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Time series vs. point processes for space-time surveillance in public health

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Abstract:

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Public health surveillance of emerging infectious diseases is an essential instrument in the attempt to control and prevent their spread. During the last 15 years a number of statistical algorithms have been proposed to perform prospective surveillance for univariate and multivariate count data time series originating from routine surveillance on country or county level. Modern data collection and visualisation methods in public health have resulted in the geographical information of surveillance data becoming more precise and timely, which has spawned a number of surveillance approaches based on spatio-temporal point processes. These allow a more flexible treatment of the time and space information than the implicit discretisation implied by time series oriented methods.

In our work we try to contrast the purely temporal and the spatio-temporal surveillance approaches using data by the German National Reference Center for Meningococci hosted by the University of Würzburg, Germany, as illustrative example. For the time series approach we use the CUSUM based methodology in Höhle and Paul (2008) and for the space-time approach the Shirayev-Roberts based work in Assuncao and Correa (2009). Both approaches are implemented in the R package "surveillance" available from the comprehensive R Archive Network (CRAN). In our comparison, we investigate in more detail two-component modelling of infectious diseases as basis for outbreak detection. Here, disease dynamics is split into endemic and epidemic components and likelihood ratio based methods are used to determine the time-point, where just an endemic component is insufficient to model the observed data and consequently an additional epidemic component is needed. For the time series approach a treatment of this procedure is given Höhle and Paul (2008) and we present very preliminary results on how a similar change-point detection can be performed in a newly space-time process based two-component infectious disease model formulated in Höhle (2009).

Literature:

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