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metagWGS: a workflow to analyse short and long HiFi metagenomic reads Taxonomic profile HiFi vs Short reads assembly

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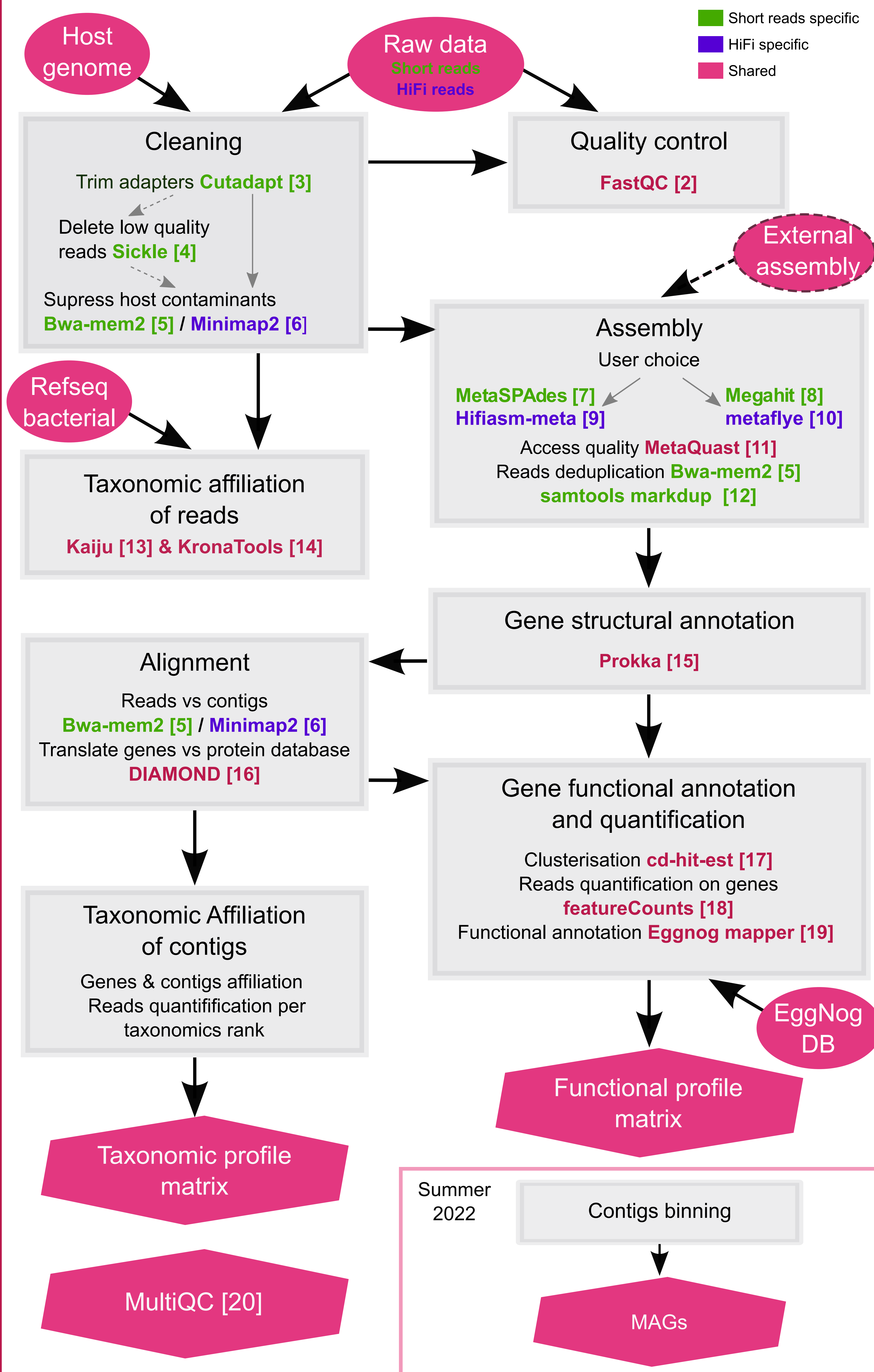
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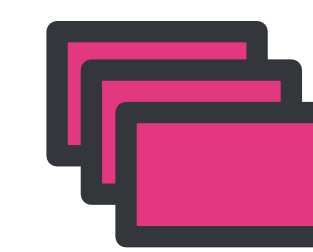
* These two authors contributed equally to this work

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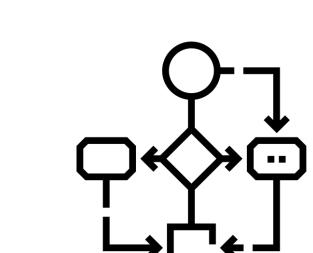
Production of whole metagenome assembly, functional and taxonomic profile



