# Multi-omics driven design of marine microbial consortia for biotechnological applications

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## Abstract

The marine microbiome is a key driver of the blue economy, making its study essential to discover, protect, and use ocean resources sustainably. It consists of microbial communities that interact with one another, often competing, but also cooperating, enabling functions beyond individual capabilities and opening avenues for biotechnological applications.
To harness this potential, we propose a computational pipeline for designing microbial consortia tailored to specific applications. As a showcase, we focus on pollutant degradation, demonstrating how microbial interactions can be leveraged to establish functional communities.

The pipeline consists of two major steps: the characterization of the metabolic capacity of strains and the inference of pairwise interactions. First, we collected 23,000 metagenome-assembled genomes (MAGs) and 6,000 prokaryotic and eukaryotic genomes from multiple databases. Each MAG and genome are characterized by the construction of genome-scale metabolic models and the retrieval of their KEGG orthologs (KOs). Candidate species are identified based on the presence of KOs related to pollutant degradation pathways, either by completing or complementing such pathways through metabolite cross-feeding.
Second, to infer interacting genome pairs, we propagate the information from a co-abundance network previously built on 234 TARA Oceans metagenomes. We link inferred interactions between TARA MAGs to isolate genomes by evaluating their similarity using Tanimoto and Hamming distances in the metabolic space. Finally, we assess the likelihood of pairwise genome interactions using a graph neural network for edge predictions and community metabolic modeling for exchanged metabolite predictions, which allows us to prioritize species selection for subsequent mono- and co-cultivation experiments.

**Keywords:** Blue economy, Multi, omics data, MAGs, microbial communities, microbial interactions, biotechnological applications, bioremediation, metabolic modeling, AI

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