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# Metagenomic assembly of complex ecosystems with highly accurate long-reads

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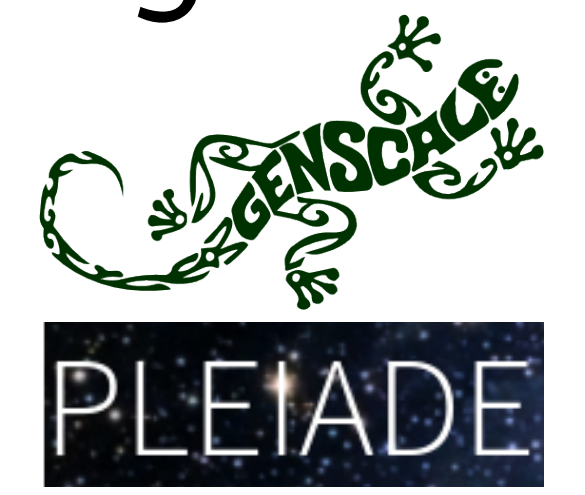
# Metagenomic assembly of complex ecosystems with highly accurate long-reads



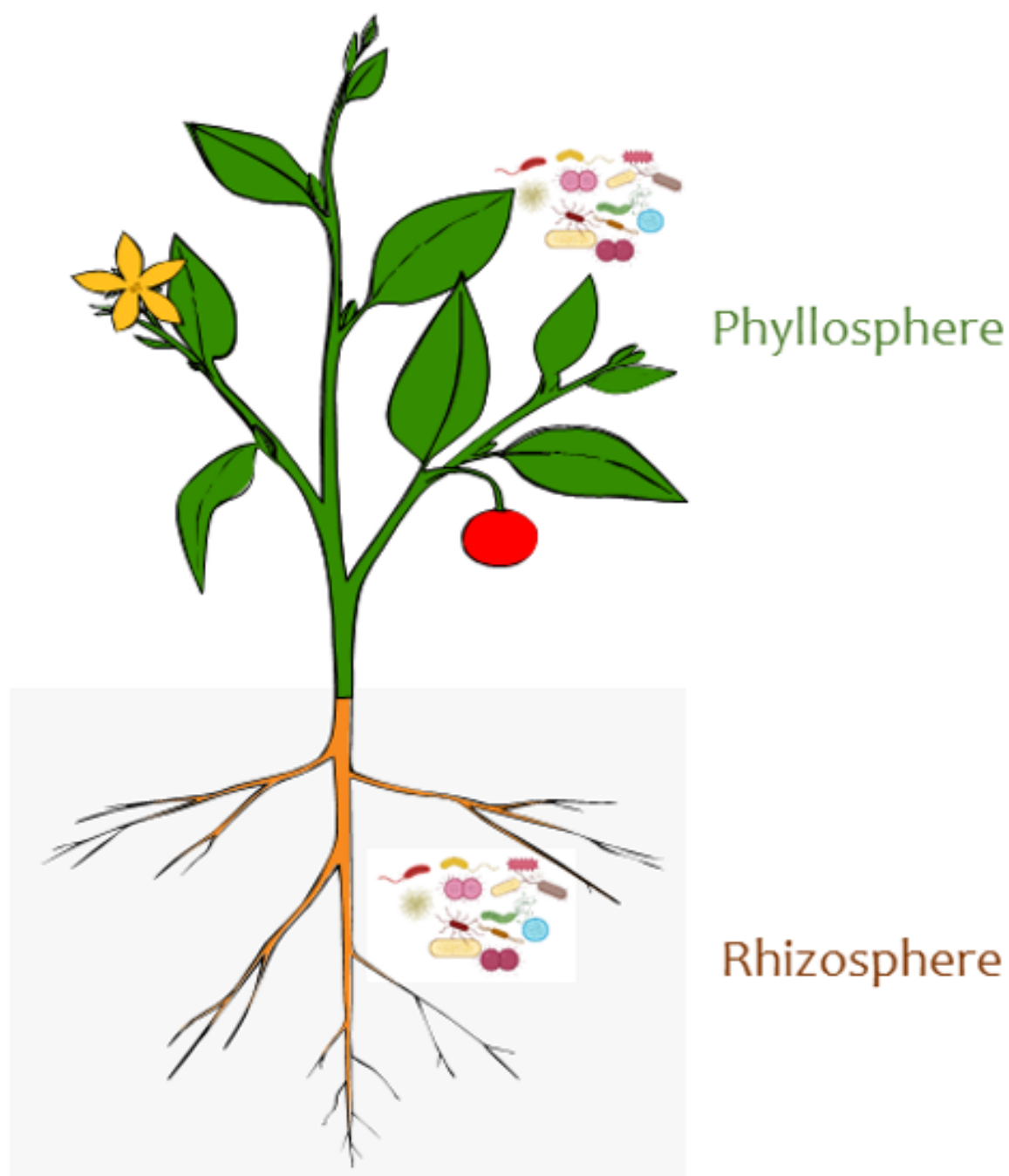
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## Context