Workflow features



Type of NGS data:
whole genome shotgun sequencing (Illumina HiSeq3000 or NovaSeq, paired, 2*150bp ; PacBio HiFi reads, single-end)



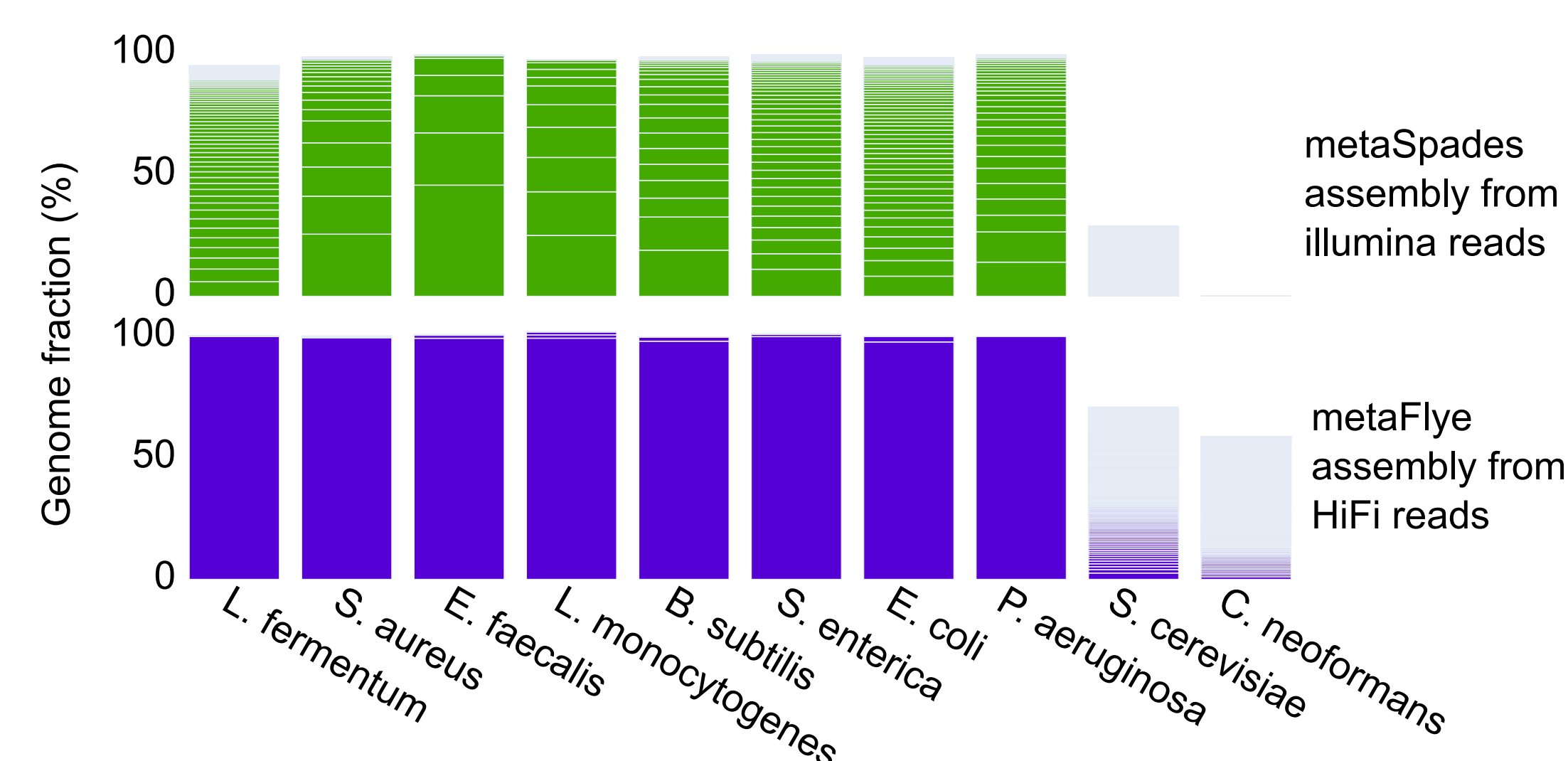
Workflow:
a scalable and reproducible metagenomic analysis with a **nextflow** [1] pipeline using **Singularity** [21] container



