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Significant multiple high-and low-risk regions in event data maps

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Objective

We describe a method to determine the partition of a map consisting of point event data, identifying all the multiple significant anomalies, which may be of high or low risk.

Introduction

The Voronoi Based Scan (VBScan) (1) is a fast method for the detection and inference of point data set space-time disease clusters. A Voronoi diagram is built for points representing population individuals (cases and controls). The number of Voronoi cells boundaries intercepted by the line segment joining two cases' points defines the Voronoi distance between those points. That distance is used to approximate the density of the heterogeneous population and build the Voronoi distance Minimum Spanning Tree (MST) linking the cases. The successive removal of its edges generates subtrees, which are the potential space-time clusters, which are evaluated through the scan statistic. Monte Carlo replications of the original data are used to evaluate cluster significance. In the present work, we modify VBScan to find the best partition dividing the map into multiple low- and high-risk regions.

Methods

In our novel approach, we use the previous VBScan recursively on the map with case-control point event data. At each recursive step, we compute two functions: (i) the likelihood ratio of the multiple components and (ii) the likelihood ratio increase since the previous step. As the first function always increases monotonically with every added component to the partition, the last function is used as a measure of the cost-benefit of adding a further region to the partition. This is done employing a multicriteria decision process, determining the nondominated partition solutions. Through Monte Carlo replications under null hypothesis, we compute the significance of the nondominated solutions and choose the best partition.

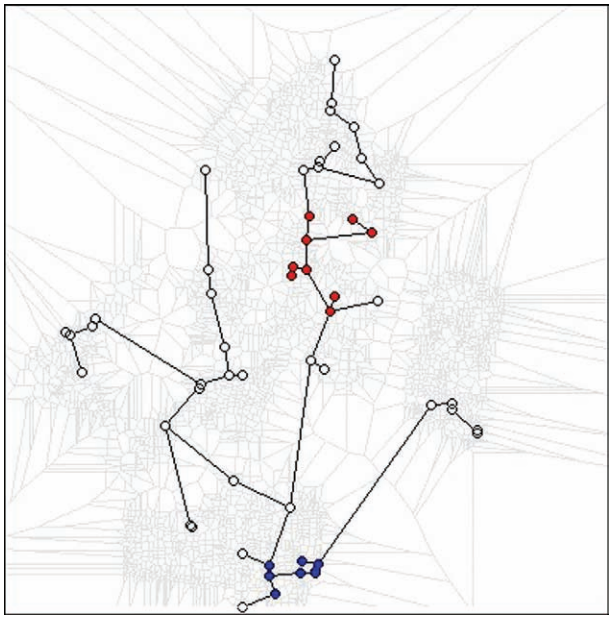

Fig. 1.

Results

Our method was tested on several different simulated maps partitioned into different numbers of components (ranging from 2 to 4). The relative risks for each component were chosen as 3 sigma, −3 sigma and 0 sigma, corresponding respectively to high-, low- and neutral-risk spots. We evaluate the power of detection and matching (a measure of overlap between the real and detected partitions) for each set of 1000 Monte Carlo replications. The average power varies from 0.686 to 0.803, and matching varies from 0.566 to 0.850 for the several sets of simulations.

We also applied the method on a case study of dengue fever in a small Brazilian town in 2010 (1). Fig. 1 shows the MST linking the 57 cases (small circles) distributed among 3929 controls. The optimal partition consists of three components: two high-risk regions (red and blue) and a low-risk region (white).

Conclusions

The proposed method is fast, with good partitions' accuracy determination. The dengue fever application's result shows that our method is in very good agreement with the previous analysis with VBScan, which indicates two significant high-risk clusters (the red region is the primary cluster with p-value 0.004, and the blue region is the secondary cluster with p-value 0.016).

Keywords

Case-control; disease cluster; spatial scan statistic; space partition; dengue fever

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Reference

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