

Workshop

Bioinformatics analysis of (bulk) RNA-seq data

Organizer

CUBiDA (Core Unit Bioinformatik, Datenintegration und Analyse) at the Universitätsklinikum Erlangen

Instructors

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Outline

The participants will receive an overview of the biological and technical background of the bulk RNA-seq technology, get practical tips about the experimental design, and know the RNA-seq analysis pipeline as well as the downstream analysis steps of the resulting data. The workshop also includes hands-on sessions to explore and perform the different analysis pipeline steps in RStudio.

Outcome

At the end of the workshop, participants will be able to run a typical RNA-seq workflow on a small dataset and understand the essential steps of data exploration, analysis, and interpretation.

Number of participants

15

Target audience

This workshop series is suitable for life and medical researchers who are new to RNA-seq. The course is beginner friendly and intended for those interested in using the command line interface for their analysis.

Prerequisites

While beginner-friendly in its approach to RNA-seq analysis, the workshop assumes basic proficiency in working with the R statistical environment. Previous experience with UNIX-based command line is an advantage but not expected.

Teaching format

The workshop will comprise a mix of interactive lectures with short hands-on exercises. Computers with preinstalled software and data will be provided to all participants. During the workshop, we will also give you access to all our teaching materials, including a software environment which can be executed on your own computer.

Provisional workshop schedule

DAY 1	
8:30-16:30	Introduction to RNA-Sequencing Viewing and interpreting FASTQ files Basic introduction to RStudio and the RStudio terminal Quality control of sequencing reads with FASTQC Adapter and quality trimming of sequencing reads with TrimGalore! Mapping sequencing reads to a reference genome/transcriptome Transcript quantification with Salmon
DAY 2	
8:30-16:30	Differential expression analysis with DESeq2 Basic visualization of differentially expressed genes Functional enrichment analysis with gProfiler2 Aggregation of reports with interactive plots for multiple bioinformatics analyses with MultiQC

At least one break will be provided each morning and afternoon.

Questions

Please, contact us at mik-cubida@uk-erlangen.de.