

Speaker: Panayiota Touloupou (University of Birmingham)

Date: 06/02/2024 at 13:15 on Microsoft Teams

Title: Scalable inference for epidemic models with individual level data

Abstract:

As individual level epidemiological and pathogen genetic data become available in ever increasing quantities, the task of analysing such data becomes more and more challenging. Inferences for this type of data are complicated by the fact that the data is usually incomplete, in the sense that the times of acquiring and clearing infection are not directly observed, making the evaluation of the model likelihood intractable. A solution to this problem can be given in the Bayesian framework with unobserved data being imputed within Markov chain Monte Carlo (MCMC) algorithms at the cost of considerable extra computational effort.

Motivated by this demand, we develop a novel method for updating individual level infection states within MCMC algorithms that respects the dependence structure inherent within epidemic data. We apply our new methodology to an epidemic of *Escherichia coli* O157:H7 in feedlot cattle in which eight competing strains were identified using genetic typing methods. We show that surprisingly little genetic data is needed to produce a probabilistic reconstruction of the epidemic trajectories, despite some possibility of misclassification in the genetic typing. We believe that this complex model, capturing the interactions between strains, would not have been able to be fitted using existing methodologies.