

RNA-seq in CLCbio Genomics Workbench

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What is CLCbio? (1/2)

- From the clcbio.com website:
 - USER-FRIENDLY BIOINFORMATICS
 - Our software is made for biologists by biologists, so it's easy to analyze, visualize, and compare DNA, RNA, and Protein data, as well as run advanced workflows with large and complicated datasets.
- Different software versions:
 - Big: Genomics workbench (a few thousand €)
 - Small: Main workbench (non NGS, few hundred €)
 - Free: Sequence viewer

What is CLCbio? (2/2)

- We use it for:
 - Quality filter RNA-seq pipeline
 - Read mapping in RNA-seq pipeline
 - Various other things. Mostly when visual inspection of read mappings becomes handy.

RNA-seq in CLCbio ()

- Samples for this demo:
 - Potato (*Solanum phureja*, double haploid)
 - 2 samples, 2 replicates (simulated)
 - Each sample 6k reads
 - Annotated reference is a part on chr 9, 25 genes

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- Steps to be taken in CLC:
 - Import fastq files (not in demo)
 - Quality trim reads (not in demo)
 - Map reads to reference. (RNA-seq module)
 - Boxplot of expression values (RPKM)
 - Quantile normalisation
 - Boxplot on normalized expression values (RPKM)
 - Start RNA-seq experiment with 2 groups
 - Start statistical analysis
 - Check DE genes
 - Perform Clustering on genes

RNA-seq in CLCbio

■ Tutorials CLC RNA-seq in online pdfs/movies:

- <http://www.clcbio.com/support/tutorials/>
- [RNA-Seq Analysis – Part I](#)
 - Covering the basics steps of running an RNA-seq Analysis with an annotated reference genome.
- [RNA-Seq Analysis – Part II](#)
 - This tutorial covers RNA-seq analysis with focus on non-specific matches and expression measures.
- [RNA-Seq Analysis – Part III](#)
 - In this tutorial we will focus on discovery of new putative exons.
- [RNA-Seq Analysis – Part IV](#)
 - This tutorial is focusing on quality control in RNA-Seq analysis