### Plant microbiota

Plants can recruit micro-organisms from the millions ( $10^3$ - $10^8$ /g) found in soil, to regulate key functions such as :

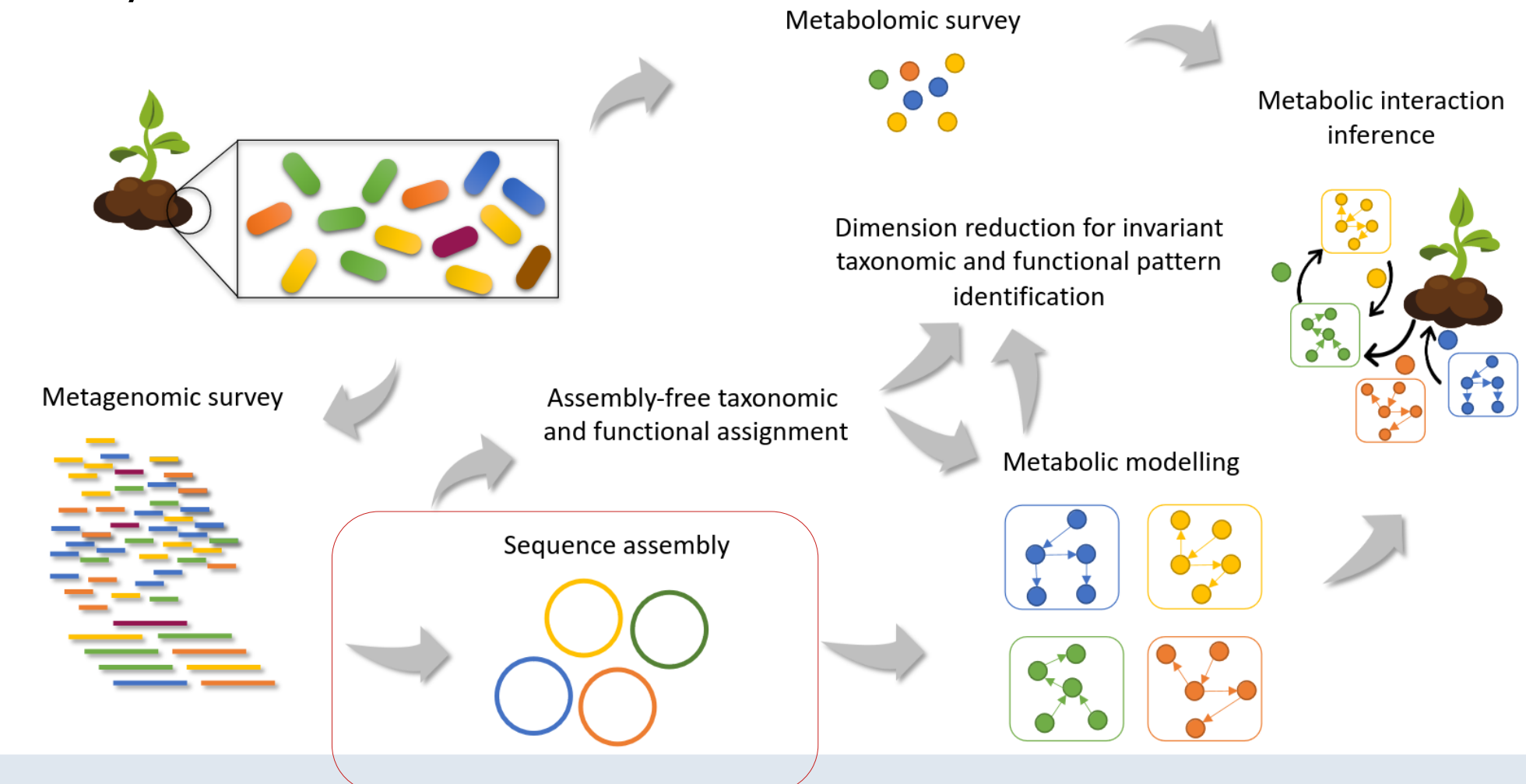
- Nutrition and growth,
- Abiotic stress,
- Biotic stress.