Fully documented
<https://forgemia.inra.fr/genotoul-bioinfo/metagwgs>

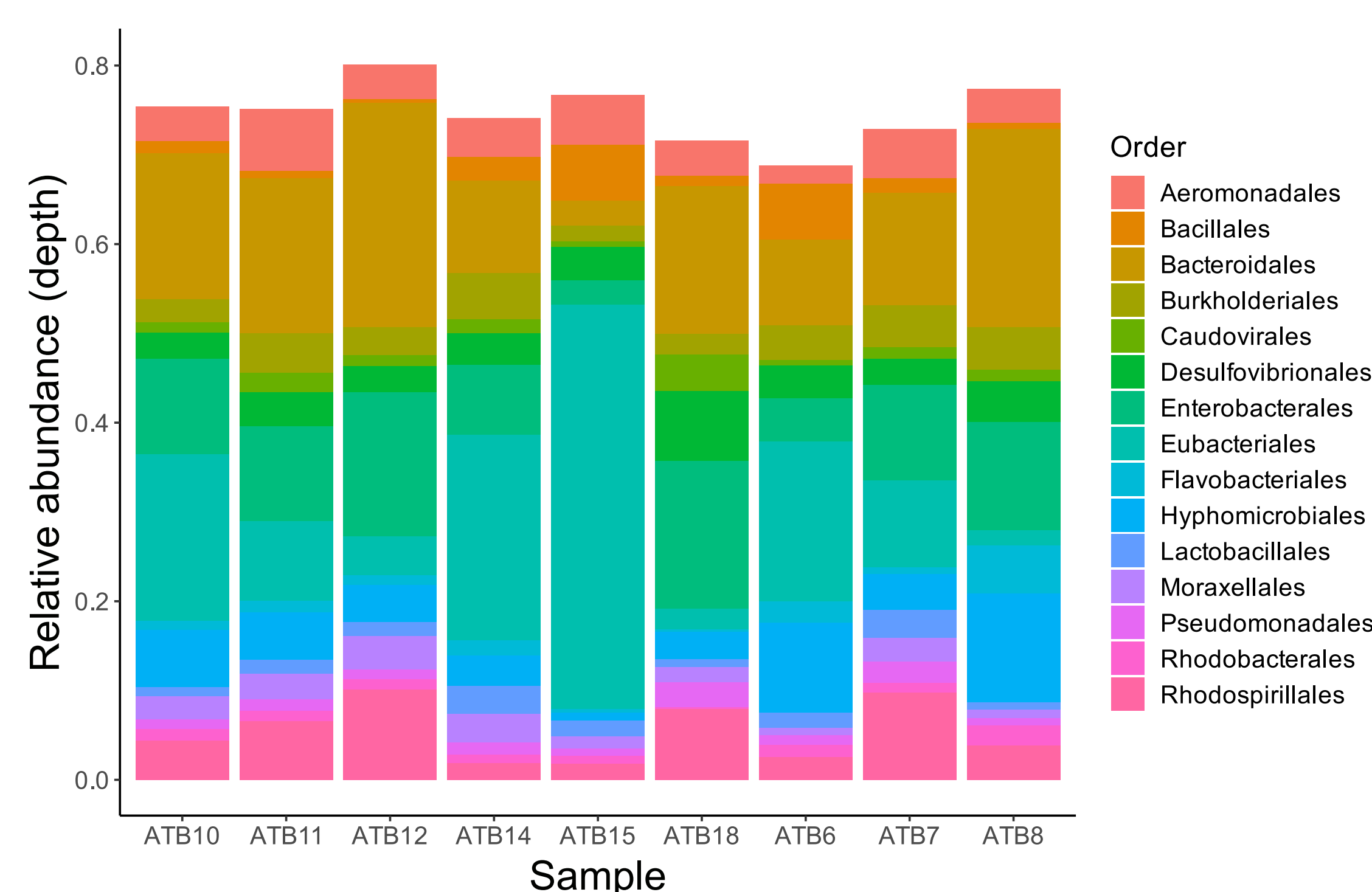
Results examples

HiFi vs Short reads assembly



Bacterial genomes of mock Zymobionics are assembled in one contig by HiFi reads. The genome fraction is the fraction of the reference genomes covers by the assembly. Each block in a bar represents a contig. Bacterial genomes are well covered by all assemblies but Illumina assembly is much more fragmented.

Taxonomic profile



Relative abundance of the 15 major orders of nine biofilms grown in bioreactors from sewage (example from ATB biofilm project). Graph made from the taxonomic profile matrix generated by metagWGS. ATB15 is a sample that was exposed to ciprofloxacin (antibiotic) during the 14 days of culture.

Perspectives

Annotation of Antibiotic Resistant Genes Annotation of mobilome genes Co-assembly

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