
Investigating metabolisms of microbial communities from metagenomics and metabarcoding data

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Abstract

A potential key to investigate the impact of microbial communities on their environments is to understand their metabolisms. Identification of these communities can be achieved through DNA sequencing approaches. Results from these approaches can be used to estimate their metabolic potentials. A major issue when analysing these communities is their high dimensionality: hundreds to thousands of micro-organisms can be associated to thousands of metabolic functions in tens of samples. Furthermore, sequencing approaches (metagenomics or metabarcoding) impacts the potential insights of these analyses.

Metagenomics approaches allow the sequencing of the genomes of the microbial communities. Thanks to these reconstructed genomes, it is possible to explore metabolic functions performed by their associated genes. Using these metagenomes, I present a method that identify potential metabolic complementarity in large-scale microbiota and generate visualisations depicting these complex interactions. In this way, the community is reduced to a set of minimal interacting organisms performing specific functions.

Metabarcoding approaches focus on a specific gene and often allow the taxonomic identification of microbial communities. Thus the metabolic functions are not directly inferred from their genomes but estimated from the closest relative organisms. I present such method and show its application to several environmental datasets. A focus will be made on predicting the impact of microbial communities on hydrogen storage.

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