Online Metagenomic data analysis platforms

https://usegalaxy.org/

https://www.mg-rast.org/

1. Quality Control

FastQC – Quality check of raw reads

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

 MultiQC

https://multiqc.info/

Trimmomatic – Adapter trimming and quality filtering

http://www.usadellab.org/cms/?page=trimmomatic

Cutadapt – Adapter trimming

https://cutadapt.readthedocs.io/

2. Host DNA Removal

Bowtie2 – Read alignment for host genome removal

http://bowtie-bio.sourceforge.net/bowtie2/

 BBMap

https://sourceforge.net/projects/bbmap/

3. Assembly

MEGAHIT – Assembler for large and complex metagenomes

https://github.com/voutcn/megahit

metaSPAdes – Metagenome-specific assembler

https://github.com/ablab/spades

Assembly Quality Assessment

Quast: https://quast.sourceforge.net/docs/manual.html

4. Binning

MetaBAT2 – Binning contigs into genomes

https://bitbucket.org/berkeleylab/metabat/src/master/

MaxBin2 – Automated binning based on coverage and marker genes

https://sourceforge.net/projects/maxbin2/

VAMB – Deep learning-based binning

https://github.com/RasmussenLab/vamb

5. Bin Quality Assessment

CheckM – Assess completeness and contamination

https://ecogenomics.github.io/CheckM/

BUSCO – Gene-based completeness estimation

https://busco.ezlab.org/

6. Taxonomic Profiling

MetaPhlAn – Species-level profiling using clade-specific markers

https://github.com/biobakery/MetaPhlAn

Kraken2 – k-mer based taxonomic assignment

https://ccb.jhu.edu/software/kraken2/

Centrifuge – Rapid taxonomic classification

https://ccb.jhu.edu/software/centrifuge/

7. Functional Annotation

HUMAnN – Functional profiling from MetaPhlAn output

https://github.com/biobakery/humann

PROKKA – Genome annotation

https://github.com/tseemann/prokka

EggNOG-mapper – Orthology and function annotation

http://eggnog-mapper.embl.de/

8. Visualization and Downstream Analysis

Krona – Interactive taxonomic visualization

https://github.com/marbl/Krona

Phyloseq (R package) – Visualization and statistical analysis

https://joey711.github.io/phyloseq/

ggplot2 – Custom plotting (R)

https://ggplot2.tidyverse.org/

9. Supplementary tools for some asks specific analysis

dbCAN3 server: https://bcb.unl.edu/dbCAN2/

MP4: Prediction of Pathogenic Proteins in Metagenomic and Genomic Datasets (https://metabiosys.iiserb.ac.in/mp4/)

Gutbug: predict the human gut bacteria-mediated metabolism and biotransformation of biotic and xenobiotic molecules (https://metabiosys.iiserb.ac.in/gutbug/)

CRCpred: predict the healthy or CRC status of an individual based on gut bacterial abundance profile (https://metabiosys.iiserb.ac.in/crcpred/app.php)

10. Other tutorials:

https://microbenotes.com/whole-genome-sequencing/

https://timkahlke.github.io/LongRead_tutorials/OV.html

https://genomics.sschmeier.com/