A promising Computational pipeline for microbial consortia analysis using Genome-scale metabolic models

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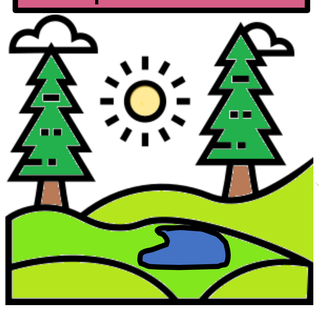
Summary

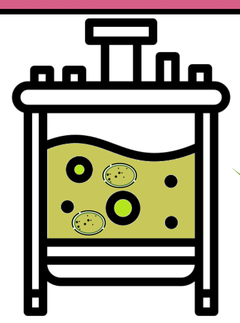
The increasing interest of complex microbial communities for biotechnological solutions requires the development of computational workflows assisting the analysis of these communities. Due to the lack of tools to achieve this goal, here, we present a reproducible bioinformatic pipeline for the functional potential of natural microbial communities and the description of their interspecific interactions using genome-scale metabolic models (**GEMs**). The analysis starts from metagenomic data like **16s rRNA amplicon sequencing** or whole metagenomic sequencing. Using the integrated, and well established tools, for taxonomic identification like **Ampliseq** or **taxprofiler**, genomic data can be retrieved and the metabolic functional information are inferred. The last step involves the translation of this information into GEMs, one of the major modeling approaches for systems-level metabolic studies to infer the interactions and allow the phenotype predictions. The result is the creation of in silico microbial consortia with modeled members and interactions. This promising analysis approach allows the study of an enriched **cyanobacterial community** with the creation of in silico microbial consortia giving promising results for optimization of a microbial consortium for biotechnological production of **Polyhydroxybutyrate** (**PHB**).

