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Chapter 1 : Trends and Spatial Patterns of Suicide Among Adolescent in Ecuador, ~ Fulltext

We analysed nationwide temporal trends, spatial and spatiotemporal high-risk clusters of NTD-related mortality. We included all deaths in Brazil between and , in which NTDs were mentioned on death certificates, either as underlying or as associated causes of death (multiple causes of death).

Most mortality maps in South Africa and most countries of the sub-Saharan region are static, showing aggregated count data over years or at specific years. Lack of space and temporal dynamics in these maps may adversely impact on their use and application for vigorous public health policy decisions and interventions. This study aims at describing and modeling sub-national distributions of age- and gender-specific all-cause mortality and their temporal evolutions from 2000 to 2010 in South Africa. Mortality information that included year, age, gender, and municipality administrative division were obtained from Statistics South Africa for the period. Individual mortality level data were grouped by three age groups: 0-14, 15-64, and 65 and over and gender male, female and aggregated at each of the municipalities in the country. The six age-gender all-cause mortality rates may be related due to shared common social deprivation, health and demographic risk factors. We undertake a joint analysis of the spatial-temporal variation of the six age-gender mortality risks. This is done within a shared component spatial model construction where age-gender common and specific spatial and temporal trends are estimated using a hierarchical Bayesian spatial model. The results show municipal and temporal differentials in mortality risk profiles between age and gender groupings. High rates were seen in 2000, especially for the 15-64 years age group for both males and females. The dynamic geographical and time distributions of subnational age-gender all-cause mortality contribute to a better understanding of the temporal evolution and geographical variations in the relationship between demographic composition and burden of diseases in South Africa. This provides useful information for effective monitoring and evaluation of public health policies and programmes targeting mortality reduction across time and sub-populations in the country. Background High-quality mortality statistics are needed in optimal health planning, decision-making, program evaluation, progress monitoring, and resource allocation [1 , 2]. These data are often only reported at high national levels of geographic aggregation but not at lower administrative levels for local public health decision making. This is despite substantial evidence pointing to variations in mortality risks at subnational levels due to, for example, age, gender, and social economic differences [3 , 4]. Additionally, their use both at national and sub-national levels has been limited, as many atlases showing geographic distribution of mortality are stationary even though the data has been collected over many years [5 , 6 , 7]. This is despite the recent developments and applications of spatial-temporal methods for disease mapping in spatial epidemiologic studies, arising from the work of Clayton and Kador, Besag, York, and Mollie, and Knorr-Held and Best [8 , 9 , 10]. These models have been extended and applied to a variety of disease settings Richardson et al. Additionally, advances in computer systems, the availability of powerful geographical information systems GIS , and the implementation of many types of spatial models in specialized software have led to a greater uptake of small-area disease mapping. Most mortality atlases fail to properly utilize the basic elements of disease mapping models to account for both spatial and time dependence in mortality risks. Most atlases use age- and gender-adjusted rates or standardized mortality rates, which for small areas or rare causes of death such as cancer, may be unreliable and unstable Manda et al. Moreover, these mortality rate indicators may be invalid when applied to different strata in subnational areas. Burden of diseases and demographic and many factors related to the wellbeing of populations are dynamic and change over time [14]. Time effects on mortality should also account for the fact that adjacent periods may have similar rates. This is justified, as mortality rates in adjacent years are more likely to be similar since both mortality counts and population denominators would not have changed considerably. Similarly, mortality rates in adjacent areas could not be assumed to be independent of each other. For rare mortality events and sparse populations, sub-population mortality rates could be very unstable. These issues could be addressed

