



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

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Joanna Fourquet, Jean Mainguy, Maïna Vienne, Céline Noirot, Pierre Martin, et al.. metagWGS: a workflow to analyse short and long HiFi metagenomic reads Taxonomic profile HiFi vs Short reads assembly. JOBIM 2022, Jul 2022, Rennes, France. Actes des exposés (keynotes, contributions orales, mini-symposia): JOBIM2022_proceedings_oral.pdf (23 Mo) et actes des posters et démos: JOBIM2022_proceedings_posters_demos.pdf (19 Mo). 10.15454/1.5572369328961167E12 . hal-03771202

HAL Id: hal-03771202

<https://hal.inrae.fr/hal-03771202>

Submitted on 7 Sep 2022

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metagWGS: a workflow to analyse short and long HiFi metagenomic reads

Joanna Fourquet^{1*}, Jean Mainguy^{1*}, Maïna Vienne¹, Céline Noiro¹, Pierre Martin¹, Vincent Darbot³, Olivier Bouchez², Adrien Castinel², Sylvie Combes³, Carole Iampietro², Christine Gaspin¹, Denis Milan², Cécile Donnadieu², Geraldine Pascal³ and Claire Hoede¹

¹ INRAE, Université de Toulouse, UR875 MIAT, Bioinfomics, PF GenoToul Bioinfo, F-31326, Castanet-Tolosan, France (doi: 10.15454/1.5572369328961167E12)

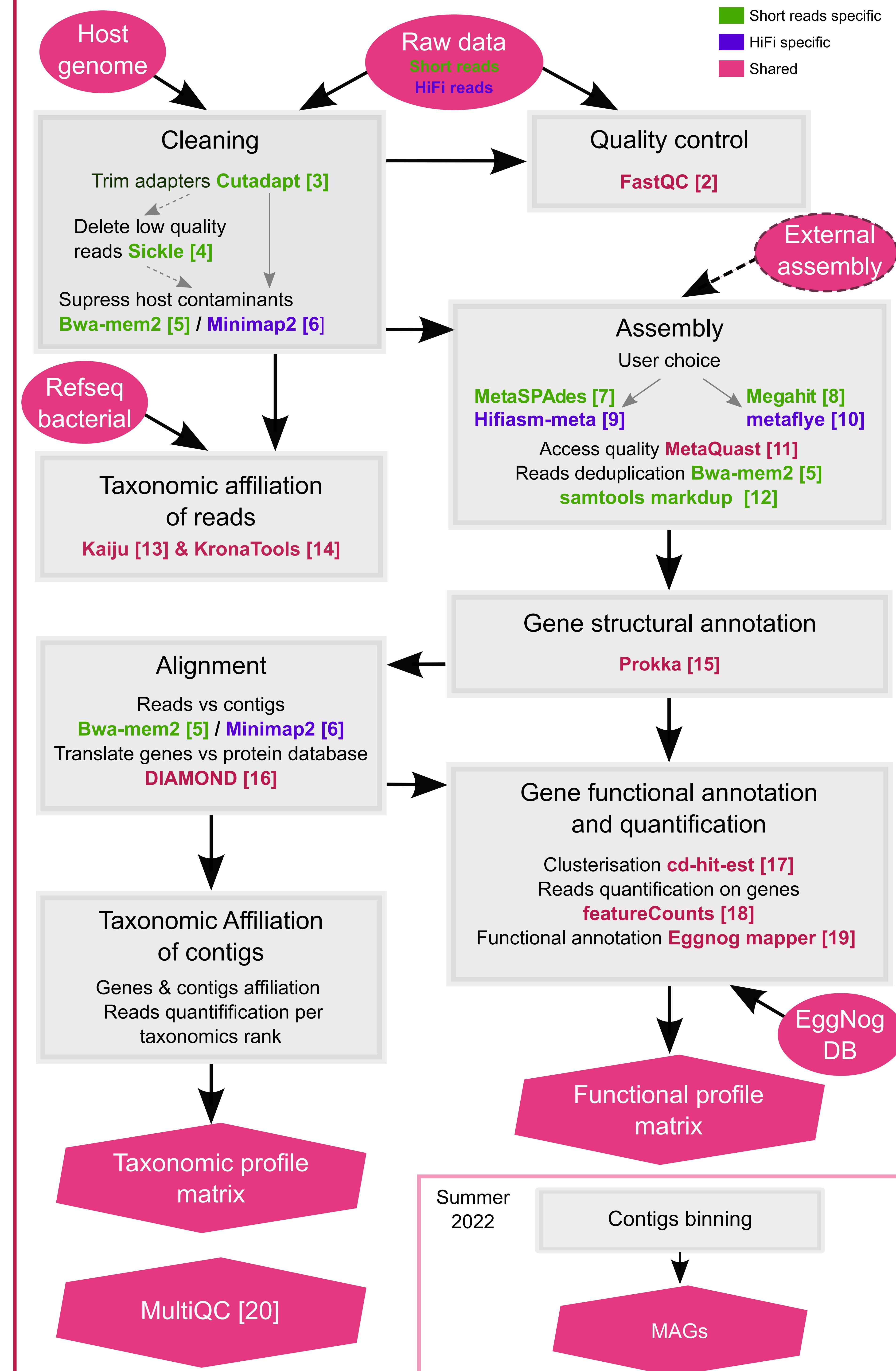
² INRAE, GeT-PlaGe, Genotoul – INRAE – 31326 Castanet-Tolosan, France (doi: 10.15454/1.5572370921303193E12)

³ GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet Tolosan, France

* These two authors contributed equally to this work

Corresponding author: claire.hoede@inrae.fr

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:

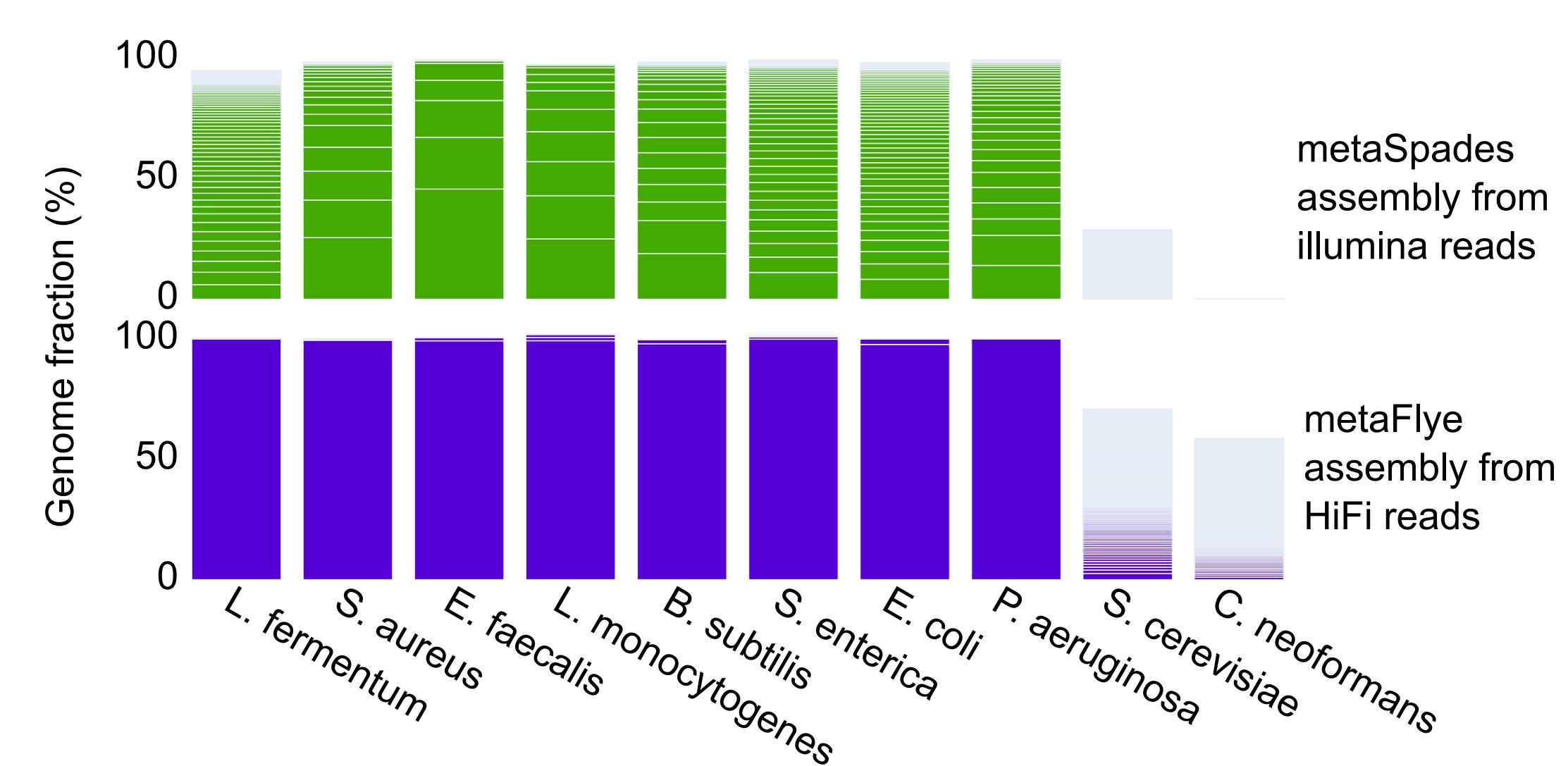
a scalable and reproducible metagenomic analysis with a **nextflow** [1] pipeline using **Singularity** [21] container

