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Joint models for site-associated species

Abstract

In ecological field surveys it is often of interest to estimate the abundance of species. It is frequently the case that unmarked animals are counted on different sites over several time occasions. A natural starting point to model these data, while accounting for imperfect detection, is by using Royle's N-mixture model (Biometrics, 2004). We extend the N-mixture modelling framework to jointly model two site-associated species abundances and propose to use the correlation between them to measure the influence of one species' abundance on the populations of the other, and study how this changes over time and space. By including a new parameter in the abundance distribution of one of the species, linking it to abundance of the other, our proposed model treats extra-variability as an effect induced by an associated species' abundance and allows one to study how environmental covariates may affect this. We illustrate our approach using data from the North American Breeding Bird Survey on bald eagles and mallards, obtained in the 2015 campaign for the states of Oregon, Washington and British Columbia. By using the joint model we were able to separate overdispersion from mallard-induced variability and hence what would be accounted for with a dispersion parameter in the univariate framework for the eagles was explained by covariates related to mallard abundance in the joint model. Our approach represents a simple way of modelling site-associated species populations jointly. We also show how to assess goodness-of-fit for these joint models using a bivariate extension of normal plots with simulation envelopes, implemented in R.