Please refer to the comprehensive workflow and the necessary software outlined in the documentation. Kindly visit the developer's website for additional details, copyright information, and licensing requirements. Ensure proper citation of all original articles.

**STEP 1: Read quality check, trimming, and host contamination removal.**

1. Raw read quality check (FastQC v0.12.0)

<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

1. Read processing, adapter removal and trimming (fastp v0.23.0)

<https://github.com/OpenGene/fastp>

1. Host contamination removal (Bowtie2 v2.5.0)

<https://github.com/BenLangmead/bowtie2>

**STEP 2: Microbial ecology and community analysis.**

1. Microbial taxonomy assignment (Kraken 2 v2.0.8)

<https://github.com/DerrickWood/kraken2>

1. Relative abundance estimation (Bracken v2.8)

<https://github.com/jenniferlu717/Bracken>

1. Visualization of microbial community result (Pavian webtool)

<https://fbreitwieser.shinyapps.io/pavian/>

**STEP 3: MAG construction, identification, completeness assessment and abundance calculations.**

1. Assembly construction from sequencing reads (metaSPAdes v3.15.5)

<https://github.com/ablab/spades>

1. Assembly statistics assessment (metaQUAST v5.2)

<https://github.com/ablab/quast>

1. Metagenome construction from assembly (metaWRAP v1.2)

<https://github.com/bxlab/metaWRAP>

1. Dereplication of MAG (dRep v3.4.5)

<https://github.com/MrOlm/drep>

1. Completeness and contamination assessment of MAG (CheckM v1.1.3)

<https://github.com/Ecogenomics/CheckM>

1. MAG annotation (Prokka v1.14.6)

<https://github.com/tseemann/prokka>

1. Taxonomic classification of MAG (Phylophlan v3.0)

<https://github.com/biobakery/phylophlan>

1. MAG abundance (Samtool v1.19)

<https://github.com/samtools/samtools>

**STEP 4: Functional profiling of shotgun metagenomic reads.**

1. Taxonomic classification of reads (MetaPhlAn v4.0)

<https://github.com/SycuroLab/metaphlan4>

1. Pathway analysis (HUMAnN v3.0)

<https://github.com/biobakery/humann>