A reading list for next generation sequencing

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Review paper about NGS

1. Shendure J and Ji H. Next-generation DNA sequencing. Nature Biotechnology (2008) 26, 1135 - 1145.

Microarray versus NGS

1. Marioni, Mason, Mane, et al. (2008), RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays. Genome Research (2008) 18(9):1509-17.

2. Su, Li, Chen, et al. (2011) Comparing next-generation sequencing and microarray technologies in a toxicological study of the effects of aristolochic acid on rat kidneys. Chem. Res. Toxicol., (2011) 19;24(9):1486-93.

Study Design

1. Conesa, Madrigal, Tarazona et al. A survey of best practices for RNA-seq data analysis. Genome Biology (2016) 26;17:13.

File Format

1. Li, Handsaker, Wysoker et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics (2009) 15;25(16):2078-9.

Alignment

1. Langmead, Trapnell, and Pop et al. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology (2009) 10:R25. (Bowtie)

2. QuasR Vignette http://bioconductor.org/packages/release/bioc/vignettes/QuasR/inst/doc/QuasR.p

3. Gaidatzis D, Lerch A, Hahne F and Stadler MB (2015). QuasR: Quantification and annotation of short reads in R. Bioinformatics, 31(7): 1130?1132. (QuasR paper)

4. Au KF, Jiang H, Lin L, Xing Y and Wong WH (2010). Detection of splice junctions from paired-end RNA-seq data by SpliceMap. Nucleic Acids Research, 38(14): 4570–4578.

RNAseq Data Analysis

1. McCarthy, J. D, Chen, Yunshun, Smyth and K. G (2012). Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. Nucleic Acids Research, 40(10) 9. (EdgeR)

2. Anders S and Huber W (2010). Differential expression analysis for sequence count data. Genome Biology, 11, pp. R106. (DEseq)

3. Trapnell C, Pachter L, Salzberg SL (2009), TopHat: discovering splice junctions with RNA-Seq", Bioinformatics, 25, 11051111. (TopHat)

4. Trapnell C, Williams BA, Pertea G, et al. (2010), Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. Nature Biotechnol. (2010) 28(5):511-5. (Cufflinks)

Single Cell RNA-seq

1. Bacher, Kendziorski. Design and computational analysis of single-cell RNA-sequencing experiments. Genome Biology (2016) 7;17:63.

2. Kharchenko, Silberstein, Scaden. Bayesian approach to single-cell differential expression analysis. Nature Methods. (2014)11(7):740-2.

DNA-seq Data Analysis: GATK

1. McKenna, Hanna, Banks et al. The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequence data. Genome Research (2010) 20(9):1297-303.