

**Title:** A Bayesian inference method to estimate transmission trees with multiple introductions applied to SARS-CoV-2 in Dutch mink farms

**Keynote Speaker:** Dr. Martin Bootsma

**Short CV:**

Martin Bootsma studied theoretical physics and mathematics at UU and did his PhD on models for the spread of antimicrobial resistance under guidance of Prof. Odo Diekmann and Marc Bonten. Ever since Martin works on models for the spread of infectious diseases and he has a joint position at the department of mathematics and at the University Medical Center of Utrecht University.

**Abstract:**

Knowledge of who infected whom during an outbreak of an infectious disease is important to determine risk factors for transmission and to design effective control measures. Both whole-genome sequencing of pathogens and epidemiological data provide useful information about the transmission events and underlying processes. Existing models to infer transmission trees assume that the pathogen is introduced only once from outside into the population of interest. However, this is not always true. For instance, SARS-CoV-2 is suggested to be introduced multiple times in mink farms in the Netherlands by the SARS-CoV-2 pandemic among humans. We have developed a Bayesian inference method combining whole-genome sequencing data and epidemiological data which allows multiple introductions of the pathogen in the population. Our method does not a priori split the outbreak into multiple phylogenetic clusters, nor does it break the dependency between the processes of mutation, within-host dynamics, transmission, and observation. On simulated data, our method identifies the number of introductions with high accuracy. When applied to data from a SARS-CoV-2 outbreak in Dutch mink farms, the method provides strong evidence for 13 introductions, which is 20 percent all infected farms. Our method, implemented in the phybreak package, allows for analysis of transmission routes of a more complex class of infectious disease outbreaks which can aid the design of effective control measures.