



Advantages and disadvantages of Genome Resolved Metagenomics



Kateryna Pantiukh¹, Reidar Anderson^{1,2}, Elin Org¹

¹Institute of Genomics, University of Tartu, Estonia ²Institute of Molecular and Cell Biology, University of Tartu, Estonia

Goal

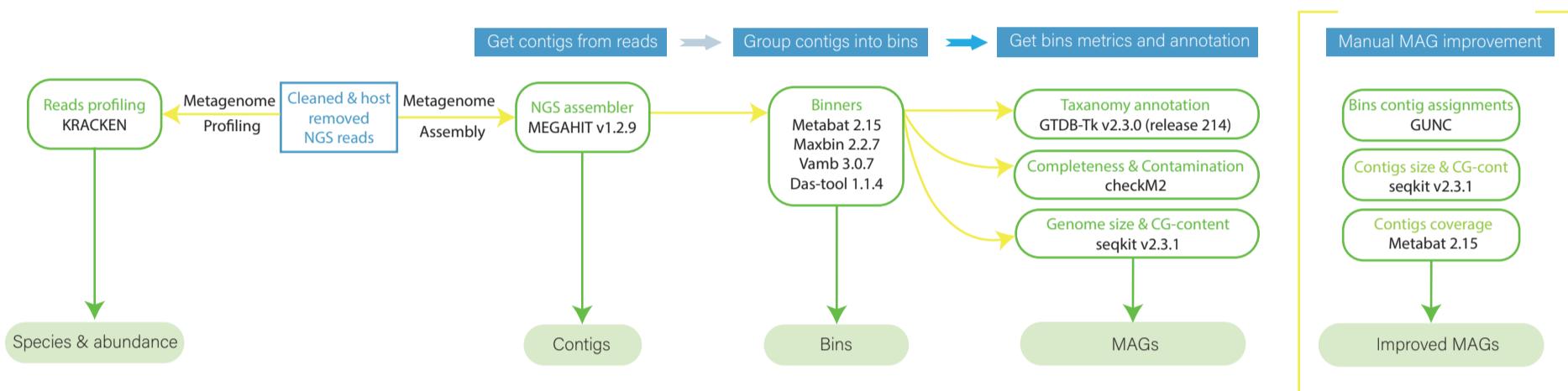
To clarify the advantages and disadvantages of the Metagenome Assembly approach so that other researchers can make informed decisions about its use.

Questions

What is the detection threshold for microorganisms using metagenomic profiling and metagenomic assemblies?
Can we improve the quality of Metagenome Assembled Genomes (MAGs) to obtain a high-quality genome for functional analysis?

Data

We use mock community data with known composition as quality data for benchmarking. A similar analysis was performed on three samples of the human gut microbiome.



Mock community

Metagenome Profiling approach allowed us to identify all microorganisms present in relative abundances between 0.005% and 19% (Fig. 1A). Metagenome Assembly approach allows us to recover the genomes of all microorganisms present in the community at a relative abundance greater than 1% (Fig. 1B).

The quality of the manually assembled genome can be improved based on the following parameters: contig taxonomy annotation and length, contig coverage, and contig CG content (Fig. 1C). After manual refinement of the genomes, the final genome size corresponds to the theoretical mock community genome size (Fig. 1D).

