

Differential gene expression analysis using RNA-Seq data and the Galaxy platform

Course description:

This course covers topics regarding experimental design, introduction and considerations for NGS sequencing, hands on sessions to get from raw sequencing data to count matrices using the Galaxy[1] platform, QCs for RNA-Seq data, sample visualizations, statistical analyses using R and the DESeq2 package[2] and the creation of reports using RStudio and R Markdown[3]. You will create an integrated report using RStudio and R Markdown [3] and have the opportunity to analyze your own data or a published dataset of interest.

References

[1] <https://galaxyproject.org>

[2] Love, Michael I., Wolfgang Huber, and Simon Anders. 2014. "Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2." *Genome Biology* 15 (12):550. <http://dx.doi.org/10.1186/s13059-014-0550-8>.

[3] <https://rstudio.com/>, <https://rmarkdown.rstudio.com>

Topics:

- Fundamentals of RNA-Seq analysis
- Processing of RNA-Seq data using Galaxy
- Visualization of sequencing data and analysis of RNA-Seq data
- Integrated RNA-Seq data analysis with R and RStudio

Methods:

Presentations, Hands-on sessions and exercises, Homework assignment, Q&A sessions

Format:

- Mode: online course on Teams
- Duration: 2 days (9 am – 5 pm)
- Language: English
- Participants: max. 12 persons

Requirements:

[Introduction to R](#) and [RMarkdown](#) or equivalent courses/experience

Dates and Application:

You can view the current dates and register for this course on [CaMS](#).