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

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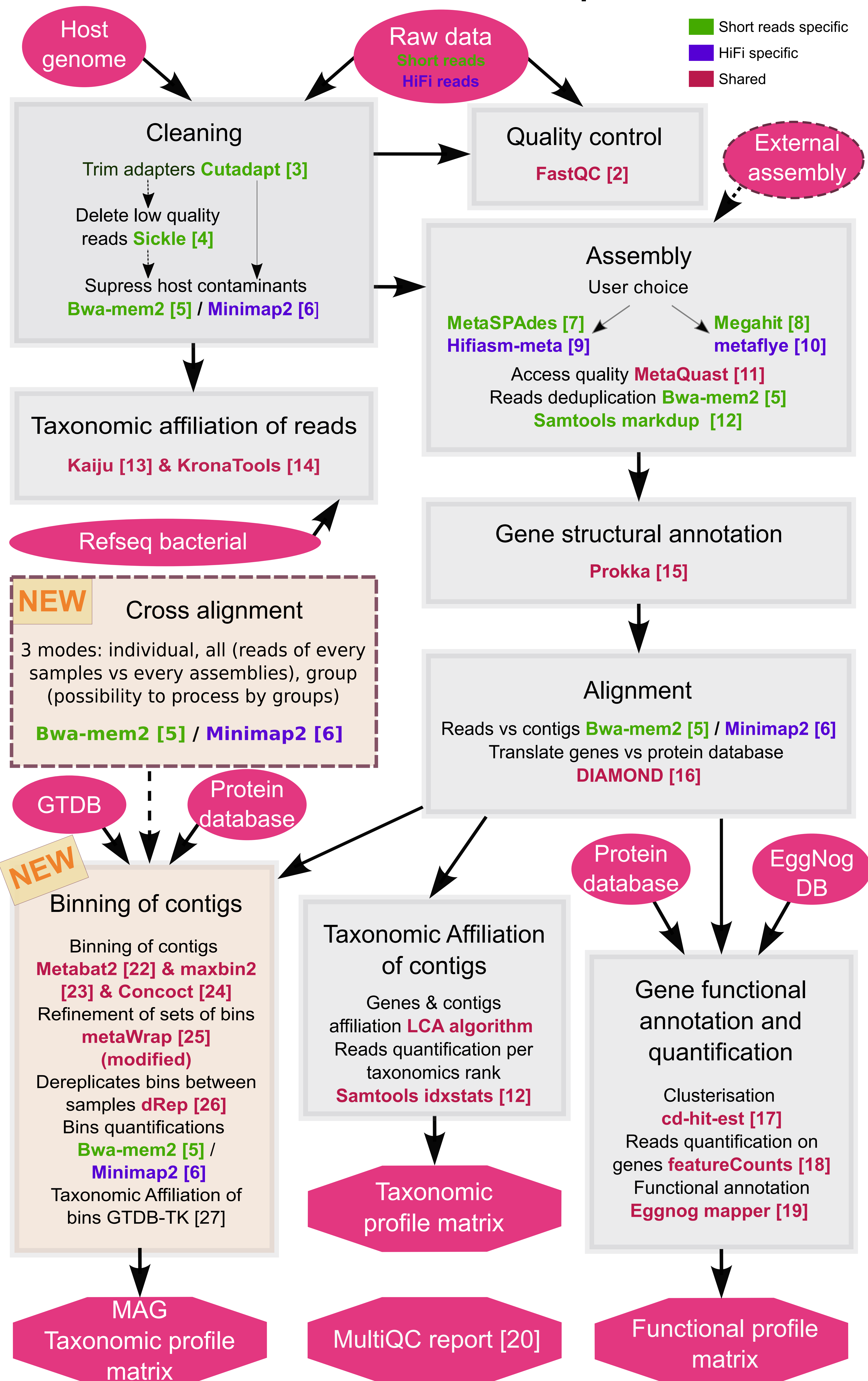
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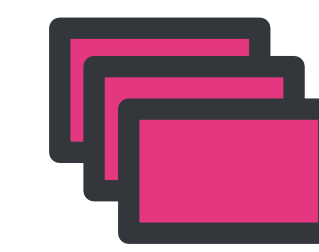
- 1 Université Fédérale de Toulouse, INRAE, BioinfOmics, GenoToul Bioinformatics facility, 31326, Castanet-Tolosan, France
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- * Present at ECCB 2022

