.

Hunsaker, C. T., Nisbet, R. A., Lam, D. C. L., Browder, J. A., Baker, W. L., Turner, M. G. & Botkin, D. B. (1993). Spatial models of ecological systems and processes: The role of GIS. In M. F. Goodchild, B. O. Parks, & L. T. Steyaert (Eds.), *Environmental Modeling with GIS* (pp. 248-264). New York: Oxford University Press.

Kane, A. S., Dykstra, M. J., Noga, E. J., Reimschuessel, R., Baya, A., Driscoll, C., Paerl, H. W., & Landsberg, J. (2000). Etiologies, observations and reporting of estuarine finfish lesions. *Marine Environmental Research, 50*(1-5), 473-477.

Maidment, D. R. (1993). GIS and hydrological modeling. In M. F. Goodchild, B. O. Parks, & L. T. Steyaert (Eds.), *Environmental Modeling with GIS* (pp. 147-167). New York: Oxford University Press.

Minitab, Inc. (2000). *Minitab Statistical Software* (Version 13.1) [Computer software]. State College, PA: Minitab, Inc.

Murie, O. J. (1974). *Animal Tracks* (2nd ed.). New York: Houghton Mifflin Company.

National Shellfish Sanitation Program. (1997). *Guide for the Control of Molluscan Shellfish.* Paper presented at the Interstate Shellfish Sanitation Conference, Sturbridge, MA, July

Rezendes, P. (1999). *Tracking & the Art of Seeing: How to Read Animal Tracks and Signs* (2nd ed.). New York: Harper Perennial, Division of Harper-Collins, Inc.

Roth, V. & Cyffka, B. (1999). Possibilities and constraints of determining and processing hydrological data—GIS as an instrument to survey water quality of stagnant water bodies. In Dikau, R. & Saurer, H. (Eds.), *GIS for Earth Surface Systems* (pp. 134-152). Berlin: Gebruder Borntraeger Verlagsbuchhandlung.

Simmons, G. M., Jr., & Herbein, S. A. (1998). *Final Report for the City of San Diego and the County of San Diego Department of Environmental Health. Potential Sources of Escherichia Coli to Children's Pool in La Jolla, CA.* Blacksburg, VA: Virginia Polytechnic Institute and State University.

Simmons, G. M., Jr., Herbein, S. A. & James, C. M. (1995). Managing nonpoint fecal coliform sources to tidal inlets. *Water Resources Update* (100), 64-74.

Swaminathan, B., Barrett, T. J., Hunter, S. B., Tauxe, R. V. & Force, C. P. T. (2001). PulseNet: The molecular subtyping network for foodborne bacterial disease surveillance, United States [On-line]. *Emerging Infectious Diseases, 7*(3). Available: www.cdc.gov/ncidod/eid/volno3/swaminathan.htm.

Water Quality, Code of Maryland Regulations. §§ 26.08.02.03-3A (1997a).

Water Quality, Code of Maryland Regulations. §§ 26.08.02.03-3C (1997b).

World Health Organization. (1999). Health-Based *Monitoring of Recreational Waters: The Feasibility of a New Approach (The "Annapolis Protocol." Outcome of an Expert Consultation, Co-sponsored by USEPA.)* WHO/SDE/WSH/99.1. Annapolis, MD, USA.

Chapter XIII

Spatial Modeling of Risk Factors for Gender-Specific Child Mortality in a Rural Area of Bangladesh

Mohammad Ali
International Vaccine Institute, Korea

Christine Ashley
University of Minnesota, USA

M. Zahirul Haq and Peter Kim Streatfield
International Centre for Diarrheal Disease Research, Bangladesh

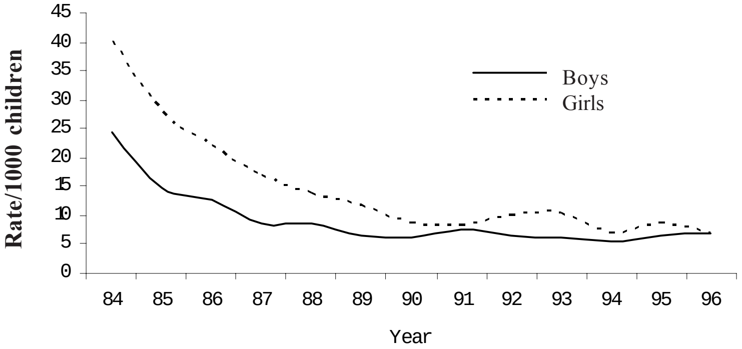
This chapter describes the use of geographic information systems to predict spatial risk of child survival problems in a rural area of Bangladesh. Demographic, health service and socioeconomic surveillance data linked with a geographic information system from the rural area were used to predict the risk of gender-specific child mortality. Temporal data from the area show that child mortality rates have declined, and that gender differences in mortality have been eliminated. However, results of the higher mortality area analysis show that this decline has not been consistent in all areas. A wide geographical variation of mortality exists within the area as well. In general, places that had no intensive child health intervention, no outside embankment and were distant from a treatment center predicted a higher risk for child *mortality. An area with Hindu predominance predicted risk for only female child mortality. The results of the analysis suggest that, with socioeconomic and cultural interventions, spatial variations in child mortality can be minimized.*

INTRODUCTION

The global reduction of child mortality has been a priority of international and national organizations for the last few decades. The Health for All by the year 2000 goal set at Alma Ata called for the equitable distribution of health services to all children, transcending geographical boundaries. Despite widespread global efforts to improve child survival, the latest UNICEF report on the *State of the World's Children 2000* (UNICEF, 2000) indicates that child mortality rates continue to remain higher in Lesser Developed Countries (LDCs), and in some areas, girls continue to die at a greater rate than boys.

Demographic surveillance data from Matlab, a rural area of Bangladesh, indicate that the mortality rates of the children (aged 1-4 years) in the area have declined greatly in the last two decades (Figure 1). The rates have also declined in other rural areas across the country (BBS, 1987, 1998), though a lesser extent than in Matlab. In Matlab, the mortality rates declined by 56% for boys and 69% for girls from 1985 to 1995, as compared to a decline of 16% for boys and 24% for girls in other rural areas nationwide. The gender mortality differential that was notoriously high in Matlab in the 1980s virtually disappeared by the mid-1990s. The

Figure 1: Temporal pattern of gender specific mortality in Matlab



larger decline of mortality in Matlab can be perhaps attributed to child health intervention programs that have been operating in a part of the area since 1982 (Fauveau, 1994).

Despite the large decline and elimination of gender disparity in child mortality, spatial variations in mortality continue to exist in Matlab (Ali *et al.*, 2001a). This variation most likely exists in the rest of Bangladesh, as well as in other Less Developed Countries (LDCs). Previous studies have attributed this variation to a variety of social, environmental, and health care factors (Ali *et al.*, 2001a; Rahman *et al.*, 1982, 1993). A multitude of social, demographic, economic, and environmental factors has been identified as contributing to the gender differential of child mortality in Bangladesh (Chen *et al.*, 1980; Koenig & D'Souza, 1986; Basu, 1989; Islam & Ataharul, 1989; Bhuiya & Streatfield, 1991; Fauveau *et al.*, 1991; Salway & Nasim, 1994; Muhuri, 1995; Muhuri & Menken, 1997; Bairagi *et al.*, 1999).

In both demographic and epidemiological transition theory, mortality decline has been attributed to modernization (Chesnais, 1992; Omran, 1971). Modernization encompasses economic, political, social and cultural changes in society (den Bosch *et al*, 2001), which may change the life style of the people and that influences their health. Since adaptation of an innovation varies across societies in Bangladesh, the modernization process must be varying spatially, and that may contribute to vary mortality decline from one place to another.

Individuals in real life do not exist in isolation, rather they live as the members of a society. This society is usually formed by a group of people living close to each other. Munshi (1996) argues that people learn from their neighbors, and that behavioral practices of individual households are influenced by them (Twigg *et al.*, 2000). Addressing such a human environment is greatly limited by the analytical tools available. The lack of an effective geocomputational environment and algorithms hindered the development of spatial analysis techniques in this area (Kwan, 2000). As a result of these constraints, unrealistic assumptions about human behavior and their environment were often made, and the methods used to operationalize the theoretical constructs were limited. Complexities arise also because of the uneven distribution of physical facilities, differences in the speed of movement in different areas and the effect of communication networks.

Health is also related to complex systems of interaction among environment, population and cultural behavior (Meade, 1988). Geographic information systems (GIS), by identifying people's residence, their cultural, social, and physical environment, can address the complex systems of interaction among those components. Spatial distribution of physical facilities, people and their cultural and socioeconomic conditions can now be modeled by creating natural boundaries of the phenomena with in a GIS. GIS has been shown as a useful tool for public health research and application, particularly in disciplines that can benefit from envisioning a spatial component, or the correlation of two or more spatial variables. It can help describe spatial variations of health and their covariation with environmental factors and health care systems (Loslier, 1998; Wilkinson, *et al.*, 1998; Anderson & Skrizhevskaya, 1996).

The chapter focuses on identifying the components creating spatial, i.e., environmental, risks for health, in particular gender-specific child mortality in a rural area of Bangladesh. The data are viewed from a geographical perspective, and natural boundaries of the phenomena are defined as models of environmentl entities.

DATA AND METHODS

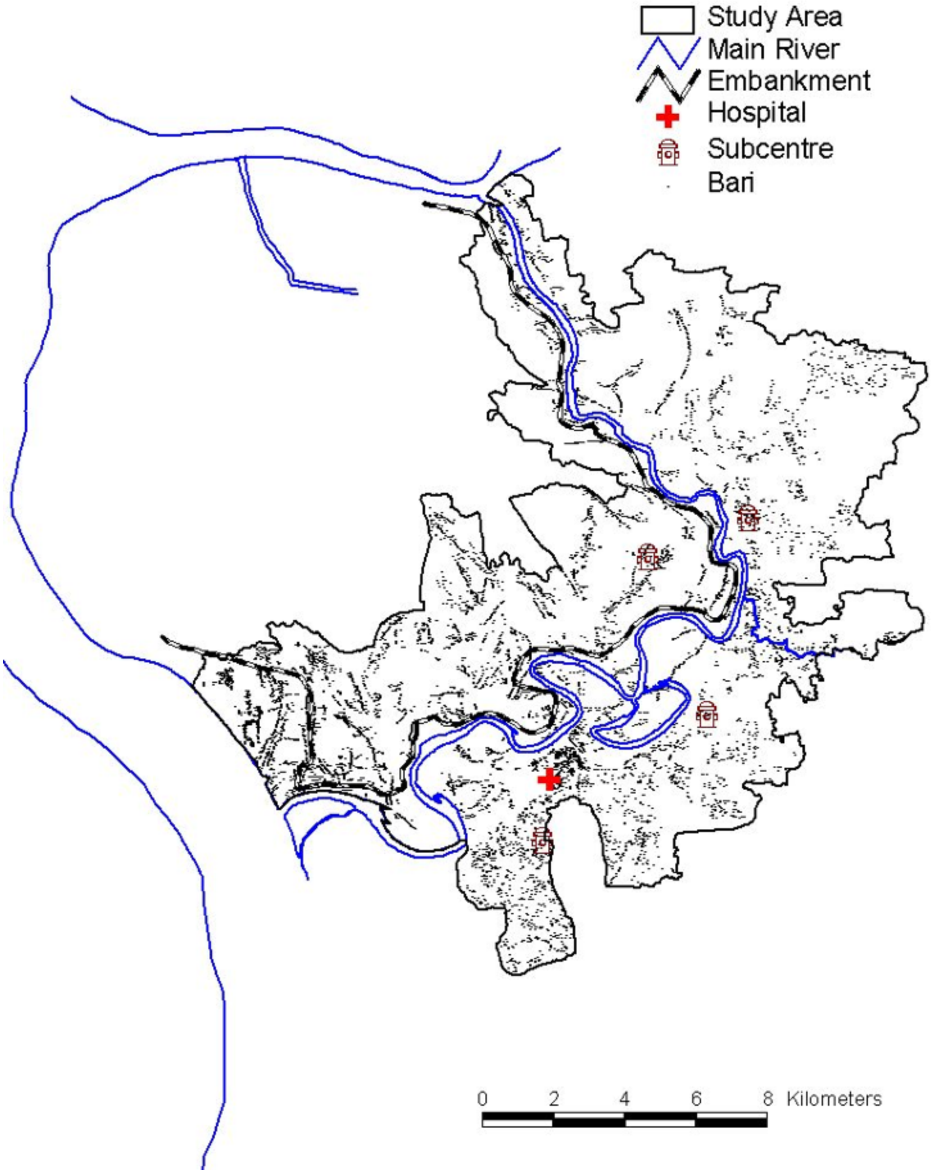
The Study Area and the GIS

The study was conducted at the International Centre for Diarrheal Disease Research, Bangladesh's (ICDDR,B) field research site at Matlab, a rural area of Bangladesh located 54 km southeast of the capital city, Dhaka. The study area is comprised of 142 villages and covers 184 km^2. The Dhonagada River intersects the study area, dividing it into nearly equal portions. In the 1980s, an embankment was commissioned alongside the main river to allow year-round agricultural activities and to provide flood protection for local communities. Since the initiation of ICDDR,B activities in 1963, a variety of health intervention programs have been undertaken in the research site. Detailed descriptions of the area and the intervention programs have been provided elsewhere (Fauveau, 1994). The intervention programs, in most cases, have been conducted in one-half of the area (intervention area); thus providing comparative figures of health status between intervention and non-intervention (comparison) areas. In the study area, a hospital and four community-based health centers (subcenters) are being operated as the part of the ICDDR,B program.

For the last three decades, a demographic surveillance system (DSS) has recorded all vital demographic events of the study area population. The population of the area is about 200,000, and the population density is approximately 1,100 people per square kilometer. The people live in clusters of patrilineally related households called *baris*. The average number of households in a *bari* is six in which approximately 30 people live. Approximately 85 percent of the population is Muslim and most others are Hindu.

In 1994, a GIS was implemented integrating the DSS components within the frame of its information systems. Figure 2 shows the geographic features of the study area. The detailed descriptions of implementing the health-based GIS are given elsewhere (Ali *et al.*, 2001b). A unique feature of the GIS is the *bari* level

Figure 2: The Matlab study area, Bangladesh



information, which allows investigating local level spatial variability of health and environmental phenomena of the study area. Both vector and raster formatted data structures are maintained in the GIS allowing a wide spectrum of spatial analysis. This study acquired data on population, mortality and socioeconomic status from the DSS and spatial data from the GIS.

Study Periods

Two time-periods, 1984-86 and 1994-96, were chosen to develop the model of spatial risk for gender-specific child mortality of the Matlab. For younger children biological factors tend to figure more prominently in gender-specific mortality rates (Islam & Ataharul, 1989). Three-year periods were selected to avoid temporal bias in the mortality rate on space. The age group 1-4 years was chosen as an indicator of the conditions of a child's environment. It is assumed that after one year of age, survival is greatly influenced by socio-environmental variables such as education, population density, socioeconomic status, access to health services and biophysical features.

Raster GIS Data

The study used raster GIS technology to exploit exploratory spatial data analysis technique as the methodological tools of this research questions. Within the raster GIS, the spatial resolution of the pixels was set to 30 meters to represent a *bari* in a single pixel. A total of 7,691 pixels of *baris* were implemented in the GIS. Within the raster system, each data set, such as population, mortality, educational status, etc., was interpreted in an image, and the data became the attribute of the pixels.

BOUNDARY MAPS OF HEALTH AND ENVIRONMENT

Health Maps (Dependent Variables)

A kernel estimation procedure described elsewhere (Bailey & Gatrell, 1995; Gatrell *et al.*, 1996) was used to compute intensity of deaths for each point of measurement (*baris*). Unlike the method described in those literatures, this study used a spatial filtering technique within a raster GIS environment (Ali *et al.*, 2002) to compute the intensity. Since the occurrence of health events depends on the size of population at risk, the intensity of deaths at a target point is adjusted by the size of population (close to 35 persons) by choosing varying sized neighborhoods from 3×3-pixel to 21×21-pixel windows.

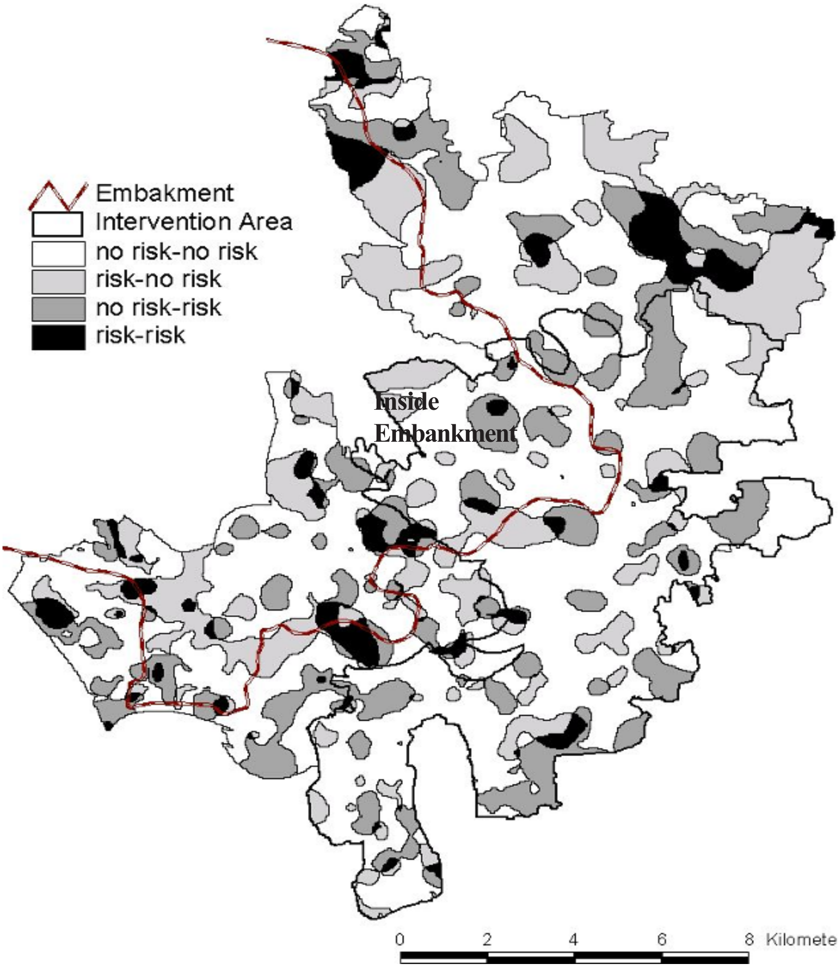
The data on estimated intensity of deaths for the point of *baris* were then used to interpolate spatially smoothed surface of mortality by using the kriging method (Oliver & Webster, 1990). In kriging, the variable that is being interpolated, Z, at a point x_0 is:

$$\hat{Z}(x_0) = \sum_{i=1}^{n} \delta_i Z(x_i)$$

where, $Z(x_i)$ is the observed data value at points i, δ_i is the weight associated with the data at point i, which is obtained from a linear predictor. Kriging uses a variogram model for interpolation of data. The underlying assumption of the variogram model is that two observations close together are more similar than two observations further apart. The closer a data point is to a measured point, the more weight it carries. The sum of the weighting factors used to calculate the value is 1.

While kriging, the grid cell size chosen was 150, thus data was interpolated at the interval of 150 meters. We then used contour mapping technique to obtain one-

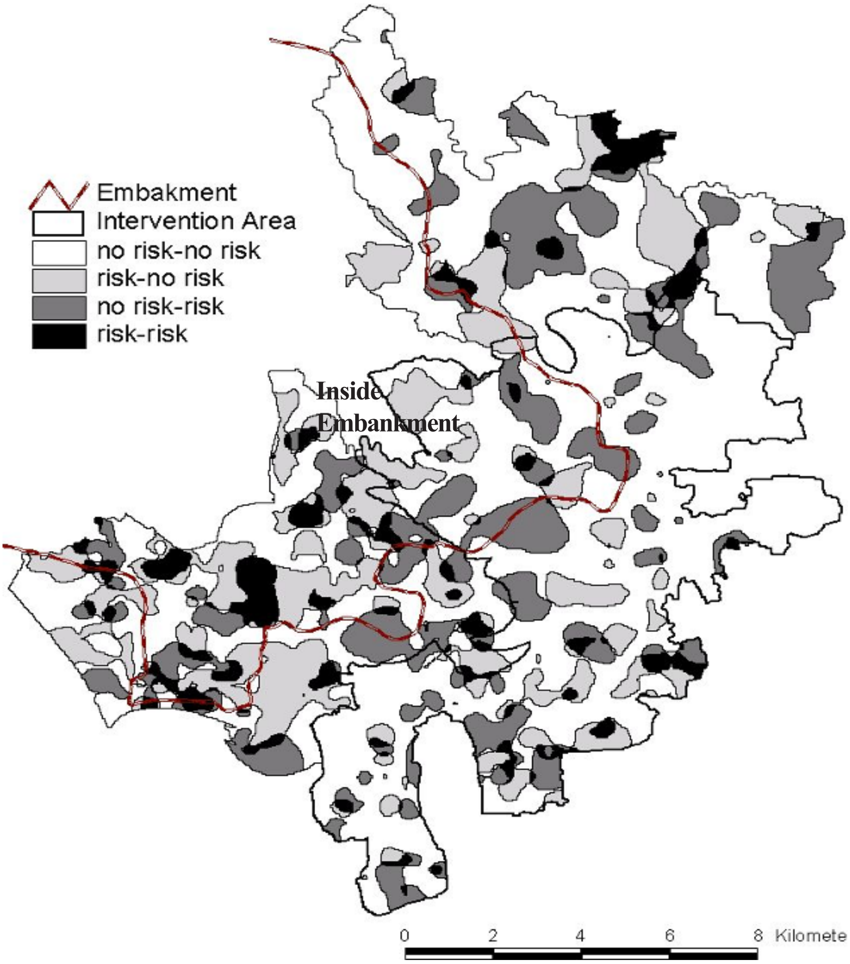
Figure 3: Cross-classification image of the high risk areas of mortality for boys with the periods 1984-86 and 1994-96, Matlab Study Area



fourth of the highest peaked surface, and the surface was defined as the higher mortality area. The surfaces of higher mortality area were obtained for both boys and girls and for the two time periods. Figures 3 and 4 show cross-classification of temporal maps of higher mortality area for boys and girls respectively.

From each of the cross-classification maps of higher mortality, four Boolean (binary) maps were created: i) risk area remains risk area, ii) risk area changed to non-risk area, iii) non-risk area changed to risk area and iv) non-risk area remains non-risk area. The area of interest was assigned the value of "1"; otherwise the assigned value was "0." The spatial logistic regression model requires that the dependent variable be employed as a probability image. A surrogate method (Eastman, 1999) using a spatial filter of window size of 7×7 - pixels was used to

Figure 4: Cross-classification image of the high risk areas of mortality for girls with the periods 1984-86 and 1994-96, Matlab study area

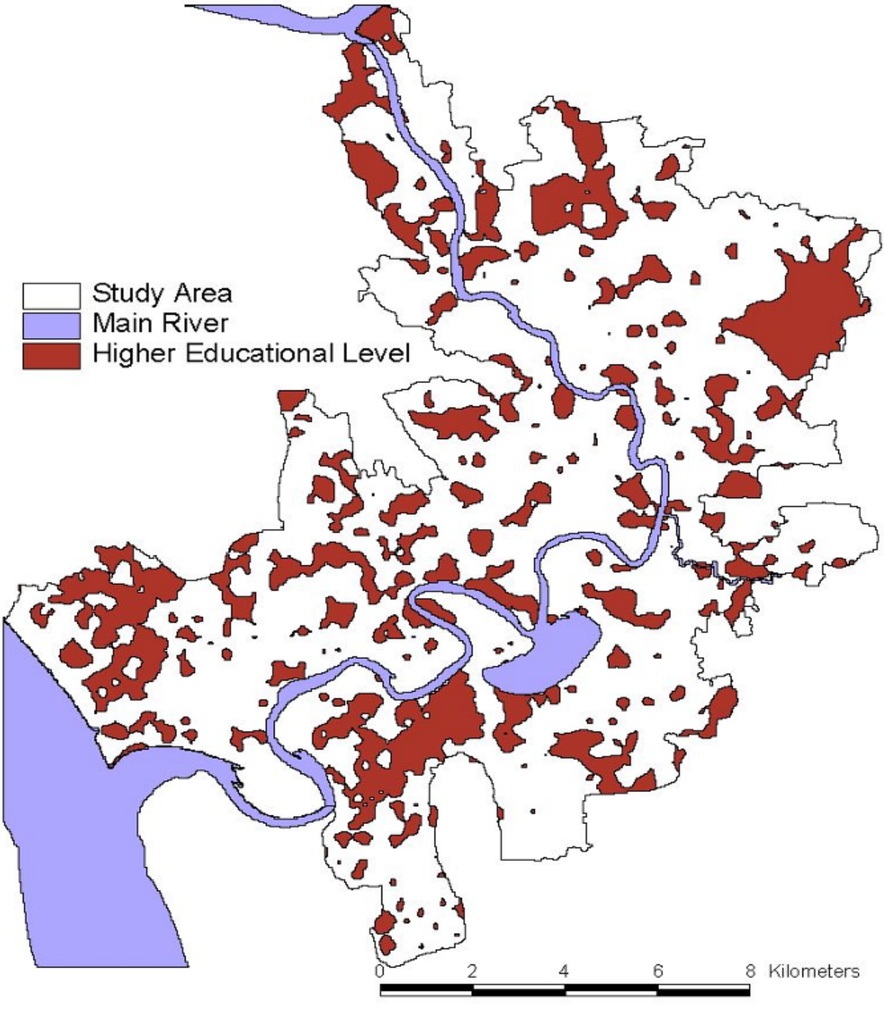


obtain the probability images. It was assumed that the size of this window would give enough variation in the surrounding areas of a pixel of the study area.

Environment Maps (Independent Variables)

The map of high education areas was created using spatial filtering. A constant size of window (7×7 - pixels) was chosen for the filtering, because it was assumed there would be no influence from neighbors after a certain distance. It was also assumed that neighbors' influence would diminish as distance increases; therefore, a distance decay function ($e^{-\text{spatial lag}}$) was used in computing it. Proportion of educated (at least four years of secular education) persons living in a *bari* was used. The method yielded a higher education for the *baris* that are surrounded by more

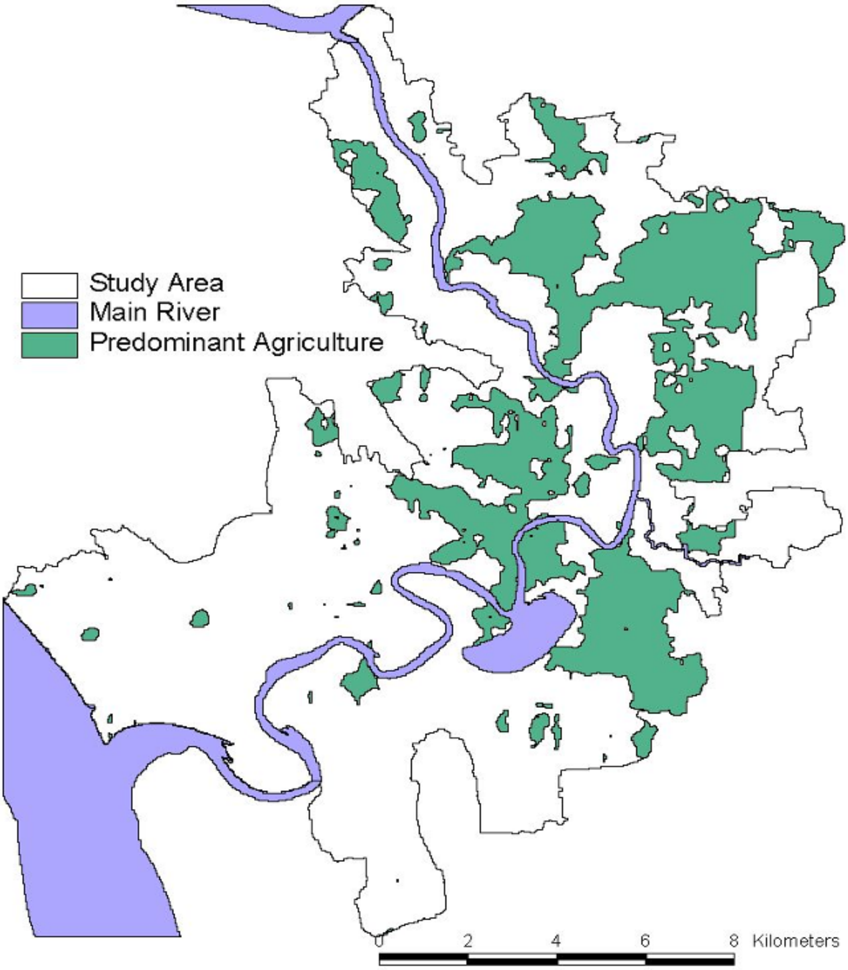
Figure 5: Map showing area of higher level of education in Matlab, 1996



educated neighbors. An edge correction term (proportion of window celling falls inside the study area) was used to remove boundary effect in the data. Using kriging and then a contour algorithm, the surface of educational status was created from which the highest elevated quarter was defined as the higher educated area. Figure 5 shows the map of higher educated areas in 1996. Similarly, higher population density and higher fertility (based on general fertility) maps were created. The population density was represented in per square kilometer dividing cumulated total of the people within the window by the size of window area (0.0441 km^2).

