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Mark H. Myer

US Environmental Protection Agency, myer.mark@epa.gov

Scott R. Campbell

Suffolk County Department of Health Services

John M. Johnston

US Environmental Protection Agency

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Spatiotemporal Bayesian modeling of West Nile virus in mosquitoes, with a focus on ecological predictors

Mark H. Myer^a, Scott R. Campbell^b, John M. Johnston^c

^a*Oak Ridge Institute of Science and Education, U.S. Environmental Protection Agency*
(myer.mark@epa.gov) ^b*Suffolk County, New York Department of Health Services* ^c*U.S. Environmental Protection Agency*

Mosquito-borne disease is a growing threat to public health, with the spread of invasive arboviral vectors and expansion of habitat zones due to changing climates driving an increased interest in predicting disease patterns. We worked with the Suffolk County, New York vector-borne disease surveillance team to develop a spatiotemporal model of West Nile virus (WNV) prevalence in *Culex pipiens-restuans* mosquitoes. Suffolk County has experienced 55 human cases of WNV since 2010, resulting in 3 deaths. Our model narrowed down a list of over 40 potential predictors of WNV including ecological, weather, and built-environment covariates. Spatial and temporal random error structure was incorporated using the R package 'R-INLA' which fits Bayesian spatial models using the stochastic partial differential equation (SPDE) method. INLA SPDE is a flexible and efficient Bayesian modeling method that is robust to unbalanced study design or missing data, can fit correlated or independent space-time models, and is suitable for small or large scales of spatial and temporal observation. We found that land cover classified as open water and woody wetlands had a negative association with WNV prevalence, while the count of septic systems near trap sites was associated with an increase. Adding the spatial and temporally correlated random errors improved model fit and predictive power, with a sensitivity of 80.9% and a specificity of 77.0% when tested against held-out 2015 data. This study confirmed findings of previous WNV models with respect to meteorological predictors and ecological determinants of public health, and suggested that wetlands provide the service of reducing WNV in mosquitoes while heavy dependence on septic systems may lead to increased risk.

Keywords: Spatiotemporal; arbovirus; West Nile; INLA; Bayesian