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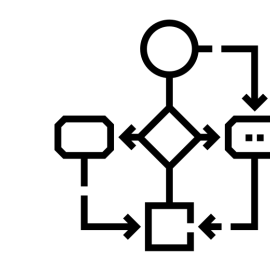
Production of whole metagenome assembly, functional and taxonomic profile



Workflow features



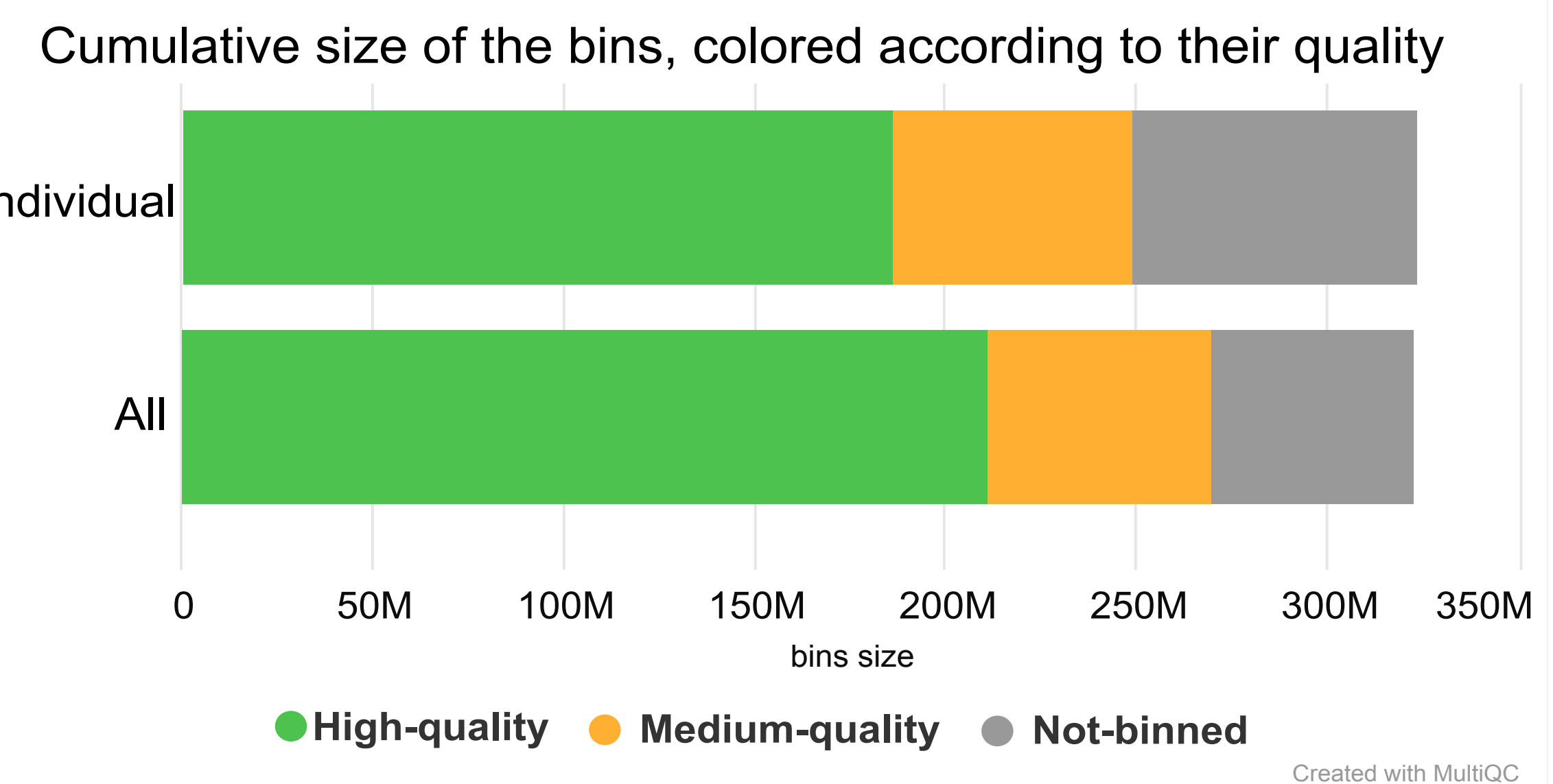
Type of NGS data:
whole genome shotgun sequencing (Illumina HiSeq3000 or NovaSeq, paired, 2*150bp ; PacBio HiFi reads, single-end)