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effectively within a spatiotemporal modelling of mortality rates to permit an assessment of the evolution of mortality dependence on both space and time. Moreover, these models help to address the problem of missing and unmeasured ecological determinants of mortality [15 , 16]. In order to provide robust perspectives of mortality over a spectrum of relevant subgroups, disease mapping models for the rates should be approached from a time dynamic perspective and address specific gender and age categories [14 , 17 , 18]. The best way to describe trends in health indicators is to evaluate the outcomes of past health policies and to ascertain the current health status of the population so that future improvements may be undertaken [19]. Most age and gender all-cause mortality risks are analyzed independently, either descriptively [7] or using disease mapping models [14 , 16 , 20 , 21]. However, several cause-specific mortality risks from certain diseases are age- and gender-dependent, for example, infectious-related deaths are more prevalent among young adults and children, and mortality from non-communicable disease are higher in the elderly [22]. Thus, independent analyses of age and gender mortality risks would not capture common and uncommon risk factor relationships between a number of age-gender mortality rates [16]. It becomes necessary to isolate common and age-gender-specific geographical patterns of mortality in a single model, which can be achieved by using the recently developed multivariate disease mapping models for multiple disease outcomes [3 , 10 , 11 , 13 , 15 , 16 , 23]. These models will enable us to assess similarities as well as differences between geographical risk patterns among age-gender groups purportedly sharing common risk profiles. These common factors may be thought of as proxies for unobserved health determinants shared by the multiple age and gender mortality risks. In the context of populations with limited resources, these methods are appealing due to the limitations of the available factors and disease data over the years. Additionally, by combining data from different age and gender groups, improvement in precisions and efficiencies of estimates, especially for rare mortality groups and causes, are obtained. There has also been a rise in lifestyle-related factors for non-communicable diseases NCDs which now account for a large proportion of adult deaths in the region. We are not aware of any previous space and time dynamics analysis of mortality in South Africa based on the Mortality Statistics vital registration data, a very rich mortality data set spanning over a long period. It is within these contexts of scarcity of such research methods and applications that this paper aims to explore geographical and temporal structures for several age and gender mortality risks jointly. In order to uncover the possibilities of unobserved ecologically distributed health services, disease burden, environmental influences and demographic factors responsible for the observed inter age-gender mortality correlations in South Africa, a shared spatial-temporal model with common and specific components is employed. These hidden factors may be reflecting the prevailing and changing distributions of age and gender mortality burden associated with changing epidemiological and demographic transitions over space and time in South Africa. Statistical Models and Data Analyses To study spatial-temporal trends of age and gender specific all-cause mortality from to in South Africa, a hierarchical Bayesian shared component spatial-temporal model [10] was undertaken using the municipality as the spatial unit for analysis.

Infant mortality is an important indicator of population health in a country. It is associated with several health determinants, such as maternal health, access to high-quality health care, socioeconomic conditions, and public health policy and practices. A spatial-temporal analysis was performed to.

Oak decline has elevated cumulative mortality of red oak species to between 11 and 15 percent in terms of relative density and basal area of standing dead oak trees, respectively. These values are three to five times higher than for white oak group and non-oak species. Oak decline and associated escalating mortality have occurred primarily in red oak species while the white oak group has maintained a relatively stable mortality rate that is comparable to non-oak species. Cross-correlation analyses indicate that mortality in the red oak group was significantly correlated with the growing season Palmer drought severity index PDSI and usually lagged two to three years following single drought events. Moreover, based on the past 17 years PDSI data, it appears that the cumulative impacts of drought may last up to 10 years. The Ozark Highlands experienced a severe drought extending from to and another milder drought from to These drought events triggered the escalation of mortality starting around year In contrast, sites with elevated white oak and non-oak mortality occurred sporadically, mainly in the southern portion Arkansas of the Ozark Highlands. Introduction Since the s, the historical woodland-savanna-glade mosaic in the Ozark Highlands of northern Arkansas and southern Missouri has been gradually replaced by large contiguous blocks of high-density oak-hickory forests. This is the result of extensive fire suppression and widespread application of other management practices that have relatively little impact on the forest overstory. As upland oak-hickory forests in the region have matured, large-scale oak decline events have increased in extent and severity. Among oaks, the red oak group species *Quercus Section Lobatae* mainly including scarlet oak *Q.* Many trees eventually die if crown dieback continues. Oak decline and mortality in red oak species occurred throughout the s [4] and earlier [5] and is prevalent throughout the Ozarks Highlands as forests reach physiological maturity [6 , 7]. Analysis of recent FIA data showed that decline-caused annual oak mortality had exceeded two percent, on average, by , which is three to five times larger than regular competition-induced mortality. The observed higher mortality of red oak group species, to varying degrees, occurred in all diameter classes compared with the steeply decreasing reverse-J mortality pattern i. A year study conducted in southern Missouri found that improvement harvests did not mitigate oak decline [8]. High red oak group mortality and the unprecedented abundance of oak borer populations associated with oak decline pose significant threats to the health and management of forests in the Ozark Highlands. Oak decline occurs over an extended temporal scale and is associated with forest succession [9]. No single cause is responsible for the oak decline syndrome and escalating mortality. Rather, oak decline is an on-going process, resulting from the interaction of multiple factors over a set of temporal and spatial scales [4 , 10]. For instance, white oaks exhibiting moderate to severe crown dieback usually are less likely to recover compared to red oaks in a year monitoring study in the Missouri Ozarks [8]. Some argue that the attack of insects like red oak borers may degrade the quality of oak trees due to the tunnels they excavated but not cause tree mortality directly [13], and improvement harvests conducted in declining oak stands may have no effect on the decline process. A mechanistic study of oak decline and mortality is necessary to explore the relationship between risk factors and symptoms and to guide forest management to restore forest health or vigor. Oak decline and mortality are inherently multi-scale issues, because the predisposing factors, inciting factors and contributing factors may interact across a variety of spatial scales. From a forest management perspective, oak decline and mortality studies mainly focus on three interrelated spatial scales: This information will allow resource managers to preemptively remove at-risk trees during intermediate harvest treatments. At the stand level, knowledge of which stands are most susceptible to oak decline will allow at-risk stands to be ranked and prioritized for treatment [14]. At the landscape level, identification of the potential extent and condition of oak decline and mortalityâ€™particularly locating future oak decline hot