Fully documented

<https://forgemia.inrae.fr/genotoul-bioinfo/metagwgs>

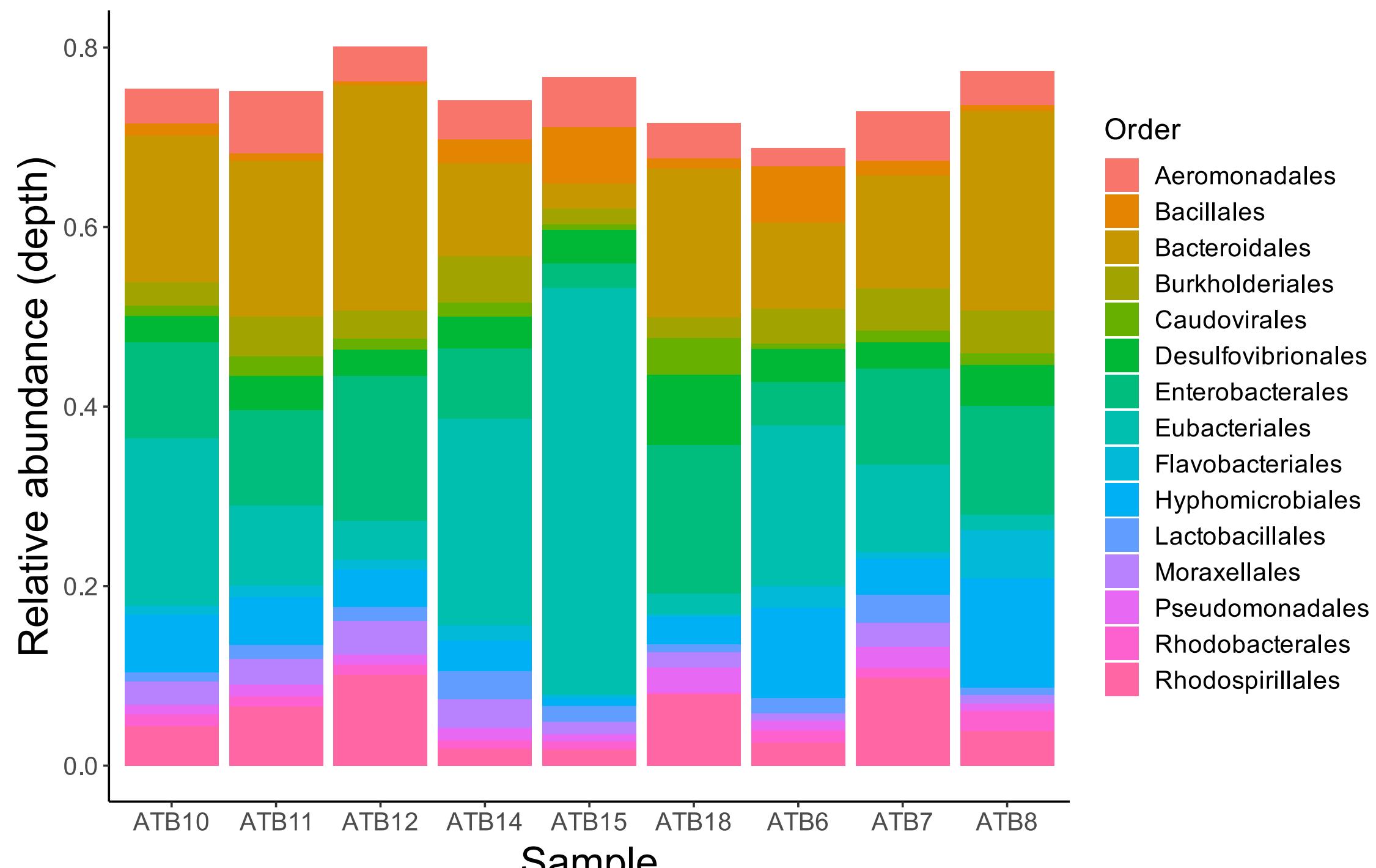
Results examples

HiFi vs Short reads assembly



Bacterial genomes of mock Zymobiomics are assembled in one contig by HiFi reads. The genome fraction is the fraction of the reference genomes covered 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 mobileome genes

Co-assembly

Acknowledgements

SeqOcIn financed by FEDER funds (Programme Opérationnel FEDER-FSE_Midi-Pyrénées et Garonne 2014-2020)

ATB_Biofilm funded by PNREST Anses, 2020/01/142

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