

Core Facility Computational Bioanalytics

RNA-Seq & Single cell RNA-Seq data analysis

Recent technological advances have made it possible to obtain genome-wide transcriptome data from single cells using high-throughput sequencing (scRNA-seq). Even though scRNA-seq makes it possible to address problems that are intractable with bulk RNA-seq data, analysing scRNA-seq is also more challenging.

In this course we will be surveying the existing problems as well as the available computational frameworks for the analysis of RNA-seq and scRNA-seq data. The course includes common analysis strategies, using state-of-the-art methods and we also discuss the central biological questions that can be addressed using RNA-seq and scRNA-seq.

Upon successful completion of this course, they will be familiar with:

- Basic RNA-seq and sc RNA-seq experimental approaches
- Quality control and alignment
- Normalization methods
- Statistics for differential gene expression

Teaching and learning method: 20% lecture and 80% interactive

Languages of instruction: English

Target audience: PhD students, technicians and researchers

Entrance qualifications: No

Costs: 150 Euro (University) / 300 Euro (Company)

Registration: zmf-sekretariat@medunigraz.at (deadline: March, 15th 2018)

As the number of participants is limited (min. 3 and max. 8), please register early to confirm your seat!

March 21th 2018 (9 am - 4 pm)

ZMF seminar room EG 086

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DFP: 7-Points