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spotsâ€™ is a top priority for resource assessment and forest planning [15 , 16]. This information will be useful to forest planning and management aimed at mitigating oak decline and mortality. The data for this study included 6, FIA plots in the Ozark Highlands of Arkansas and Missouri that contained oak species and were measured and remeasured from through Table 1. Tree dbh, species, crown ratio, damage class, plot slope, aspect and elevation were measured or recorded. Number of plots within each species group used in analysis.

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Chapter 3 : International Handbook Of Adult Mortality by RoyRapp - Issuu

Objective. Maternal and neonatal mortality are important public health issues in low-income countries. This study evaluated spatial and temporal maternal and neonatal mortality trends in Brazil between and

Characteristics of host, pathogens and environment contributing to infectious disease epidemics Role of interactions in disease transmission These factors are all connected to each other through interactions. This can transpire either human-human, agent-agent, agent-human, agent-vector, vector-human or others. It is shown in the figure below. Unique interactions among these are human-human which help in spreading the epidemic. Agent-agent is where two variants or subspecies of a pathogen can combine to form a new mutant. This is also problematic. A prime example of this is the Influenza virus which continuously evolves and mutates into a new variant. Interactions between host, agent, vector and environment leading to disease transmission. They are caused by different factors. There are three major factors that lead to outbreak in a community WHO, This is shown in the figure below. Major factors leading to outbreak of infectious diseases Source: WHO Therefore, interaction patterns and environmental characteristics play a significant role in outbreak of diseases. Knowledge about these factors is advantageous in analysis and prediction of epidemiological data Ughade Moreover, government can plan control and prevention strategies keeping in mind these factors. Studying the factors that contribute directly or indirectly to disease outbreak. It can also help determine risks of population or population sub-groups. Moreover, it can assist in understanding extent of contribution. Planning and prediction of success of control or prevention strategies can be done. Such models can help study interaction dynamics existing within a population. Mainly, agent or pathogen, host and environmental features contribute to disease outbreaks and spread. Each of them belongs to a different class of organisms. Pathogens or agents possess intrinsic characteristics that dictate their pathogenicity, host range and mode of transmission. Extrinsic characteristics of pathogens based on host-agent interaction include: Host-specificity, Infectivity ability of pathogen to invade and multiply in host , Infective dose no. These factors contribute to pathogenicity. In emerging infectious diseases the ability of the pathogen are very important. These abilities include adaptation and evolution in hosts or vectors through mutation and human contact Leventhal et al. Characteristics of hosts responsible for disease outbreaks One of the prominent factors driving infectious disease epidemiology is host resistance or susceptibility. Resistance or susceptibility naturally depends upon state of immune system. This includes both specific and non-specific immunity. Besides this, demographic profile like age, gender, race and genetic makeup of a population affect infection. Extrinsic factors of hosts include behaviors like diet and history of infection. Environmental factors leading to disease outbreaks The major environmental factors leading to disease outbreak are climate and extreme natural events. Anthropogenic factors like sanitation, utilities also play a role WHO These factors influence the behavior and ranges for agent, vectors and hosts. Agent reservoirs are also affected. Physical factors include climate humidity, temperature, precipitation trends and topography of area. Biological factors include plants and animals that humans frequently interact with. Finally, socioeconomic factors of environment influence human behavior and interaction and hence diseases transmission. Challenges posed by interaction behaviors One can determine causative factors through observation and laboratory analysis. However the complex interactions existing between all organisms and factors are hard to interpret. When multiple factors simultaneously lead to disease transmission, the route of transmission is hard to determine. Knowledge about these interaction patterns is important in predicting success of control strategies. Governments should spread knowledge at individual, societal and environmental levels. Moreover, prediction of future events or early warning systems also requires comprehensive knowledge about associated factors and the risks they pose. Therefore, risk prediction based on associated or causative factors are needed along with interaction studies or modeling in disease epidemiology research. Concepts of Disease Occurrence. An Introduction to Applied Epidemiology and Biostatistics. Evolution and emergence of infectious diseases in theoretical and real-world networks. Nature Communications, 6, p. Mathematical

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modeling of infectious disease dynamics. *Virulence*, 4 4 , pp. Influenza virus evolution, host adaptation, and pandemic formation. *Cell Host and Microbe*, 7 6 , pp. Statistical modeling in epidemiologic research: Clinical Epidemiology and Global Health, 1 1 , pp. Environmental Health in Emergencies: