A Flexible Scan Statistic for Spatial Cluster Detection: A Dengue Fever Case Study in Southern Taiwan

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Abstract

Dengue fever remains a major mosquito-borne viral disease, with over 50–100 million infections annually and a disproportionate burden in the Asia-Pacific region. Taiwan illustrates both the successes and challenges of control: stringent quarantine and vector management kept incidence low from 2003 to 2014, yet global resurgence led to large epidemics in 2014–2015 and again in 2023. These recurring outbreaks underscore the urgent need for improved surveillance and cluster detection methods.

Geographical cluster analysis has become central to identifying hotspots, but existing approaches often fail to adjust for spatial autocorrelation and environmental covariates, producing biased or unstable results. To overcome these limitations, we introduce SEMSCAN, a framework embedding scan statistics within a spatial error model. This integration allows simultaneous estimation of covariate effects and spatial clustering, while directly accounting for residual spatial dependence. SEMSCAN improves robustness, reduces computational burden, and enhances the validity of hotspot detection in heterogeneous risk environments. This framework offers a practical and rigorous tool for strengthening dengue surveillance and guiding targeted vector control strategies.

Keyword: Spatial Epidemiology, Spatial Scan Statistics, Disease Hotspot Detection, Spatial Autocorrelation