

Tools for pre-processing Illumina raw reads:

Trimmomatic- <https://github.com/usadellab/Trimmomatic>

Cutadapt- <https://cutadapt.readthedocs.io/en/stable/installation.html>

Tools to check the quality of fastq reads:

Fastqc- <https://github.com/s-andrews/FastQC>

Tools to preprocess Nanopore reads:

Porechop- <https://github.com/rrwick/Porechop>

Tools to assemble Illumina/hybrid reads:

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

MIRA: <https://github.com/bachev/mira>

Unicycler (prokaryotic alone)- <https://github.com/rrwick/Unicycler>

Tools to assemble Nanopore reads alone

Flye (Prokaryotic)- <https://github.com/fenderglass/Flye>

Canu- <https://github.com/marbl/canu>

Miniasm (prokaryotic) : <https://github.com/lh3/miniasm>

RAST: (Prokaryotic): <https://rast.theseed.org/>

Tools for post assembly quality control:

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

DFAST: <https://dfast.ddbj.nig.ac.jp/>

Gvolante: <https://gvolante.riken.jp/>

Genome annotation tools:

Prokka (Prokaryotic): <https://github.com/tseemann/prokka>

Augustus: <https://github.com/Gaius-Augustus/Augustus>

BRAKER: <https://github.com/Gaius-Augustus/BRAKER>

Miscellaneous tools and websites:

TYGS: <https://tygs.dsmz.de/>

BWA: <http://bio-bwa.sourceforge.net/>

Minimap2: <https://github.com/lh3/minimap2>

Samtools: <http://www.htslib.org/>

Seqtk: <https://github.com/lh3/seqtk>

CGview: <http://cgview.ca/>

Mauve: <https://github.com/nconrad/mauve-viewer>

Tools for metagenomics:

Assembly:

Spades:

Flye:

MEGAHIT: <https://github.com/voutcn/megahit>

Classification tools:

MG RAST- <https://www.mg-rast.org/>

KRAKEN: <https://github.com/fbreitwieser/krakenuniq>

KAIJU: <https://github.com/bioinformatics-centre/kaiju>

MEGAPHLAN: <https://huttenhower.sph.harvard.edu/metaphlan/>

HUMANN: <https://huttenhower.sph.harvard.edu/humann/>

16s amplicon method:

QIIME: <https://docs.qiime2.org/>