Spatio-temporal patterns of Nephropathia epidemica and Lyme disease incidence in Belgium

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Lyme disease (LD) and Nephropathia epidemica (NE) are zoonoses resulting from two different transmission mechanisms and the action of two different causal agents, the bacteria Borrelia burgdorfori and the Puumala hanta virus, respectively. Recently, a remarkable increase of reported cases has been observed in Belgium and other European countries.

The occurrence patterns in both diseases, although caused by different pathogenic organisms, have the common aspect of being strongly dependent on environmental conditions, vegetation dynamics and landscape characteristics.

The formulation of hypotheses explaining the observed temporal and spatial patterns in disease outbreaks can be supported by the utilization of information sources in which vegetation, climate and landscape features are recorded across the temporal and/or spatial dimension. In this respect, land cover maps are a valuable source of information concerning regional landscape configuration.

As part of a larger research initiative on several aspect of these epidemiological diseases, this study explores the links between the observed spatial pattern of a local Bayesian risk estimator for NE and LD across the period 1996-2007 and landscape features. By means of geographically weighted regression, the relation of estimated risk and landscape configuration metrics is assessed.

The study is largely based on count data at municipal level provided by the Belgian Institute for Public Health and landcover data from the CORINE land cover map as well as national landcover data sources.

Preliminary results of this on-going analysis confirm that the increasing number of infected cases for both diseases corresponds also to a clear spatial expansion. Moreover, patches metrics for certain cover classes (broad-leaved forest, herbaceous vegetation, urban areas, amongst other) revealed the aspects of landscape configuration that may be influencing infection risk. These findings underline the need of incorporating spatial covariates in existing outbreak modelling schemes.