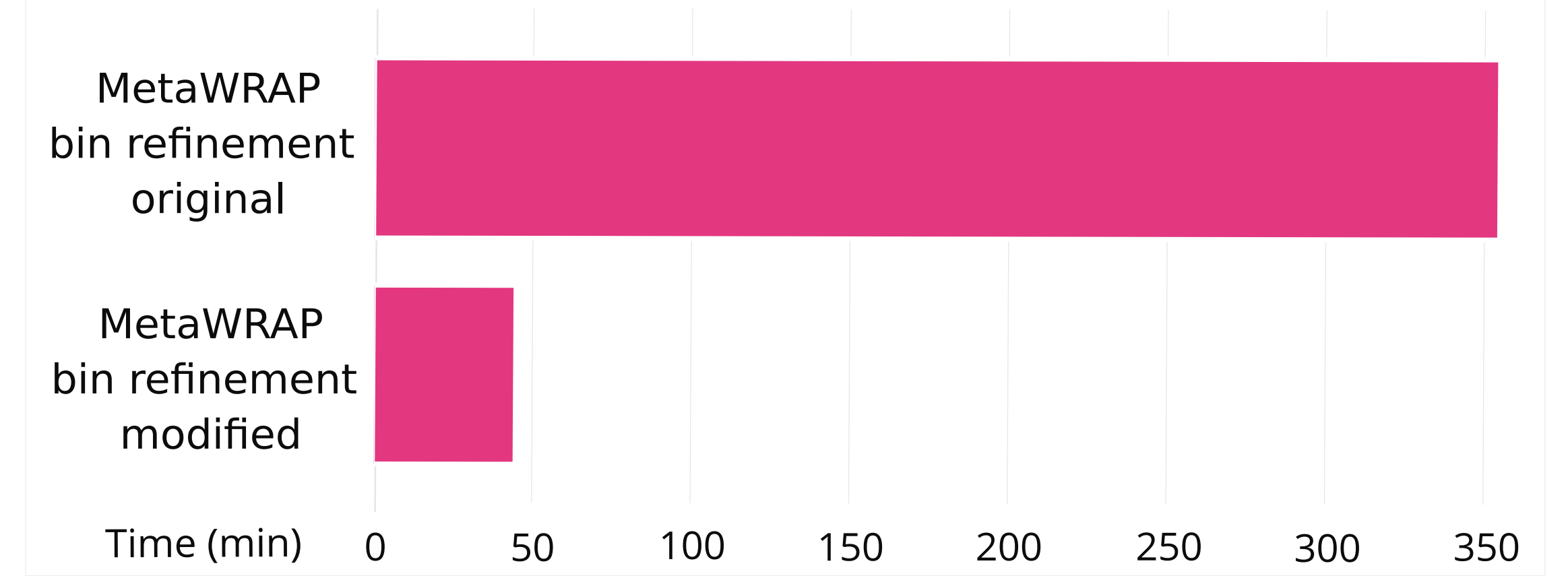
Workflow:
a scalable and reproducible metagenomic analysis with a **nextflow** [1] pipeline using **Singularity** [21] containers



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



The strategy of aligning reads of every samples (**Cross-alignment: All**) against each assembly improved the quality of binning. Tests were done on a synthetic mock composed of 142 bacteria and archea genomes with 3 samples of 66.651.100 Illumina paired-end reads (2x150bp).



The improved version uses Checkm2 [28] instead of Checkm1 [29] and takes advantage of a custom resume parameter. The modified version gives very similar results.

Conclusion

The new version of **metagWGS (2.3)** allows the analysis of **Illumina short reads** or **PacBio HiFi long-reads sequencing data** and brings as a **major new feature the binning of contigs**.

The workflow proposes to use the abundance information contained in nearby samples to **improve the binning by implementing cross-alignment per sample set**.

We have also improved the performance of the **bins refinement step by dividing the execution time by 7**.

References



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Perspectives

Better assembly of the minority species when the sequencing depth is not sufficient: implementation of co-assembly (by giving the possibility to normalize data first).

Improve the performance of the workflow: replacing Prokka [15] with other tools.

Long term perspectives: enable the annotation of antibiotic resistance genes and of the mobileome