Still, both ecosystems are poorly characterised, as culturomics, transcriptomics and short-read metagenomics cannot recover enough complete genomes needed to modelise and characterise those communities.

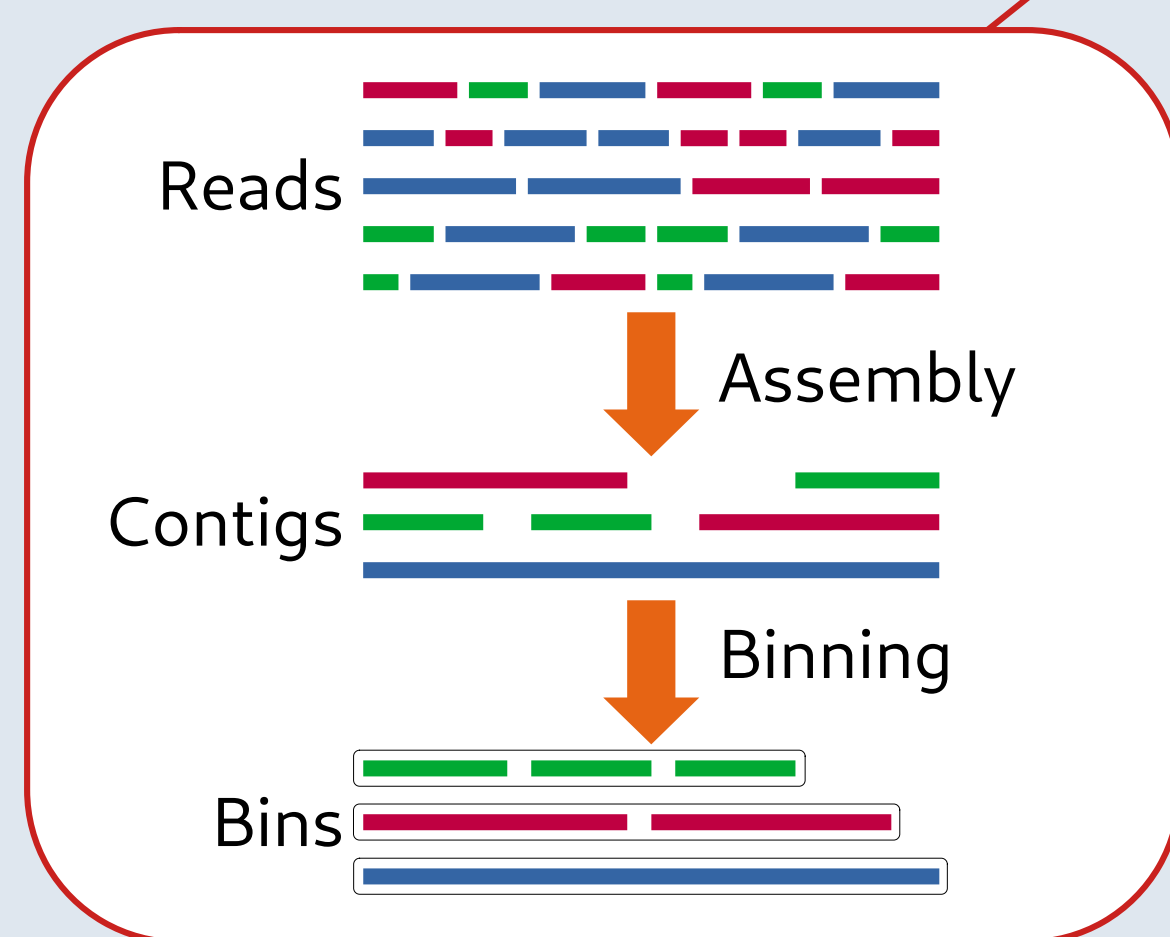
### MISTIC Project : [project.inria.fr/mistic](http://project.inria.fr/mistic)

Methodological development for microbial community dynamics modelling

- WP1 : Top down approach from large-scale data on natural communities,
- WP2 : Bottom up approach, building dynamic models of increased complexity under controlled conditions.



