Spatial-temporal Risk Analysis of Case-control Studies of Cancer

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Abstract

Exploring spatial-temporal patterns of disease incidence through cluster analysis can identify areas of significantly elevated risk, providing potential clues about disease risk. There are, however, several relevant methodological issues that arise in space-time cluster analysis of cancer. Typical spatial cluster studies with aggregate data are plagued by issues of poor spatial resolution, population migration, and confounding. In contrast, applying modern statistical analysis of case-control studies with residential histories can account for population mobility, disease latency, and known risk factors. As an example, we present a spatial analysis of a population-based case-control study of non-Hodgkin lymphoma (NHL) in four National Cancer Institute registries. Using 20-year residential histories, we used generalized additive models adjusted for known environmental and genetic risk factors to model spatially the probability that an individual had NHL and to identify clusters of elevated NHL risk. We found that the best model fit was for residential locations 20 years prior to diagnosis and there were statistically significant areas of elevated risk of NHL in three study areas.

Keywords: Cancer; Generalized additive model; Spatial-temporal; Clusters.

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