Socioeconomic maps were created with the major occupations, such as agriculture, fishing and business. Figure 6 shows the area of predominant agriculture in 1982. Using cross-classification of the maps of major occupations, seven maps

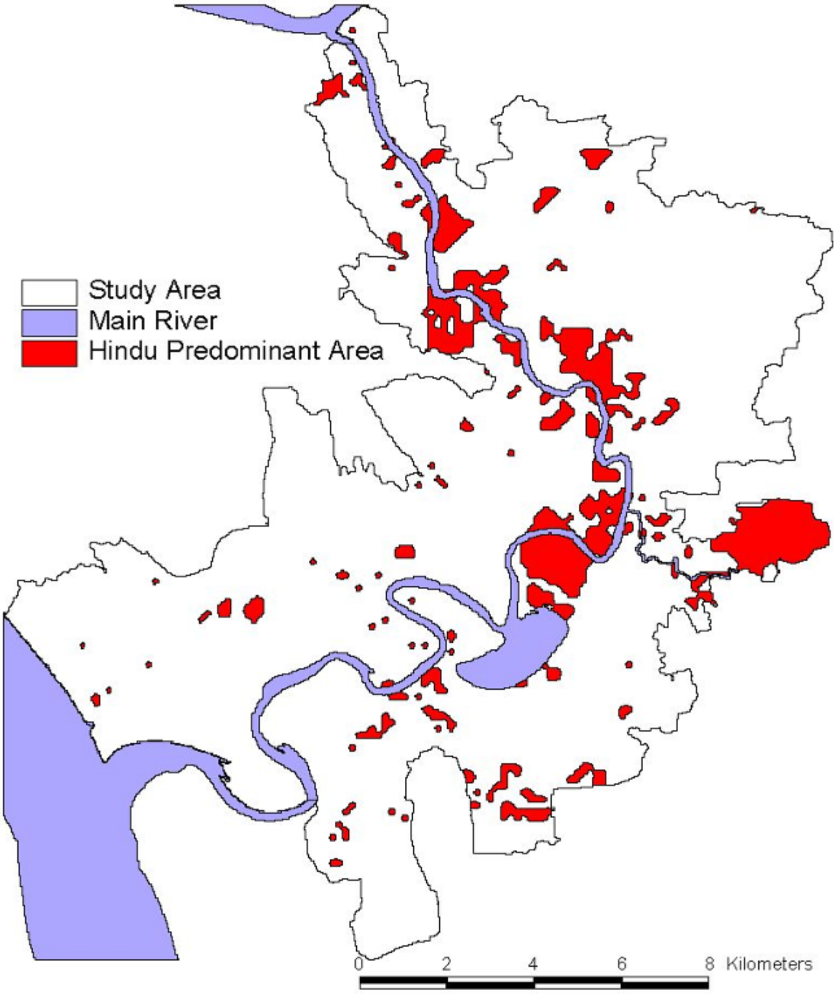
Figure 6: Map showing area of predominant agriculturist in Matlab, 1982



of all possible combinations were created. The cultural map was created identifying the Hindu predominant areas. The map (Figure 7) shows the Hindu communities live along the main river, as fishing is their predominant profession.

All maps were described in binary (Boolean) category. The binary maps were used to create distance surfaces from the islands (elevated quarter surface) of the phenomena. In the distance surface, the closer a pixel is to the island, the smaller the attribute value of the pixel is; the pixels fall in the islands was attributed to "0." A binary image was created for embankment attributing the pixels outside the embankment as “1,” and “0” otherwise. Similarly, the comparison area (non-intervention area) and intervention area were described by “1” and “0” respectively. The map of accessibility to heathcare was the cost distance (in time) to the nearest

Figure 7: Map showing Hindu predominant area in Matlab, 1996



treatment center (TC). In computing the cost distance, river and canals were treated barriers, and accounted their cost (time) five times higher than that of the ground.

Analytical Methods

Logistic regression was employed to determine predictive risk factors for gender-specific child mortality. The regression model takes the form:

$$\text{logit}(p)=\ln(p/1-p)=a+b_1x_1+b_2x_2+\ldots\ldots+b_nx_n$$

where p is the dependent variable expressing the probability of the outcomes, which are a) risk area remained risk area (R-R), b) risk area changed to non-risk area (R-N), c) non-risk area changed to risk area (N-R), and d) non-risk area remained non-risk area (N-N). The kappa statistic was also used to ascertain the agreement in the risk areas of mortality between boys and girls.

RESULTS

The thresholds to define higher mortality areas for boys and girls are given in Table 1. The cross-classification of higher mortality areas between boys and girls reveals poor agreement for both the time-periods (kappa statistic <0.20). In Matlab, the majority of the deaths were associated with infectious diseases: in 1985, 43% of the total child deaths were attributed to diarrhea, 14% to measles, and 4% to respiratory diseases. In 1995, approximately 33% of the deaths were attributed to diarrhea and 11% were due to respiratory diseases. Drowning was also one of the major causes of child deaths in both the periods, which was also reported elsewhere (Myaux *et al*., 1996; Ahmed *et al*., 1999).

The regression was done in two steps. In the first step, the simple logistic regression was used, and the factors showing a minimum of 2% variation in explaining spatial risk for gender-specific mortality were used in a multiple logistic regression in the second step. The results of the multiple logistic regression show that the combined effects of the factors explain 11% of the total variations in predicting N-R for male child (Table 2). Being in an area outside an embankment is the most important factor in predicting risk for male child mortality followed by areas of multiple groups of professionals. A high fertility rate also predicts spatial risk for

Table 1: Thresholds (deaths/1,000 children) for defining high risk areas of child mortality

Gender	1984-86	1994-1996
Male	30.4	9.0
Female	41.4	10.5

Table 2: Results of the multiple logistic regression (spatial) of the male child mortality. Models: Non-risk area changed to risk area (N-R) and non-risk remains non-risk area (N-N)

Variables	Model: Non-risk to Risk (N-R)		Model: Non-risk to Non-risk (N-N)	
	Regression coefficient	t-test	Regression coefficient	t-test
Intercept	-3.817858	-250.14736	2.690645	166.0446
multiple groups of professionals	0.000090	39.580791	-0.000058	-26.80997
high educational status	0.000362	18.031919	-0.000044	-2.516286
high fertility	0.000106	10.347898	0.000123	13.851040
comparison area	0.170880	17.679539	-0.058213	-6.269722
outside embankment	0.469618	51.742344	-0.306266	-35.09447
cost distance to TC	0.001229	21.177443	-0.000528	-9.392699
high density of population	0.009980	1.036064	0.054325	5.873418
Hindu dominance	0.001021	17.087276	-0.000358	-6.205904
Adjusted R^2	**0.114470**		**0.034517**	

male child mortality. Areas of higher population density show the lowest spatial risk among the factors. On the other hand, the same factors do not predict much (only 3% of total variations) in explaining N-N.

Since the spatial regression yielded no direction of relationship (positive or negative), a logistic regression was done outside the GIS environment using the *bari* level data to understand the direction of relationship. The results of the analysis reveal that *baris* in the area of multiple groups of professionals, higher educational level, comparison area, cost distance to TC and outside embankment have a positive relationship with N-R. In contrast, fertility, population density and Hindu community show a negative relationship with N-R. Since no variables predicted N-N, the *bari* level analysis was not employed for it.

The results of the analysis for predicting R-R and R-N of male child are presented in Table 3. In the table, the model R-R shows that the comparison area predicts higher spatial risk for male child mortality. The effect of an embankment in predicting spatial risk is also significant. The distance to treatment centers and areas dominated by multiple groups of professionals also influence risk areas to remain risk areas. Overall, the combined effect of the variables explains 16% of the total variation for male child mortality. Table 3 also shows that the factors included in predicting R-R do not predict R-N. According to the *bari* level data, all the factors included in the model, such as multiple groups of professionals, comparison area, outside embankment and the cost distance to TC, show a positive relationship with the R-R.

The results of regression analysis for N-R and N-N of female child mortality are given in Table 4. In this case, the combined effect of the factors explains 10% of the total variations in predicting N-R. The comparison area predicts the highest risk among all factors of mortality included in the model followed by embankment

Table 3: Results of multiple logistic regression (spatial) of the male child mortality. Models: Risk area remains risk area (R-R) and risk area changed to non-risk area (R-N)

Variables	Model: Risk to Risk (R-R)		Model: Risk to Non-risk (R-N)	
	Regression coefficient	t-test	Regression coefficient	t-test
Intercept	-4.086931	-178.4538	2.057620	71.24044
multiple groups of professionals	0.000044	12.188567	-0.000017	-5.028326
comparison area	0.808863	50.562550	-0.233676	-16.77735
outside embankment	0.382884	26.844124	-0.115347	-8.904040
cost distance to TC	0.001489	16.102747	0.000166	1.993834
Adjusted R^2	**0.162250**		**0.012257**	

Table 4: Results of multiple logistic regression (spatial) for female child mortality. Models: Non-risk area changed to risk area (N-R) and non-risk remains risk area (N-N)

Variables	Model: Non-risk to Risk (N-R)		Model: Non-risk to Non-risk (N-N)	
	Regression coefficient	t-test	Regression coefficient	t-test
Intercept	-3.753035	-240.24765	2.534480	153.52201
multiple groups of professionals	0.000050	20.524385	-0.000021	-9.178230
high educational status	0.000396	20.178802	-0.000223	-12.881060
high fertility	0.000060	5.703178	0.000164	18.772718
comparison area	0.369911	38.578598	-0.190321	-20.605009
outside embankment	0.306635	32.521801	-0.114156	-12.863127
cost distance to TC	0.001503	25.077888	-0.000688	-12.130284
high density of population	0.216925	21.126863	-0.117856	-12.287079
Hindu dominance	0.001357	21.803726	-0.000698	-11.900236
Adjusted R^2	**0.101230**		**0.028542**	

and then cost distance to the TC. However, modeling N-N with these factors has little impact on the outcome. The *bari* level data indicate that educational status, comparison area, outside embankment, cost distance to TC, population density and Hindu community have a positive relationship, while *baris* located in multiple groups of professionals and in high fertility areas have a negative relationship while predicting N-R.

Table 5 presents the results of the analysis of R-R and R-N for female child. Of the factors, the comparison area influences the highest mortality followed by multiple groups of professionals and embankment in predicting R-R. Educational status, distance to the TC and Hindu community explains 19% of the total variations

Table 5: Results of multiple logistic regression (spatial) for female child mortality. Models: Risk area remains risk area (R-R) and risk area changed to non-risk area (R-N)

Variables	Model: Risk to Risk (R-R)		Model: Risk to Non-risk (R-N)	
	Regression coefficient	t-test	Regression coefficient	t-test
Intercept	-4.393467	-194.85032	2.253702	75.933701
multiple groups of professionals	0.000100	31.636171	-0.000045	-14.123897
high educational status	0.000302	10.860458	0.000152	6.076112
comparison area	0.555219	40.760643	-0.186226	-14.012320
outside embankment	0.243221	20.090242	-0.064532	-5.284036
cost distance to TC	0.001201	13.869790	-0.000286	-3.372448
Hindu dominance	0.001133	12.658359	-0.000239	-2.746511
Adjusted R^2	**0.191666**		**0.019756**	

in predicting R-R for girls. However, these factors did not show any influence in predicting R-N. According to the *bari* level data, multiple groups of professionals, educational status, comparison area, outside embankment and cost distance to TC have a positive relationship, while Hindu predominance has a negative relationship with the R-R.

DISCUSSIONS AND CONCLUSIONS

By modeling spatial risk for gender-specific child mortality, we identified several predictors for this rural area of Bangladesh. The cross-classification analysis of temporal data on higher mortality areas shows that, although the mortality rates have declined over time, they have not declined consistently over the entire study area. About 25% of the areas that experienced lower child mortality in the 1980s shifted to higher mortality areas in the 1990s. On the other hand, a major part of the higher mortality area of the 1980s became lower mortality areas in the 1990s. The shift of one type to another type of mortality area resulted in the wide geographical variation of mortality in Matlab. The cross-classification of gender-specific mortality maps also indicates significant spatial variability in mortality between boys and girls. The variability implies that human environmental processes of mortality for boys and girls are not the same.

The comparison areas where no intensive intervention was carried out, areas outside an embankment, areas distant from a treatment center and the areas predominated by multiple groups of professionals predict a higher risk for male child mortality for both the models (N-R and R-R). The results are somewhat similar to previous studies (Myaux *et al.*, 1997; Rahman *et al.*, 1982). Areas of higher educational status, lower fertility level, lower population density and non-Hindu areas predict spatial risk for male child mortality when modeling N-R.

The positive association of the areas of higher educational status with higher male child mortality indicates that neighbors' education status did not play any role in declining mortality to the extent that was anticipated. It suggests that education may not be a good predictor of mortality reduction, as it did not influence the outcome when modeling mortality with R-R. Similarly, areas of higher fertility show a negative association with higher mortality when modeling N-R, but do not show any significant influence on mortality when modeling R-R for male children. The lower mortality in Hindu-dominance area is perhaps related to their settlement pattern near the main river, which facilitates them year-round easy access to treatment centers by their own boats. However, further study is required for a better understanding of the relationships between distance to treatment centers and mortality rates.

When predicting R-R and N-R for female children, areas of higher educational status, the comparison area of no intensive intervention, being outside an embankment and greater distance to a TC were the common factors for higher mortality. Areas with multiple groups of professionals show a contrasting picture in predicting mortality when modeling the data with N-R and R-R for female. Predicting areas of mortality with the N-R model, the Hindu community shows a negative association for males and a positive association for female child mortality indicating a gender bias in seeking health care services. According to Hindu laws, the daughters cannot inherit their father's property—thus causes dowry systems existing during marriage. In many instances, the parents of the bride have to sell their assets to get the dowry demanded by the groom's family. Thus, a female child is not desirable in this society, and is received less attention by their parents.

This chapter has identified several socioeconomic and cultural factors that predict spatial risk for gender-specific mortality in Matlab. However, a large amount of variation is left unexplained in modeling spatial risk for mortality. This was anticipated, as we know that health is influenced by many factors (Wilkinson *et al.*, 1998). However, this paper has unveiled the unequitable reduction in child mortality in Matlab, and has identified associated socioeconomic and cultural factors for it. Appropriate measures targeted to specific areas may reduce the geographic variation of gender-specific child mortality.

Geographical analysis of health variation and its determinants have an important role in the design of equitable health programs. Understanding the influence of the factors on child mortality at a spatial scale can help decision makers develop an effective strategy for area-based health programming. In conclusion, although this chapter describes the Matlab study area in Bangladesh, the findings of this study may provide insight into the barriers for ensuring child survival elsewhere in the country and the region.

ACKNOWLEDGMENTS

This research was funded by DFID and ICDDR,B: Centre for Health and Population Research which is supported by countries and agencies which share its concern for the health problems of developing countries. Current donors providing unrestricted support include: the aid agencies of the Ggvernments of Australia, Bangladesh, Belgium, Canada, Japan, The Netherlands, Sweden, Sri Lanka, Switzerland, the United Kingdom and the United States of America; international organizations include United Nations Children's Fund. The authors are grateful to Mr. Mamunur Rashid for his assistance in data processing and map generating activities.

REFERENCES

Ahmed, M.K., Rahman, M., & van Ginneken, J. (1999). Epidemiology of child deaths due to drowning in Matlab, Bangladesh. *International Journal of Epidemiology*, 28(2), 306-311.

Ali, M., Emch, M., Tofail, F., & Baqui, A.H. (2001a). Implications of health care provision on acute lower respiratory infection mortality in Bangladeshi children. *Social Science and Medicine*, 52(2), 267-277.

Ali, M., Emch, M., Ashley, C., & Streatfield, P.K. (2001b). Implementation of a medical geographic information system: Concepts and uses. *Journal of Health, Population, and Nutrition*, 19(2), 100-110.

Ali, M., Emch, M., & Donnay, J.P. (2002). Spatial filtering using a raster geographic information system: Methods for scaling health and environmental data. *Health & Place* (in press).

Anderson, V. & Skrizhevskaya, E. (1996). Solving medical geographical problems with GIS: The case of South Ukraine. In Second Joint European Conference & Exhibition on Geographical Information. Barcelona, Spain. pp. 857-861.

Bailey, T.C. & Gatrell, A.C. (1995). Interactive Spatial Data Analysis. Essex, England: Longman Scientific & Technical.

Bairagi, R., Sutradhar, S., & Alam, N. (1999). Levels, trends and determinants of child mortality in Matlab, Bangladesh, 1966-1994. *Asia-Pacific Population Journal*, (June); 51-68.

Basu, A.M. (1989). Is discrimination in food really necessary for explaining sex differentials in childhood mortality? *Population Studies*, 43, 193-210.

BBS. (1987). *Statistical Yearbook of Bangladesh.* Bureau of Statistics, Ministry of Planning, Government of Bangladesh.

BBS. (1998). *Statistical Yearbook of Bangladesh*. Bureau of Statistics, Ministry of Planning, Government of Bangladesh.

Bhuiya, A. & Streatfield, K. (1991). Mother's education and survival of female children in a rural area of Bangladesh. *Population Studies*, 45:253-264.

Chen, L., Rahman, M., & Sardar, A.M. (1980). Epidemiology and causes of death among children in a rural area of Bangladesh. *International Journal of Epidemiology*, 9(1), 25-33.

Chesnais, J.C. (1992). The demographic transition: Stages, patterns and economic implications. Oxford: Clarendon Press.

den Bosch, J.H.W., van Poppel, F.W.A., Looman, C.W.N., & Mackenbach, J.P. (2001). The role of cultural and economic determinants in mortality decline in The Netherlands, 1875/1879-1920.24: A regional analysis. *Social Science & Medicine*, 53, 1439-1453.

Eastman, J.R. (1999). *Idrisi 32 Tutorial.* Clarks Labs, Worcester, Clark University. MA..

Fauveau, V., Koenig, M.A., & Wojtyniak, B. (1991). Excess female deaths among rural Bangladeshi children: An examination of cause-specific mortality and morbidity. *International Journal of Epidemiology*, 20(3), 729–735.

Fauveau, V. (1994). Introduction. In V. Fauveau (eD.), *Matlab: Women, Children and Health.* Dhaka, ICDDR,B, Bangladesh.

Gatrell, A.C., Bailey, T.C., Diggle, P.J., & Rowlingson, B.S. (1996). Spatial point pattern and its application in geographical epidemiology. *Transactions of the Institute of British Geography,* NS 21, 256-274.

Islam, M. & Ataharul, M. (1989). Assessing homogeneity and association in male and female mortality in Bangladesh, *Rural Demography*, 16(1-2), 1-7.

Koenig, M.A. & D'Souza, S. (1986). Sex differences in childhood mortality in rural Bangladesh. *Social Science and Medicine*, 22(1), 15-22.

Kwan, M. (2000). Analysis of human behavior in a GIS environment: recent development and future prospects. *J Geograph Syst*, 2, 82-90.

Loslier, L. (1998). Geographical information system (GIS) for a health perspective: Spatial and temporal analysis of epidemiological data. In *GIS for Health and the Environment*, IDRC Books, http://www.idrc.ca/books/focus/766/nobre.html.

Meade, M.S., Florin, J.W., & Gesler, W.M. (1988). Medical geography. New York: The Guilford Press.

Muhuri, P.K. & Menken, J. (1997). Adverse effects of next birth, gender, and family composition on child survival in rural Bangladesh. *Population Studies*, 51(3), 279-294.

Muhuri, P.K. (1995). Health programs, maternal education, and differential child mortality in Matlab, Bangladesh. *Population and Development Review*, 21(4), 813-834.

Munshi, K.D. (1996). Farmers as Econometricians: Social Learning and Technology Diffusion in Indian Green revolution. Boston University, mimeo.

Myaux, J., Iqbal, A., Uzma, A., Chakraborty, J., Ali, M., & Hossain, M. (1996). Environmental hazards as a leading cause of death in children from Bangladesh. *International Child Health*, VII(4), 49-52.

Myaux, J.A., Ali, M., Chakraborty, J., & de Francisco, A. (1997). Flood control embankments contribute to the improvement of the health status of children in rural Bangladesh. *Bulletin of the World Health Organization*, 75(6), 533-539.

Oliver, M.A. & Webster, R. (1990). Kriging: A method of interpolation for geographical information systems. International Journal of Geographical Information Systems, 4: 313-332.

Omran, A.R. (1971). The epidemiologic transaction; A theory of the epidemiology of population change. *Millbank Memorial Fund Quarterly*, 49, 509-538.

Rahman, M.M., Aziz, K.M.S, Munshi, M.H., Patwari, Y., & Rahman, M. (1982). A diarrhea clinic in rural Bangladesh: Influence of distance, age, and sex on attendance and diarrhoeal mortality. *American Journal of Public Health*, 72(10), 1124-1128.

Rahman, S.A.H.M., Huq, S.M.M., & Saleheen, M.U. (1993). Spatial pattern of mortality in Bangladesh. *Social Science and Medicine*, 36(10), 1325-1330.

Salway, S.M. & Nasim, S.M.A. (1994). Levels, trends and causes of mortality in children below 5 years of age in Bangladesh: Findings from a national survey. *Journal of Diarrhoeal Disease Research*, 12(3), 187-193.

Twigg, L., Moon, G., & Jones, K. (2000). Predicting small-area health-related behaviour: A comparison of smoking and drinking indicators. *Social Science & Medicine,* 50, 1109-1120.

UNICEF. (2000). *The State of the World's Children 2000*. New York: UNICEF.

Wilkinson, P., Grundy, C., Landon, M., & Stevenson, S. (1998). GIS in public health. In Gatrell, A. & Löytönen, M. (Eds.). Taylor & Francis, *GIS and Health (GISDATA Series 6)*,

SECTION IV:

HOSPITALS
&
HEALTHCARE

Chapter XIV

Using GIS to Unveil Distance Effects on Hospitalizations in Victoria[1]

Ge Lin
West Virginia University, USA

In this chapter, we examine travel distance and its effect on total and avoidable hospitalizations using data from the capital health region in British Columbia, Canada. We developed a GIS procedure to connect distance-to-hospital with socioeconomic contexts of patient locations. The procedure includes geo-coding hospital locations and patient locations to determine travel distance for each hospitalization, generating several geographic barriers, such as mountain crossing, to assess their impedance, and linking patient neighborhood locations to socioeconomic variables of their locations. It was found that the overall hospitalization rates have an inverse relationship with distance-to-hospital, and living too close to a hospital may encourage utilization of hospital resources. Even though low-income patients are more likely to be hospitalized for avoidable conditions, the income effect influences different dimensions to those affected by the distance effect. Thus, it explicitly confirms the two aspects of the inverse of healthcare law that work simultaneously: those with lower socioeconomic status and those living in greater distance to hospitals tend to be less likely to access hospital care. Furthermore, the inclusion of physical barriers to our evaluation enhanced our understanding of local conditions and how they may affect hospitalizations.

INTRODUCTION

Access to healthcare includes at least two dimensions: economic access in terms of affordability, and geographic access in terms of proximity to providers (Gold, 1998). The so-called inverse care law—those most in need tend to have the least access to healthcare services—also includes social and geographic dimensions (Hart, 1971). The geographic aspect of access suggests that everything else being equal, people tend to seek healthcare at a closer distance than at greater distance (Gesler & Meade, 1988). Further, people may be discouraged from seeking health care if they have to travel beyond a certain distance (Brustrom & Hunter, 2001; Parkin, 1979; Williams et al., 1983); otherwise, other aspects of their lives might be adversely affected (Yantzi et al., 2001). In the Canadian context, while efforts to reduce socioeconomic barriers to access to health care have been ongoing, policies aimed at reducing physical barriers have been less persistent, especially for hospital care. The 1970s saw the construction of numerous smaller hospitals outside of larger urban centers to help address the problem of geographically unequally distributed hospitals. However, in the late 1980s and early 1990s, many small hospitals were subsequently closed as a means of cutting costs (Liu et al., 2001).

The changes evident in the policy arena reflect a lack of understanding of the role of geography in terms of accessibility, which is due, in part, to a lack of routine data collected on geographic access measurements (e.g., distance variables) and limited methodologies. While most methodological developments using distance measurements have dealt with either potential accessibility or efficient ways of allocating hospital resources (Love & Lindquist, 1995; Mayhew & Leonardi, 1982), effective engagement requires multiple linkages and several different data sources. This could prove challenging for data collection and manipulation. With the advent of geographic information systems (GIS), greater accessibility of georeference data from multiple sources and renewed interests in local participation in healthcare planning, it is now possible to evaluate geographic accessibility based on actual distance and other geographic variables. This process also provides a mechanism whereby dialogue between geographic and socioeconomic perspectives on access to health services can begin.

This chapter explores methods for assessing distance effects on hospital utilization of GIS technologies. Previous studies (see Goodman & Fisher, 1997) generally find that hospitalization rates decline as distance to hospital increases. However, most of studies deal with a specific type of hospitalization (Mollsop, 1969) or specific population group (Mooney et al., 2000). In our case studies of general and avoidable hospitalizations, we examine the general patient population for all types of hospitalizations. In addition, both physical barriers and socioeconomic variables are included in the analyses. Our approach is similar to that used by Goodman and Fisher (1997), but draws on actual rather than potential distance to hospitals. In the remaining sections, we first describe the data and data manipulation procedures undertaken to construct the geographic variables. Next, we document the distance effect on hospitalizations and model it in a multivariate framework with the intent of bringing geographic and socioeconomic perspectives together. Finally, we offer some concluding remarks in terms of the methodological and substantive findings.

DATA AND SAMPLE SELECTION

Database and Sample Area

Data for this study are drawn from the British Columbia Linked Health Data Resource (BCLHD—Chamberlayne et al., 1998) which includes person-specific data on the utilization of publicly funded health services, such as physician claims, acute care hospital separations, continuing care services (home-based and residential care), mental health services, pharmacare, as well as vital statistics (births and deaths). These data were also linked to 1996 Canadian Census data using various geographic indicators such as health region, local health area, census tract, census division (or subdivision) and census enumeration area. From the BCLHD , the current study relies on data available from hospital separation files for a 10% random sample of the BC population in the Capital Health Region (CHR) who were registered with the provincial health services plan from April 1, 1990, to March 31, 1998. The CHR is an area of approximately 2,317 square kilometers encompassing 12 municipalities, 15 aboriginal communities and unincorporated territory in four electoral areas. The region, which is organized into four local health areas, is situated on the southern tip of Vancouver Island and includes the southern Gulf Islands and the provincial capital city of Victoria. The Victoria metropolitan area is the largest urban center extending to a radius of approximately 15 kilometers from the downtown core. In 1997, the CHR served a total resident population of 334,541 people (8.4% of the total population).

