## Approach 1

**DUST (BLAST) MetAMOS** Input fastq file Classify and label Removing low-Metagenomic the metagenomic complexity assembly with metagenomics dataset dataset associated genomes sequences

kraken2

## Approach 2

Get sequence ID of Remove Compare files by Get 2 output files contaminations from contaminating taxonomy ID from kraken2 species reads

- 1. Standard output file contains taxonomy ID and sequence ID
- 2. Report file contains taxonomy ID and information about species