Bayesian joint species distribution modelling using Stan

Joint species distribution modelling (jSDM) has shown increasing popularity with ecologists over the past few years as it allows for the modelling of species responses to environmental factors simultaneously with interspecies correlations. Within this presentation we will introduce a new R package for Bayesian jSDM that provides an interface for fitting these models within the Stan language. Currently supported jSDM types include multivariate generalised linear mixed models (i.e. where the entire species covariance matrix is fitted) and generalised linear latent variable models (i.e. where the species covariance matrix is approximated by a small number of latent variables). Using the Stan probabilistic programming language allows us to exploit the Stan implementation of Hamiltonian Monte Carlo for more efficient and robust exploration of the model parameter space. This presentation will demonstrate how to use this package to simulate data according to these jSDMs, fit models and return useful diagnostics and summaries. Package performance in recovering parameters from simulated data will be presented for a range of species and site numbers, along with varying average rarity of species, in order to identify some of the strengths and limitations of these models. We hope that this package will provide a valuable tool for ecologists wishing to fit joint species distribution models in a Bayesian context.