Hauptseminar Bioinformatik – Themen

Aktuelle Methoden für Next-Generation-Sequencing

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WS 2017

1. **Bowtie and Bowtie2:**
    – *Langmead, et al. (2009) Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol 10:R25*
    – *Langmead and Salzberg. (2012) Fast gapped-read alignment with Bowtie 2. Nature Methods, 9:357-359*

2. **BWA**
    – *Li and Durbin. (2009) Fast and accurate short read alignment with Burrows-Wheeler Transform. Bioinformatics, 25:1754-60*
    – *Li and Durbin. (2010) Fast and accurate long-read alignment with Burrows-Wheeler Transform. Bioinformatics, 26: 589-595*

3. Genome assembly with de Bruijn graphs
   - *Compeau et al. (2011) How to apply de Bruijn graphs to genome assembly. Nature Biotechnol. 29, 987–991*
   - *Zerbino, D.R. & Birney, E. (2008) Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18, 821–829.*

4. String Graph Assembler (SGA)
   - *Simpson and Durbin (2012) Efficient de novo assembly of large genomes using compressed data structures, Genome Res. 22: 549-556*
   - *Simpson, J.T., (2012) Efficient sequence assembly and variant calling using compressed data structures, PhD thesis, chapter 2*

5. STAR
   – *Dobin et al. (2012) STAR: ultrafast universal RNA-seq aligner. Bioinformatics, 29: 15-21*

6. ContextMap
   – *Bonfert et al. (2015) ContextMap 2: fast and accurate context-based RNA-seq mapping. BMC Bioinformatics, 16:122*
   – *Bonfert et al. (2017) Prediction of Poly(A) Sites by Poly(A) Read Mapping. PLoS One. 2017 Jan 30;12(1):e0170914.*

7. HISAT
   – *Kim et al. (2015) HISAT: a fast spliced aligner with low memory requirements. Nature Methods, 12,357–360.*

8. Transcript reconstruction

   – *Trapnell, C. et al. (2010) Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nat. Biotechnol. 28, 511–515*

   – *Guttman et al. (2010) Ab initio reconstruction of cell type–specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnol. 28,503–510*

9. Alternative polyadenylation

– *Xia, Z., et al. (2014) Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3'-UTR landscape across seven tumour types. Nature Communications 5, 5274.*

10. circRNAs

– *Gao et al. (2015) CIRI: an efficient and unbiased algorithm for de novo circular RNA identification. Genome Biology, 16:4*

– *Cheng et al. (2016) Specific identification and quantification of circular RNAs from sequencing data. Bioinformatics 32:1094-6*