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

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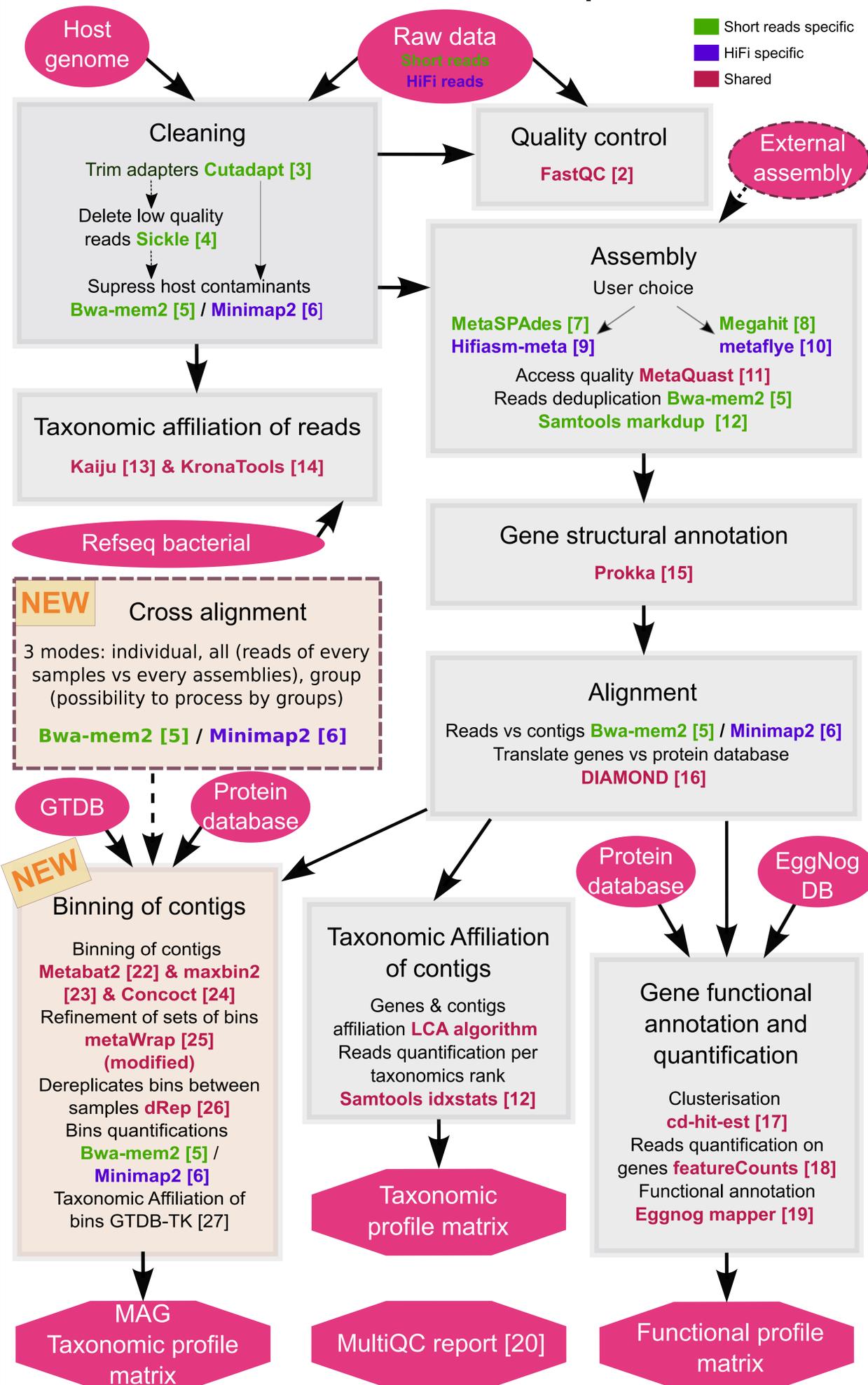
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Production of whole metagenome assembly, functional and taxonomic profile



Workflow features



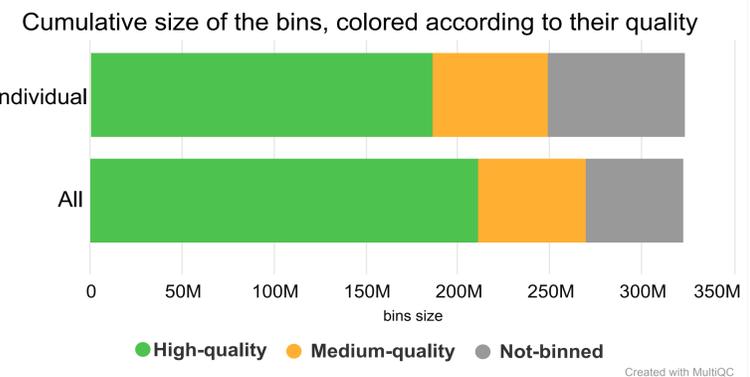
Type of NGS data:
whole genome shotgun sequencing (Illumina HiSeq3000 or NovaSeq, paired, 2*150bp ; PacBio HiFi reads, single-end)



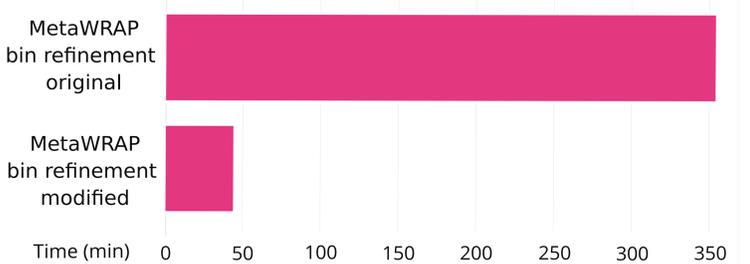
Workflow:
a scalable and reproducible metagenomic analysis with a **nextflow** [1] pipeline using **Singularity** [21] containers



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).



Execution time in minutes of the original MetaWRAP bin refinement module [25] compare to the improved version implemented in metagWGS, on the synthetic mock. 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