Taxonomic & functional classification

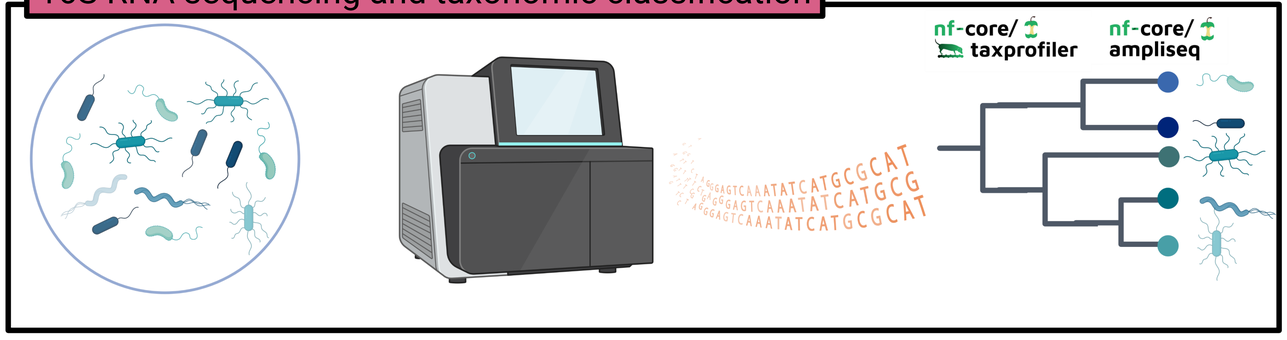
Sample collection



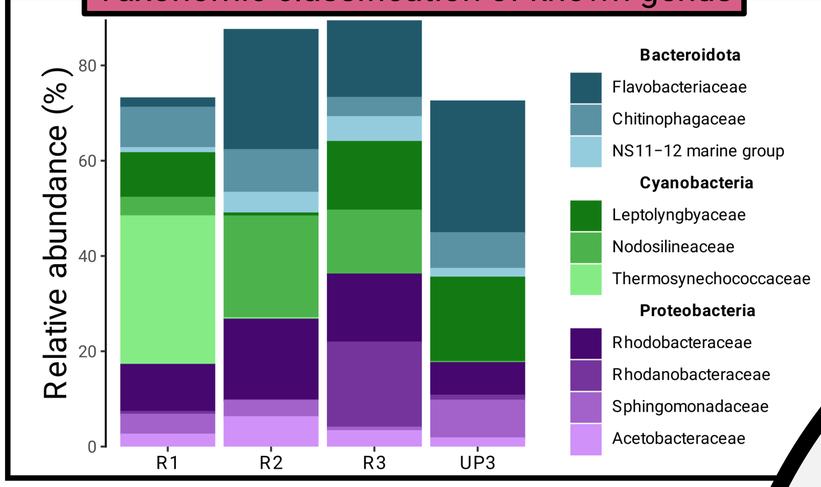
Cyanobacterial enrichment



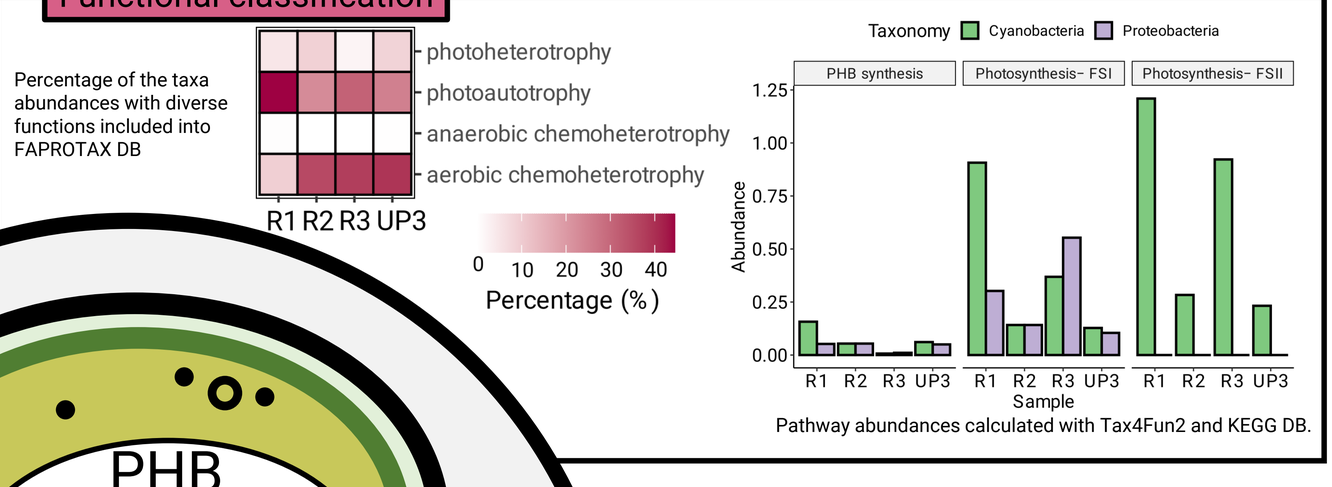
16S RNA sequencing and taxonomic classification

