Deep Learning for biodiversity monitoring through eDNA Metabarcoding

Letizia Lamperti*†[1,2]

[1]Centre d'Ecologie Fonctionnelle et Evolutive – Ecole Pratique des Hautes Etudes, Centre National de la Recherche Scientifique, Institut de Recherche pour le Développement, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement, Institut Agro Montpellier, Université de Montpellier, Université de Montpellier Paul-Valéry – France

[2]Centre National de la Recherche Scientifique – CNRS, CNRS – France

Abstract

With the growing threats to global biodiversity, understanding the spatio-temporal variations in ecological assemblages has become essential for ecosystem management and biodiversity conservation. Environmental DNA (eDNA) metabarcoding is one of the emerging and promising tools for monitoring biodiversity changes, particularly in marine ecosystems. However, traditional analysis methods often struggle to detect and visualize these variations and diversity patterns because the data linked to eDNA metabarcoding are highly complex. This complexity and the difficulties in analysis thus limit potential ecological and biogeographical interpretations. To overcome these limitations,we developed advanced machine learning (ML) and deep learning (DL) techniques for the analysis of eDNA metabarcoding data. These techniques allow the detection of biodiversity variations and patterns and ecosystem monitoring. ML and DL approaches surpass traditional methods in managing large datasets and modeling non-linear relationships within eDNA metabarcoding data. The tools developed offer new possibilities for biodiversity monitoring using eDNA metabarcoding, thereby improving the study of biodiversity and biodiversity management strategies.

Keywords: Environmental omics

*Speaker

†Corresponding author: letizia.lamperti@univ-grenoble-alpes.fr