



*9° Congresso della Società Italiana di
Biologia Evoluzionistica*

Book of abstracts

Ancona, 4-7 September 2022

*Department of Life and Environmental Sciences and Department of
Agricultural Sciences, Food and Environment, Marche Polytechnic University,
Via Brecce Bianche, 60131, Ancona*

Niche Modeling (ENM) and estimated habitat dynamics during the Pleistocene in Europe. The models were produced with the R software “ENMeval” using the geographical coordinates of the sightings of the species from 1960 to 2021, and both recent and Pleistocene bioclimatic data. These models allowed prediction of habitat characteristics from four different periods: early Holocene, last glacial maximum, last interglacial period and Marine Isotope Stage 19 interglacial. Results from ENM were then compared to effective population size (N_e) fluctuations estimated using a Pairwise Sequentially Markovian Coalescent method (PSMC) from heterozygosity values of the reference genome of *E. orbicularis*. Preliminary data suggest a reduction in habitat availability during the last glacial maximum. However, the demographic history of the species showed a relatively constant trend until the early Holocene. Here, a significant N_e reduction was recorded despite estimates of good habitat conditions. This pattern suggests possible anthropogenic factors affecting the demography of *E. orbicularis*.

Exploring fungal biodiversity using a comprehensive python package for automatic (multi-marker) barcode analyses

1,3_Tatti Alessia, 2,3_Piccinno Riccardo, 1_Fusco Giuseppe, 2,3_Rota-Stabelli Omar

alessia.tatti@studenti.unipd.it

1_Dipartimento di Biologia, Università di Padova, via Ugo Bassi 58B, I-35131 Padova, Italy, 2_Center Agriculture Food Environment (C3A) University of Trento, San Michele all'Adige (TN) Italy, 3_Research and Innovation Centre Fondazione Edmund Mach San Michele all'Adige (TN) Italy

Fungi play a pivotal role in all ecosystems: they regulate nutrient cycles, influence soil structure and ecosystem multifunctionality, and undergo symbiotic associations with plants, algae, and animals. Despite their importance in shaping and maintaining ecosystems, it is estimated that we currently know only 3-8% of worldwide fungal biodiversity. Fungi can be detected in environmental DNA samples, but it is difficult to metagenomically extract their typically long polyploid genomes in the absence of reference genomes for mapping reads. For fungi, primary databases are still a hidden source of new information in a classical DNA barcode fashion. However, existing barcoding tools lack a comprehensive pipeline, can be very time-consuming and do not take full advantage of metadata associated with sequences.

To tackle these issues, we developed a comprehensive Python package for the automatic barcode analysis of fungi. The pipeline is composed of different scripts which cover consecutive steps: data retrieved from multiple sources; selection of samples based on length, quality and occurrence; construction of chimeric sequences using sequence identifiers, automatic cleaning of the alignment; concatenation of different markers, barcode gap estimation and visualisation; detection of outliers; inference of phylogenetic tree. The package has been successfully used to define cryptic species and to identify misled samples in various fungal taxa.

Our package is a useful tool for the quick detection of new taxa from often understudied or unbinned nucleotide collections. It is scalable to any type of organism and to many markers for multi-marker barcoding and phylogenomic studies. It may ultimately contribute to improving our understanding of fungi and other organism diversity.