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SÉMINAIRE

Exploring "dark" omics: a crucial step to study adaptive and evolutionary processes in natural communities

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Our understanding of the microbial world is undergoing a paradigm shift. Metagenomics and metatranscriptomics offer unprecedented measures of the taxonomic and functional biodiversity of communities. However, as current inference tools are mainly based on species names or function names, a significant part of the (meta-)omic sequences is ignored. Advances in culture methods and an increase in the number of model organisms are helping to reduce the proportion of unknown molecular sequences (sequences that can not be taxonomically and/or functionally assigned), but these costly solutions are difficult to implement quickly. Today, bioinformatics methods are available that can exploit the enormous amount of known and unknown sequences, thus overcoming our still incomplete view of communities. I will present the methods used in my team to explore the microbial dark omics. In particular, I will present case-studies (e.g., one on dinoflagellates (ubiquitous marine unicellular eukaryotes, bearing an extensive diversity of protein families), one on planktonic communities from the open-ocean) using sequence similarity networks and machine learning. These methods allow to study without a priori the adaptive and evolutionary processes that shape the taxonomic and functional diversity of non-model organisms, notably in the environment, and offer new perspectives to stimulate and enrich models describing population dynamics in the ecosystems or biogeochemical cycles. Keywords: (meta)genomics, (meta)transcriptomics, non-model organisms, sequence annotation (taxonomical, functional), organismal traits, networks, machine learning