

Data-driven modeling of epidemics
a minisymposium given in the
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Abstract

Currently, an increasing amount of data concerning contact- and transport networks is made available and additionally, population measurements of various granularity are gathered for scientific purposes. In this minisymposium we are interested in the increased level of detail of epidemiological modeling which is made possible using such data, be it in animal or in human populations. This includes large-scale simulation of realistic models in disease spread, multi-scale modeling aspects, powerful visualization tools, and inference about hidden states. Additionally, risk assessment or scenario evaluations could be important contributions to the general topic.

Schedule

The reserved slot is **Tue 17th of June, 11:40–15:30**.

11:40 – 12:05 S. Widgren

12:05 – 12:30 E. Vergu

12:30 – 12:55 T. Britton

Lunch 13:00 – 14:00

14:00 – 14:25 U. Wennergren

–15.30 Time for discussions

Efficient data-driven simulation of infection spread in the Swedish cattle population

Speaker: Stefan Widgren

Contributors: Pavol Bauer, Stefan Engblom

One of the most important routes for the spread of infectious diseases in animal populations is movement of live animals. European Union legislation requires all bovine animals to be registered in national databases. Moreover, the databases must also contain date of birth, identification number of the holding where the animal was born, identification numbers of all holdings where the animal has been kept and dates of each change of holding and date of death and slaughter.

The use of real population and event data enables realistic disease spread modeling of the spatio-temporal dynamics due to age structures, trade patterns, population size and slaughter. However, performing detailed data driven simulations requires efficient algorithms and data structures to handle the complex network of herds and events.

Verotoxinogenic *Escherichia coli* O157:H7 (VTEC O157:H7) is a zoonotic pathogen of great public health interest. VTEC O157:H7 is capable of causing severe enterohemorrhagic colitis in humans, notably children. Cattle is considered to be a major reservoir of the pathogen and shed the bacteria in feces without showing any clinical signs of disease.

In this work we study spatio-temporal models of the spread of VTEC O157:H7 in the Swedish cattle population where epidemiological processes are formulated as continuous-time Markov-chains. To accelerate computations in our discrete-event simulator SimInf we divide work among cores of shared memory multiprocessors by using the models inherent parallelism in between transport events gathered from actual data. We will present the epidemiological model and study the overall parallel efficiency of the simulation.

Pathogen spread and control on the network of French cattle movements through coupling of intra- and inter-herd models

Speaker: Elisabeta Vergu

Contributors: Pauline Ezanno, B. L. Dutta, Mathieu Moslonka-Lefebvre

Going beyond farm areas, enzootic diseases spread in livestock populations at a regional scale through animal movements between holdings and neighboring relationships. Because animal trade networks are time varying, it is important to be studied over several years to identify if structural patterns underlying pathogen spread are stable in time. In addition, at the intra-herd scale, potentially large heterogeneities occur in the infection prevalence over time (determined by the time since infection and the rate of external exposure), and among herds in a region (with respect to herd specificities such as size and degree of connectivity). Therefore, the intra-herd infection dynamics may have to be accounted for when modelling the risk of pathogen spread to in-contact herds. We first analyzed the French cattle movement network from 2005 to 2009 using tools from graph theory, for different spatial granularities (farms or communes as nodes) and temporal windows (month, year) to investigate the stability of its main descriptors. Proxies for pathogen spread (at the national or regional scales, on the entire network or on subsets of it), such as percolation and reachability ratio, accounting for its time-varying properties, were also computed. Second, we coupled intra- and inter-herd infection dynamics, described by stochastic models in discrete time, to model the spread of bovine viral diarrhoea virus (BVDV), as an example of bovine pathogen, on the sub-network of dairy herds in Brittany (France), a main region for dairy cattle farming systems. The location of virus introduction in the region as well as herd specificities highly influenced BVDV spread. The relative roles in inter-herd transmission of neighborhood relationships (occurring in high-density area with long lasting pasture periods) and animal trade were also investigated through sensitivity analysis. Third, we evaluated control strategies related to the indirect knowledge of the source herd infection status, such as the level of antibodies in the bull tank milk, or the imperfect and delayed knowledge of the animal infection status at movement occurrence. The model is currently under extension to account for the heterogeneity in herd farming systems as encountered in a region.

Inferring global network properties from egocentric data with applications to epidemics

Speaker: Tom Britton

Contributor: Pieter Trapman

Social networks are often only partly observed. It may be desirable to induce global properties of the network from “egocentric” data. In the talk we study different types of egocentric data, and show what global network properties are consistent with data. Two global network properties are considered: the size of the largest connected component (the giant), and the size of an epidemic outbreak taking place on the network. The main conclusion is that in most cases, egocentric data allow for a large range of possible sizes of the giant and the outbreak. The asymptotic size of the giant and the outbreak is also characterised assuming the network is selected uniformly among networks with prescribed egocentric data.

Modeling animal disease spread: including several paths of disease spread in a bayesian data-driven approach

Speaker: Uno Wennergren

Contributors: Peter Brommesson, Tom Lindström, Annie Jonsson

The spread of animal disease between farms mainly occurs through the movement of animals between farms or by a local diffusion like process. This diffusion process is known to consist of several separate modes — ranging from wind spread to veterinarians visiting the farms. We will show how such a process interacts with the process governed with animal movement. We will present examples from US, UK, Sweden, and Italy. We will also show the effect of movement to slaughterhouses and when including markets in the movement process. Sweden do not use markets in the national movement structure while the other countries does. By using a Bayesian approach to analyze data on movements one can include the uncertainty given in the data throughout the model and display it in the simulation results. We will also show how to scale up partial datasets as in the US case. The Bayesian modeling may also include a hierarchical approach to include for example both distance dependence and classes of farms. The classes can be size of farm or production type. We also present some analysis of movement differences between seasons and regions.