

Core Facility Computational Bioanalytics

Introduction to NGS data analysis

Next-generation sequencing has become an essential tool in genetic and genomic analysis. Therefore it is important to equip the experimental scientists with adequate bioinformatics skills to understand and analyze the large volume of sequencing data generated with NGS.

This course will provide an introduction in NGS with specific focus on principles of bioinformatics and analysis of the data generated in NGS for genomics. The participants will acquire knowledge about the tools and all necessary steps to guarantee reliable results. Hands on examples will include obtaining data from various databases, quality control and pre-processing (raw data management, quality check, filtering short reads, mapping sequences to a reference, visualization of sequence data, database search etc.).

Upon successful completion of this course, participants will be able to understand NGS data and start using the appropriate tools for its analysis.

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: basic computer skills

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

Registration: zmf-sekretariat@medunigraz.at (deadline: October, 8th 2019)

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

October 22th 2019 (9 am - 4 pm)

ZMF seminar room ground floor EG-087

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DFP: 7-Points