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New statistical methods for eDNA data

Environmental DNA (eDNA) is a survey tool with rapidly expanding applications for assessing presence of a wildlife species at surveyed sites. eDNA surveys consist of two stages: stage 1, when a sample is collected from a site, and stage 2, when the sample is analysed in the lab for presence of species' DNA. The methods were originally developed to target particular species (single-species), but can now be used to obtain a list of species at each surveyed site (multi-species/metabarcoding).

In this talk, I will present a novel Bayesian model for analysing single-species eDNA data, while accounting for false positive and false negative errors, which are known to be non-negligible, in both stages of eDNA surveys. All model parameters can be modelled as functions of covariates and the proposed methodology allows us to perform efficient Bayesian variable selection that does not require the use of trans-dimensional algorithms. I will also discuss joint species distribution models as the starting point for modelling multi-species eDNA data and will outline the next steps required to obtain a unifying modelling framework for eDNA surveys.