## Motivations



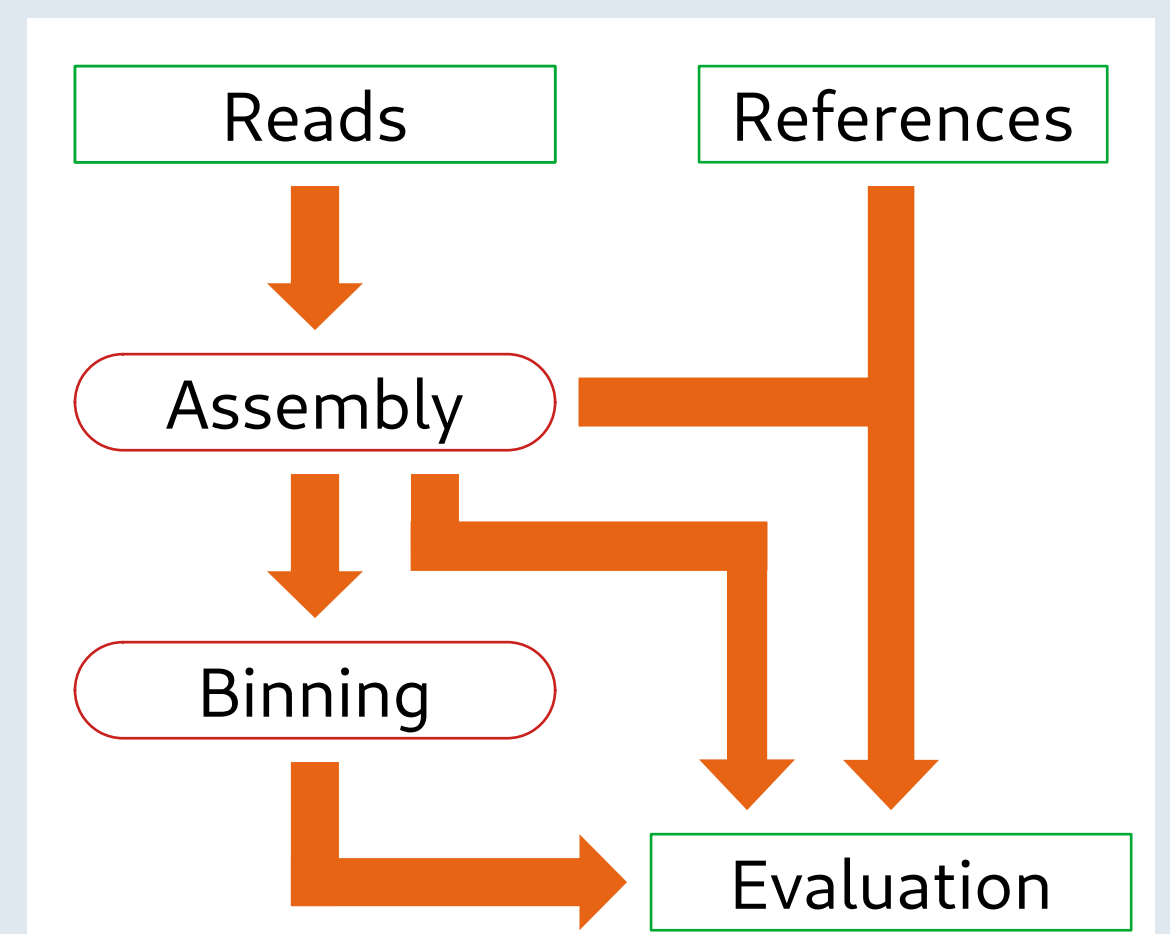
### Emerging sequencing technologies

	Read type	Read length (bp)	Error rate
Illumina	Short reads	151 bp	~0.1
ONT R9.4	Long reads	~20kb	~10%
PacBio CLR		~10kb	~10%
ONT R10.4	Highly accurate	~20kb	~1%
PacBio Hi-Fi	long reads	~10kb	~1%

Higher quality reads lead to higher quality assemblies.

