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SEP.
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🕐 de 13h à 14h

Robust diversity measures for metabarcoding - Parameter inference for stochastic models

Sylvain Moinard
Université Grenoble Alpes

Metabarcoding is increasingly used to study environmental DNA, especially for biodiversity monitoring purposes. However, this technique induces many biases in the resulting data. I will present two projects of my PhD on the acquisition of quantitative metabarcoding data and on the taxonomic attribution of the observed DNA sequences to species.

Secondly, I will present the Fixed Landscape Inference MethOd (flimo), a new inference algorithm for stochastic models used in ecology. It is a simulation-based likelihood-free algorithm with a specific management of the random variables generation. Flimo works in a framework similar to Approximate Bayesian Computation (ABC) algorithms. In the studied applications, flimo allows a strong reduction of the inference time for similar performances compared to existing methods.