

Modelling spatial species distributions with Bayes rule

Species distribution models are a popular tool to predict the (potential) distribution of species as a function of environmental variables. Even though the maps produced by these methods are easy to read, the methods are usually optimised for obtaining good predictive performance leading to a loss of interpretability of the fitted relationships. We introduce a novel method for species distribution modelling that allows for greater flexibility, interpretability and testing of model hypotheses.

This method models the available presence-background data directly by fitting density functions to both datatypes and infers probability of presence by application of Bayes' rule. Flexibility is given to the modeller in determining the density functions for both presence and background distributions. Covariance between independent variables can be modelled by addition of copulas or through fitting multivariate kernel density functions.

The major strength of this method lies in increased interpretability of the model, and in the ability to test different biological hypothesis on the distribution of different species or groups within species. The possibility of model generalization along with hypothesis testing can lead to improved use of available (limited) data. All of this is expected to lead to more transparent species distribution models, an important demand from the policy domain.

In this presentation we showcase progress on the development and application of this method to several case studies, as well as on establishment data of invasive tree pests in Europe.