**How to exploit those highly accurate long-reads to recover high-quality genomes from complex environments such as soil and rhizosphere ?**

## Mapler : [gitlab.inria.fr/mistic/mapler](http://gitlab.inria.fr/mistic/mapler)



### Pipeline

Built with Snakemake and Slurm integration.

Benchmarks three highly accurate long reads assemblers :

- Metaflye<sup>1</sup>,
- Hifiasm-meta<sup>2</sup>,
- MetaMDBG<sup>3</sup>.

### Datasets

	Total size (Gb)	Median size (Kb)	Taxonomic complexity
Zymo D6331	18.0	8.1	Mock community
Human gut	15.2	8.4	+
Rhizosphere	19.5	5.8	++
Soil	13.4	6.0	+++

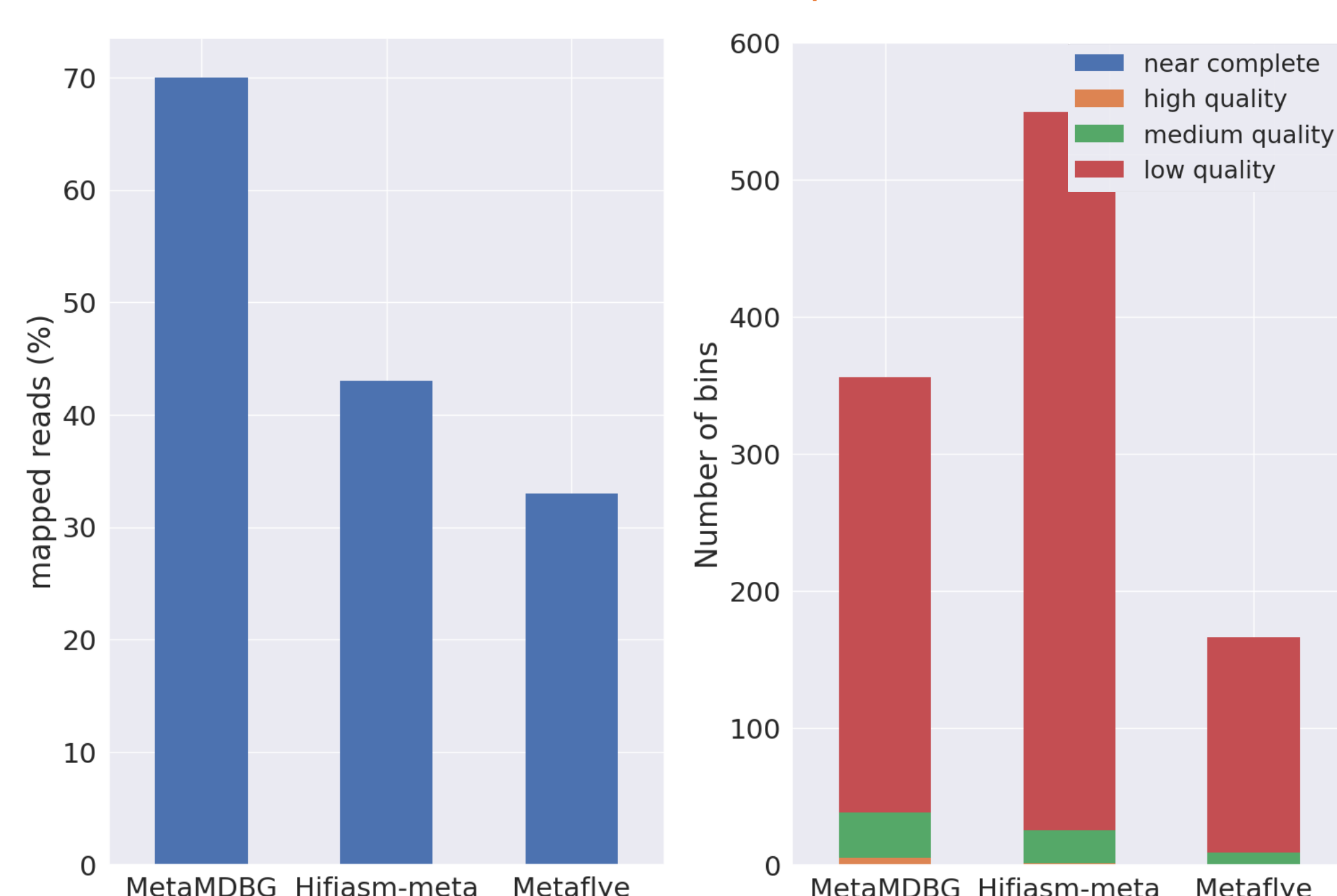
### Evaluation metrics

- Aligning contigs on reference genomes, if available : NGA50 and genome fraction,
- Aligning reads on contigs : counting reads that map to the assembly,
- Evaluating the bins completeness and contamination with marker genes, then categorizing bins by level of quality.

