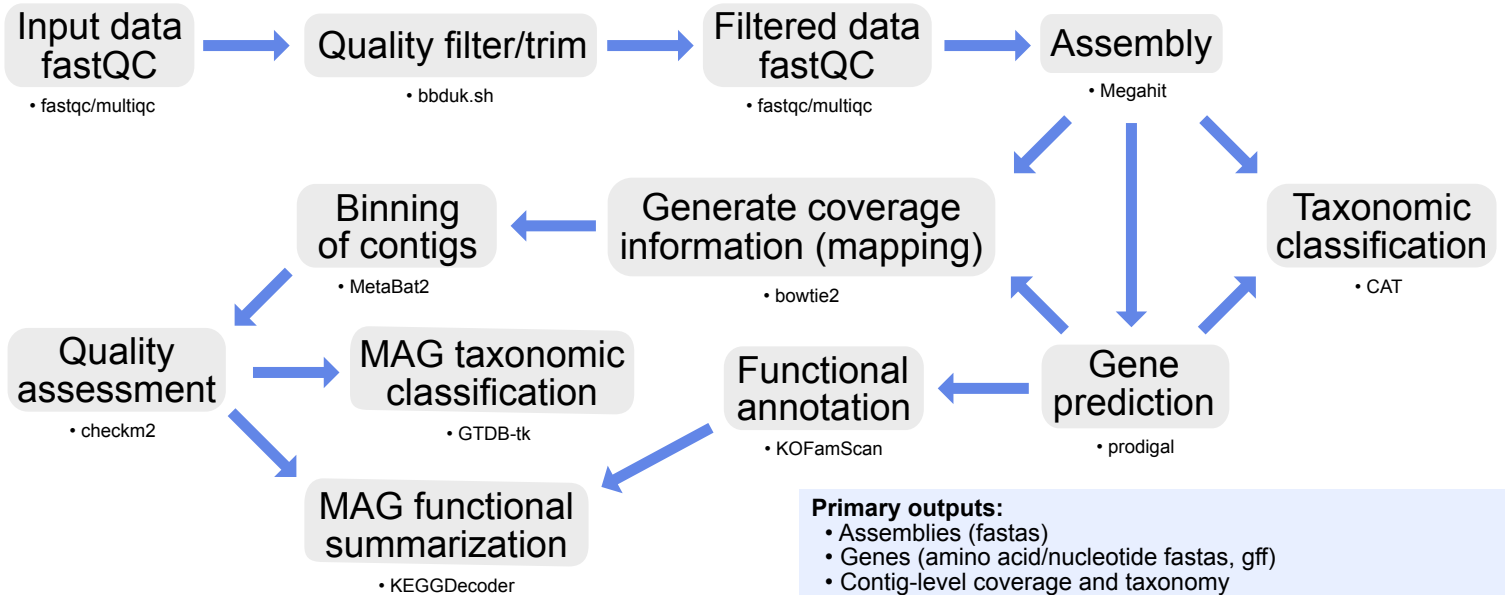


# *bit* metagenomics workflow



## Primary outputs:

- Assemblies (fastas)
- Genes (amino acid/nucleotide fastas, gff)
- Contig-level coverage and taxonomy
- Gene-level functional annotation, coverage, and taxonomy
- KEGG KO all-sample combined table with coverages
- Combined all-sample taxonomy table with coverages
- High-quality **Metagenome-Assembled Genomes** (MAGs, fasta)