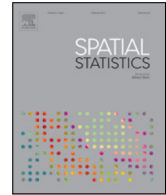




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Spatial Statistics

journal homepage: www.elsevier.com/locate/spasta

A probabilistic predictive Bayesian approach for determining the representativeness of health and demographic surveillance networks



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ARTICLE INFO

Article history:

Received 29 January 2016

Accepted 13 May 2016

Available online 21 June 2016

Keywords:

Bayesian inference

BIC

Central clustering

Finite Gaussian mixture model

Gibbs sampling

Predictive clustering

ABSTRACT

Health and demographic surveillance systems, formed into networks of sites, are increasingly being established to circumvent unreliable national civil registration systems for estimates of mortality and its determinants in low income countries. Health outcomes, as measured by morbidity and mortality, generally correlate strongly with socioeconomic and environmental characteristics. Therefore, to enable comparison between sites, understand which sites can be grouped and where additional sites would aid understanding of rates and determinants, determining the environmental and socioeconomic representativeness of networks becomes important. This paper proposes a full Bayesian methodology for assessing current representativeness and consequently, identification of future sites, focusing on the INDEPTH network in sub-Saharan Africa as an example. Using socioeconomic and environmental data from the current network of 39 sites, we develop a multi-dimensional finite Gaussian mixture model for clustering the existing sites. Using the fitted model we obtain the posterior predictive probability distribution for cluster membership of each 1×1 km grid cell in Africa. The maximum of the posterior predictive probability distribution for each grid cell is proposed as the criterion for representativeness of the network for that particular

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grid cell. We demonstrate the conceptual superiority and practical appeal of the proposed Bayesian probabilistic method over previously applied deterministic clustering methods. As an example of the potential utility and application of the method, we also suggest optimal site selection methods for possible additions to the network.

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1. Introduction

Health and demographic indices related to births, deaths, migration, economic activity, morbidity and child mortality are used by governments and many other organizations for effective planning, health policy formulation and other decision-making processes (Ngom et al., 2001; WHO, 2013). The data used for estimating these indices are usually obtained from censuses and national civil registration systems. However, data from these sources in low-income countries are often inconsistent and unreliable (Sankoh and Byass, 2012; Ye et al., 2012). To circumvent this problem, longitudinal data collection systems known as Health and Demographic Surveillance Systems (HDSS) were established to provide more informative and accurate long-term monitoring data. Such systems involve the description of a target population through an initial census, which is then succeeded by regular collection of vital statistics and other relevant data. To provide a comprehensive picture of health and population dynamics across much wider geographical areas, many HDSS sites have joined networks such as the International Network of field sites with continuous Demographic Evaluations of Populations and Their Health (INDEPTH) (Baiden et al., 2006; Sankoh and Byass, 2012). At the time of writing, the INDEPTH network comprises of 52 HDSS sites, of which 39 are located in sub-Saharan Africa.¹ Moreover, new networks are being established, such as the Child Health and Mortality Prevention Surveillance Network (CHAMPS),² a network of disease surveillance sites in developing countries.

With networks of surveillance sites attempting to provide standardized and representative data on a range of health and demographic indicators, and pooling data to provide information on wide-area demographic patterns and their determinants, understanding the coverage and representativeness of the network becomes important. This is particularly necessary when it is of interest to determine where additions to the networks would help improve utility and coverage or to characterize the uncertainty associated with extrapolations using information from the network. Also, when performing site selection for establishing new networks of sites, understanding how the network can be effectively configured to capture the range of variabilities that exist in the regions of interest can be valuable.

Morbidity, mortality and health equity measures generally correlate and are influenced strongly by socioeconomic and environmental conditions. These have therefore previously been used as surrogate measures for assessing the coverage and representativeness of the INDEPTH network (Tatem et al., 2006; Jia et al., 2015). These studies used deterministic approaches such as hierarchical clustering (Ward, 1963) for grouping the sites based on gridded datasets depicting factors such as temperature, rainfall and population density, and the Euclidean metric for mapping the socioeconomic and environmental coverage of the sites. These studies provided a basic assessment of the similarities between existing sites, representativeness of the network and grouping of sites in terms of available gridded covariate layers, but did not account for or quantify the uncertainties inherent in undertaking this.

¹ See http://www.indepth-network.org/index.php?option=com_content&task=view&id=1306&Itemid=1070 for details.

² See <http://www.gatesfoundation.org/Media-Center/Press-Releases/2015/05/Child-Health-and-Mortality-Prevention-Surveillance-Network>.

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