.

Hospital Utilization

The hospital separation data include patient age-group (in five-year intervals), sex, date of admission, date of separation, and the international disease codes (ICD-9) by principal and primary diagnoses for admission. To calculate hospitalization rates at the enumeration area (EA) level, we would ideally have patient registries for the entire potential patient population similar to the ones in the UK and

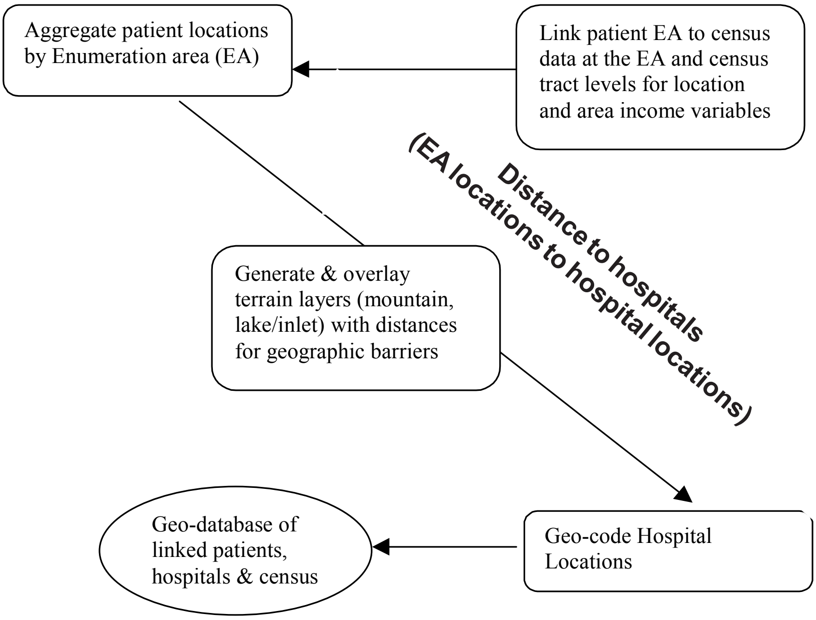
Manitoba (Haynes, et al., 1995; Roos & Nicol, 1999). These registries allow one to compare hospitalized patients to the population at-risk accurately within each geographic unit. Since they are not available in British Columbia, we rely instead on the 1996 census for these figures. This sample is restricted to those admitted during the three-year period between 1994-96 so that the patient sample is close to the 1996 census year. We use the three-year (1994-96) hospital admissions as the sample basis and the 100% population counts of the 1996 census as the exposure to calculate hospital admission rates. Over the three years, the sample registered 18,947 hospital separations across 49 EAs, with each EA having about 627 residents on average. Note also that patients may be hospitalized several times during the study period, and the hospitalization rates to be calculated therefore include multiple hospitalizations during the study period with each admission being counted as a single event.

We used Weissman, Gatsonis and Epstein's (1992) definition of avoidable hospitalizations—conditions for which hospitalizations can be avoided if ambulatory care is provided in a timely and effective manner. There are 12 conditions included in the measure (ruptured appendix: 540.0, 540.1; asthma: 493; cellulitis: 681, 682; congestive heart failure: 428: diabetes: 250.1, 250.2, 250.3, 251.0; gangrene: 785.4; hypokalemia: 276.8; immunizable conditions: 032, 033, 037, 072, 045, 055; malignant hypertension: 401.0, 402.0, 403.0, 404.0, 405.0, 437.2; pneumonia: 481, 482, 483, 485, 486; pyelonephritis: 590.0, 590.1, 590.8; perforated or bleeding ulcer: 531.0, 531.2, 531.4, 531.6, 532.0, 532.2, 532.4, 532.6, 533.0, 533.1, 533.2, 533.4, 533.5, 533.6). If one of the 12 conditions was identified as the principal or primary diagnosis for admission, it was coded as an avoidable hospitalization (AH=1). Admissions for other reasons were coded as AH=0. In total, there were 1,185 (6.3%) avoidable hospitalizations.

PUTTING HEALTH DATA INTO GEOGRAPHIC CONTEXT

In this section, we develop a geo-processing procedure for contextual measurements. In order to evaluate distance effects, we first geo-coded each patient and hospital so that distance to hospital could be calculated and put into socioeconomic and geographic contexts. However, in the process of seeking hospital care, a patient must overcome socioeconomic and physical access barriers. From a socioeconomic perspective, income is an important indicator of access to care. From a geographic perspective, various physical barriers should be considered especially when the Euclidean distance is used. Some even suggest that it is not distance, but other geographic barriers that affect people's propensity for seeking healthcare (Kreher et al., 1995). Figure 1 provides a flow chart for various tasks in the process of modeling individual and contextual effects on hospital admission. At the first step, it is critical to review all the meta-data, so that common projection and an acceptable level of precision can be established. To assess the contextual effect of neighborhoods, we begin by linking patients' residential locations with census variables at the level of census enumeration area (EA). Next, we geo-coded each hospital location by latitude and longitude so that distance from each EA (representing patient location) to a hospital could be determined. Furthermore, given the terrain characteristics of the three health regions, getting to a hospital may be complicated by having to cross a mountain, sea or other physical barriers. In order to represent these barriers, we generated dummy variables using various geographic data obtained digitally through BC Land Resources at the original scale of 1 to 250,000. In particular, we generated barrier themes, such as water-body, mountains and hills, and then overlaid with the distance feature. Originally, we implemented all GIS procedures in ArcInfo 8.0, and then replicated most procedures in ArcView 3.2a, a desktop GIS package; the detailed procedures reported in the following sections are based on the ArcView GIS.

Figure 1: Data manipulation for assessing distance effects



Geo-Referencing Patient Locations

The BCLHD includes geographic identifiers from the larger health region, to mid-level census tract or census subdivision in rural areas, to the smallest unit, census enumeration area (EA), which is comparable to block group in the US Census. All geographic identifiers, regardless of size, are identifiable from their respective geographic center (centroid) in latitude and longitude from the 1996 Census of the population. Thus, by linking each EA in the hospital file with the EA in the census file using the unique enumeration id, patients' residential location can be identified in terms of their respective EA centroids. These, in turn, can be used to generate a point theme.

Income Variable

Census data come from the 1996 Census Profile Series, a series of tables that represent over 100 selected census variables and are presented at different geographic levels. The majority of variables are concerned with the demographic structure of the population. However, there are some income-related variables indicative of the socioeconomic status of an area. While multiple indicators or a single indicator derived from multiple indicators are perhaps better alternatives to a single-item indicator for demonstration purposes, median household income was selected as a proxy measure of socioeconomic status. However, approximately 17% of the EAs have suppressed incomes in the 1996 Census due to small populations and a concern for confidentiality. Even though less than half of EAs with missing incomes affect our patient sample, we decided to impute missing values using a method similar to Frohlich and Mustard (1996) that uses the geographic unit one level higher than the EA (i.e., census subdivision—CSD). Generally speaking, if income for a particular EA is missing, the average of incomes from adjacent enumeration areas is assigned to it.

To classify neighborhoods with regard to income, we initially tried to assess absolute deprivation (e.g., poverty level) at the census EA level. However, there is a lack of empirical literature in the Canadian context that compares individual and area deprivations, let alone for the province of BC. Although this in itself is an important research project, we decided to use the relative measure of four income quartiles as the basis for the classification. The lowest income quartile includes those living in an EA with average annual household income below $38,414, the second between $38,414 and $47,360, the third between $47,360 and $57,453, and the highest above $57,453.

Geo-Coding Hospital Locations

It is necessary to geo-code all the hospitals in the province as patients in the Victoria region could seek hospital care anywhere in the province. Digital hospital location files for British Columbia are available from both provincial and federal governments; however, the accuracy level is relatively poor when we selected some sample locations from these files. For this reason, we decide to geo-code each hospital location (longitudes and latitudes) from a 1:50,000 topographic map, and these coordinates were then used to generate the hospital location theme or layer. Most hospitals are clearly marked on the maps. If a map at the requested scale was not available, a map at the next level (1:100,000, or in rare instances 1:250,000) was obtained. If a hospital was not on a map, the hospital was called directly and asked to identify the nearest street intersection as its location. Using this procedure, 106 hospitals in the province were geo-coded, all of which were identifiable on a map scale of 1:250,000 or larger.

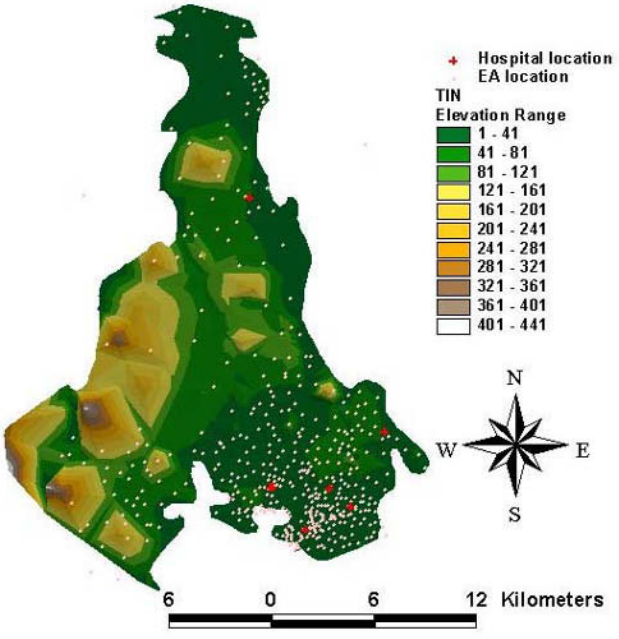
Calculating Euclidean Distance

In geographic analyses, distances to a hospital can either be potential or actual. Potential distance is hypothetical: it is assumed that patients will access a hospital based on some rational criteria (e.g., closest hospital). However, patients do not always go to the closest hospitals as demonstrated by Gesler and Meade (1988). Actual distance is based on the hospital actually used by a patient although exact travel mode (e.g., car, transit, walk), and routes may not necessarily be known. Here, we know both potential and actual hospital location for each hospitalization, However, our distance calculation is based on the actual rather than potential distance. If a patient was hospitalized twice in two different hospitals during the study period, two different measures of distance-to-hospital are calculated even though the patient lived in the same EA. Likewise, if a patient moved during the study period, the hospitalization is measured from the associated EA. We chose Euclidean distance over other distance measurements, as real network distance is almost impossible to determine. For many of the study areas, patient populations are sparsely settled on mountains and islands, and the centroids of the EA may not be close to any network, not even when detailed road networks are available. Given the large geographic coverage at the provincial level, it is not feasible for us at this stage of the study to use road-network to measure distance to hospital (Love & Lindquist, 1995). It is important to note though that Euclidean distance-to-hospital is assumed to be in proportion to real network distance. Empirical evidence has shown that real network distance tends to be consistently 20-25% greater than the Euclidean distance, or half-way between Euclidean and rectilinear (Manhattan) distances (Francis et al., 1992). This assumption is unlikely to affect our assessment qualitatively as we emphasize relative rather than the absolute magnitude of distance effects.

Generating Geographic Barriers

For simplicity, three types of barriers—steep hill, lake or inlet and island without a hospital—were identified. Conceptually, if we treat the straight line between the EA and hospital as the Euclidean distance, then the box in the middle of Figure 1 is the barrier. If a line crosses any of the barriers, a dummy variable is assigned. First, data from a digital elevation model (DEM) were used to generate TIN (triangulated irregular network) terrain for each study region. The DEM was provided with elevation readings that included x-y coordinates comparable to the resolution of a 1:250,000 topographic-map. ArcView 3D extension was used to generate TIN from the DEM table. The resulting TIN model was identical to the TIN generated by ArcInfo. However, one needs to covert the TIN to a polygan coverage by retaining hill slope and elevation attributes. A steep hill can then be defined using a 12% slope or elevation difference of 200 meters or more between the highest passing elevation to either points of the distance line (EA or hospital location). If an Euclidean distance line crossed a steep hill, a dummy variable—hill crossing—was coded one, otherwise, it was coded zero. Likewise, lake or inlet barriers were defined when a Euclidean distance line appeared across (intersect with) either one. Finally, patients living on an island without a hospital must use a ferry, thereby imposing additional constraints on travel to hospital. Figure 2 provides a graphical example of TIN with the hospital and sample locations of EA

Figure 2: Patient (EA) and hospital locations in Victoria, BC



centroids for a portion of one of the three health regions studied. Using this figure, one can eyeball each EA location and identify whether or not a patient needs to cross an inlet for hospital care. Note that the map can only provide a visual impression of the relative location and general landscape, as one cannot determine which patients went to which hospitals simply from the map.

For the most part, the implementation of the above procedure is straightforward. However, there is also a need to convert digital sources of different projections to the same projection system. The UTM-N9 was used to realign the road network, one or two reference layers from different UTM zones to UTM-N9 and several digital layers (DEM, Lakes, coastal lines) of the Albere conformal project to the UTM. The key in ArcView is to convert all layers to longitude and latitude, and then re-project them to the desired projection system. Although new variables can be easily added through linkage of tables with a common field, or though spatial joining (e.g., map overlay), careful documentation is needed along the way. Without this documentation, it is very easy to lose track of the level of geography (e.g., census tract, EA) from which new variables are derived. The final step is to attach the new variables to each patient identifier, along with their respective hospital records. This is discussed in the following section.

ANALYZING DISTANCE EFFECTS ON HOSPITALIZATIONS

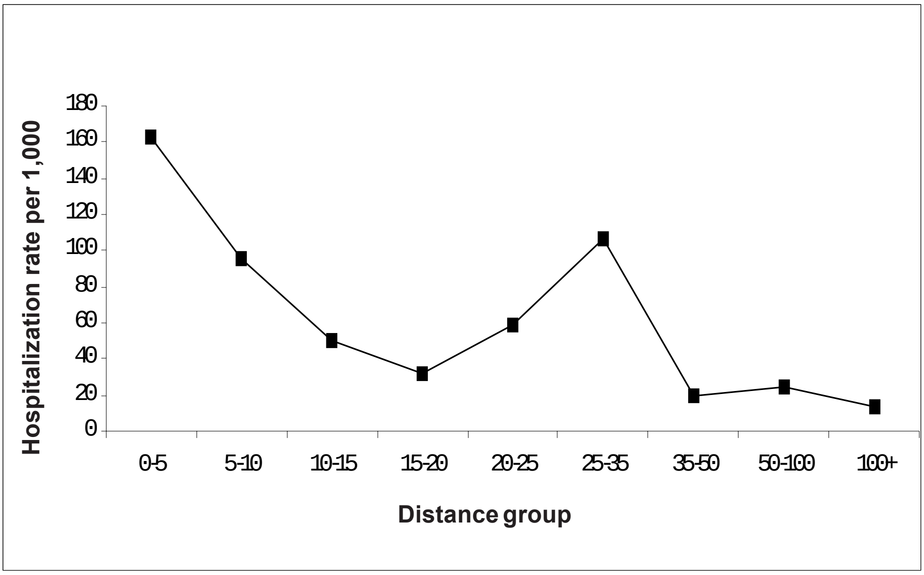
In this section, we analyze hospitalizations in the context of socioeconomic condition of neighborhood and geographic accessibility. We first provide some descriptive pictures on hospitalizations and then model income and distance effects under a multivariate framework. At the descriptive level, we use EA total population as the exposure to derive hospitalization rates for several distance-to-hospital ranges (Pappas et al., 1997). Rate-based multivariate analyses, however, require either population-based survey or aggregate analytical models (e.g., Poisson regressions). Neither of these are appropriate in this particular case, as we do not have an at-risk population (exposure) that corresponds to patient-level variables (e.g., age, sex, income). For this reason, we adopt logistic regression for the multivariate analysis.

Descriptive Analysis of Overall Hospitalizations

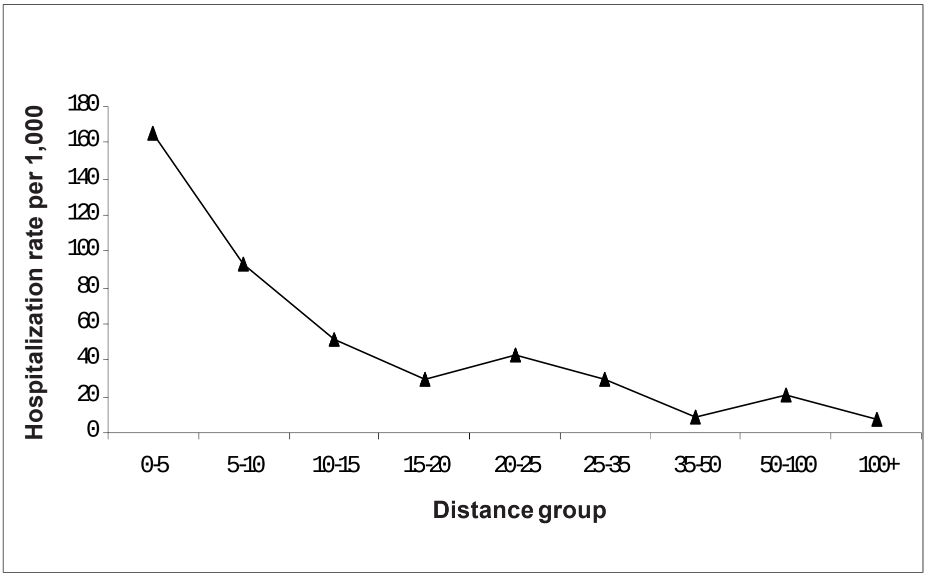
From a population health perspective, hospitalization rates should be more or less evenly distributed if patient populations are distributed evenly across geographic space. The degree to which rates vary across different geographic dimensions reflects level of accessibility from a provider's point of view, and ability

Figure 3: Annual average of hospitalization rates per 1,000 by distance in Capital Health Region

a. Overall rates including all communities



b. Adjusted rates excluding satellite communities



and willingness to travel from a patient's point of view. Figure 3a shows the three-year average (1994-96) hospitalization rate according to distance-to-hospital. Overall, the hospitalization rate declines as distance increases with a reverse trend and small peak around 20 to 35 km. It seems that residents located near a hospital are either sicker or more willing to seek hospital care than residents at greater distance. Given the magnitude of the difference, this pattern is likely to persist even when potential confounding factors, such as age, sex and income, are introduced into the model.

To determine why there are small peaks of hospitalization rates between 25-35 km, it is important to understand local geography. As noted earlier, the primary urban area for Victoria is within 15 kilometers to the city center. A community located 25 kilometers beyond an urban center often represents a separate catchment area rather than a continuous suburb to the urban core. For example, Sooke, which does not have a hospital, is a town (population approximately 3,000) located approximately 30 kilometers from Victoria and is separated by hills and forest. While 20-30 kilometers may not be overly burdensome to go to a hospital, it may not be particularly convenient either. Therefore, even though there is no co-payment associated with hospital care, people in these communities may not be as likely to access hospital care as those who live closer by.

In the migration literature, neutral migration rates are used to describe a region with an average propensity of in and out migration (Liaw, 1990). Borrowing from this concept, we may want to try to determine a hospitalization rate when the distance effect is neutralized (i.e., potential convenient hospital shoppers (patients) are deterred by travel distance and cost). If there are sizeable communities located 20-35 kilometers away from a major urban center and hospitals, the average hospitalization rates among these communities may provide a reference point for a “reasonable” hospitalization rate with neutralized distance effects (Imbens & Angrist, 1994). For convenience, we label them "satellite communities." and operationally define them as those with populations above 2,500 which are either located on an island without any hospitals, or are communities from 20 to 30 km away from a major urban center and separated by farms, mountains or water bodies. Indeed, if we delete observations from these communities, the local peaks in Figure 3a become negligible (Figure 3b).

The influence of satellite communities on hospitalization rates provides an important clue for multivariate modeling. In urban geography, it is known that population density around an urban center is inversely related to distance from the urban center. If there are satellite cities located within 20 kilometers of a major center, a small peak will be evident in the urban density function around 20 km. Since the amenity that a hospital provides only takes effect when people suffer some fairly serious illness or injury, we suspect that living fairly close to a hospital induces greater propensity for going to a hospital, and living relatively far from a hospital deters some necessary hospital care. Satellite communities represent a more or less median distance range to hospital, therefore, a reasonable hospitalization rate in terms of neutralized distance effect. If we take this reasoning seriously, we can compare satellite communities with all other communities. However, subsequent comparisons between satellite and other communities found little differences (e.g., sex, income). The only exception to this is the distribution of the elderly population, with satellite communities having a greater proportion of elders (56% versus 53%). This difference, however, is not sufficient to generate a substantial difference in terms of hospitalizations.

Multivariate Analysis of Avoidable Hospitalizations

From the previous case study, it was determined that satellite communities appear to be "outliers," and if we can control for them, the overall hospitalization rates display an inverse relationship to distance-to-hospital. Based on this finding and the fact that more than 94% of hospitalizations are unavoidable, we can compare avoidable and other hospitalizations, treating other hospitalizations as

Table 1: Logistic regression for avoidable hospitalization

Control variables	Odds-ratio	Odds-ratio	Odds-ratio
Old (35-55 referent)	2.870**	2.849**	2.878**
Young (35-55 referent)	1.438**	1.429**	1.439**
Sex (male referent)	0.741**	0.735**	0.735**
Satellite communities	1.197**	1.206**	1.177**
Distance (0-5 km referent)			
5-10	0.758**	0.805**	0.792**
10-15	0.671**	0.727**	0.709**
15-20	0.921	0.944	0.92
20-25	0.687**	0.732	0.737**
25-35	0.536**	0.540**	0.505**
35-50	0.751**	0.749**	0.727**
50-100	0.761**	0.797**	0.752**
100+	0.926	0.953	0.924
Socioeconomic			
lower 25% (top 25% referent)		1.296**	1.321**
mid-low 25% (top 25% referent)		1.246**	1.258**
mid-up 25% (top 25% referent)		1.106	1.101
Physical Barriers			
Lake/inlet crossing			0.923
Hill crossing			1.164**

Note:
* and ** indicate the significant levels of 0.05 and 0.01 respectively

known and "normal" following distance decay while explicitly controlling for satellite communities. Under the logistic regression framework, the dependent variable is the likelihood of having an avoidable hospitalization versus an unavoidable hospitalization. We run three nested logistic regression models (Table 1) starting with a simple model (Model 1) controlling for age, and sex, while looking at the distance effects. In Model 2, socioeconomic variables are introduced to see if some of the distance effects can be explained by income gradients along with distance to hospital. Finally, in Model 3, a number of physical barriers are added to shed some light on the overall geographic determinants of avoidable hospitalization.

Evidently, age effects are markedly different: compared to those 35-55 years of age, those in both younger and older age groups are more likely to experience avoidable hospitalizations. In addition, males are more likely than females to have an avoidable hospitalization. Further, we find that avoidable hospitalizations generally decline with distance for the first few distance categories, and then fluctuate somewhat for the further distance categories. Compared to the 0-5 km distance category, being 5-10 km from the hospital reduces the odds of avoidable hospitalization by 0.758, while being an additional 5 km further away reduces the odds still further to 0.671. Since the total hospitalization rate follows a distance decay curve, avoidable hospitalizations seem to have a steeper curve, although not quite as smooth as all other hospitalizations. Controlling for satellite communities, the local peak originally found around 20 km loses statistical significance. However, the lowest avoidable hospitalization rate appears in the 35-50 km category rather than in the further distance categories as was evident with regard to overall hospitalization rates.

Although the introduction of the income variable has little impact on the distance effects (Model 2), the results are consistent with general expectation. Patients from the two lowest income groups are approximately 1.25 times as likely to be hospitalized for avoidable conditions as those in the highest income group. For those in the second highest income group, there is no significant difference from the highest income group in terms of avoidable hospitalization.

Finally, we introduce in Model 3 two physical barriers: inlet/lake and mountain crossings generated from GIS operations. Relatively speaking, crossing an inlet or lake does not have significant effect. However, crossing a mountain or hill increases the likelihood of an avoidable hospitalization. To interpret these effects, we also need to consider distance and local geography. For instance, people from many distance communities need to cross a steep hill to get to the hospital. When the hill crossings are included, they not only increase the likelihood of an avoidable hospitalization, but also reduce odds for the last few distance categories (e.g., 50-10). Thus, steep hill crossings may take away some of the distance effects from farther distance categories.

CONCLUSIONS AND DISCUSSIONS

In this chapter, we developed a GIS procedure to generate variables for modeling distance-to-hospital in geographic and socioeconomic contexts. Since individual-level SES variables were not available, we created a socioeconomic context by linking census data with individual patient data. In addition, we believe that physical barriers, such as lakes, inlets, mountains, hills and islands, will complicate simple Euclidean distance measures, and should somehow be accounted for. To this end, we introduced a number of variables reflecting several layers of physical features, and let them intersect with distance-to-hospital. We believe that new insight can be gained by creating and incorporating physical barriers into access to care measures.

Through careful examination of local conditions, we unraveled "neutral hospitalization rates" represented by satellite communities. These rates tend to be slightly below the regional average. When we simply plotted hospitalization rates along distance to hospital, we observed a small peak on the distance decay curves. When we controlled for the impact of residence in satellite communities, the overall hospitalization rates had an inverse relationship with distance-to-hospital. This finding is robust when additional control variables are included. However, it is hard to imagine that people will find a hospital attractive enough to prompt them to go more often, as is the case with regard to regular shopping (Pellegrini, Fotheringham & Lin ,1997). In a healthcare system without gate fees, distance-to-hospital may be an obvious deterrent to hospital care either because one is less able or willing to travel the required distance or because referrals by physicians for those living far away from a hospital are less frequently given (Mellsop, 1969). A well-defined neutral hospitalization rate could serve as a yardstick for assessing the consequences of the distance effect on hospitalizations. If satellite communities and communities near a hospital tend to have similar health outcomes while differing substantially in hospitalization rates, then we can perhaps conclude that living close to a hospital may encourage utilization of hospital resources.

We found that avoidable hospitalizations generally follow similar variations in distance to the non-avoidable hospitalizations with slightly greater distance deterrent effects for 5-10 and 10-15 km categories. Consistent with previous literature (Laditka & Johnston, 1999; Pappas et al., 1997), low-income patients are more likely to be hospitalized for avoidable conditions. We also confirmed that the income effect influences different dimensions to those affected by the distance effect, since the inclusion of income variables does little to change the distance effects. Finally, to demonstrate the use of physical barrier variables, we included crossing hills, lakes or inlets. The inclusion of these variables not only changed some distance effects, but also offered some insight into avoidable hospitalizations. For instance, crossing hills or mountains significantly increases the likelihood of having an avoidable hospitalization. Since we know that the majority of villages or small communities in mountain areas or on islands often lack primary and ambulatory care services, it is expected to see a greater likelihood of avoidable hospitalization (Casanova & Starfield, 1995).

There are several limitations to this study. First, the simplicity of Euclidean distance comes with some compromises. We assume that the Euclidean distance to a hospital is in proportion to the true network distance to the hospital. Even though we included additional physical barriers to correct the measurement, we should only interpret distance effects in relative terms. If a health region intends to quantify distance effects for planning purposes, it is important to gauge the absolute magnitude of the distance effects, or at least convert Euclidean distance effects into network distance effects. In this situation, we will have to resort to more accurate network distance measurements to calibrate the distance effect (Mayhew & Leonardi, 1982; Hansen & Schwab, 1987). Second, we did not include the hospital context in our design, which could be an important omission. A complete conceptualization of distance-to-hospital should bring individual characteristics, neighborhood characteristics, travel conditions and hospital characteristics into the same modeling framework. Finally, since we did not have a complete roster of all those registered with the Medical Services Plan, we had to rely on census data to generate the population figures necessary to calculate hospitalization rates. This limited our level of confidence in the hospitalization rates for small areas. Despite these limitations, the study represents an important step in understanding the integration of geographic and socioeconomic approaches to health services accessibility. Methodologically, the use of the GIS to generate contextual variables for both socioeconomic and physical environments has expanded GIS applications, and has helped to generate new hypotheses (e.g., neutral hospitalization rate). Substantively, it explicitly confirms the two aspects of the inverse of healthcare law that work simultaneously: those with lower socioeconomic status and those living in greater distance to hospitals tend to be less likely to access hospital care. Further studies are needed to disentangle various distance decay effects in relation to other healthcare services, and their planning implications for new and existing hospital locations in relation to other health facilities.

ENDNOTE

[1] This research was conducted as part of the project, “Health Care Restructuring and Community-Based Care: A Longitudinal Study,” funded by the Canadian Health Services and Research Foundation, 1998-2001 (LOI 97-054). I appreciate support and comments provided by Richard Stanwick, the

medical chief officer, from the Capital Health Region, and Diane Allen for data processing.

REFERENCES

Brustrom, J. E., & Hunter, D. C. (2001). Going the distance: How far will women travel to undergo free mammography? *Military Medicine*, 166 (4); 347–9.

Casanova C, & Starfield, B. (1995). Hospitalizations of children and access to primary care: A cross-national comparison. *International Journal of Health Service*. 25(2): 283-94.

Chamberlayne, R, Green, B, Barer, ML, Hertzman, C, Lawrence, WJ, and Sheps, SB. (1998). Creating a population-based linked health database: A new resource for health services research. *Canadian Journal of Public Health*. 89(4): 270–3.

Francis, RL, McGinnis LF. & White, JA. (1992). *Facility Layout and Location: An Analytical Approach*. Englewood Cliffs, NJ: Prentice Hall.

Frohlich, N & Mustard, C. (1996). A regional comparison of socioeconomic and health indices in a Canadian province. *Social Science and Medicine*. 42: 1273–1281

Gesler, WM, & Meade, M. (1988). Locational and population factors in health care-seeking behavior in Savannah, Georgia. *Health Services Research*. 23(3): 443-62.

Gold, M, (1998). Beyond coverage and supply: Measuring access to healthcare in today's market. *Health Services Research*. 33(3): 625-52.

Goodman, DC, and Fisher, E. (1997). The distance to community medical care and likelihood of hospitalization: Is closer always better? *American Journal of Public Health*. 87:1144–1150.

Hansen, S, and Schwab, M. (1987). Accessibility and urban travel. *Environment and Planning A*. 19(6):735–48.

Hart, JT. (1971). The inverse care law. *Lancet,* I:405–412.

Haynes, RM, Lovett, AA, Bentham, G, Brainard, JS, & Gale, SH. (1995). Comparison of ward population estimates from FHSA patient registers with the 1991 Census. *Environment and Planning A*. 27: 1849–58.

Imbens, GW, and Angrist, JD. (1994). Identification and estimation of local average treatment Effects. *Econometrica*. 62(2) 467–75.

Kreher, NE, Hickner, JM, Ruffin MT, and Lin, CS. (1995). Effect of distance and travel time on rural women's compliance with screening mammography: An UPRNET study. *Journal of Family Practice*. 40(2):143-7.

Laditka, SB, & Johnston JM. (1999). Preventable hospitalization and avoidable maternity outcomes: Implications for access to health services for Medicaid recipients. *Journal of health and Social Policy*. 1991 11(2):41–56.

Liaw, KL. (1990). Neutral migration process and its application to an analysis of Canadian migration data. *Environment and Planning A*. 22: 333–43.

Liu, L, Hader, J, Brossart, B, White, R, & Lewis, S. (2001). Impact of rural hospital closures in Saskatchewan, Canada. *Social Science & Medicine*. 52:1793–1804.

Love, D, & Lindquist, P. (1995). The geographic accessibility of hospitals to the aged: A geographic information systems analysis within Illinois. *Health Service Research*. 29:629–649.

Mayhew, LD, & Leonardi, G. (1982). Equity, efficiency, and accessibility in urban and regional health systems. *Environment and Planning A*. 14:1479-507.

Mellsop, GW. (1969). The effect of distance in determining hospital admission rates. *The Medical Journal of Australia*. 2:814–17.

Mooney, C, Zwanziger, J, Phibbs, CS, & Schmitt, S. (2000). Is travel distance a barrier to veterans' use of VA hospitals for medical surgical care? *Social Science & Medicine*. 50:1743–1755.

Pappas, G, Hadden, WC, Kozak, L J, & Fisher, GF, (1997). Potentially avoidable hospitalizations: Inequalities in rates between US socioeconomic groups. *American Journal of Public Health*. 87: 811–816.

Parkin, D. (1979). Distance as an influence on demand in general practice. *Journal of Epidemiological Community Service*. 33:96–99.

Pellegrini, P., Fotheringham, S., & Lin, G. (1997) Parameter sensitivity to choice set definitions in shopping destination choice models. *Papers in Regional Science: The Journal of Regional Science Association International*. 76: 257–284.

Roos LL, & Nicol JP.(1999). A research registry: Uses, development, and accuracy. *Journal of Clinical Epidemiology*. 52: 39–47

Weissman, JS, Gatsonis, C, & Spstein, AM. (1992). Rates of avoidable hospitalization by insurance status in Massachusetts and Maryland. *Journal of the American Medical Association*. 268 (17):2388–2394.

Williams, AP, Schwartz, W B, Newhouse, J P, & Bennett, BW. (1983). How many files to the doctor? *The New England Journal of Medicine*. 309(16):958–63.

Yantzi, N. Rosenberg, M W., Burke, S O, & Harrison, M. (2001). The impact of distance to hospital on families with a child with a chronic condition. *Social Science and Medicine*. 52:1777–1791.

Chapter XV

Spatial Accessibility to Primary Care and Physican Shortage Area Designation: A Case Study in Illinois with GIS Approaches

Wei Luo and Fahui Wang
Northern Illinois University, USA

This chapter introduces two new GIS-supported methods of measuring accessibility to primary healthcare. The improved floating catchment method defines the service area of physicians by a threshold travel time while accounting for the availability of physicians. The gravity-based accessibility method considers two factors: travel times from service providers (a nearby supply is more accessible than a remote one) and competition intensity by residents for such a service (measured by gravity-based potential). The methods are applied to examining accessibility to primary care in the northern Illinois region in 1990 and 2000. The GIS-based methods may be used to help the U.S. Department of Health and Human Services and state health departments define health professional shortage areas.

INTRODUCTION

Access to healthcare is affected by where physicians locate (supply) and where people reside (demand). The geographic distribution of physicians does not necessarily match that of population. Some areas experience physician surplus, and others have physician shortage. The shortage has been especially pronounced in rural areas and impoverished urban communities (Council on Graduate Medical Education or COMGE, 2000; Rosenblatt & Lishner, 1991). The U.S. federal government spends about $1 billion a year on programs designed to alleviate access problems, including awarding financial assistance to providers serving designated shortage areas (General Accounting Office or GAO, 1995).

These federal programs depend on two main systems for identifying shortage areas (GAO, 1995; Lee, 1991). One designates Health Professional Shortage Areas (HPSAs), the other Medically Underserved Areas or Populations (MUA/MUPs). Both systems use the ratio of the number of providers to population within a geopolitical unit (usually a county) as a primary indicator. Neither system, however, adequately reflects the fact that the availability of services depends not only upon the supply of resources in a community, but also the supply of such resources in neighboring communities, and the distance and ease of travel among them (Klienman & Makuc, 1983, p. 543). This limitation of HPSA or MUA/MUP could easily overestimate shortage in some areas and underestimate shortage in others so that funding may not be channeled to where it is most needed (GAO, 1995). Despite efforts to improve the methods (Department of Health and Human Services or DHHS, 1998), two geographic problems have not been addressed appropriately: (1) not accounting for the actual spatial distributions of physicians and population within the areal unit (e.g., county), and (2) not considering the actual road network travel time between supply and demand and travel across geopolitical boundary. Better methods for defining physician shortage areas are needed to help direct the limited federal resources to the truly underserved population.

While we are aware that socio-demographic characteristics including ethnicity and socioeconomic status may also influence healthcare accessibility, this chapter will focus primarily on spatial accessibility. Identifying the spatial mismatch between healthcare supply and demand is the first step towards an improved healthcare delivery system. The purpose of this chapter is to show how the existing DHHS designation systems for physician shortage areas can be improved by applying GIS technology to data at a finer geographic resolution. Specifically, two new methods will be used: the improved floating catchment method and the gravity-based accessibility method. Both involve the analysis of travel time through a road network and better reveal the spatial access to healthcare. Physician shortage areas are more accurately identified by the methods.

EXISTING METHODS

A geographic area is designated as a primary care HPSA if the following three criteria are met (see DHHS, 1980; Lee, 1991; GAO, 1995; and http://bphc.hrsa.gov/dsd/default.htm for detail):

I. The area is a rational area for the delivery of primary medical care services, which is one of the following:
   (a) A county (or parish in Louisiana; census area in Alaska; municipio in Puerto Rico) or a group of contiguous counties whose population centers are within 30 minutes travel time of each other;
   (b) A portion of a non-metropolitan county or an area made up of portions of more than one county, whose population, because of topography, market or transportation patterns, distinctive population characteristics or other factors, has limited access to contiguous area resources, as generally measured as travel time greater than 30 minutes from other resources;
   (c) Established neighborhoods or communities within metropolitan areas that display a strong self-identity (as indicated by a homogeneous socioeconomic or demographic structure and/or a tradition of interaction or interdependency), have limited interaction with contiguous areas and have a minimum population of 20,000;

II. One of the following conditions prevails within the area:
   (a) The area has a population to full-time-equivalent (PTE) primary care physician ratio of at least 3,500:1.
   (b) The area has a population to PTE primary care physician ratio of less than 3,500:1 but greater than 3,000:1 and has unusually high needs for primary care services or insufficient capacity of existing primary care providers.
   An area is considered to have unusually high needs if:
      (i) The area has more than 100 births per year per 1,000 women aged 15-44;
      (ii) The area has more than 20 infant deaths per 1,000 live births;
      (iii) More than 20% of the population (or of all households) have incomes below the poverty level;
   An area is considered to have insufficient capacity of existing primary care providers if two or more of the following criteria are met:
      (i) There are more than 8,000 outpatient visits per year per FTE primary care physician serving the area;
      (ii) There are unusually long waits for routine appointments (e.g., longer than 1 hour for a pre-scheduled appointment);
      (iii) There is excessive emergency services use for routine primary care;

(iv) Two-thirds or more of the area's physicians do not accept new patients;
(v) There is abnormally low utilization of health services, as indicated by an average of 2 or less office visits per year;

III. Primary medical care professionals in contiguous areas are overutilized, excessively distant or inaccessible to the population of the area under consideration. They are considered so if one of the following conditions are met:
(a) Primary care professional(s) in the contiguous area are more than 30 minutes travel time from the population center(s) of the area being considered for designation;
(b) The contiguous area population to FTE primary care physician ratio is in excess of 2000:1;
(c) Primary care professional(s) in the contiguous area are inaccessible to the population of the area under consideration because of specified access barriers, such as: significant differences between the demographic (or socio-economic) characteristics of the area under consideration and those of the contiguous area and a lack of economic access to contiguous area resources (i.e., where more than 20 percent of the population or the households have incomes below the poverty level).

An MUA/MUP is designated based on four factors of health service need (see Lee, 1991; GAO, 1995; and http://bphc.hrsa.gov/dsd/default.htm for detail):

I. Primary care physicians-to-population ratio;
II. Infant mortality rate;
III. Percentage of the population with incomes below the poverty level;
IV. Percentage of the population aged 65 and older.

These four variables are applied to county or small area data to obtain a single Index of Medical Underservice (IMU) score between 0 and 100 assigned to each area, with 0 representing the most underserved and 100 the best-served area.

Both DHHS methods of identifying physician shortage areas, then, consider using a variety of spatial and non-spatial criteria. Both also use predefined geopolitical boundaries, in most cases counties, as the basic unit for calculating the physician to population ratio. The implied assumptions of the spatial criteria used are that: (1) people within the rational service area have equal access to the physicians within that area, and (2) people within the rational service area do not go beyond that area to seek care. Yet these assumptions are among the most criticized features of the spatially related criteria for identifying physician shortages (GAO, 1995; COGME, 1998). The first assumption of this methodology leads to the majority of the HPSAs (68% in 1997) and most of the MUA/MUPs being whole counties or a group of counties (COGME, 1998; GAO, 1995). Only occasionally are portions of a county (e.g., a community or a population group) or a facility (e.g., a prison or hospital) designated as an HPSA. It is clearly possible for pockets of population within a county not designated as a shortage areas to have severe access problems (an underestimate), and similarly, for pockets of population within a designated shortage county to have adequate access (an overestimate). The second assumption means that the methods fail to fully account for the fact that people often seek care in adjacent or nearby geopolitical units (Klienman & Makuc, 1983; Wing & Reynolds 1988; GAO, 1995). Although Step III of the HPSA method is intended to consider the adjacent areas, the physician-to-population ratios are still calculated within their respective geopolitical boundaries, and the actual interaction across boundaries is not accounted for. Even in the most recent proposed revision of the shortage area designation, the rational health service areas are still primarily based on fixed and predefined geopolitical boundaries (DHHS, 1998).

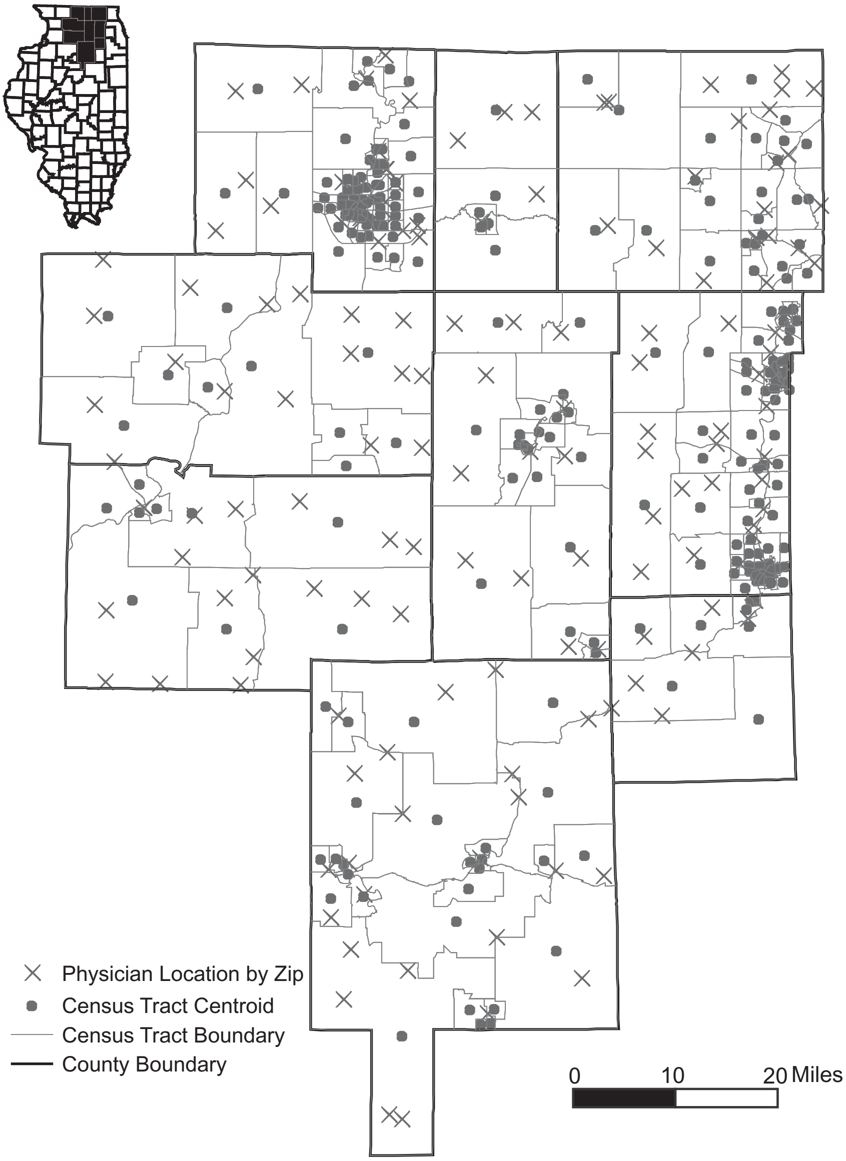
The problems of using a predefined geopolitical boundary as the basic unit to determine the adequacy of supply of a service or resource relative to its demand have long been recognized in geography but are still not well resolved (e.g., Openshaw & Taylor, 1981). This is partially due to the complexity of the problem, i.e., both the supplies and demands are spatially distributed and are likely overlapping, and competitions exist among the supplies and the demands (e.g., Huff, 1963, 1964). In addition, the scarcity of available data at fine geographic scales made previous attempts to more accurately identify shortage areas technically difficult (Makuc et al., 1991). The increasing abundance of digital data (e.g., socioeconomic data, street and road network, physician database) and advancement of GIS technology now make it possible to locate physicians more accurately and identify population distribution at finer resolutions (Love & Lindquist, 1995; Kohli et al., 1995; Parker & Campbell, 1998).

STUDY AREA AND DATA

A group of counties surrounding DeKalb, of Illinois, are chosen as the study area (only for demonstrating the methodology). See Figure 1.

The 1990 population data at the census tract level were obtained from the U.S. Census Bureau. The 1999 population data (to approximate the year 2000 population while the new 2000 Census data were unavailable), estimated by CACI International, Inc., were extracted from the Environment System Research Institute (ESRI) Data and Maps Compact Disk. The study covers two years in order to examine the temporal changes. For simplicity, the centroid of a census tract is used to represent the location of all population in the tract.

Figure 1: Census tracts and physician locations by Zip in the study area



The primary care physician data of Illinois for the year 1989 and 2000 were purchased from the Physician Master File of the American Medical Association via Medical Marketing Service, Inc. The 1990 physician data were not available. The 1989 physician data were used to match the 1990 Census population data, and the

2000 physician data were used to match the 1999 estimated population data. Primary care physicians include family physicians, general practitioners, general internists, general pediatricians and some obstetrician-gynecologists (Cooper, 1994). This case study focuses on primary care physicians because these physicians are an integral component of a rational and efficient health delivery system and they represent the first line of defense for the population. Only after seeing one of these physicians are many of the ill sent to see specialists. With soaring healthcare costs, the need for primary care physicians also increases, because prevention is at the heart of primary care and good primary care can avoid or reduce costly, unnecessary diagnostic and treatment intervention by specialists (Lee, 1995). The methodology can be easily adapted to identify shortage areas of other healthcare specialties, and at state and national levels.

Ideally, the physician locations should be geo-coded by their street addresses with GIS software, a process of converting the address information to x and y coordinates of a point on the map by matching address name and interpolating the address range to those stored in a digital map (e.g., TIGER line file). However, a significant number of records in the Physician Masterfile only have "P. O. Box" addresses, which are not feasible for geo-coding. To illustrate the methods, this study simply uses the centroid of Zip Code of a physician's preferred address to represent the physician's location. Zip Code represents a finer resolution than county and has been used extensively in health research (e.g., Ng et al., 1993; Parker & Campbell, 1998; Knapp & Harwick, 2000). See Figure 1.

The GIS methods discussed in the next two sections utilize travel time between any pair of population and physician locations. Travel time is assumed to be the shortest time driven through a road network composed of all levels of roads. Specifically, the network includes all roads with CFCC codes between A11 (interstate highway) and A48 (neighborhood road). The CFCCs (census feature class codes) are used by the U.S. Census Bureau in its Topologically Integrated Geographic Encoding and Reference (TIGER) line files. Speed limits, corresponding to various CFCC codes, are used to determine the impedance value for each road in the network quickest path computation. See Wang (2000) for more details.

THE IMPROVED FLOATING CATCHMENT METHOD

The floating catchment method has been used in job accessibility studies (e.g., Peng, 1997; Wang, 2000). Based on Radke and Mu (2000), an improved floating catchment method is developed. The method is implemented in seven steps:

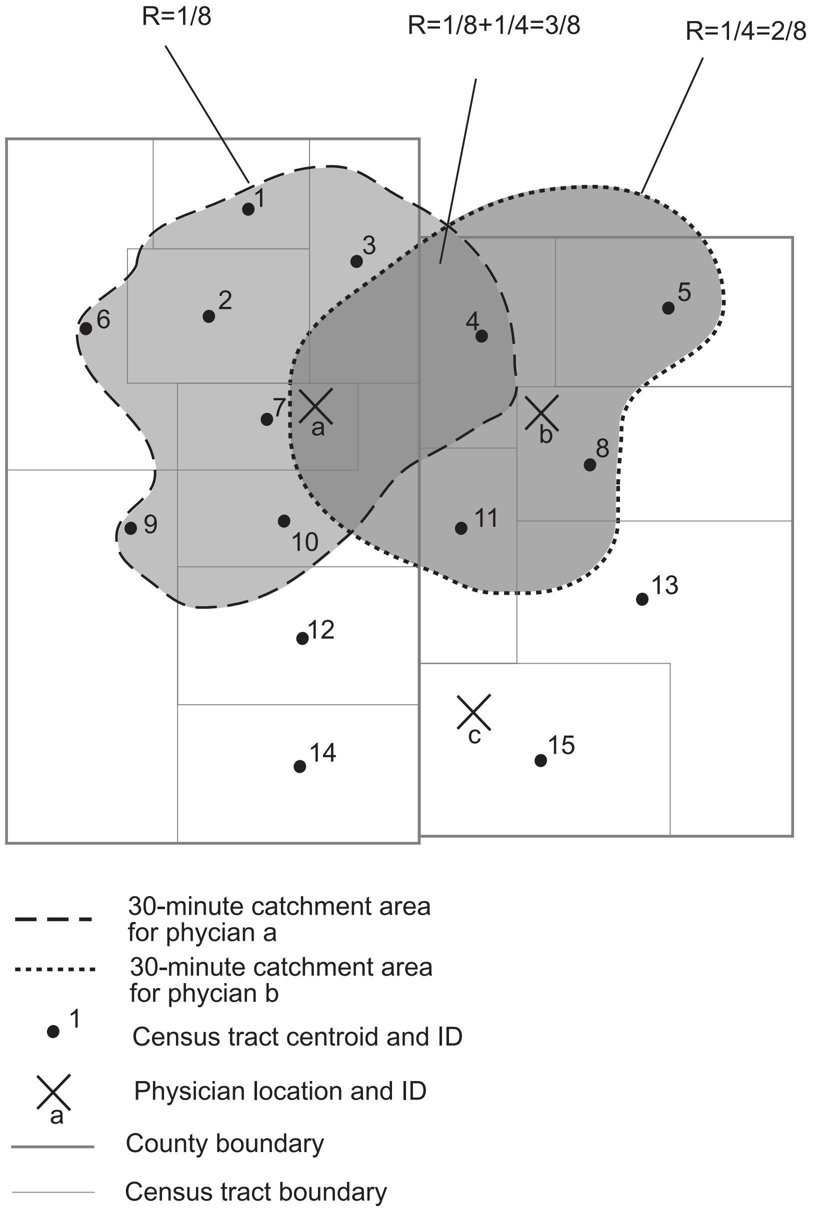
a) Use GIS street network analysis to compute the travel time between any pair of physician location (taken as the Zip Code area centroid) and population location (taken as the census tract centroid).
b) For each physician location *k*, select population locations that are within a reasonable travel time (e.g., 30 minutes) of that physician location, defining an imaginary catchment area for physician location *k* (referred to as catchment *k* hereafter).
c) Compute the physician-to-population ratio for catchment *k* (R_k) using the number of physician(s) at the physician location *k* (Phy_k) and the sum of population within catchment *k*:

$$R_k = \frac{Phy_k}{\sum_{t \in C_k} Pop_t} \tag{1}$$

where Pop_t is the population of tract *t* whose centroid falls within catchment *k*, and C_k identifies all these tracts.
d) Repeat steps b) and c) for all physician locations.
e) For each population location *i*, search all physician locations that are within the reasonable travel time (e.g., 30 minutes), and sum up the physician-to-population ratios at these locations.
f) Repeat step e) for all population locations.
g) Run a GIS query to identify all the census tracts with a ratio less than the DHHS standard (1:3,500 for primary care) as the shortage areas.

Figure 2 shows an example of this method. For illustration purposes, assume that each census tract has only one person residing at its centroid and each physician location has only one physician practicing there. Also assume the reasonable travel time is 30 minutes. The different shades of the polygons represent different physician-to-population ratios. Under our assumption, the catchment around physician location *a* (or simply catchment *a* hereafter) has one practicing physician there and eight persons (eight black dots) residing within the catchment. Therefore the physician to population ratio for catchment *a* is 1/8. All the centroids within catchment *a* (1, 2, 3, 4, 6, 7, 9, 10) will be assigned an initial ratio of 1/8. Similarly, all the centroids within catchment *b* (4, 5, 8, 11) will be assigned an initial ratio of 1/4. Residents at centroids 1, 2, 3, 6, 7, 9 and 10 have access to physician *a* only and thus their ratios remain as 1/8; and residents at centroids 5, 8 and 11 have access to physician *b* only and thus their ratios remain as 1/4. However, centroid #4 is located in the overlapping area formed by catchment *a* and *b*, and has access to either physician *a* or *b*, and therefore the physician-to-population ratio there is the sum of the initial ratios in catchments *a* and *b* (i.e., 1/8 + 1/4 = 3/8).

Figure 2: A simple example of the improved floating catchment method



Several features need to be noticed in the improved floating catchment method:

(1) The catchment is centered on physician location rather than on population location, thus the travel time between physicians and any person within the catchment does not exceed the reasonable travel time.

(2) The physician-to-population ratio is calculated using only the physicians practicing at the center of each catchment rather than by counting all the physicians within the catchment. Those physicians nearby (in or outside the catchment but not at the center, e.g., physician *a* in catchment *b*) will each have their own service area, which may overlap with the catchment under consideration, and thus their service will not be available to all the population within the catchment under consideration.

(3) The contributions of nearby physicians are included only in the ratios for the overlapping areas of catchments since people living there can be served by physicians at either location (e.g., people residing at centroid #4 can be served by physicians at either location *a* or location *b*) and thus they enjoy a higher accessibility than those who live in the non-overlapping area (e.g., people residing at centroids #5 or #9).

The improved floating catchment method has several advantages over the conventional method of identifying physician shortage areas. It uses smaller areal units for population and physician distributions (i.e., census tracts and Zip Code areas instead of counties); considers potential interaction between patient and physician across administrative border; and accounts for the travel time between patients and physicians. However, it draws an artificial line (say, 30 minutes) between an accessible and inaccessible physician. Physicians within that range are counted equally regardless of the actual travel time (e.g., 5 minutes versus 25 minutes). Similarly, all physicians beyond that range are defined as inaccessible, regardless of any differences in travel time. In other words, the competition of health care is confined within the range. A better approach is to define accessibility using a gravity model. In a gravity model, the intensity of interaction (e.g., frequency or likelihood of visiting a physician) is inversely related to travel time (or distance), and the measure is *continuous* rather than *dichotomous*.

THE GRAVITY-BASED ACCESSIBILITY METHOD

We start with a simple gravity model to illustrate the concept. Hansen (1959) proposes the following model for accessibility (A_i) at location i:

$$A_i = \sum_{j=1}^{n} Phy_j d_{ij}^{-\beta} . \tag{2}$$

where Phy_j is the number of physicians at location j, d_{ij} is the travel time between population location i and physician location j, β is the travel friction coefficient (an empirically determined constant) and n is the number of physician locations. In the model, a physician nearby is considered more accessible than a remote one. This index measures how far residents are from all physicians. The higher the value of A_i, the closer the residents at location *i* are to physicians.

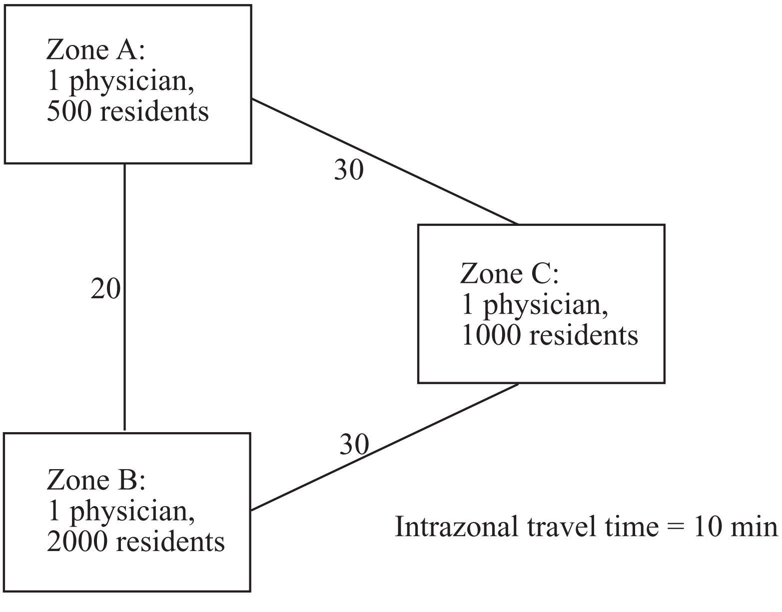
To illustrate the model, we use a simplified example with three zones. In Figure 3, each of the three zones A, B and C has one physician. Zone A has 500 residents, Zone B has 2,000 residents and Zone C has 1,000 residents. Assume the intrazonal travel time is 10 minutes (i.e., residents in Zone A on average travel 10 minutes to see the physician in Zone A itself) for all three zones, 20 minutes between A and B, and 30 minutes between A and C or between B and C. Assuming β=1 for simplicity, we have:

$$A_A = \frac{Phy_A}{d_{AA}} + \frac{Phy_B}{d_{AB}} + \frac{Phy_C}{d_{AC}} = \tfrac{1}{10} + \tfrac{1}{20} + \tfrac{1}{30} = 0.183, A_B = 0.183, A_c = 0.166.$$

We may conclude that residents in zones A and B are closer to physicians than those in Zone C.

One limitation of equation (2) is that it only considers the "supply side" of physicians, and not the "demand side"—the competition for available physicians among residents. In Figure 3, with one physician in each zone, zone A has 500 residents and zone B has 2000 residents (and the same travel time from zone C). Obviously we would expect that zone A should have a better accessibility to physicians than zone B.

Figure 3: A simplified example illustrating gravity accessibility with three zones



Among others, Joseph and Bantock (1982) improve the measurement by also considering the demand side—competition for healthcare services among people. With the essence of their model unchanged, we restructure the model as follows for easier interpretation:

$$A_i = \sum_{j=1}^{n} \frac{Phy_j d_{ij}^{-\beta}}{V_j}, \text{ where } V_j = \sum_{k=1}^{m} Pop_k d_{kj}^{-\beta} . \tag{3}$$

This new index re-scales the proximity to a physician location *j* by the location's service competition intensity (V_j), and V_j is a measure of the potential of physicians at location *j* to all populations (Pop_k, $k=1, 2, ..., m$). Again d_{ij} is the travel time through the actual road network, and β is the travel friction coefficient. A similar approach is used for defining job accessibility in Shen (1998) and Wang (2001).

Using the same example in Figure 3, we first compute a zone's physician competition intensity V based on its relative location to residents in all zones:

$$V_A = \frac{Pop_A}{d_{AA}} + \frac{Pop_B}{d_{AB}} + \frac{Pop_C}{d_{AC}} = \tfrac{500}{10} + \tfrac{2000}{20} + \tfrac{1000}{30} = 183, V_B = 258, V_c = 183.$$

Since Zone B has more residents than others, V_B is the highest among three zones. Equation (3) rescales the supply-side-only physician proximity in (2) by the demand competition intensity V, and yields a comprehensive accessibility index:

$$A_A = \tfrac{1}{10}/183 + \tfrac{1}{20}/258 + \tfrac{1}{30}/183 = 0.0009221, A_B = 0.0008430, A_c = 0.0008578.$$

This clearly identifies that Zone A is most accessible to physicians, Zone C the second, and Zone B the least.

This accessibility index may be interpreted similarly to the physicians/population ratio. Indeed the weighted average of accessibility in all locations (population as weight) is equal to the physicians/population ratio in the whole study region (see Shen, 1998, for a proof). The larger the value of A_i, the better accessibility the people at location *i* enjoy.

RESULTS AND DISCUSSION

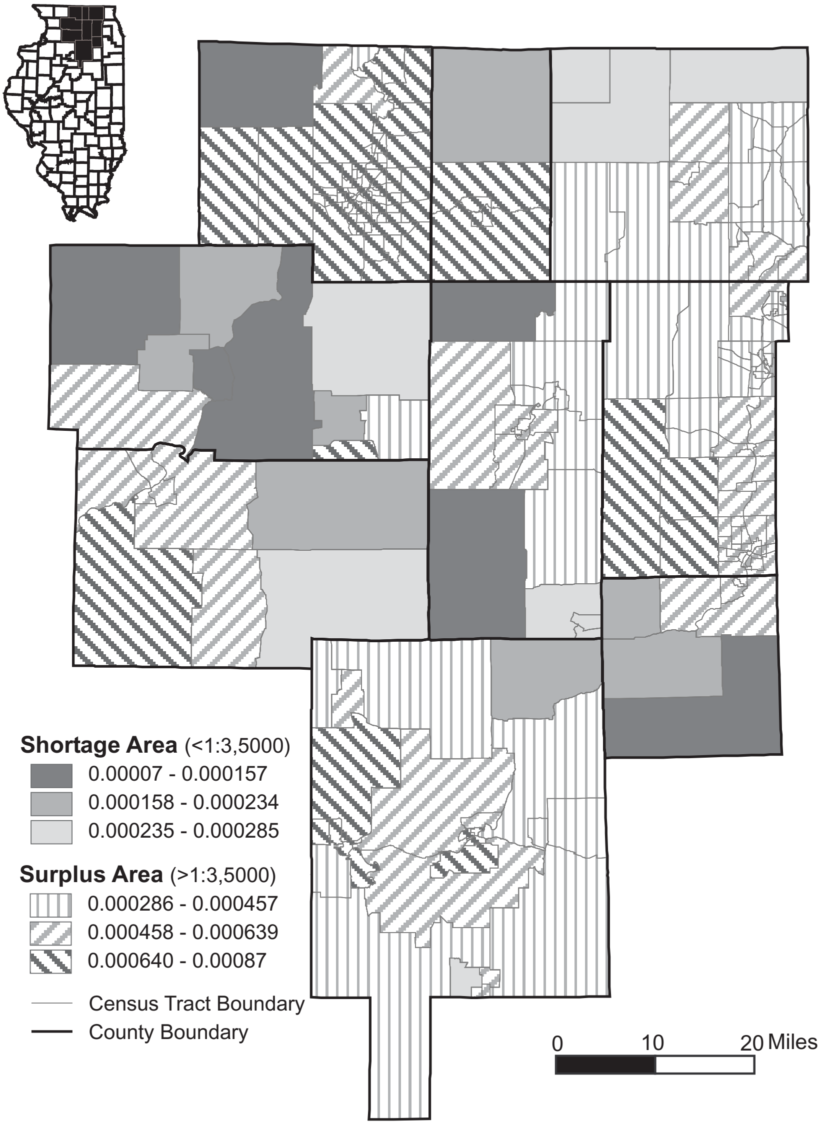
The focus of this chapter is on the methodology. Not every aspect of the DHHS shortage designation methods is considered (e.g., the possibility of using a lower ratio than 1:3,000 for areas showing special needs or using FTE concept for physician count). The results shown here are not directly comparable with those generated by DHHS methods (DHHS, 1990, 1999).

The results of applying the two GIS methods are presented in Figures 4-7. One may use actual primary care physician visit data to determine the β value in the gravity-based accessibility method using a regression such as:

$$T_{ij} = aPop_i Phy_j d_{ij}^{-\beta} \qquad (4)$$

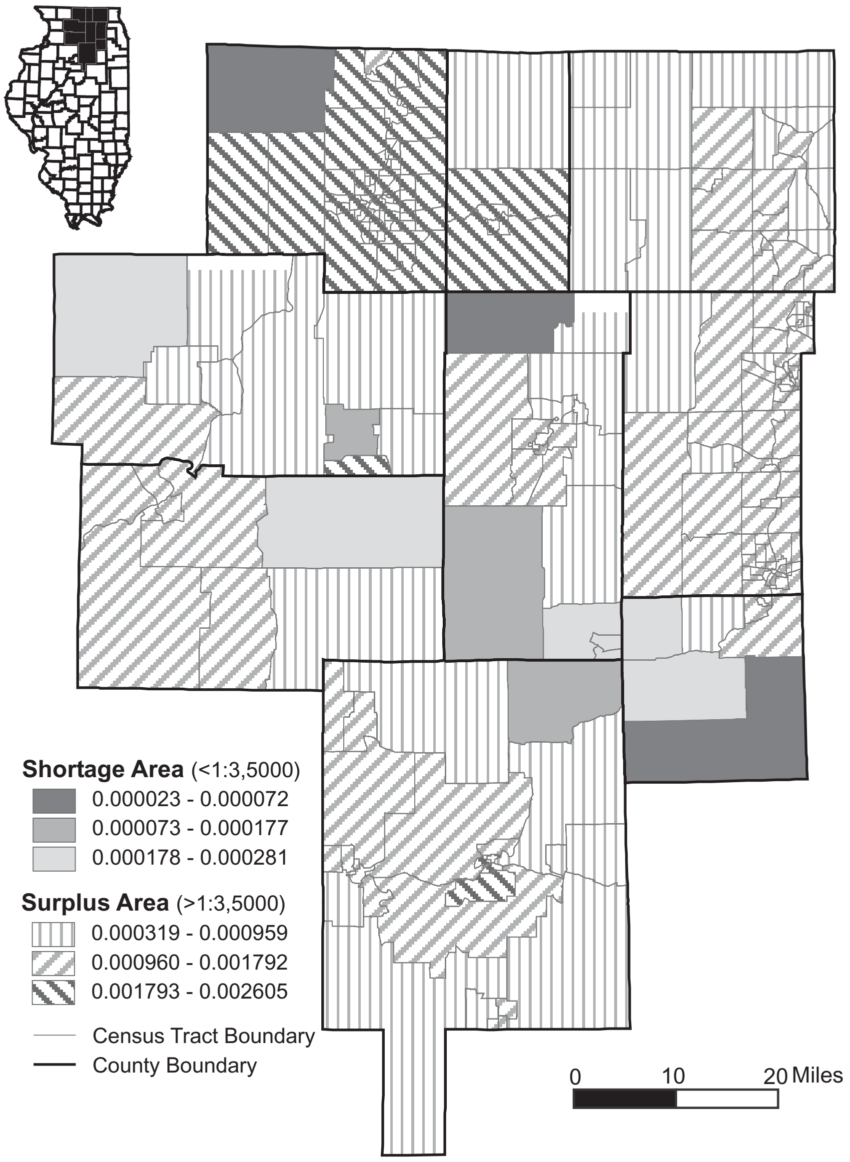
where T_{ij} is the number of patient visits between population location i (Pop_i) and physician location j (Phy_j), and a is constant. We do not have access to such data for this study, and have experimented a number of values (0.6, 0.8, 1.0, 1.2 and 1.4) based on job commuting analysis (Wang, 2000). The result shown in figures 6-7 are based on $\beta = 0.8$. Using other β values generates very similar patterns.

Figure 4: Results from applying improved floating catchment method to 1990 data



The following observations can be made. First, both GIS methods reveal more detailed spatial variation within each county than the conventional methods, and clearly reveal both the severity of shortages and the level of surpluses. Second, both methods consider potential interactions between physicians and patients across county boundaries, and thus remove the limitation of using predefined geopolitical boundaries in the traditional methods. Third, the overall healthcare accessibility in

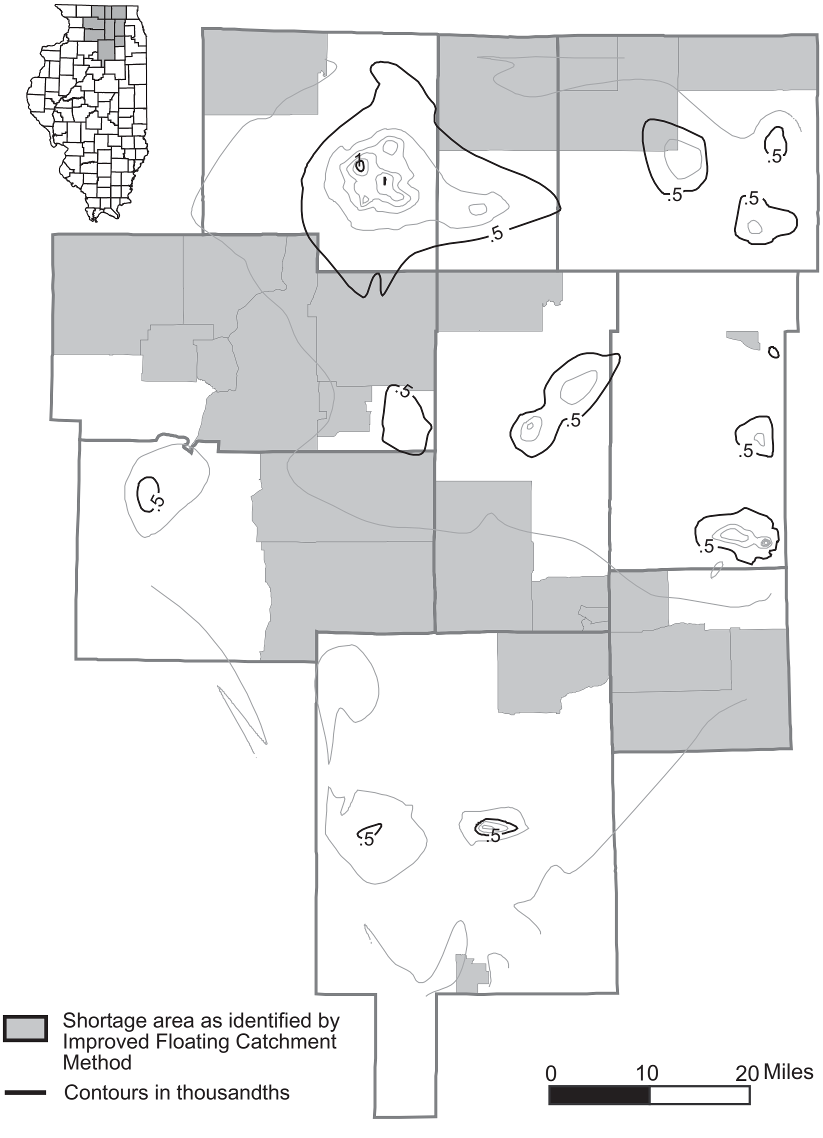
Figure 5: Results from applying improved floating catchment method to 2000 data



2000 has apparently improved significantly compared with that in 1990 (Figures 4-7). Fourth, the majority of the shortage areas are rural areas outside of urban centers (e.g., Rockford). Fifth, since the study area is limited to the DeKalb and surrounding counties, the actual health care status for the areas on the edge of the study area may not be accurately reflected since data from neighboring states are not included.

The two methods generate similar physician shortage patterns. The gravity-based accessibility method is more accurate than the floating catchment method

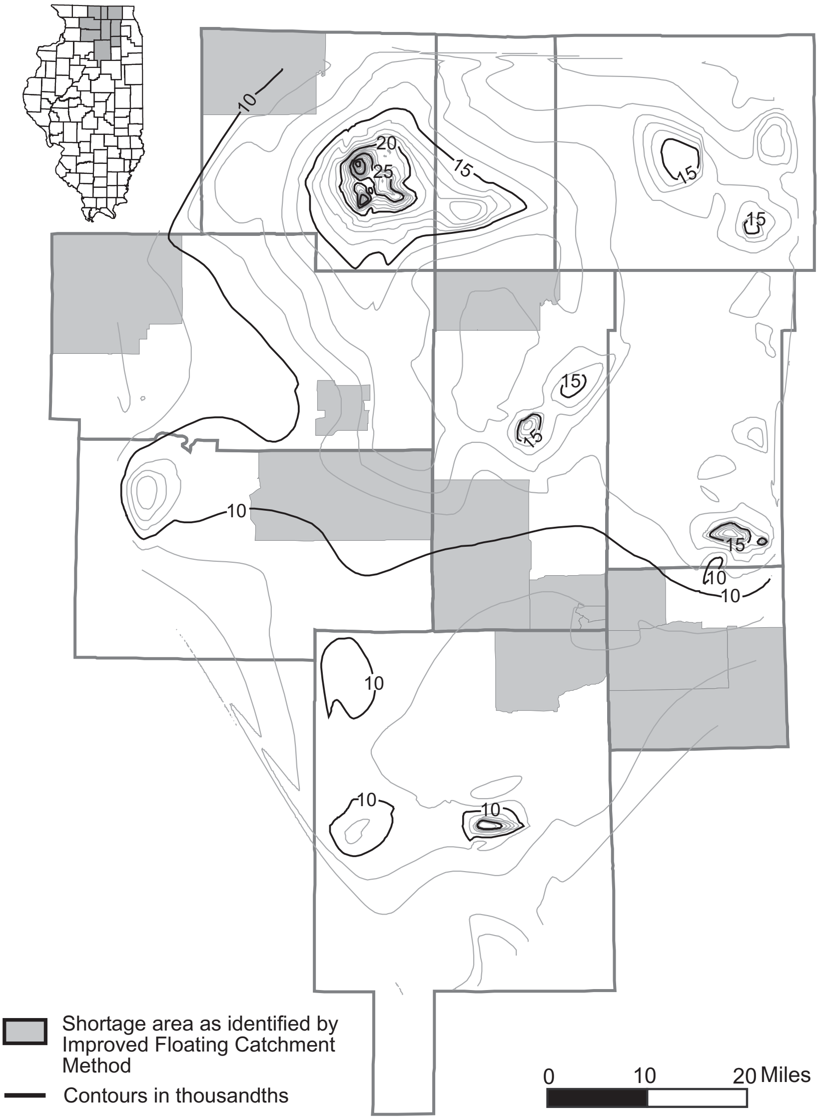
Figure 6: Results from applying gravity accessibility method to 1990 data (Assuming β = 0.8)



because the floating catchment method uses a dichotomous measure. However, the gravity-based accessibility method also involves more computation, and the determination of friction coefficient β values requires more data. The floating catchment method generates physician-to-population ratios, which are comparable to conventional methods and are easy to interpret.

In summary, by taking advantage of GIS technology and population data at a fine geographic resolution, the two methods presented here consider the interaction

Figure 7: Results from applying gravity accessibility method to 2000 data (assuming β = 0.8)



between physicians and patients across geopolitical borders and account for travel time for determining areas of physician shortage. Results by the methods show the spatial variation of accessibility to healthcare within counties. While the gravity-based accessibility method seems to be more accurate than the floating catchment method, the latter is simpler and generates results easier to interpret. It can, therefore, be argued that by incorporating these new methods into existing designation practices, areas of healthcare shortage could be more accurately delineated, enabling limited federal resources to be more appropriately directed to underserved areas.

ACKNOWLEDGMENT

This research is supported by the U.S. Department of Health and Human Services, Agency for Healthcare Research and Quality, under Grant 1-R03-HS11764-01. Points of view or opinions in this chapter are those of the authors, and do not necessarily represent the official position or policies of the U.S. Department of Health and Human Services. Partial support from the 2000-2001 Faculty Fellowship, Social Science Research Institute, Northern Illinois University to the first author is also gratefully acknowledged.

REFERENCES

Cooper, R. A.. (1994). Seeking a balanced physician work force for the 21st century. *Journal of the American Medical Association,* 272, 680–87.

Council on Graduate Medical Education (COGME) 10th report. (1998). *Physician Distribution and Health Care Challenges in Rural and Inner-City Areas*, Washington DC.

Council on Graduate Medical Education (COGME) Resource Paper Compendium. (2000). *Update on the Physician Workforce*. Washington, D.C.: U.S. Department of Health and Human Services, Health Resources and Services Administration.

General Accounting Office (GAO) (1995). Health Care Shortage Areas: Designation Not a Useful Tool for Directing Resources to the Underserved, (GAO/HEHS-95–2000), Washington D. C.

Hansen, W. G. (1959). How accessibility shapes land use, *Journal of the American Institute of Planners* 25, 73–76.

Huff, D. L. (1963). A probabilistic analysis of shopping center trade areas, *Land Economics* 39, 81–90.

Huff, D. L. (1964). Defining and estimating a trading area, *Journal of Marketing* 28, 34–38.

Joseph, A. E., & Bantock, P. R. (1982). Measuring potential physical accessibility to general practitioners in rural areas: A method and case study, *Social Science and Medicine* 16, 85–90.

Kleinman, J. C. & Makuc, D. (1983). Travel for ambulatory medical care, *Medical Care* 21, 543–557.

Knapp, K. K. & Hardwick, K.. (2000). The availability and distribution of dentists in rural Zip codes and primary care health professional shortage areas (PC-HPSA) Zip Codes: Comparison with primary care providers, *Journal of Public Health Dentistry* 60, 43–49.

Kohli, S., A. Sivertun, & Wigertz, O. (1995). Distance from the primary health center: A GIS method to study geographical access to medical care. *Journal of Medical Systems* 19, 425–434.

Lee, P. R.. (1995). Health system reform and generalist physician. *Academic Medicine* 70, S10–S13.

Lee, R. C. (1991). Current approaches to shortage area designation, *Journal of Rural Health* 7, 437–450.

Love, D. & Lindquist, P. (1995). The geographical accessibility of hospitals to the aged: A geographic information systems analysis within Illinois, *Health Services Research* 29, 629–651.

Makuc, D. M., Haglund B., Ingram, D. D., Kleinman J. C. & Feldman, J. J. (1991). The use of health service areas for measuring provider availability, *Journal of Rural Health*, 7(4): 347–356.

Ng, E., R. Wilkins, & Perras, A. (1993). How far is it to the nearest hospital? Calculating distances using the Statistics Canada Postal Code Conversion File, *Health Report* 5, 179–188.

Openshaw, S. & Taylor, P. J. (1981). The modifiable areal unit problem, in N. Wrigley and R.J. Bennett (Eds), *Quantitative Geography: A British View*, Routledge, London.

Parker, E. B. & Campbell, J. L. (1998). Measuring access to primary medical care: some examples of the use of geographical information systems, *Health and Place* 4, 183–193.

Peng, Z. (1997). The jobs-housing balance and urban commuting, *Urban Studies* 34, 1215–1235.

Radke, J. & Mu, L. (2000). Spatial decomposition, modeling and mapping service regions to predict access to social programs, *Geographic Information Sciences* 6, 105–112.

Rosenblatt, R. A. & Lishner, D. M. (1991). Surplus or shortage? Unraveling the physician supply conundrum, *Western Journal of Medicine* 154, 43–50.

Shen, Q. (1998). Location characteristics of inner-city neighborhoods and employment accessibility of low-income workers. *Environment and Planning B: Planning and Design* 25, 345–365.

U.S. Department of Health and Human Services (DHHS). (1980). Criteria for designation of health manpower shortage areas: Final regulations. *Federal Register* 45, 50436–50439.

U.S. Department of Health and Human Services (DHHS). (1990). List of designated primary medical care health manpower shortage areas (HMSAs), *Federal Register* 55, 27010–27027.

U.S. Department of Health and Human Services (DHHS). (1998). Designation of medically underserved populations and health professional shortage areas: Proposed rule, *Federal Register* 63, 46537–46555.

Department of Health and Human Services (DHHS). (1999). Lists of Designated Primary Medical Care, Mental Health, and Dental Health Professional Shortage Areas, *Federal Register,* 64, 50873–50922.

Wang, F. (2000). Modeling commuting patterns in Chicago in a GIS environment: A job accessibility perspective, *Professional Geographer* 52, 120–133.

Wang, F. (2001). Explaining intraurban variations of commuting by job accessibility and workers' characteristics, *Environment and Planning B: Planning and Design* 28, 169–182.

Wing, P. & Reynolds, C. (1988). The availability of physician services: A geographic analysis, *Health Services Research* 23, 649–667.

Chapter XVI

Using GIS with Publicly Available Data for Hospital Market Share Analysis

Evan R. Wolarsky
Healthcare Consultant, USA

Publicly available data of all hospital discharges has been available since Medicare changed to a case-based reimbursement system. A non-confidential version of this dataset contains a Zip Code identifier for each discharge, in addition to diagnoses, procedures, payer information, hospital charges and basic demographic data. The method for converting the raw data into a useful marketing database is described. An application of this database in conjunction with GIS is presented here. In this application, the market share of a community hospital is analyzed. A series of maps shows that geography plays an important role in hospital choice, and a linear regression model provides quantitative evidence of this pattern. Finally, bivariate maps are used for more complex analysis.

INTRODUCTION

A dataset of all hospital discharges has been available for many years. This chapter describes the dataset and shows one of its potential applications with GIS. This application analyzes the market share of a community hospital and identifies potential opportunities for further hospital growth.

THE DATASET

In 1965, Medicare legislation was passed after many years of debate concerning national health insurance. During the succeeding 15 years, it became apparent that the original projections of hospital cost had been too low. In an attempt to control these costs, the Health Care Financing Administration (HCFA) changed to a radically different payment scheme. Rather than paying hospitals for their ongoing costs for each admission, they would reimburse hospitals with a fixed payment for each diagnosis. The goal was to shift some of the financial risk back to the hospitals. Thus, a hospital would be paid a previously decided upon amount for acute appendicitis, irrespective of the cost of the actual care given.

In order to implement the program, HCFA adopted a classification of diseases called Diagnostic Related Groups (DRGs). This classification scheme provided a way to group all hospital discharges into a few hundred diagnoses on which Medicare could base all its hospital payments. Upon discharge, the patient's physician lists all the pertinent discharge diagnoses and procedures in the medical record. This sheet then goes to a "coder," an individual who converts each diagnosis and procedure into an "ICD9," number. A computer program called a "grouper" then aggregates all the ICD9 codes into a single DRG number on which payment is made. In general, there are paired diagnoses for most major conditions–one code for the uncomplicated case and another for the more complex case. The system thus allows for two levels of severity of illness.

In order to implement the system, a dataset called UB82, for Uniform Bill, was constructed. This dataset has recently been updated to UB92 but has remained relatively stable for many years. Of great importance is that many states and fiscal intermediaries have adopted this dataset. The dataset contains several hundred fields of data, including the patient's demographic data, age, sex, race, insurance coverage, as well as up to nine diagnoses, six procedures, length of stay, and the calculated DRG. There are several fields listing all the various hospital charges. Many states make their data publicly available in a non-confidential dataset that masks the ability to identify the individual patient, and often the individual physician. While individual street addresses are masked, Zip Codes are included in the dataset.

As a result of the availability of this data, many applications have been found for its use. Dr. John Wennberg at Dartmouth has developed a series of atlases showing the geographical variations in hospital care based on this dataset, as well as other claims data.

A more complex and controversial use of this dataset has been the efforts to analyze quality of hospital and physician care. Algorithms to assign a severity rating of illness to cases have been constructed by weighting the various diagnostic and procedure codes, along with variables such as age and sex. After assigning a severity rating to each case, the utilization of hospital resources and outcomes such as length of stay have been analyzed. In this manner, statistical analysis of the norms and outliers for each diagnosis has been produced. These efforts have been controversial because of the inconsistencies of coding patterns in hospitals, as well as the complex logistic regression analyses employed for the design of the severity ratings.