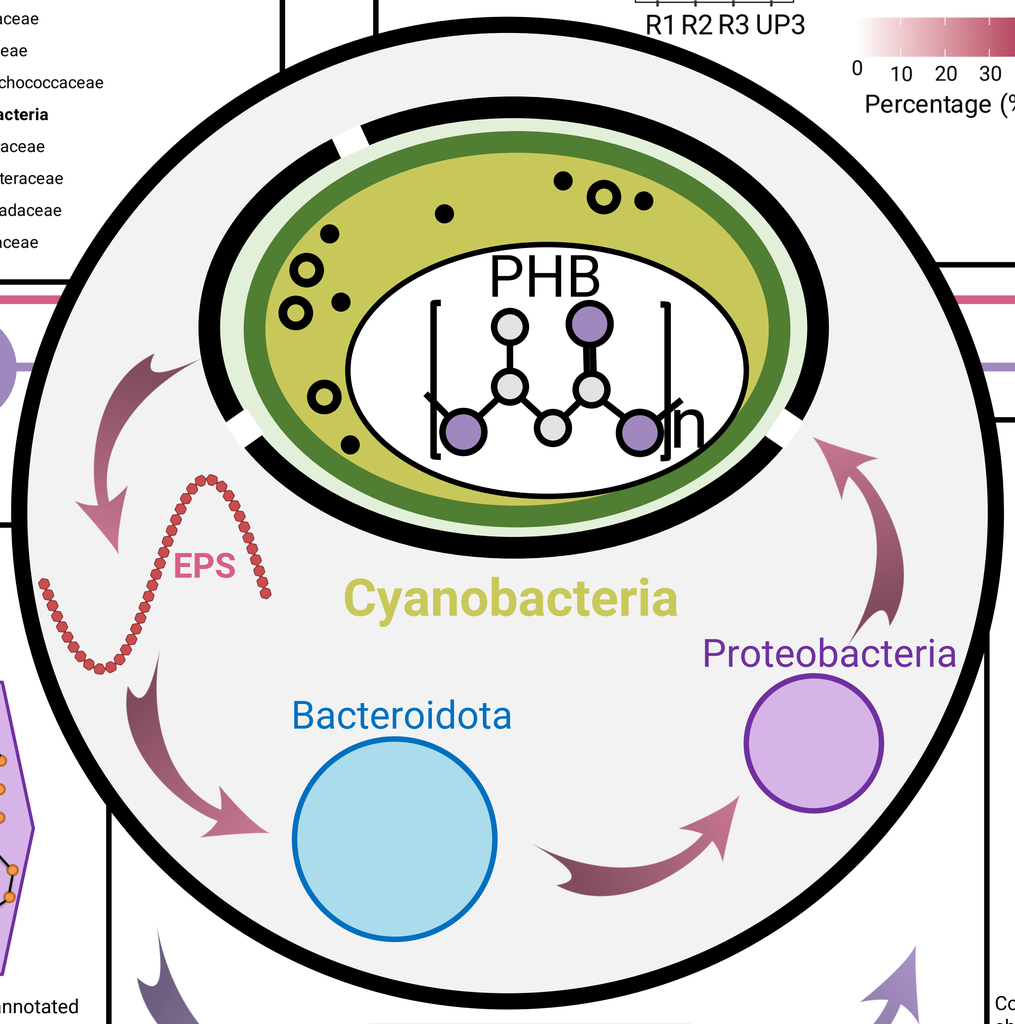


Taxonomic classification of known genus



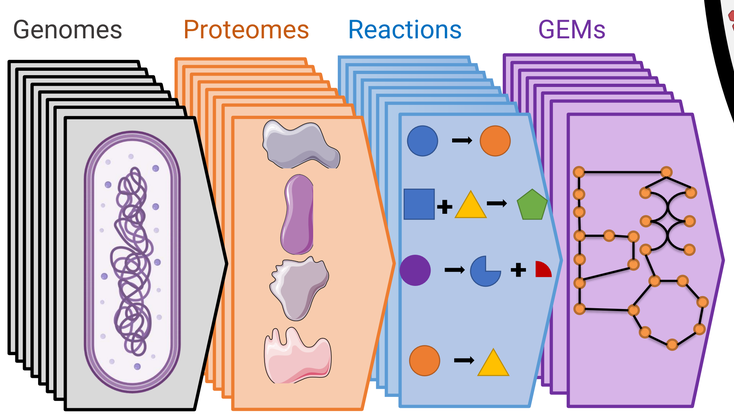
Functional classification





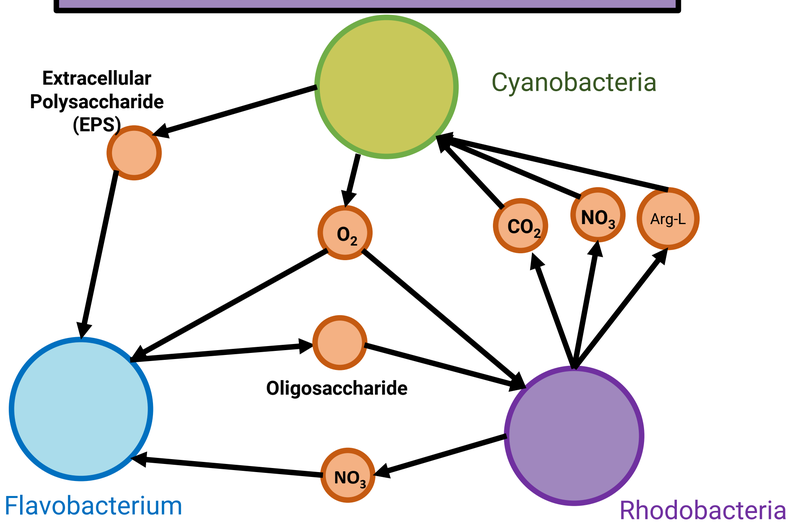
Metabolic Modelling

Metabolic modelling (genus level)



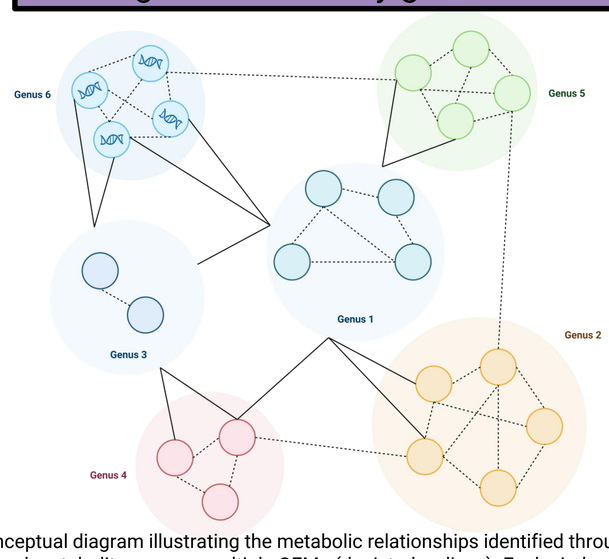
Schematic description of automatic creation of draft GEMs at genus level. The annotated genomes associated of the desired genus are downloaded from NCBI database

Identification of metabolic connections



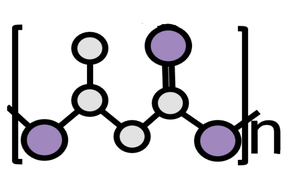
Metabolic interactions identified in the enriched cyanobacterial samples. The direction of the arrows indicate if the metabolite (Orange circles) is consumed or produced.

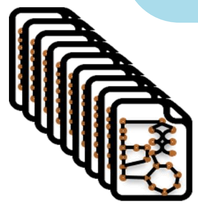
Predictions of Metabolic interactions among the community genus

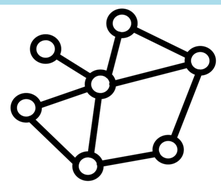


Conceptual diagram illustrating the metabolic relationships identified through shared metabolites across multiple GEMs (depicted as lines). Each circle represents an individual GEM, while the colored areas indicate sets of GEMs belonging to the same genus

Summary of results







4 Functional potential of PHB microbial consortia

3 Draft metaGEMs database

Prediction of microbial community **metabolic links**

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