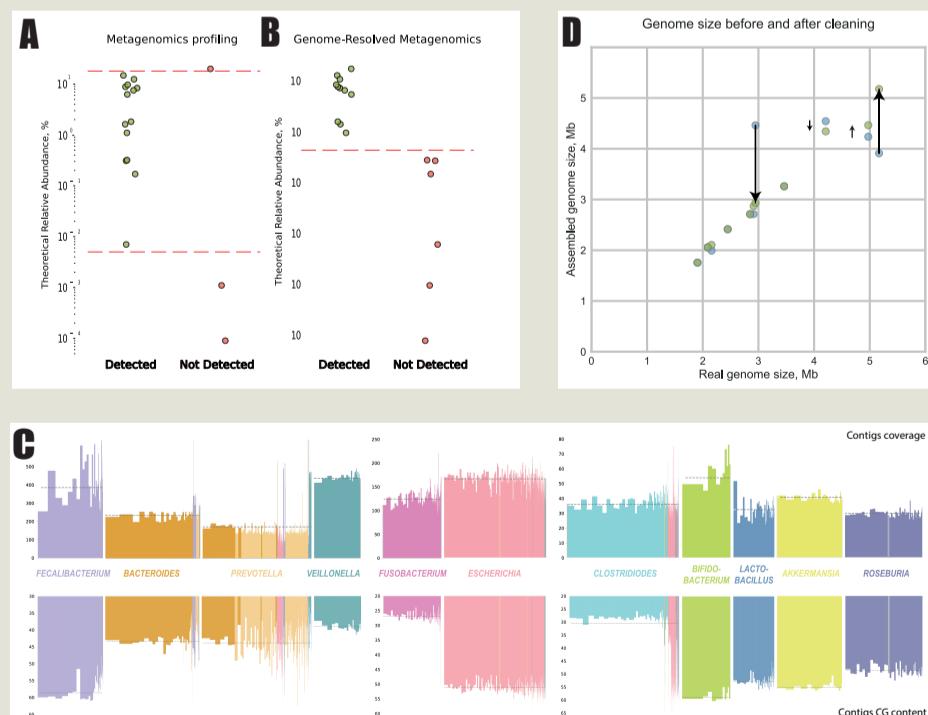


Figure 1 Metagenome analysis of mock community sequencing data.

Human gut microbiome community

By metagenomic profiling, the relative abundance of bacterial species in samples was estimated to range from 0.00009% to 26.73% (Fig. 2A). Abundance of assembled genomes bacteria were in range from 0.0078% to 14.41% (Fig 2B).

For some MAGs, genome quality can be improved. As an example, we selected the low quality (LQ) bin with 100% completeness, 82.92% contamination and unknown taxonomic annotation and performed the same analysis in the mock community. Based on the results, we divided this LQ bin into 2 bins represents *Lachnospira* and *Eubacterium* genera (Fig. 2C). Both new MAGs were rated as high-quality MAGs.

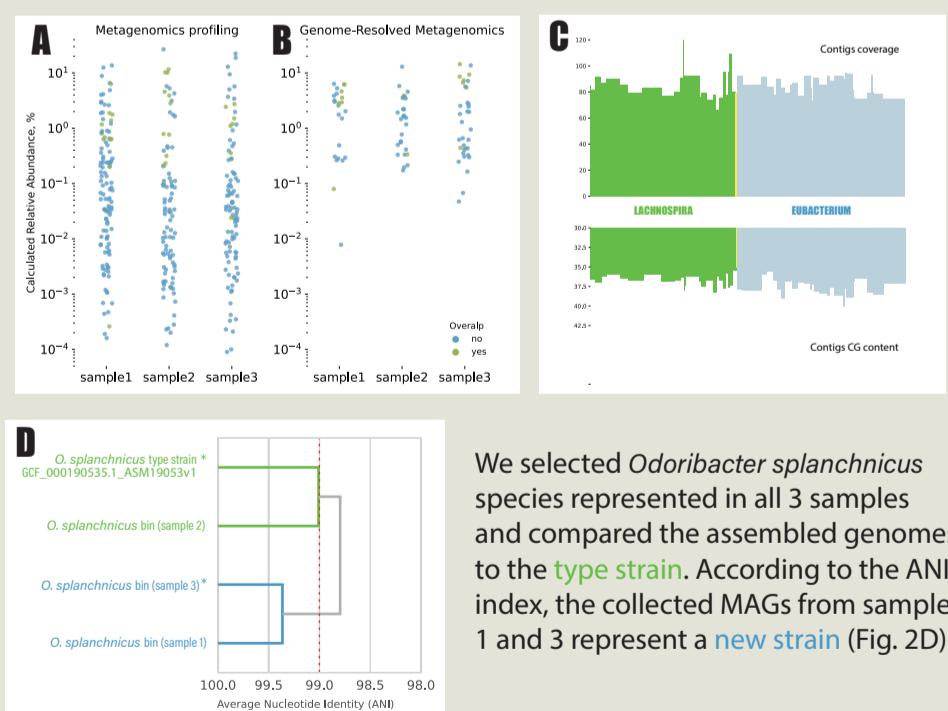


Figure 2 Metagenome analysis of human gut metagenome samples.