## Mapler : Results

### Assembler comparison

On the soil sample

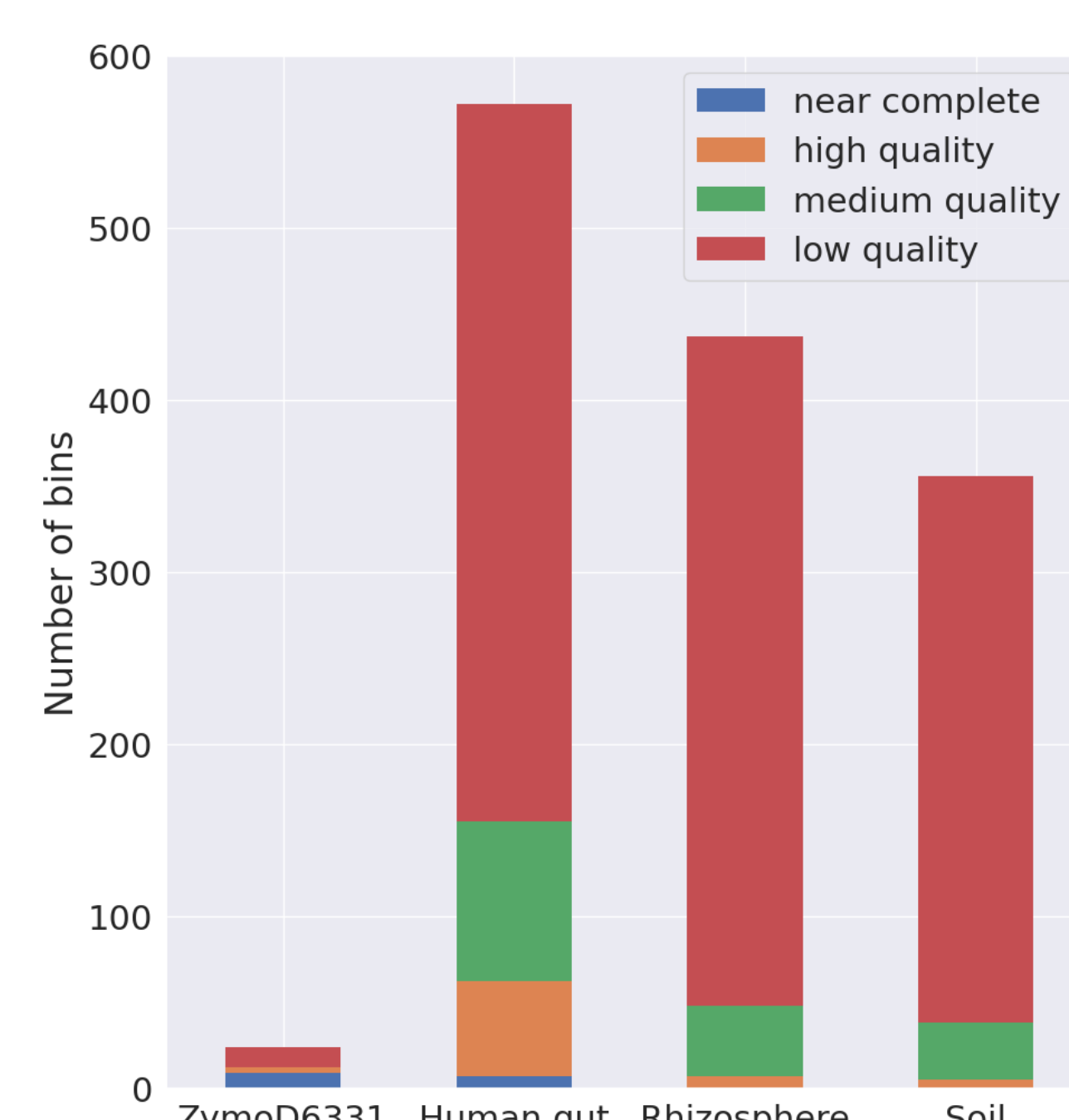


MetaMDBG captures :

- A greater proportion of reads,
- More high-quality bins,
- More medium-quality bins.

