

Project Topic: Reconstruction of microbial genome using long-reads

Project Partner: GFZ Deutsches Geoforschungszentrum Potsdam

Sample type: Enrichment cultures and isolates from soil

Target Molecule: DNA

Laboratory Analysis:

DNA extraction and Nanopore sequencing using the MinION device

Bioinformatic Analysis:

High Accuracy (HAC) basecalling

Genome assembly

Plasmid detection

Binning and draft genome polishing

Publish genome at NCBI

Summary:

Oxford Nanopore Technologies (ONT) offers long read sequencing by nanopore sequencing. Long reads are well suited for genome reconstruction, still the workflow requires careful execution of different computational steps from basecalling to binning of final genome. Some steps of this workflow have a high influence on the size and quality of the final genome.

More details: available soon ...

(a) Alignment of a single reads that was generated with different basecalling accuracy: high accurate - HAC(top row), super high accurate - sHAC (mid row), fast (bottom row).



(b) Completeness, contamination and size in BP of final bin/genome for different basecalling accuracy

