

## 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](mailto:zmf-sekretariat@medunigraz.at) (deadline: April, 2<sup>nd</sup> 2018)

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

April 10<sup>th</sup> 2018 (9 am - 4 pm)

**ZMF seminar room 3rd floor 03-012**

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DFP: 7-Points