USING THE DATA

States vary in the way in which they release the UB82/92 data. Many now provide data on CD-ROM that enable personal computer users easy access to the dataset. The main impediment to using the dataset is the ability to use a relational database program, such as Microsoft Access. The reason is that the released data contains millions of records in which all the text entries are coded, i.e., in numerical form. Instead of a text entry to hospital name or diagnosis, there is a three-digit code for hospital name and a five-digit ICD9 code for diagnosis. It is thus necessary to import the raw data into a relational database program that will link each coded field to a matching table listing the code numbers with the associated text entries.

The second impediment to the use of the data is that one must be familiar with Medicare jargon. While it is not difficult to figure out that "provider number" refers to "hospital name," there have been a number of changes over the years, which have modified the DRG groupers and other fields. The easiest solution to this problem is to identify the individual at a nearby hospital who is the keeper of the codes.

Once the dataset has been converted into a database of hospital discharges, one can then query the database. This can be done from within the database program, or by sending the query from GIS software–depending on the software being used. A simple query, for example, might be to count the number of discharges per Zip Code. The database program then returns an answer with two columns– a list of Zip Codes and an associated number of discharges. It is then easy to save this answer in a format recognized by the GIS program, and import the table into the GIS. One then links the Zip Code column of the data table to the geographical file in the GIS and can easily produce maps of the discharges. A more complex, but extremely useful query, is the cross tabulation query. Here, one asks the database to provide a count of discharges per hospital per Zip Code. One then has a table with a Zip Code in each row, and a hospital name in each column. When this is linked to a Zip Code geographical file, each hospital appears as an attribute for each Zip Code. It is then simple to scroll through the hospitals and provide a series of thematic maps for each one. Similarly one can provide maps for any of the pieces of data contained within UB82/92 such as individual diagnoses, procedures, hospital charges, length of stay or insurance carriers.

Once the database is constructed, it is of enormous value for planning or marketing purposes, as the dataset reflects the entire hospital use for a given geographic area. One shortcoming of the dataset, however, is that is does not include outpatient data. As more and more care has migrated into the outpatient setting, the dataset thus includes less of the total hospital care provided.

MARKET SHARE APPLICATION

One application of this method is the analysis of market share for Hunterdon Medical Center, a community hospital in Hunterdon County, New Jersey. Hunterdon County is a relatively rural county in the western part of central New Jersey, bordering on Pennsylvania. While it is the only hospital in the county, it is surrounded by a series of other hospitals within an easy drive of Hunterdon County.

Using the 1997 UB82/92 dataset, it was determined that the overall market share of Hunterdon Medical Center was 63% for residents of Hunterdon County. In other words, of all residents of the county needing hospital admission, 63% were admitted to Hunterdon Medical Center. A basic principle of marketing is to attempt to segment the market. Thus one could query the database as to patterns of admission by diagnosis, procedure, age, sex and insurance carrier. In this particular application, the role of geography was to be addressed. Simply, to what extent does location of patient residence explain the hospital of choice for admission?

While maps were prepared for all the surrounding hospitals, three are shown here as examples. There are thematic maps for admissions to Hunterdon Medical Center, as well as its two closest hospitals and main competitors, Somerset Medical Center and Warren Hospital. In order to facilitate comparison, these three maps were prepared with similar scales and legends. The maps show the outline for Hunterdon County with Zip Code boundaries indicated. Each map then shows the admissions to its respective hospital by Hunterdon County Zip Code. Locations of the hospitals in Hunterdon, Somerset and Warren counties are indicated by the capital "H" symbols.

The first map, "Hunterdon Medical Center Admissions," shows the location of the hospital in the central portion of the county, with Somerset County to the east and Warren County to the west. The Zip Code thematic map clearly shows that most admissions came from the Zip Code in which the hospital is located, with a further distribution as indicated by the shading. It should be noted that one disadvantage of using Zip Code boundaries in thematic maps is that the Zip Codes are of uneven size, population and may extend across county lines. Nonetheless, they are the only geographic variable in the publicly available dataset.

The second map, "Somerset Medical Center Admissions," shows the pattern

Figure 1: Hunterdon Medical Center admissions

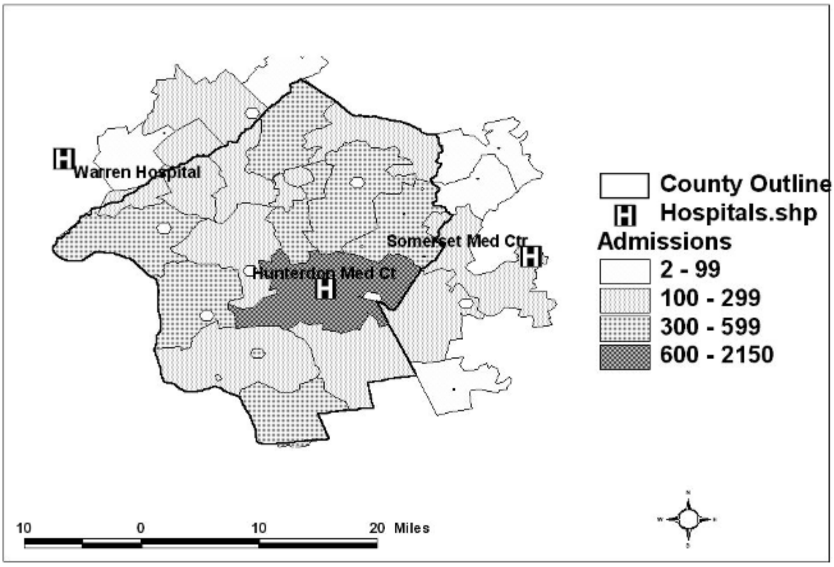
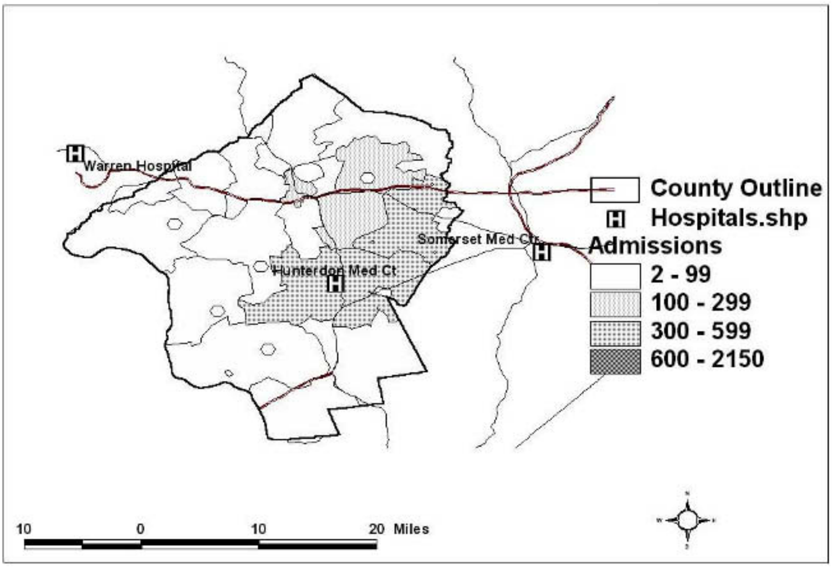
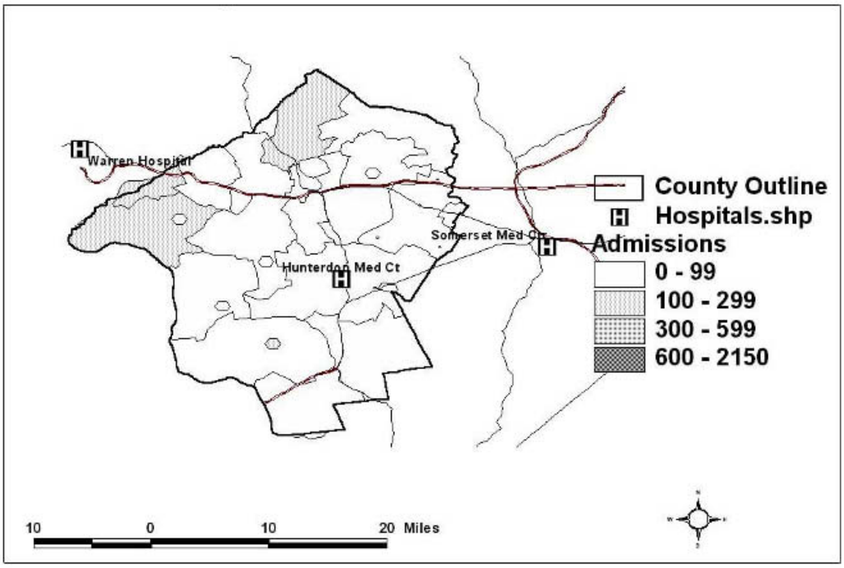


Figure 2: Somerset Medical Center admissions



of admissions to this hospital from Hunterdon County. A striking feature is that the overwhelming majority of patients come from Zip Codes contiguous with Somerset County. The major roads are included in this map to show that there is an interstate road and two other major highways providing access for patients from Hunterdon

Figure 3: Warren Hospital admissions



County to Somerset Hospital.

The third map, "Warren Hospital Admissions," similarly shows that admissions again are largely from Zip Codes contiguous to Warren County. It should be noted that the admissions here are less than to Somerset Hospital. One reason may well be that there are fewer good access roads in this part of the county.

Maps of the other hospitals surrounding Hunterdon County reveal a similar picture–geography is an important variable in determining which hospital people choose. Given all the possible factors that might affect a person's choice, it is clear that proximity is of significant importance.

A quantitative approach to this subject was taken by Phibbs and Robinson (1983). They studied hospitals in California in order to determine hospital market size for use primarily in antitrust analysis. They measured the distance between each hospital and the centroid of each Zip Code. Using publicly available data, they then calculated the average radius to provide 75% and 90% of each hospital's market share. Their findings concluded that the median distance to capture 75% of hospital admissions was 7.33 miles, and 14 miles for 90% of admissions. This study confirms that local geography plays an important role in hospital choice.

BUILDING A MODEL

In order to gain further insight into the role of geography, an attempt was made to build a multiple linear regression model. Such a model asks whether the results of a dependent variable, such as admissions from each Zip Code, can be predicted from a variety of independent variables. In this case several demographic variables were chosen from census data. These included population of each Zip Code, elderly population, housing value and mean income. In order to test the geographic component, the distance from each Zip Code was measured to Hunterdon Medical Center, as well as the distance to the nearest other hospital. These two measurements were included in the model. Finally, since physicians play an important role in hospital access, the number of primary care physicians in each Zip Code was included in the model as an independent variable.

The model was run in SPSS, and an R-squared of .67 was obtained–that is, 67% of the variability of admissions to Hunterdon Medical Center from each Zip Code could be explained by the variables selected by the model. The final model included three variables–population of each Zip Code, distance of each Zip Code from Hunterdon Medical Center and number of primary care physicians in each Zip Code. The regression model thus confirmed the impression that geography and geographic variables play an important part in determining hospital admission.

FURTHER ANALYSIS USING BIVARIATE MAPS

At this point, one could argue that while the maps are interesting, the conclusion that most people would rather go to a nearby hospital rather than a distant one is fairly intuitive. The map, “Market Share Percent,” shows the percentage of Hunterdon Medical Center market share for each Zip Code. Clearly the market share is highest in the Zip Code of the hospital and in the contiguous central Zip Codes of the county.

A different view of this data is obtained, however, if one maps two thematic variables per Zip Code. This is done by attaching one set of numeric attributes to a Zip Code boundary file, and a second set to the Zip Code centroid point file. In this case, market share is mapped by three symbols–star, circle, and square–each representing a third of market share. As indicated in the legend, the star represents the highest third of market share. A second variable, out-migration, is mapped by the underlying shades of gray in each Zip Code. Out-migration refers to the number of cases admitted to other hospitals per Zip Code, rather than market share percent. At first glance, one sees that market share is generally higher in the southern part of the county and lower in the northern half. In keeping with this, out-migration is generally lower in the southern half. One extremely surprising finding, however, is in the Zip Code of Hunterdon Medical Center. Here it can be seen that while the market share is high, it also has the highest number of patients leaving the county for care elsewhere. This counter-intuitive finding results from the fact that Zip Codes,

Figure 4: Market share percent

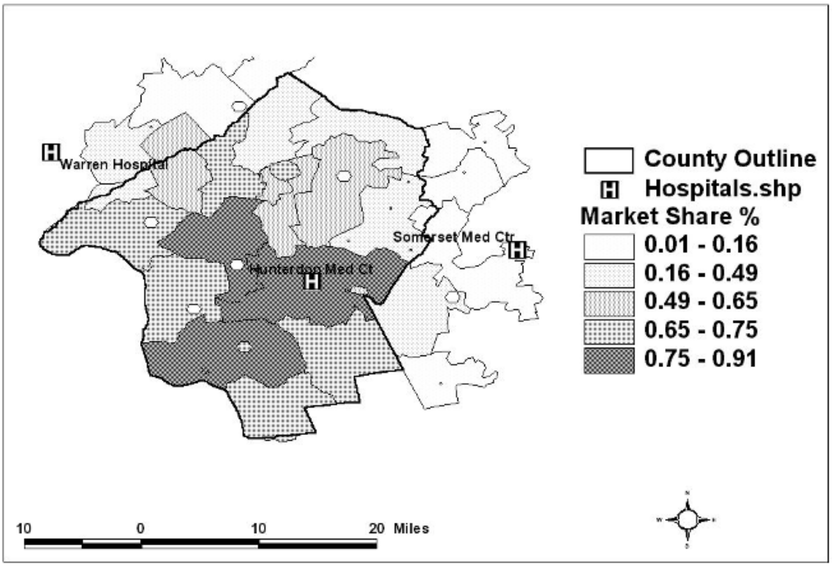
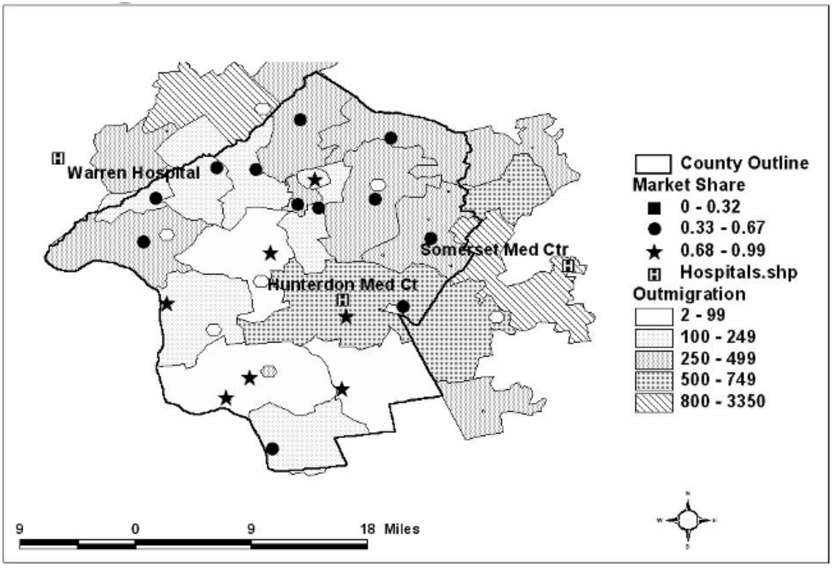


Figure 5: Outmigration and market share



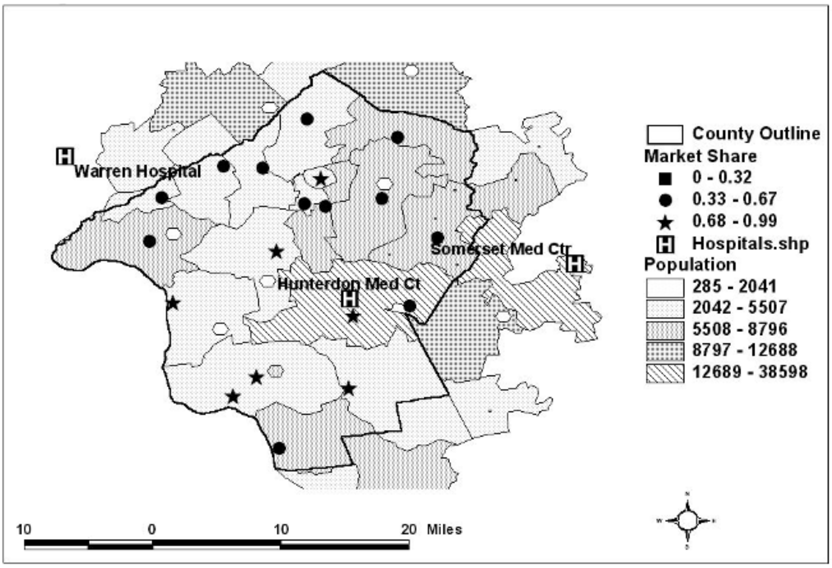
again, are not of uniform size. In fact, the Zip Code of the hospital is several times the size of most of the other Zip Codes. Thus while the market share in this Zip Code is 80%, this Zip Code has approximately 500 patients seeking care elsewhere–far greater than in other Zip Codes. This finding provides an opportunity for further research in this interesting observation.

MARKETING THEORY

This finding proved to be of importance in terms of constructing a general theory of market share for the hospital. There were several new physicians who were interested in locating in Hunterdon County and sought advice as to where they might locate. At the time of the analysis, the dominant thought was that the hospital should expand centrifugally by placing physicians in the distant parts of the county, and even in surrounding counties. The research results, however, indicate a market share model, which includes proximity to the hospital as an important variable. In order to attempt to determine where new physicians might establish offices, another bivariate map was used. Since the regression model indicated hospital admissions were greatest in the Zip Codes with large populations close to the hospital, a map was made with two thematic variables. The variable indicated by the solid symbols was again market share. However, in this bivariate map, the underlying thematic variable was population. The figures were based on census numbers and census estimates for future growth in the county.

Analysis of the map reveals several important facts. First, the market share, as seen in the previous map, shows a clear difference between the northern and southern halves of the county. The population, however, shows a clear pattern in which the Zip Codes of maximal population are in the northeastern quadrant of the county and extend into Somerset County. Third, as seen previously, this region of

Figure 6: Population and market share



the county is traversed by a series of roads that led directly to Somerset Medical Center. It thus became quite clear that there was an area of low market share and high population within easy driving distance of both Hunterdon Medical Center and Somerset Medical Center. It thus made marketing sense to place more emphasis on this portion of the county than on peripheral areas elsewhere. Furthermore, a map including physician locations (not included here) enabled more detailed study of where opportunities might exist for new physician offices.

SUMMARY

1. The publicly available UB82/92 dataset is of value in the analysis of patterns of hospital use. The raw data has to be converted into a usable database, but then facilitates analysis using any of the included variables.
2. Geographic location is an important variable in segmenting the hospital population. Despite all the factors that might influence choice of hospital, proximity is extremely important.
3. Geographical analysis with the dataset and GIS is a powerful tool for analyzing the hospital market. Besides showing basic patterns of hospital uses, bivariate geographical analysis can be used for more complex analysis.

REFERENCE

Phibbs, C.S. & Robinson, J.C. (1993). A variable-radius measure of local hospital market structure. *HSR: Health Services Research, 28(3)*, 313–324.

Chapter XVII

Mapping Accessibility to General Practitioners

Lars Brabyn and Paul Gower
University of Waikato, New Zealand

Accessibility to general practitioners (GPs) is an important health issue that has financial, cultural and geographical dimensions. This chapter concentrates on a Geographical Information System method for assessing geographical accessibility using network analysis but begins with an overall review of health accessibility literature, followed by a more detailed review of GIS solutions to assessing geographical accessibility. A procedure based on ArcInfo software is described and demonstrated using cost path analysis to determine the minimum travel time and distance to the closest GP via a road network. This analysis is applied to approximately 36,000 census centroids in New Zealand and this enables travel time and distance to be linked to the population distribution. Statistics can be generated on what is the average time spent traveling or the average distance traveled if everybody visited a GP once. These statistics can be generated for different management areas and enables comparisons to be made between regions. This accessibility model is intended for decision support for health planners assessing the distribution of GP services. It can also be easily adapted for other services such as access to hospitals and cancer screening centers.

INTRODUCTION

Accessibility to general practitioners (GPs) is a major contentious issue in many countries (Perry & Gesler, 2000). Poor access to primary health services, such as GPs, can result in people with simple health problems not being advised by GPs and subsequently developing more complex problems with considerable discomfort that can be expensive to treat (Haynes et al., 1999). Health planners and policy developers require information on accessibility to GPs so that procedures and policies can be developed to address inequity. An important consideration for such decision making is where people are living, and their travel distance and time to the closest GP.

Geographical access models developed using network analysis functions in a GIS have enormous potential for informing policy development and grounding debate on how to achieve social equity of primary healthcare access. However, accessibility to health services is a complex subject and it is important that this is well understood before developing such models. There are many political and cultural considerations of accessibility that GIS cannot easily model. GIS can model geographical accessibility and this complements other considerations.

This chapter begins with a general discussion on the meaning of accessibility and the many facets to this term. The discussion then narrows to geographical accessibility and the GIS capabilities available to model this. An example of a GIS method for estimating the geographical accessibility of GPs is then comprehensively described and demonstrated. This example uses least cost analysis to determine the minimum travel time and distance to the closest GP via a road network. This analysis was applied to approximately 36,000 census enumeration district (meshblock) centroids in New Zealand, and this enabled travel time and distance to be linked to the population distribution. Statistics were generated on what is the average time spent traveling or the average distance traveled if everybody visited a GP once. These statistics can be generated for different management areas and enables comparisons to be made between regions.

A difficulty with calculating travel times is determining the travel speeds for different roads. Road layers often contain information that describes the road characteristics, and additional information on the bendiness of the roads can be obtained from calculating the sinuosity of the roads. A process for calculating sinuosity and estimating road travel speeds is described.

This chapter finishes with a discussion on the application of this accessibility model. This process can be easily adapted for other services such as access to hospitals and cancer screening centers.

ACCESSIBILITY

> *"Accessibility is ... a slippery notion ... one of those common terms that everyone uses until faced with the problem of defining and measuring it."* (Gould, in Moseley, 1979)

Few would suggest that a simple measure of Euclidean or network distance from an origin point to a destination is sufficient as a measure of accessibility. Moseley (1979, p.56) suggests that when we talk of something being "accessible," we are simply referring to the degree to which it is "get-at-able." This crude, yet helpful proposition leads us to an understanding of accessibility that is larger than a simple measure of distance.

In the past the accessibility problem has been examined by a number of geographers. Hagerstrand (in Moseley, 1979) outlined accessibility as being made up of two components, legal/social and the physical. Legal/social accessibility is described as barriers that exist around a supply point including such variables as age, training, ability to pay and support from others. Physical accessibility is a derived measure of the physical "distance" from an individual to the desired supply point. The separation of these two components of accessibility on a conceptual level fails to recognize the interactions that take place between the physical and legal/social in real-life situations. For example a young person having a certain birthday may mean that they are able to drive alone and therefore have greater physical accessibility. Nevertheless, this conceptual framework makes explicit the complex nature of accessibility and identifies physical proximity to a location as simply a part of the accessibility measure of that location.

The difference between mobility and physical accessibility has been the matter of discussion by a number of geographers. Daly states (in Moseley, 1979) that accessibility must be measured in relation to 'distant but necessary destinations.' This suggests that a desired destination must be required in order to measure accessibility. Mitchell and Town (in Moseley, 1979), in talking of accessibility existing in relation to 'a given activity,' also hold to the notion of accessibility requiring a desire to access a specific destination. Opposing the 'desired' component of accessibility is Ingram (1971), who defines accessibility as being the ability to overcome some spatially operating form of friction. Moseley (1979) suggests that a synthesis of two components, 'units of separation' and 'usefulness of various destinations' make up physical accessibility measurements. Therefore, such a combination of elements is most appropriate in analysis and measurement of physical accessibility.

This brief examination of 'accessibility' theory is sufficient to be able to suggest that accessibility is a complex concept, with a contested meaning. A further field of literature will now be examined to place the question of access in a primary health context.

ACCESSIBILITY AND PRIMARY HEALTH

The World Health Assembly's Declaration of Alma-Ata championed the concept of access to primary healthcare on the international stage in 1978 (WHO/UNICEF, 1978). In this declaration, accessibility is identified as being contingent on four interrelated components--geographic, financial, cultural and functional accessibility. Each component examines a different aspect of the accessibility equation. Geographic accessibility considers the physical separation of population from a desired location. Financial accessibility describes the ability for a population to pay for the desired service, whereas cultural accessibility appraises centers not only in relation to ethnic exclusion but also in terms of personal perceptions in respect to accessing the desired service. Functional accessibility is simply "…care is available on a continuing basis to those who need it, whenever they need it, and that it is provided by the health team required for its proper delivery" (WHO/UNICEF, 1978). The above framework for considering accessibility to services is undoubtedly comprehensive and surpasses the dualistic conceptual model proposed by Hagerstrand.

A further accessibility model for primary health situations has been developed by Hulka (1978) and has recently been widely used by American and British researchers (Coster & Gribben, 1999). Hulka proposed that accessibility was made up of three components of accessibility, acceptability and availability. The first component, accessibility, refers to physical distance to the desired location. Acceptability refers to the cultural and social perceptions, and appropriateness of a desired service. The third component, availability, highlights the fact that there are capacity limits to services, and these limits need to link with demand for the service within an appropriate physical distance.

Joseph and Phillips (1984), in perhaps the seminal text on the topic of geographic patterns of health service delivery, present 'locational' and 'effective' accessibility as the defining components of any accessibility description. 'Locational' accessibility refers to the physical proximity of the service. This measure is inherently geographical and relatively easy to measure using GIS processes. However 'effective' accessibility is somewhat more problematic as it includes opening hours of a service, social and financial availability of the service, and personal space-time budgets. Each of these measures is more difficult to model using GIS and generally available data sets.

PREVIOUS RESEARCH

From the above discussion it can be noted that accessibility is a multifaceted concept, one that is firstly difficult to define and resultantly difficult to measure. This chapter will focus on a least cost path method to measure physical accessibility to GPs for aggregated census populations. A number of previous studies have used Geographic Information Systems (GIS) to modeling accessibility to healthcare services, and these will be reviewed.

Wilkinson, Grundy, Landon and Stevenson (1998) suggest that there are two related conceptual models of access, which are relevant to healthcare organizations and analyzable using GIS. These are 'access to services' and 'equity in service provision'. Each model uses a fundamentally different approach yet are complementary in describing accessibility.

A GIS method that uses the 'access to services' approach tends to produce outcomes based on Euclidean distance, Thiessen polygons or travel time and distances measures using transport networks. Non-GIS research undertaken by Shannon, Skinner and Bashshur (1973) has shown that consideration of travel time and distance independently, as accessibility measures of healthcare facilities, produces different results. Lovett, Haynes, Sunnenburg and Gale (2000) substantiate this finding in stating that the accessibility measure closest to an individual's experience is that of travel time.

There have been a number of studies that have used Euclidian distance and Thiessen polygons. Kohli, Sahlen, Silvertun, Lofman, Trell and Wigertz (1995) used an areal distance measure in their small-scale analysis in the Ostergotland province of Sweden. Twigg (1990) employed Thiessen polygons to model catchment areas of general practitioners. Zwarenstein, Kringe and Wolff (1991) also used a Thiessen polygon-based approach in the assessment of access to hospitals by different ethnic populations in Natal, South Africa. Perry and Gesler (2000) used 5km buffers to represent possible travel distance by walking one hour in their study of Andean Bolivia. This method did not take into consideration topology of land or use of networks of paths or roads. Road networks have a fundamental effect on accessibility, therefore models based just on Euclidian distance and Thiessen polygons, although claiming objectivity, only provide a crude measure of accessibility.

Accessibility studies involving the use of network models are increasing in number. This is probably a reflection of the increased computing power that is affordable and the increased availability of geo-referenced data. Lovett et al. (2000) conducted a comprehensive, large-scale study of travel times to GPs based on both private and public transport. A complex 12-speed class road network was used to generate travel times. Bus timetables were analysed to assess frequency of service and areas were then classified based on number of bus services in a day. This project was based in East Anglia and represented a population of 2,144,921.

New Zealand-based examples have been produced in main by Critchlow Associates (1995 and 1996) under contract for Central and Southern Regional

Health Authorities respectively. These studies utilized a simple three-speed class road network. This network was used to develop service areas by which census-based population data was then merged and tabulated.

The use of density mapping in accessibility measurement is based on identifying and quantifying inter-regional variability. This measure uses simple mathematical ratios of service supply to population demand and is helpful in identifying inter-regional differences in rates of servicing. Joseph and Phillips (1984) discuss the problematic nature of using such methods and identify boundary definition and scale of analysis as sources of imprecision. There is a long history of generating such measures of access variability using both larger provincial (Roos, Gaumont & Horne, 1976; Spaulding & Spitzer, 1972) and smaller, localized urban scales (Barnett, 1978; Stimson, 1981). General practitioners per population and utilization rates are visualized using simple choropleth mapping techniques. This technique fails to describe patterns of variance found within the regional boundary, and consequently this technique has a smoothing and generalizing effect of statistical reality. Clumping of either GPs or populations is harder to identify. These spatial patterns are often only noticed at certain scales of spatial unit aggregation. This technique also fails to take into consideration any cost to the user in accessing the GP service. Travel-time is one such cost that can greatly affect utilization of a service yet fails to be described by density maps.

LEAST-COST PATH ANALYSIS

Least-cost path analysis theory and techniques can be traced back to Dantzig who in the 1940s developed linear programming. Linear programming is concerned with finding optimum solutions to problems such as the minimum cost of travel. From such techniques Dijkstra (1959) developed his simple path-finding algorithm. Least cost path commands in Arc/Info are based on the Dijkstra algorithm and are described in Arc/Info user manuals (ESRI, 1992). Analysis using least-cost techniques can be performed using any impedance (cost) variable. Such analyses are used to describe the shortest distance to a service for a population or a travel time to the closest service. The shortest path by distance may be totally different to the shortest path by time (Shannon et al., 1973).

There is a large body of technical literature that describes network systems and least cost path algorithms (Pollack & Wiebenson, 1960; Moore, 1959; Rapaport & Abramson, 1959). These tend to fall into the category of literature informing what has been commonly called ‘the transportation problem,’ which is concerned with minimizing transport goods for delivery. With the ever-expanding road networks and associated databases of contemporary society, there is continuing need to modify shortest path or least cost algorithms. In this respect, Zhan (1996) has explored the use of 'fast' shortest path algorithms for particular use on large road networks.

MODELLING MINIMUM TRAVEL DISTANCE TO THE CLOSEST GP

The following text describes a population-based approach used to calculate the travel distance to the closest GP. The calculation of travel time requires some additional modelling and this is described later in this section.

Three input layers were used for the analysis: a road network, meshblock centroids and point locations of the GPs. Fortunately, the NZ Government has recently relinquished its demand for royalties for access to the national 1:50,000 topographic data set, which means that a comprehensive road network of NZ is now available to all researchers. This road network contains various information on road characteristics but does not contain information on travel speed or time for each road segment. To calculate travel distance, road segment length is required and this is easily computed with GIS.

Meshblocks are the smallest areas used in the distribution of census data and there are approximately 37,000 in the 1996 Census release with a median population of 90 people per meshblock (Statistics New Zealand, 2001). The unique identification number for each meshblock links these small areas to population census data, which facilitates demographic analysis. The meshblock centroids were generated from Statistics New Zealand's meshblock areas.

The network analysis capabilities in *ARC/INFO* were used to calculate accessibility. The key command used was called *nodedistance*, which computes the distances between all possible combinations of origin and destination nodes. This command uses Dijkstra's least cost path algorithm. In this study, road network nodes closest to the meshblock centroids were the origin nodes, and the nodes closest to the GPs were the destination nodes. The nodes closest to the meshblock centroids and GPs were identified using the *near* command, which also calculates the Euclidian distance to the nodes.

The *nodedistance* command provides a table of minimum distances via a network between all possible combinations of origins and destinations. It also provides identification numbers of the origins and destinations for each record and the Euclidean distance. The *nodedistance* function not only identifies distances but can also be used on any specified field, such as travel time. To identify the closest GP for a given meshblock centroid, the *statistic* function in Arcinfo was used to identify the minimum distance for each origin to the closest destination.

The minimum distance to the closest GP for each centroid was calculated by summing the network distance (obtained from the *nodedistance* command and subsequent statistics) plus the distance from the centroid to the closest road node (obtained from the *near* command) plus the distance from the GP to the closest road node (also obtained from the *near* command).

The calculation of minimum travel distance to the closest GP is easy to understand and Arc/Info provides some powerful commands that make this possible. This process produces many output tables and the most difficult part of developing this process was linking all the tables through common identification fields so that the identified closest GPs and their distances can be linked back to the meshblock centroids.

The process for calculating the minimum travel time to the closest GP is similar to the minimum distance process, except road travel time was used instead of distance. The difficulty with this process was determining what the travel times were for travelling along the road segments. The method for calculating this is described below. The travel times from meshblock centroids and from GPs to the closest road node were calculated using distance (obtained from the GP-distance modelling process) and a travel speed of 50 km/hour.

The processing time for both travel distance and time was approximately eight hours using two 750 MHz CPU standard desktop PC computers.

ROAD NETWORK TRAVEL TIMES

The estimated road network travel times were based on whether the road was inside or outside an urban area, whether or not it was a motorway, the number of lanes, the surface and the bendiness (sinuosity).

Urban roads were identified from integrating the road network with a Landcover layer (Thompson, 1998). Motorways were identified by using the field "*name*" and searching for the name "Motorway," and also by manually locating "open speed limit" roads in the Wellington and Auckland urban areas. The number of lanes a road has and the road surface were provided with the road layer.

Sinuosity indexes have been used in hydrology to describe the meandering of river channels. A simple formula for sinuosity is observed length divided by expected straight-line (direct) length (Haggett & Chorley, 1969). GIS easily provides observed lengths of lines. The straight-line length was calculated for each road segment by creating a new road layer that was a generalization of the original road layer. This generalization involved removing vertices from the road arcs so that there was only one vertex per 500m. This had the effect of straightening the road segments. The lengths of the straightened road segments were then calculated and joined to the original road network using arc IDs. The sinuosity index was calculated by dividing the original length by the straight length. If a road was originally straight, then the sinuosity index will be 1. If a road is bendy then the sinuosity index will be above 1. A very bendy road that turns back on itself (hairpin corners on a hill) may have a high sinuosity score of 4. A sinuosity threshold of more than 1.02 was used to identify bendy roads. This threshold was determined by graphically viewing the sinuosity indices of roads in New Zealand and identifying what threshold was required to distinguish roads that are known to be bendy.

The estimated travel speed for each road segment was calculated as follows:

- Sealed urban roads - average speed: 30km/hr
- Urban motorway- average speed: 80km/hr
- Non urban, 2 lanes, sealed, straight roads- average speed: 80 km/hr
- Non urban, 2 lanes, sealed, bendy roads- average speed: 60 km/hr
- Non urban, 1 lane, sealed, straight roads- average speed: 70 km/hr
- Non urban, 1 lane, sealed, bendy roads- average speed: 40 km/hr
- Metalled straight roads- average speed: 50 km/hr
- Metalled bendy roads- average speed: 30 km/hr

This classification of road speeds is more detailed than that used by Critchlow Associates (1995), which was based on only three classes of roads speed - 80km/h for motorways and high-speed rural roads, 60km/h for slow rural roads, and 35km/h for urban and minor rural roads. The travel time study of GPs in East Anglia (UK) (Lovett et al., 2000) used 12 classes of travel time, but because traffic and road conditions are different in the UK, it is not valid to compare them with NZ roads.

The road segment travel times were calculated from arc lengths and estimated travel speeds. It needs to be emphasized that the road segment travel times are estimations only. The travel speeds for different road types are not based on scientific empirical evidence but instead on approximations based on personal experience. This process does not take into account urban expressways where average travel speeds could be more than 35km/hr. It also does not consider the effects of traffic congestion and difficult intersections. The network distance and travel times ignore one-way streets.

The travel times of the road network were tested against travel times between major towns published by the New Zealand Automobile Association (AA). The major towns that the AA used were entered into a GIS and least cost path analysis generated travel times between each town using the derived road network. Overall the GIS-generated travel times were 5.08% less than the AA times. The absolute difference in time, calculated as a percentage of the AA time, was 8.85%. This was considered to be an acceptable difference.

Many meshblock centroids are located on offshore islands or out at sea. These centroids are used to represent people on boats or isolated islands. The distance to the closest GP from these centroids is based on the Euclidian distance to the closest road and the network distance along the road to the closest GP. Sometimes the closest roads to these centroids were roads on islands that did not connect to roads near GPs. This caused a problem that was resolved using two approaches. First, road networks on large islands were connected to the main road network by an arc that represented a ferry service route. The travel times for these ferry routes were then estimated from timetable schedules. The second approach was to then delete all roads that were not connected to the main road network in the South or North Islands. The *Trace* and *Nselect* commands were used to identify these roads.

RESULTS AND APPLICATIONS

The travel distance and time to the closest GP for each meshblock centroid is represented in Figures 1 and 2. These figures show the raw data that results from the analysis. This data can be aggregated to many different regional management units, such as Territorial Local Authorities or District Health Boards (DHB).

Figure 1: Travel distance to the closest GP by meshblock centroid

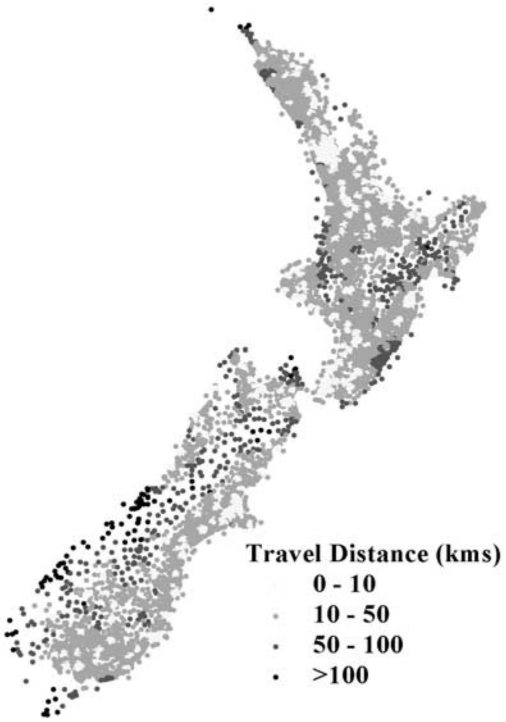


Figure 2: Travel time to the closest GP by meshblock centroid

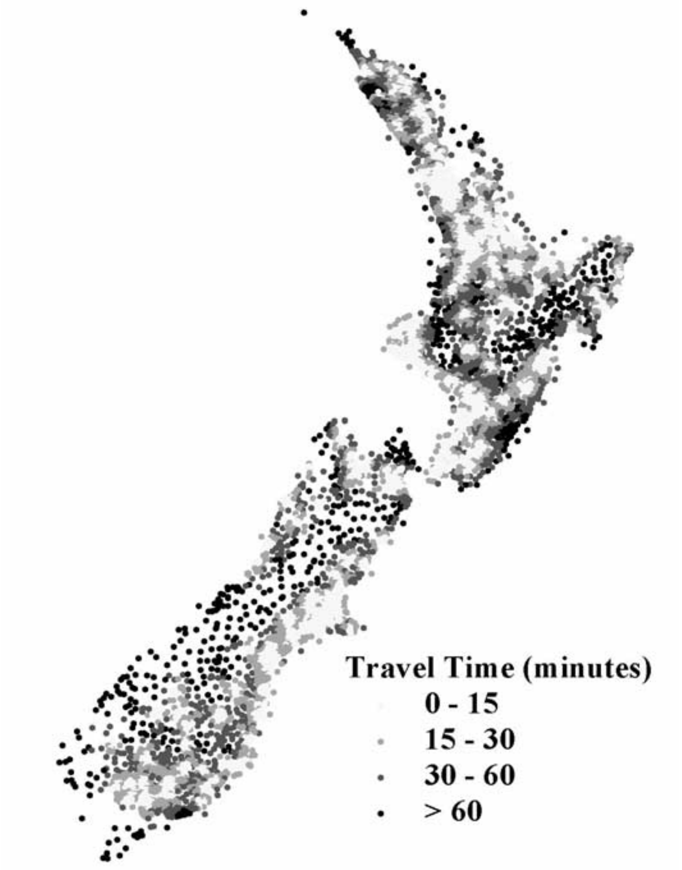
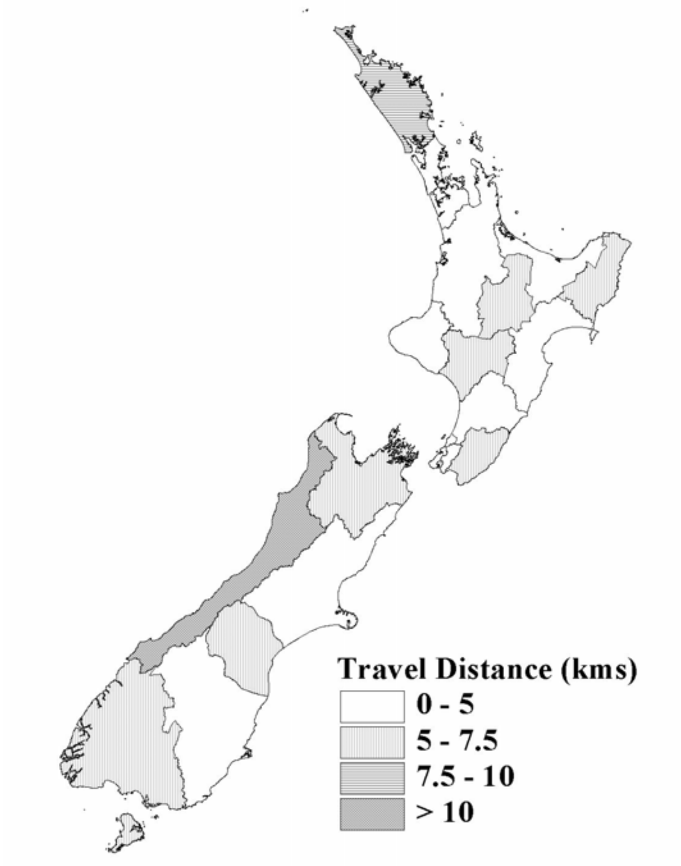


Table 1 shows the average meshblock travel distances and times for each DHB. A more meaningful representation of this data would be to also consider the spatial distribution of the population, because there are many areas in New Zealand that have low population densities. Population census data is aggregated to meshblocks therefore it is easy to obtain the population for each meshblock and multiply these by the travel distance or travel time. These products can then be summed for each DHB, and Table 1 also shows these sums ("Total Population Distance" and "Total Population Time"). These totals can then be divided by the population of each DHB to provide the average population distance and the average population time. These averages are shown in Table 1 and illustrated in Figures 3 and 4.

Table 1: Summary of Travel Distance and Time by District Health Boards

District Health Board	Population (1996)	Population per GP	Average Meshblock Distance (kms)	Average Meshblock Time (minutes)	Total Population Distance (kms)	Total Population Time (hours)	Average Population Distance (kms)	Average Population Time (minutes)	Average Speed (kph)
Northland	136,515	1,128	11.97	14.6	1,304,604	26,688	9.56	11.7	49
Waitemata	394,059	1,327	2.28	3.3	861,514	21,011	2.19	3.2	41
Auckland	346,551	871	1.05	1.9	325,147	9,816	0.94	1.7	33
Counties Manukau	341,439	1,284	3.91	4.7	1,079,335	22,452	3.16	3.9	48
Waikato	312,744	1,298	7.73	9.2	1,541,797	31,760	4.93	6.1	49
Bay of Plenty	163,665	1,177	5.89	7.2	702,072	14,523	4.29	5.3	48
Lakes	95,103	1,235	7.75	8.9	498,354	10,080	5.24	6.4	49
Tairawhiti	45,999	1,353	12.16	14.6	324,410	6,378	7.05	8.3	51
Taranaki	106,917	1,353	5.89	6.7	409,013	8,162	3.83	4.6	50
Whanganui	67,593	1,379	8.37	10.3	375,902	7,769	5.56	6.9	48
MidCentral	157,911	1,436	7.71	8.5	733,205	14,125	4.64	5.4	52
Hawke's Bay	142,692	1,297	7.82	9.2	687,153	13,545	4.82	5.7	51
Wairarapa	38,508	1,540	8.09	9.3	214,893	4,283	5.58	6.7	50
Hutt	132,852	1,510	1.73	3.0	223,402	6,704	1.68	3.0	33
Capital and Coast	234,615	1,096	1.30	2.2	306,579	8,936	1.31	2.3	34
Nelson-Marlborough	116,721	1,216	10.36	12.5	657,428	13,319	5.63	6.8	49
West Coast	32,502	1,625	23.54	24.0	529,108	8,971	16.28	16.6	59
Canterbury	411,150	1,052	4.46	5.2	1,058,413	22,139	2.57	3.2	48
South Canterbury	54,255	1,466	15.36	16.0	400,904	7,447	7.39	8.2	54
Otago	173,058	1,055	7.43	8.8	763,177	15,860	4.41	5.5	48
Southland	111,351	1,428	13.37	16.3	808,825	16,114	7.26	8.7	50

Figure 3: Average distance to closest GP by District Health Board



The "Average Population Time" is the average amount of time spent travelling per person in each DHB if everybody visited the closest GP once. These statistics, based on the population distribution, provide a means of comparing accessibility of different regions throughout New Zealand. The average travel times appear to be very low, especially in some DHBs such as Auckland. It needs to be emphasized that these travel times only include actual driving time, not time required to get in the car and finding a car park near the GP. Most people in Auckland would require more time than 1.7 minutes to get to their closest GP because it takes time to load the car (especially if you have children), get the car out the garage, find a car park within the vicinity of the GP and walk into the GP's medical centre. These extra activities could conservatively add 10 minutes to a journey.

Figure 4: Average time to closest GP by District Health Board

The raw output data can be tabulated to localised scales that show variation within a DHB. Figure 5 shows the average population travel times by New Zealand's Territorial Local Authorities (TLA). This map uses the same class intervals and shading as Figure 4, which is based on the DHB scale, but looks totally different. The MacKenzie TLA and the Westland TLA have Average Population Travel Times of 46 and 34 minutes respectively. Most DHBs contain large cities where Average Population Travel Time is low, and this reduces the Average Population Travel Times of the whole DHB even though parts of the DHB may have high Average Population Travel Times.

Figure 5: Average time to closest GP by Territorial Local Authority

The raw output data produced from the least-cost analysis can be applied in many different ways when combined with population data to produce many interesting maps and statistics. However, it is not appropriate to present many maps in this chapter. The main intention of this chapter is to describe the process used to create the base results, rather than demonstrate applications. It is possible to compare the accessibility of elderly people or different ethnic groups. It can be safely assumed that elderly people need to visit GPs more frequently than other age groups. When calculating total travel times, it is possible to put extra weighting on elderly people. Using such weightings and statistics, it would be possible to examine and display aspects of social equity in provision of GP services.

The analysis process not only calculated the distance and time to the closest GP, but also identified the name of the closest GP based on both distance and time (sometimes these were different). The number of visits each GP would receive if everybody visited the closest GP once can be easily tabulated and a catchment area for each GP can also be mapped. The average travel speed per GP visit can also be calculated and Table 1 shows the average travel speed by DHB.

DISCUSSION AND CONCLUSION

GIS accessibility models based on least cost path analysis are a critical resource that can be used by health service planners to prioritise the location and allocation of health services. These models are fairly straightforward, and new health services can be added and the models reprocessed quickly on a desktop computer, even for large data sets.

The example of a GIS accessibility model described and demonstrated in this chapter does not take into consideration all factors relevant to assessing access to GP services. Firstly, it only considers physical accessibility and does not provide insight into financial, cultural or functional barriers. Even just considering physical accessibility, the example does not include consideration of the availability and cost of public transport. This can be important because not everyone is able to use a private car. The travel times associated with roads, although based on least cost path analysis, also included assumptions about travel speed that are only estimations. Further empirical research is required to improve information on road travel speeds in New Zealand. Nevertheless, this GIS accessibility model does provide decision support and a relatively consistent method.

When one is developing GIS processes using relatively large data sets and many operations, careful consideration needs to be given to the possibility of error. Logical errors associated with the process and inaccurate data sets can have major effects on the results, and considerable caution and cross-checking is required. With powerful computer analysis that is often conducted by one individual, it is imperative that studies be repeated and validated by independent researchers.

The least cost path algorithm used in this analysis was based on an algorithm developed several decades ago, but what has changed is the availability of large national spatial databases and computer processing power. The example described in this chapter has demonstrated that it is now practical to compute accessibility over large networks using thousands of demand points and thousands of supply points. This research has raised the awareness of many public servants of what can be done with GIS, and many are now thinking of other services that should be analysed for accessibility using this approach. Examples from within the health sector alone can be identified as hospitals, mental health centres, eye specialists, ontologists and maternity services. Health planners are now starting to think of the importance of maintaining geographical databases relating to such services.

ACKNOWLEDGMENTS

We would like to thank Dr. Chris Skelly and Ron King, from Public Health Intelligence, Ministry of Health for their help in supplying GP locations and assisting in reviewing the analysis results.

REFERENCES

Barnett, J.R. (1978). Race and physician location: Trends in two New Zealand urban areas. *New Zealand Geographer, 34*, 2–12.

Coster, G. & Gribben, B. (1999). *Primary Care Models for Delivering Population Based Health Outcomes.* Wellington: National Health Committee.

Critchlow Associates. (1995). *Access to Healthcare and Disability Support Services—Time, Distance, Cost Report.* Unpublished paper.

Critchlow Associates. (1996). *Accessibility of Health and Disability Support Services.* Unpublished paper.

Dijkstra, E. W. (1959). A note on two problems in connexion [sic] with graphs. *Numeriske Mathematik, 1.*

Environmental Systems Research Institute. (1992). *Network Analysis ARC/INFO User's Guide 6.1.* ESRI Press.

Fotheringham & O'Kelly. (1989). *Spatial Interaction Models: Formulations and Applications.* Kluwer Academic Publishers.

Haggett, P.& Chorley, R. (1969). *Network Analysis in Geography.* London: Edward Arnold.

Haynes, R., Bentham, G., Lovett, A., & Gale, S. (1999). Effects of distance to hospitals and GP surgery on hospital inpatient episodes, controlling for needs and provision. *Social Science and Medicine, 49,* 425–433.

Hulka, B.S. (1978). Epidemiologic applications to health services research. *Journal of Community Health, 4(2).*

Ingram, D.R. (1971). The concept of accessibility: A search for an operational form. *Regional Studies, 5(2),* 101-107.

Joseph, A.E.,& Phillips D.R. (1984). *Accessibility and Utilization-Geographical Perspectives on Health Care Delivery.* New York: Harper and Row.

Kohli, K., Sahlen, K., Silvertun, A., Lofman, O., Trell, E. & Wigertz, O. (1995). Distance from the primary health center: A GIS method to study geographical access to healthcare. *Journal of Medical Systems, 19(6),* 425–436.

Lovett, A., Haynes R., Sunnenburg, G. & Gale, S. (2000). *Accessibility of Primary Healthcare Services in East Anglia.* Norwich: School of Health Policy and Practice, University of East Anglia.

Malcolm, L. & Clayton, C. (1988). Recent rends in the availability, distribution, utilisation and cost of general practitioner services. *New Zealand Medical Journal,* (December), 818–821.

Malcolm, L.A., Higgins, C.S. & Barnett, J.R. (1980). The availability, distribution and utilisation of general practitioners in New Zealand. A study based on GMS claims. *New Zealand Medical Journal,* (28 May), 396–399.

Moore, E.F. (1958). The shortest path through a maze. *Annals of the Computation Laboratory of Harvard University, 30.* Harvard.

Moseley, M.J. (1979). *Accessibility: The Rural Challenge,* London: Methuen & Co. Ltd.

Perry, B. & Gesler, W. (2000). Physical access to primary healthcare in Andean Boliva. *Social Science and Medicine, 50,* 1177–1188.

Pollack, M. & Wiebenson, W. (1960). Solutions of the shortest-route problem: a review. *Operations Research, 8,* 224–230.

Rapaport, H. & Abramson, P. (1959). An analogue computer for finding an optimum route through a communications network. Institute of Radio Engineers. *Transactions on Communication Systems, CS-7,* 37–42.

Roos, N.P., Gaumont, M. & Horne, J.M. (1976). The impact of the physician surplus on the distribution of physicians across Canada. *Canadian Public Policy, 2,* 169–191.

Shannon, G.W, Skinner, J.L. & Bashshur R.L. (1973). Time and Distance: The journey for medical care. *International Journal of Health Services, 3(2),* 237–244.

Spaulding, W.B. & Spitzer, W.O. (1972). Implications of medical manpower trends in Ontario, 1961-1971. *Ontario Medical Review, 39,* 527–533.

Statistics New Zealand. (2001). *Glossary of Terms* [Online]. Avalable:http://www.stats.govt.nz [2001, August 13].

Stimson, R.J. (1981). The provision and use of general practitioner services in Adelaide, Australia: Application of tools of locational analysis and theories of provider and user spatial behaviour. *Social Science and Medicine, 15(D),* 27–44.

Thompson, S. (1998). *Today's Actions Tomorrow's Landscapes, Proceedings of the 25th Anniversary Conference of the New Zealand Institute of Landscape Architects.* Wellington, New Zealand.

Twigg, L. (1990). Health based geographical information systems: Their potential examined in the light of existing data sources. *Social Science and Medicine, 30(1),* 143–155.

WHO/UNICEF. (1978). *Primary Health Care-Report of International Conference at Alma Ata,* Geneva. World Health Organisation.

Wilkinson, P., Grundy, C., Landon, M. & Stevenson, S. (1998). GIS in Public Health. In Gatrell & Loytoren, M. (Eds.), *GIS and Health.* London: Taylor and Francis Ltd.

Zhan, F.B. (1996). A set of shortest path algorithms that run fastest on real road networks. *Proceedings GIS/LIS 96.* Falls Church, VA: ACSM/ASPRS. 755–764.

Zwarenstein, M., Kringe, D. and Wolff, B. (1991). The use of a geographical information system for hospital catchment area research in Natal / Kwazulu. *South African Medical Journal, 80,* 467–500.

About the Authors

Omar A. Khan has a keen interest in the field of health and GIS, and has served as Co-Chair of the First and Second International Health Geographics Conferences. His academic background includes training in conservation biology, public health and medicine. His interests include healthcare for the under-served and an active research interest in international health. Omar has a faculty appointment at the Johns Hopkins University School of Public Health. He served as the first Director of the South Asia Infectious Disease Network (SAIDNET) and presently works with the South Asia Public Health Forum as well. He has served as a consultant for the US Department of Health and Human Services, as well as international disease control programs such as the AIDS International Training & Research Program (AITRP), through the University of Alabama School of Public Health. Omar has an active applied research collaboration with colleagues in South Asia on issues of HIV/AIDS epidemiology, prevention and control. He serves on the editorial board of the *International Journal of Health Geographics*, as a referee for the *Journal of Epidemiology & Community Health* and *AIDS*, and on the Publications Board of the American Public Health Association. He has served as an Honorary Adviser to the Indian Council for Medical Research and is a member of the Board of Directors of The Naz Foundation USA. He is active in a variety of public health and medical societies.