### Sample comparison

Using metaMDBG

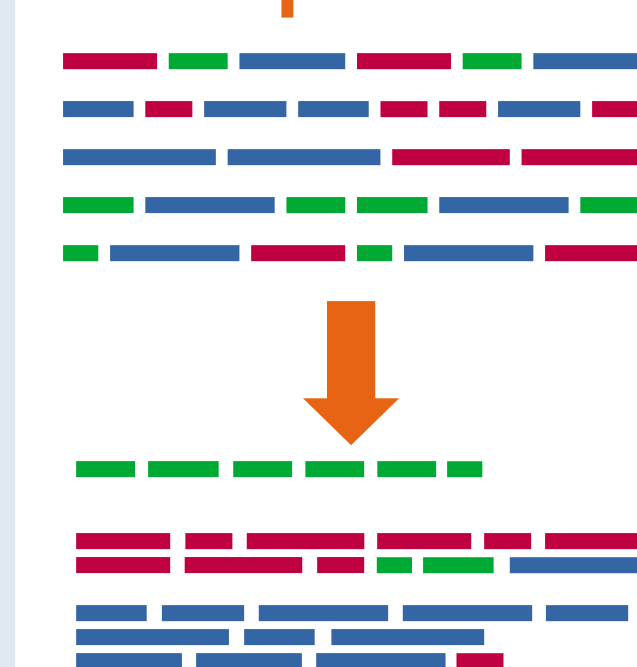


As taxonomic complexity increases :

- Quality of bins decreases,
- Proportion of captured taxa decreases.

## Methodological avenues of improvement

### Read partitioning

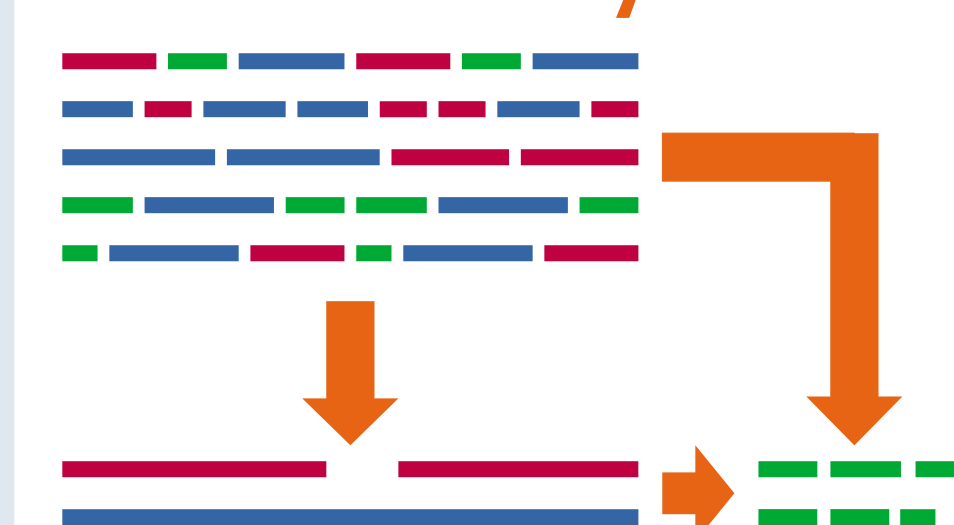


By partitioning the reads into smaller sets via :

- Taxonomic assignation,
- Composition-based clustering,
- Abundance-based clustering.

We could reduce the complexity of each subset, simplifying the assemblies.

### Read recovery



By mapping the reads on contigs, we could extract unassembled reads, and assemble those separately with reduced complexity.

### Hybrid assembly or binning

Highly accurate long reads could be complemented by a higher coverage of short reads, which could be used to better assess the abundance of each long-read, leading to a better assembly or binning.

[1] M.Kolmogorov et Al. metaFlye: scalable long-read metagenome assembly using repeat graphs, 2020

[2] X. Feng et Al. Metagenome assembly of high-fidelity long reads with hifiasm-meta, 2022

[3] G. Benoit et Al. High-quality metagenome assembly from long accurate reads with metaMDBG, 2024