



SEMINAR

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Hosted by Assoc Prof Ryan Chisohlm

Data integrating statistical models for prediction tasks in ecology and infectious diseases

Tianxiao August Hao

*Senior Research Officer,
The Kids Research Institute Australia*



Statistical models are widely used in biological sciences for predicting patterns of interest across space and time, including for example species abundance and infectious disease prevalence. In these applications, the model typically learns the pattern in the data, but does not explicitly separate the process of data observation from the true underlying biological process of interest. However, the same biological process can often be observed by different and complementary data collecting processes – integrating different types of data in one model can allow us to make more accurate and useful predictions. In this talk, I will present three recent infectious disease and ecology applications that use data-integrating models to predict quantities difficult to directly observe in real life: 1) integrating clinical immunological assay and population observation data to predict the waning of vaccine effectiveness in real-world populations; 2) integrating multiple streams of disease surveillance data to reconstruct infection prevalence history in a population; and 3) integrating species and community occurrences to predict the distribution of soil biocrusts in Australia. I will explain how the underlying biological questions and explicit observation processes are modelled in these examples, and discuss practical considerations in building data-integrating models.

Tianxiao (August) Hao is an early-career statistical modeller based at The Kids Research Institute Australia and The University of Melbourne. He is a member of the Infectious Disease Ecology and Modelling team lead by Prof Nick Golding (The Kids; University of Western Australia) and the Australia-Aotearoa Consortium for Epidemic Forecasting & Analytics (ACEFA). He received a PhD in quantitative ecology in 2022, and has since worked on Bayesian inference models with applications in COVID-19 pandemic response, antimalarial drug resistance, and conservation & landscape ecology. His methodological focus lies strongly in innovating established phenomenological and correlative model approaches to incorporate first-principle-based mechanisms and dynamics where possible, whilst retaining the flexibility to fit to complex and noisy real-world data. He is interested in model applications across biological domains, including human immune responses, mosquito ecology & biology, global human mobility, and the biogeography of fungi and other understudied soil-surface organisms.