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Clustering Metabarcoding Data: a Model-Based Approach

Authors:

Luisa Ferrari^{1*†}, Maria Franco-Villoria¹, Garritt L. Page²
Alex Laini³

¹ University of Modena and Reggio Emilia

² Brigham Young University

³ Università di Torino

* Corresponding author † Presenter

Contact: luisa.ferrari5@unibo.it

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Abstract:

Analyzing species occurrence data is extremely relevant for monitoring biodiversity and designing conservation plans. The traditional method used to collect this type of data consists of capturing a sample using traps, followed by morphological identification by an expert. Obviously, this methodology is very time-consuming, and for this reason, the datasets collected in the field of ecology are usually quite small. Metabarcoding is a relatively novel technique based on genetic identification, which makes it possible to rapidly retrieve a large amount of information about the occurrence of multiple species from a single sample. The deployment of metabarcoding represents a complete paradigm shift in the study of ecological communities. Metabarcoding-generated datasets represent the future of research in this field, and therefore, new statistical tools specifically designed to address their challenges must be developed. In particular, these datasets consist of binary entries representing the presence or absence of a large number of species across multiple sampled sites. In this work, we focus on model-based clustering methods to explore ecological patterns within metabarcoding data. This can be useful to discover groups of species with similar occurrence patterns, as well as to identify sites with similar species composition—that is, biogeographical areas. Specifically, we consider the Bernoulli Mixture Model, which has already been successfully applied in the fields of image and text mining. We propose to extend the basic model to include environmental covariates collected at the different sampling locations. This allows us to investigate the relationship between the identified clusters and habitat characteristics. Additionally, we consider an informative prior on the number of clusters using the asymmetric Dirichlet prior recently proposed in the literature. To evaluate the soundness of our approach, we first conduct a simulation study comparing the performance of the current standard model in the literature—that is, the basic Bernoulli Mixture Model—with our extended version. Finally, we apply our model to a metabarcoding dataset recording the presence or absence of dung beetle species in the Northwestern Alps of Italy, in order to uncover potential clustering patterns and support ecologists in better understanding the ecological structure of the area.