* * *

Mohammad N. Akhter, MD, MPH (pronounced “actor”) is Executive Director of the American Public Health Association, the oldest and largest organization of public health professionals in the world. Prior to joining APHA, Dr. Akhter was a Senior Advisor at the U.S. Department of Health and Human Services. Dr. Akhter is a physician with board certification in preventive medicine and is a Clinical Professor in the Department of Family and Community Medicine at Georgetown University Medical School in Washington, DC. and also an Adjunct Professor of international public health at the George Washington University School of Public

Health and Health Services. Dr. Akhter has served in many public health leadership positions, including the Director of the Missouri State Department of Health and as Health Commissioner in the nation's capitol. Under his leadership, APHA has developed strategic priorities, expanded its continuing education programs and adopted global health as an integral part of its mission. He has also broadened public awareness of public health issues through media coverage, enhanced the collaboration between medicine and public health, and expanded APHA's links with other organizations in the public and private sector. He is now actively expanding the association's scientific base, strengthening the affiliates and enhancing its advocacy role to protect the health of the American people in the 21st century.

Mohammad Ali is Scientific Systems Analyst at the International Vaccine Institute (IVI) in Seoul, Korea, where he conducts geographic research for vaccine-related studies. Before joining the IVI, he worked as the Head of the Geographic Information Systems Unit at the International Centre for Diarrhoeal Disease Research, Bangladesh. He has published many medical geography papers on cholera, other diarrheal diseases, acute lower respiratory infection and family planning. Dr. Ali received his PhD in the Department of Geomatics at the University of Liege in Belgium.

Christine Ashley, MA, is a PhD student of the University of Minnesota, USA. She is interested in geographical studies on health.

Lars Brabyn is a GIS lecturer at Waikato University, New Zealand. He has been collaborating with the Ministry of Health and the local District Health Board on a number of Health GIS projects. Besides researching health accessibility analysis techniques, he has been investigating methods for representing and mapping disease occurrences. He completed his PhD in 1996 at Canterbury University, which was on automated landscape classification.

Scott Carlin is an Associate Professor of the Environmental Studies at Southampton College, Long Island University, and Co-Director of the Institute for Sustainable Development at Long Island University. The Institute conducts research and education projects related to community and environmental sustainability on Long Island. Dr. Carlin works with regional breast cancer organizations to explore how to most effectively use GIS technologies to map and explain spatial patterns of breast cancer. Dr. Carlin received his PhD in Geography from Clark University in 1995.

Andrew Curtis, PhD is an Assistant Professor in the Department of Geography and Anthropology, Louisiana State University. Dr. Curtis teaches classes in GIS, Spatial Statistics and Medical Geography. His primary research involves identifying patterns of infant risk in Baton Rouge. Other research projects include using GIS to analyze patterns of rabies, lyme disease and encephalitis. Dr. Curtis has also been using GIS and spatial statistics to model and animate epidemic disease patterns from the 1800s.

George Davis is currently Professor of Microbiology and Tropical Medicine at George Washington University Medical Center. He is concurrently Editor-in-Chief of *Malacologia, the International Journal of Malacology*. He is currently Co-P.D. for an NIH funded Tropical Medical Research Center located in Shanghai, China. His research focuses on the evolution and coevolution of snail-borne diseases with emphasis on schistosomiasis in Asia. His work involves molecular genetics, biogeography and epidemiology.

Michael Emch is an Assistant Professor in the Department of Geography at Portland State University. He specializes in health and environmental applications of geographic information systems and satellite remote sensing. He has conducted research at the International Centre for Diarrheal Disease Research, Bangladesh, and has published many papers on the spatial aspects of cholera and other diarrheal diseases. Other medical geographic studies that he has conducted have been on visceral leishmaniasis, acute lower respiratory infection and vaccine methods.

M. E. Folkoff is a Professor in the Department of Geography and Geosciences, and an Adjunct Professor of Environmental Health Science at Salisbury University (SU). He has a BA from SUNY New Paltz, an MA from the University of Albany, New York, and a PhD from the University of Georgia. His research centers on soil, hydrology, geomorphology and cartographic applications.

Mark Frana is a Professor in the Department of Biological Sciences at Salisbury University. Dr. Frana joined the faculty of SU in 1988 and holds a BS degree in Microbiology from the University of Iowa and a PhD in Microbiology from the University of Kansas. His current research interests involve the use of molecular biological techniques for the detection of microorganisms.

Peng Gong is currently a Professor in the Department of Environmental Science, Policy & Management at the University of California at Berkeley, where he teaches courses in Photogrammetry and Remote Sensing, Introduction to GIS and Mapping, Advanced Remote Sensing of Natural Resources and Advanced GIS for Natural Resources Studies. Dr. Gong is Co-Director of the Center for the Assessment and Monitoring of Forest and Environmental Resources at the University of California, Berkeley. His research interests include Photo Ecometrics, Hyperspectral Data Analysis, Global Change Modeling and GIS Data Uncertainty Determination, Representation and Modeling.

Dennis M. Gorman is an Associate Profession in the Department of Epidemiology at The Texas A&M University Health Science Center School of Rural Public Health. He received his PhD from the University of Essex in Great Britain in 1988. In addition to his interest in the spatial dynamics of alcohol availability and violent crime, he also conducts research into alcohol and drug prevention policy and programs. He is especially interested in the roles that schools play in drug prevention, and has published a number of papers on this topic in addiction, public health and policy journals and books.

Paul Gower is a Masters Scholar at Waikato University interested in the application of GIS to social justice issues. He is currently analyzing the social impact of the first casino in Hamilton, and is a member of the Salvation Army.

Paul J. Gruenewald, PhD, is a Senior Research Scientist and Associate Director at the Prevention Research Center (PRC) of the Pacific Institute for Research and Evaluation and is the Director of the Spatial Systems Group at PRC. Dr. Gruenewald's research focuses upon: (1) ecological models of the availability and use of alcohol, (2) geostatistical models of the geographic distribution of alcohol problems, and (3) mathematical models of alcohol use and related risks. Within these areas he has participated in (1) formative studies demonstrating the impacts of alcohol availability upon alcohol use, choices of drinking venues and related risks, (2) the development and application of geostatistical techniques to the study of the geography of alcohol problems in community settings; and (3) the development and application of Stochastic Drinking Theory to the measurement of drinking patterns and problems.

Xueguang Gu is currently a Professor in the Department of Schistosomiasis at the Sichuan Institute of Parasitic Diseases in Sichuan, China. He is also Director of the Department of Schistosomiasis at the Institute, Director of the Training and Research Center on Schistosomiasis in Mountainous Regions, and serves as the Chair of the Sichuan Expert Committee on Schistosomiasis.

Daikwon Han is a graduate student in the Department of Geography, SUNY at Buffalo, and a Research Assistant at the National Center for Geographic Information and Analysis. His research interests are in spatial analysis and GIS, especially in the applications of GIS in the studies of environmental health. He is currently working on a PhD on evaluating the role of human mobility on disease clustering.

Cathleen A. Hanlon, VMD, PHD, is currently a Veterinary Medical Officer in the Rabies Section at the Centers for Disease Control and Prevention. Dr. Hanlon joined the Rabies Unit of the Wistar Institute in 1985 and engaged in basic and applied research on rabies. From 1994 through 1996, she was Deputy and Acting State Public Health Veterinarian for the New York State Department of Health, with a primary focus on rabies prevention in humans and domestic animals, and initiating oral rabies vaccination of free-ranging raccoons in New York. In her current position she specializes in rabies epidemiology, pathogenesis and prevention, through the use of genetically engineered vaccines and development of alternatives for rabies immune globulin.

M. Zahirul Haq, MSc, is the GIS Database Manager of the ICDDR,B (Centre for Health and Population Research), Dhaka, Bangladesh.

Daniel W. Harris has been a Lecturer in the Department of Geography and Geosciences at Salisbury University, in Salisbury, Maryland, since 1996. He completed his Bachelor of Arts degree in Geography at the University of North Carolina—Chapel Hill in 1991 and received his Master of Arts degree from Appalachian State University in Boone, North Carolina, in 1996. His research interests include remote sensing, geographic information science, applied climatology, and hydrology.

Xurxo Hervada-Vidal has an MD in medicine from the University of Santiago de Compostela, Spain; a general degree in public health from the National School of Public Health; and a combined course in Medical Statistics and Epidemiology from the London School of Hygiene and Tropical Medicine. At the present time he is the head of the service of information about public health in the Public Health Department of the regional autonomous government of Galicia, in Santiago de Compostela. His research interests include epidemiological surveillance, information systems, mortality analysis and spatial disease mapping.

Michael Leitner, PhD is an Assistant Professor in the Department of Geography and Anthropology, Louisiana State University. His main research interests are in the visualization of data quality and its impact on spatial decision support, and in the science and application of GIS and Spatial Analysis for geo-marketing and the spatial analysis of crime. Dr. Leitner teaches classes in computer cartography, spatial statistics and GIS.

Ge Lin is an Assistant Professor at the Department of Geology and Geography, West Virginia University. He obtained his PhD from the State University of New York at Buffalo, specialized in GIS applications, population geography, medical geography, demography and spatial statistics. His research interests include developing novel methods and approaches for various geographic problems. He has several research grants, most recently from NIH, and the Bureau of the Census.

Robert Lipton, PhD, is an Associate Research Scientist at the Prevention Research Center of the Pacific Institute for Research and Evaluation. He is an Epidemiologist with interests in the areas of substance use and abuse, and associated health and social problems. He has developed research in the area of the spatial relationships between violence and alcohol outlets. Dr. Lipton is a Research Associate to the Spatial Systems Group and supports studies in geographic epidemiology.

Mária Esther López-Vizcaíno has a Master of Science in statistics and a Bachelor of Science in Mathematics from the University of Santiago de Compostela, Spain. She also attended PhD courses in spatial statistics. At present, she is working in the Galician Statistical Institute of the Regional Autonomous Government of Galicia, in Santiago de Compostela. Her research interests include statistical applications in economics and regional analysis, spatial disease mapping and Bayes methods for mortality analysis.

Wei Luo is an Assistant Professor in the Department of Geography at Northern Illinois University. His research interests include physical geography, hydrology, computer simulation geomorphic and hydrologic processes, and applying GIS to a variety of areas, including healthcare and linguistic geography. He has published articles in *Geographic Information Sciences*, *Computers and Geosciences*, *Journal of Geophysical Research* and other journals.

Jane McCall holds a master's degree in Public Health in Epidemiology and a Certificate in Geographic Information Systems. She is a Research Biostatistician and Spatial Epidemiologist at Baystate Medical Center, in Springfield, Massachusetts. Her current focus is on GIS applications in healthcare, particularly the use of census data to investigate the relationship of social and demographic factors and health. In addition to GIS, her previous work encompasses extensive research in cancer, cardiovascular and trauma epidemiology; nosocomial infection surveillance methodology and resident education. Ms.McCall has published over 50 references in the medical literature (primarily under Jane L. Garb), including a book entitled: *Understanding Medical Research: A Practitioner's Guide*.

Karl J. McCleary, PhD, MPH, is a member of the faculty in the Department of Health Policy and Administration at The Pennsylvania State University, University Park Campus. Before joining Penn State, he was on the faculties of Loma Linda University School of Public Health, and the University of Missouri-Columbia. He received his Master's of Public Health (MPH) in Health Policy and Management from Emory University and a Doctor of Philosophy (PhD) in Health Services and Organizational Behavior from the University of Alabama at Birmingham. His research interests include interdisciplinary teams and care management systems, organ procurement and transplantation effectiveness, and organizational change.

Susanne Montgomery, PhD, MPH, is a member of the faculty at the School of Public Health and the Department of Preventive Medicine at Loma Linda University. She received her graduate training in Germany in Nutritional Science and from the University of Michigan in Public Health. She has many years experience in funded and non-funded community based research, and she is and has been the PI or a CO-PI of several National Institute on Drug Abuse (NIDA) funded projects. These range from designing and evaluating school- and community-based alcohol, tobacco or drug (ATOD) abuse prevention projects, to trying to better understand the needs of homeless runaway and drug injecting youth and young adults. She is also a COI on an NIH-funded study of lifestyle and cancer among Seventh Day Adventists. While she is committed to conducting rigorous research studies, she is cognizant and sensitive to the need for the translation of research findings to a community level and therefore is a member of a number of local and area community coalitions, planning groups and advisory groups. As a member of these groups, she uses her expertise and access to data to enhance the planning processes and decision making regarding future directions. She teaches research and evaluation methods classes as well as a violence class on the graduate level, and publishes on a national level in peer-reviewed publications about her work.

Gregory Pappas is current Deputy Director for Health of ORC Macro that conducts the Demographic and Health Surveys. These national population-based surveys have been conducted in over 70 developing nations and serve as the basic health information for many nations. Dr. Pappas is involved in developmental activities with the DHS, including expanding capacity to monitor the HIV/AIDS epidemic, adult health and the use of biomarkers in surveys. Previously Dr. Pappas was Senior Policy Advisor to Surgeon General David Satcher in the Department of Health and Human Services. Dr. Pappas worked in a number of areas including disparities in health and global health (HIV/AIDS, other infectious diseases and health information systems development). Dr. Pappas has directed the Office of International and Refugee Health, Department of Health and Human Services. Dr. Pappas received his MD and PhD (Anthropology) from Case Western Reserve in Cleveland, Ohio. After doing his clinical training, he came to Washington DC, first in a fellowship in Epidemiology, then continuing as a scientist at the National Center for Health Statistics/CDC. Dr. Pappas is author of numerous articles, including his work in the *New England Journal of Medicine* on the increasing disparity in mortality between socioeconomic groups in the United States and his book with Cornell, *The Magic City: Unemployment in a Working Class Community*. Most recently he has published a book with the government of Pakistan, *A Health Profile of the Pakistani People* which is based on a national health examination survey of 18,000 people. Dr. Pappas is on the faculty of the Johns Hopkins School of Hygiene and Public Health in the Department of Health Policy and Management. Dr. Pappas is Chair of the Science Board of the American Public Health Association and a Member of the Executive Board of APHA.

Amy Pasini is the Manager of GIS and Injury Prevention in the Department of Surgery at Baystate Health System. She has worked for the past five years to implement the GIS program at Baystate Medical Center. She is the City of Springfield's Violence Prevention Co-Chairperson and worked with the Office of the Vice President's national "SafeCities" partnership. Her work has focused on surveillance and injury control in violence, and traumatic injuries utilizing GIS. She holds a BS from Springfield College and is completing her Master's in Public Administration.

Dongchuan Qiu is currently a Professor of the Sichuan Institute of Parasitic Diseases in Sichuan, China. He is also Deputy Director of the Institute and Head of the Department of Schistosomiasis.

Patrick A. Rivers, PhD, MBA, is a member of the faculty at the College of Business at Arizona State University and at the Arizona Graduate Program in Public Health, University of Arizona Health Sciences Center. Before joining Arizona State University, he was an Agency for Health Care Research and Quality (formerly AHCPR) Postdoctoral Fellow in the UCLA Department of Health Services in the School of Public Health in Los Angeles, California, and RAND Corporation in Santa Monica, California. He received his Master's of Business Administration

(MBA) in Finance, Investment and Banking from the University of Wisconsin-Madison and Doctor of Philosophy (PhD) in Health Services and Strategic Management from the University of Alabama at Birmingham. His research interests include healthcare financing, total quality management, access to medical care for working poor, hospital competition, quality of care, medical errors and patient safety managed care systems, top management teams and hospital performance. Dr. Rivers is a Faculty Associate of the American College of Healthcare Executives. He is a member of Association of Health Services Research and the Academy of Management (Health Care Administration Division).

Peter A. Rogerson is Professor of Geography at the University at Buffalo, State University of New York. He is also a member of the National Center for Geographic Information and Analysis. His interests are in the areas of spatial analysis and spatial statistics. His recent research has focused upon the development of methods for the detection of geographic clustering in spatial data, and on the development of surveillance methods for detecting change in geographic patterns over time. He is also the author of *Statistical Methods for Geography*, by Sage Publications.

Mária Isolina Santiago-Pérez has a Master's of Science in Statistics and a Bachelor of Science in Mathematics from the University of Santiago de Compostela, Spain. At present time she is working in the Public Health Department of the Regional Autonomous Government of Galicia, in Santiago de Compostela. Her research interests include software for epidemiological analyses, statistical applications in mortality analysis, spatial disease mapping and Bayes methods for such projects.

Michael Scott is an Assistant Professor of Geography and Geosciences at Salisbury University. He first received his Bachelor of Science degree in Geography at Salisbury University. He then attained his master's and PhD in Geography from the University of South Carolina, specializing in geographic information science and environmental hazards.

Edmund Y. W. Seto is currently a Researcher in the School of Public Health at the University of California at Berkeley. His research interests stem from his dissertation work on schistosomiasis transmission in China, and include the temporal dynamics and geographic patterns of disease occurrence and transmission. Specifically these interests encompass the use of mathematical modeling, geographic information systems, global positioning systems and remote sensing to understand spatio-temporal aspects of disease.

Ric Skinner is the Senior GIS Coordinator in the Geographic Information System Program in the Department of Surgery at Baystate Medical Center, Springfield, Massachusetts, USA. Ric provides overall coordination of GIS activities at BMC and with BMC's community, state and national partners, as well as supports GIS Program staff, in the application of GIS to healthcare. Ric has over 30 years of professional experience: 12 years in the utilization of GIS in healthcare and environmental areas, and over 20 years pursuing research in environmental management and assessment. Prior to BMC, he was a Research Scientist in the New Jersey Department of Health and Senior Services providing GIS support on epidemiology studies, specifically in cancer control and prevention. He was also the department's GIS Coordinator and Representative to the Interagency GIS Team. In the mid-1990s, Ric was an independent consultant providing GIS services to several hospitals in eastern Pennsylvania and a major healthcare information provider in Virginia. The majority of his professional career was spent in environmental monitoring and surveillance for electric power companies in Michigan and Pennsylvania. During this time he also designed, constructed and operated three aquatic bioassay laboratories. Ric initiated and co-chaired the First International Health Geographics Conference in 1998 in Baltimore, MD, and co-chaired the Second International Health Geographics Conference in 2000 in Washington, DC. He is on the Editorial Board of the *International Journal of Health Geographics*. He has authored or co-authored over 100 publications, reports and presentations on such topics as GIS, health geographics, and environmental management and assessment.

Sam Soret, PhD, MS is member of the faculty at Loma Linda University School of Public Health, Department of Environmental Health, where he is also Program Coordinator of the Health Geographics BSPH, and Director of the Health GIS Laboratory. Before joining Loma Linda University, he was a Post-Doctoral Fellow at the GIS Laboratory and at the Statewide Air Pollution Research Center, University of California, Riverside. Dr. Soret is a specialist in the application of GIS and spatial analysis to health issues, frequently offering GIS expertise to campus, local, state and national groups and agencies. He is currently involved in several GIS research projects on disease pattern analysis in California and healthcare geographics.

Robert C. Spear is currently a Professor of Environmental Health Sciences in the School of Public Health at the University of California at Berkeley. Dr. Spear is the Founding Director of the University's Center for Occupational and Environmental Health and has served as Associate Dean of the School of Public Health and of the College of Engineering at Berkeley. His research interests focus on the assessment and quantification of human exposures to toxic and hazardous agents in the environment, principally the occupational environment. His early work concerned the exposure of agricultural workers to pesticides. More recently, his research has taken a more theoretical turn, and he is currently working on the use of mathematical and statistical techniques in the assessment and control of exposures to both chemical and biological agents.

Peter Kim Streatfield, PhD is the Head of the Health and Demographic Surveillance Programme of the ICDDR,B (Centre for Health and Population Research), Dhaka, Bangladesh.

Enrique Vázquez-Fernández has an MD and a PhD in Medicine from the University of Santiago de Compostela, Spain, and a MPH from the University of Antioquia, Colombia. He was working in the Public Health Department of the Regional Autonomous Government of Galicia, Spain. His activities were focused on information systems, mortality analysis and epidemiological methods. At present time he has joined the Pan American Health Organization as Epidemiologist in Buenos Aires, Argentina.

Elichia A. Venso is an Associate Professor and Director of the Environmental Health Science Program at Salisbury University. She came to the university in 1993 after receiving a doctorate in Environmental Sciences from the University of Texas School of Public Health in Houston, Texas. Prior to returning to UT to pursue advanced degrees, she was a Petroleum Geologist for Getty Oil Company and Texaco, Inc. Dr. Venso's research interests center on exposure assessment of and measurement methods for environmental contaminants, particularly those found in ground and surface waters.

Carmen Lucía Vidal-Rodeiro has a Master of Science in Statistics and a Bachelor of Science in Mathematics from the University of Santiago de Compostela, Spain. She was working in the Public Health Department of the Regional Autonomous Government of Galicia, in Santiago de Compostela. At the present time she is submitting a PhD in Statistics supported by a National Institutes of Health (USA) grant in the Department of Mathematical Sciences of the University of Aberdeen, UK. Her research interests include measurement error models, statistical applications in mortality analysis, information systems, spatial disease mapping and Bayes methods for such projects.

Richard Wait is currently Chairman of Surgery at Baystate Medical Center in Springfield, Massachusetts, and Clinical Professor of Surgery at Tuft's University School of Medicine in Boston. He maintains a practice in surgical oncology and a career-long interest in basic science research which includes several national grants and numerous academic honors. A strong advocate for new technologies in medical education, he helped establish the GIS program at Baystate. His current clinical research centers on breast cancer in minority populations and the use of GIS in injury prevention and cancer screening. A member of numerous medical and scientific societies, he has authored more than 70 articles in scientific journals, and serves as editorial reviewer for several.

Fahui Wang is an Assistant Professor in the Department of Geography at Northern Illinois University. His research interests include transportation and urban geography, GIS applications, and spatial statistics in crime and healthcare analyses. He has published articles in *Environment and Planning A & B*, *Papers in Regional Science*, *Professional Geographer*, *Regional Science and Urban Economics*, *Socioeconomic Planning Sciences*, *Urban Studies* and other journals.

Seth Wiafe is a Health Geographics major in the BSPH Program at Loma Linda University School of Public Health (LLUSPH), California. He is also a Research Assistant at LLUSPH GIS Laboratory. A native of Ghana, Mr. Wiafe earned diplomas in Medical Technology from Malamulo College of Medical Sciences (1991), Malawi; and in Health Education from Kenya College of Communication Technology (1998). Until 1999, he served in various positions as Clinical Instructor of the Biochemistry Department, Malamulo College of Medical Sciences; Director of Clinical & School of Laboratory Technology, Gimbie Adventist Hospital, Ethiopia; and Public Health Educator at West Wollega Oromia Health Bureau, Ethiopia.

William F. Wieczorek is the Director of the Center for Health and Social Research and Professor of Geography and Planning at Buffalo State College. In addition to the spatial analysis of alcohol and drug-related topics, his research interests include drinking and delinquency, drinking and driving, substance use and health, gambling and substance use, and the evaluation of educational improvement initiatives. His awards from the National Institute on Alcohol Abuse and Alcoholism include a First Independent Research and Transition (FIRST) Award, an Independent Scientist Award and several research project grants. Also involved in international research, he is Visiting Professor and Co-Director (with President Jiang Chao) of the Dalian Medical University-Buffalo State College Institute of Behavioral Medicine at Dalian Medical University in the People's Republic of China.

Evan R. Wolarsky served as Vice-President of Medical Affairs at Hunterdon Medical Center from 1991-1999. During that time, he developed an interest in using publicly available claims data to study patterns of hospital utilization in the hospital's market area. Dr. Wolarsky received his undergraduate education at Harvard College, an MD at the University of Pennsylvania and an MBA at The Wharton School. He is currently a healthcare consultant.

Weiping Wu is Associate Professor at the Institute of Parasitic Diseases, Chinese Academy of Preventive Medicine. His research interests are in the application of Remote Sensing and GIS in schistosomiasis surveillance and control, epidemiology of schistosomiasis and health economics evaluation of parasitic diseases.

Bing Xu is currently a doctoral student in the Department of Environmental Science, Policy & Management at the University of California at Berkeley. Her research interests include remote sensing image processing, analysis and application, and GIS theory, techniques and application. Bing Xu's PhD research is on the use of remote sensing and GIS for schistosomiasis control in Sichuan, China.

Index

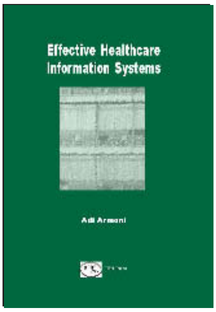
New Books on Healthcare Information Systems

Effective Healthcare Information Systems

Adi Armoni, Ph.D., Tel Aviv University, Israel

Health and medical informatics encompass a very broad field that is rapidly developing in both its research and operational aspects. The discipline has many dimensions, including social, legal, ethical and economic. This book, ***Effective Healthcare Information Systems*** puts a special emphasis on issues dealing with the most recent innovations such as telemedicine, Web-based medical information and consulting systems, expert systems and artificial intelligence.

ISBN: 1-931777-01-2; eISBN: 1-931777-20-9; Copyright: 2002
Pages: 295 (s/c); Price: US $59.95

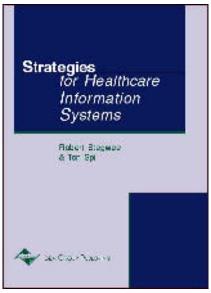


Strategies for Healthcare Information Systems

Robert Stegwee, Ph.D., University of Twente, The Netherlands
Ton Spil, University of Twente, The Netherlands

Information technologies of the past two decades have created significant fundamental changes in the delivery of healthcare services by healthcare provider organizations. ***Strategies for Healthcare Information Systems*** provides an overall coverage of different aspects of healthcare information systems strategies and challenges facing these organizations.

ISBN: 1-878289-89-6; Copyright: 2001; Pages: 232 (s/c); Price: US $74.95

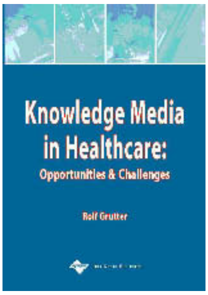


Knowledge Media in Healthcare: Opportunities and Challenges

Edited by Rolf Grutter, Ph.D., University of St. Gallen, Switzerland

Because the field of healthcare reflects forms of both explicit and tacit knowledge such as evidence-based knowledge, clinical guidelines and the physician's experience, knowledge media have significant potential in this area. ***Knowledge Media in Healthcare: Opportunities and Challenges*** is an innovative new book which strives to show the positive impact that Knowledge Media and communication technology can have on human communication within the field of healthcare.

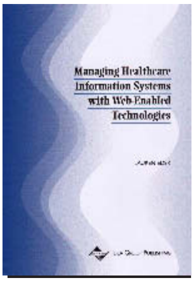
ISBN 1-930708-13-0; eISBN: 1-59140-006-6; Copyright: 2002; Pages: 296; Price: US$74.95



Excellent additions to your library–
Please recommend to your librarian.

Managing Healthcare Information Systems with Web-Enabled Technologies

Lauren Eder, Ph.D., Rider University, USA

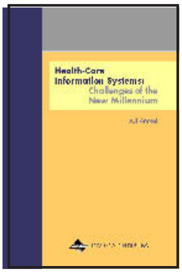


Healthcare organizations are undergoing major adjustments to meet the increasing demands of improved healthcare access and quality. ***Managing Healthcare Information Systems with Web-Enabled Technologies*** presents studies from leading researchers focusing on the current challenges, directions and opportunities associated with healthcare organizations and their strategic use of Web-enabled technologies.

ISBN: 1-878289-65-9 ; eISBN:1-930708-67-X; Copyright: 2000
Pages: 288 (s/c); Price: US $69.95

Healthcare Information Systems: Challenges of the New Millennium

Adi Armoni, Ph.D., Tel Aviv University, Israel



Healthcare information sysstems are crucial to the effective and efficient delivery of healthcare. ***Healthcare Information Systems: Challenges of the New Millennium*** reports on the implementation of medical information systems.

ISBN: 1-878289-62-4; eISBN: 1-930708-55-6; Copyright: 2000
Pages: 256 (s/c); Price: US $69.95

It's Easy to Order! Order online at www.idea-group.com

or call our toll-free hotline at 1-800-345-4332!
Mon-Fri 8:30 am-5:00 pm (est) or fax 24 hours a day 717/533-8661

Idea Group Inc.
Hershey • London • Melbourne • Singapore • Beijing