
Modelling and surveillance of infectious diseases - or why there is an R in SARS

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Abstract. This talk will focus on how R could assist in two aspects of the continuing efforts to better understand and control infectious diseases - be it in human, plant or veterinary epidemiology.

Firstly, stochastic modelling is an important tool in order to better understand the dynamics of infectious diseases. A key epidemic model in this process is the stochastic susceptible-exposed-infectious (SIR) model. The R package `RLadyBug` contains a set of functions for the simulation and parameter estimation in spatially heterogeneous SIR models. Simulation is based on the Sellke construction or Ogata's modified thinning algorithm, while estimation is based on maximum likelihood or - when the disease is only partially observed - Markov Chain Monte Carlo.

Secondly, routine surveillance of public health data often boils down to the on-line detection of change-points in time series of counts. Surveillance has hence a close connection to problems from statistical process control. The R package `surveillance` contains an implementation of some of the most common surveillance methods such as the Farrington procedure or cumulative sums. Data and results can be temporally and - in case of multiple time series - spatio-temporally visualized.

Both packages are introduced and their use is illustrated by means of examples and R-code.

References

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Keywords

infectious disease epidemiology, SIR model, outbreak detection