

METAGENOMICS: FROM PARTS LISTS TO ECOLOGY

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Meta-omics (metagenomics, metatranscriptomics, metaproteomics) are powerful tools for the analysis of the (unculturable fraction of) microbial communities. Because of its complexity, meta-omics data has required the development of novel computational analysis tools to determine the functional and phylogenetic composition of the sampled community (Raes et al., Curr Opin Microbiol 2007).

However, to go from a metagenomic 'parts list' (i.e. a bag of genes) to an initial understanding of the ecosystem structure and functioning, current tools are not sufficient (Raes & Bork, Nat Rev Microbiol 2009). I will present a range of approaches to analyze metagenomes, infer ecological parameters, extract species interaction and competition relationships, interpret metabolic changes and identify biologically relevant features from meta-omics data with applications in diverse environments. I will specifically focus on data coming from the Tara oceans expedition, integrating multi-omics approaches with detailed oceanographic measurements from viruses to fish larvae.