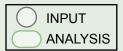
DRAM for genomes

FASTA of genomes, MAGs, or assemblies



Call genes with Prodigal Hvatt. et al. 2010

Annotate

genes with

JniProt

MEROPS

VOGDB

Count number of tRNAs with tRNAscan-SE Lowe, et al. 2016

Identify 5S, 16S, 23S with barrnap github.com/tseemann

Annotate genes with USFR database

Úserdefined Taxonomy Input

Userdefined Completion Input

Distilled & Refined Annotation of MAGs

Raw

each gene nucleotide and amino acid sequence with annotations (.faa, .fna, .tsv, .qbk)

Distillate

taxonomy, quality statistics, and key metabolisms summarized by genome (.xlsx, .tsv)

Product

genome metabolisms classified by key functional gene, with gene FASTAs output (.html, .fna, .faa)

Metabolism Distillation Levels