

Genome-centric Metagenomics

- QC of raw reads using **bbduk**
- Assembly of raw reads into contigs using **Megahit** or **Metaspades**
- Mapping of short reads using **bowtie2** or **bbmap**
- Annotation using **MetaErg**
- Binning of contigs using **Metabat**
- Assessment of bin quality using **CheckM**
- Taxonomic assignment of bins using **Gtdb-Tk**
- Extraction of bin annotation from **MetaErg** output

