EPSRC DTP PhD Research Project

Project Title: Efficient Bayesian inference for infectious disease models

Primary Supervisor details:
Trevelyan McKinley

t.mckinley@exeter.ac.uk,

https://medicine.exeter.ac.uk/people/profile/index.php?web_id=TJ_McKinley

Additional Supervisory team details:
Theo Economou**,** t.economou@exeter.ac.uk

Dave Hodgson, D.J.Hodgson@exeter.ac.uk,
https://biosciences.exeter.ac.uk/staff/profile/index.php?web_id=david_hodgson

Collaborator: Dez Delahay, University of Exeter and the Animal and Plant Health Agency.

Department: Clinical and Biomedical Sciences

Location: RILD Building, Barrack Road, Exeter

PhD Programme: PhD in Clinical & Biomedical Sciences

Project Description:

Infectious diseases can result in significant welfare and conservation costs to human and animal populations, and where they infect livestock or are zoonotic they can also have substantial impacts on the farming industry and public health respectively. Performing robust statistical inference for infectious disease systems is challenging, requiring cutting-edge computational methods, which are difficult to implement and scale. As such, improving the efficiency of these methods could have substantial impacts for improving the utility of such methods for understanding mechanisms of disease spread, and informing disease management and response strategies.

This studentship will build upon recent work that utilised a new advance in computational statistical inference methods—the individual forward filtering backward sampling (iFFBS) algorithm—in order to fit dynamic transmission models of bovine tuberculosis (bTB) infection to individual-level data in wild badgers. This project utilised a unique long-term ecological survey of bTB in badgers from Woodchester Park in Gloucestershire, and has successfully integrated key complex processes such as age-dependent mortality with

censoring, stochastic capture-mark-recapture data, imperfect diagnostic testing and spatio-temporal meta-population structures. This work has provided unique biological insights into the epidemiology of this important disease in a wildlife reservoir, and the iFFBS framework provides a flexible, powerful and efficient way to fit models to infectious disease data sets in small- to medium-size populations where individual-level data is available.

This PhD project will develop this methodological framework further, with various avenues that could be pursued, for example:

- Using different sampling schemes to allow the iFFBS algorithm to be made more efficient in larger populations and thus extending its utility to a wider range of problems.
- Utilising recent advances in performing Bayesian model choice with the iFFBS sampler and applying these to quantify the weight-of-evidence in favour of competing models.
- Embedding model discrepancy into the inference framework to account for unobserved and unmodelled sources of infection and interaction.
- Integrating recent advances in model diagnostics, such as latent class residuals, which could be readily utilised within this framework for diagnosing model misspecification.

Within the context of bTB spread in badgers, these methodological advances would allow us to:

- Build models to understand important epidemiological questions, such as whether there are sex- or age-specific impacts on key parameters such as transmission potential or the probability of being a superspreader; infection-related changes in mortality risk; or whether more sophisticated between-group transmission structures could be incorporated.
- Build models to understand key questions for disease management. Current models have been fitted to data retrospectively, and there is potential for future work to explore key questions relating to the efficacy of potential management strategies such as targeted vaccination by performing simulations using the fitted model parameters.

These algorithms would also have much wider applicability than just bTB, and could thus become a useful tool in modellers' toolboxes when in comes to modelling infectious disease systems in general.

Konzen et al. (2024); McDonald et al. (2017); Buzdugan et al. (2017); Hudson et al. (2019); Touloupou et al. (2020).

Project specific entry requirements:

This project will suit students with an interest in developing and implementing computational methods, preferably with a background in mathematics, statistics or computer science, or an equivalent STEM subject area. A background in R / C / C++, or a similar programming language such as Python is essential.

Project specific enquiries:

For informal enquiries, please contact Trevelyan McKinley at t.mckinley@exeter.ac.uk.