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/rrwick/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)