Exploring the dark side of molecular sequences in environments

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Résumé

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 sequences, 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 methods used to explore the microbial dark omics. In particular, I will present work using sequence similarity networks, co-occurrence networks and machine learning. These methods allow us to study without a priori the adaptive and evolutionary processes that shape the taxonomic and functional diversity of non-model organisms in the environment, and offer new perspectives to stimulate and enrich models describing population dynamics or biogeochemical cycles.
As a case study, results from a holistic study of carbon fixation in oceanic ecosystems will be presented.

Mots-Clés: Meta, omics, Unknown sequences, Functional annotation, Plankton, Carbon fixation

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