

DNA-Tools

Inhalt nach Stichwort

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- **Flye** is a de novo assembler for single molecule sequencing reads (<https://github.com/fenderglass/Flye>)
- **SMARTdenovo** is an ultra-fast de novo assembler using long noisy reads (<https://github.com/ruanjue/smartdenovo>)
- **bwa** - Burrows-Wheeler Alignment Tool for mapping low-divergent sequences against a large reference genome (<http://bio-bwa.sourceforge.net/>)
- **FREEC** is a tool for the detection of copy-number changes and allelic imbalances using deep-sequencing data (<https://docs.hpc.qmul.ac.uk/apps/bio/freec/>)
- **MergeMap** constructs accurate consensus genetic maps from a set of individual genetic maps using DAGs (<http://www.oligospawn.org/mgmap/>)
- **Canu** is a hierarchical assembly pipeline for high-noise single-molecule sequencing (<https://github.com/marbl/canu>)
- **Racon** is a genomic consensus module to correct raw contigs generated by rapid assembly methods (<https://github.com/lbcb-sci/racon>)
- **Unicycler** is an assembly pipeline for bacterial genomes (<https://github.com/rwrick/Unicycler>)
- **PanGenie** - Genotyping based on k-mers and pangenome graphs (https://bitbucket.org/jana_ebler/pangenie/src/master/)
- **Jellyfish** is a tool for fast, memory-efficient counting of k-mers in DNA (<https://github.com/gmarcais/Jellyfish>)
- **Long Ranger** is a set of analysis pipelines that processes Chromium sequencing output to align reads (<https://support.10xgenomics.com/genome-exome/software/pipelines/latest/what-is-long-ranger>)
- **Salmon** is a tool for quantifying the expression of transcripts using RNA-seq data (<https://combine-lab.github.io/salmon/>)
- **HOME** (histogram of methylation) is a python package for differential methylation region (DMR) identification (<https://github.com/ListerLab/HOME>)
- **MUMmer** is a versatile alignment tool for DNA and protein sequences (<https://github.com/mummer4/mummer>)
- **AlphaFold** is a package for highly accurate protein structure predictions (<https://github.com/deepmind/alphafold>)