

Core Facility Computational Bioanalytics

Data management

In this workshop critical concepts and practical methods to support planning, collection and dissemination of data in clinical and medical research are presented. Participants learn how to structure their research data, how to merge different files, import and export data. Merging data, coding and labelling data in a meaningful manner is essential and provides the basis for later data analysis. Additional topics: Convert string variables to a numeric variables, convert categorical string variables to labeled numeric variables, create categorical variables from continuous variables, create a new variable that is calculated from other variables, create date variable from a date that is stored as a.

Questions that are addressed in this workshop: What to do with missing values? How can I identify and remove duplicate observations? How to deal with outliers? How can I better structure my data in excel? How should I arrange my data file depending on my research design? What is important in the data collecting process? Do I have to consider the proposed statistical methods during the data management process?

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: no

Costs: free of charge

Registration: zmf-sekretariat@medunigraz.at (deadline: April 6th 2018)

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

April 13th 2018 (9 am – 11 pm)

ZMF seminar room ground floor EG-086

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
<https://zmf.medunigraz.at>

Core Facility Computational Bioanalytics

Advanced R for Life Sciences

R is a language and computational environment for statistics, advanced data analysis, machine learning and visualization; it is the most widely used programming language in bioinformatics.

Due to technological advances in molecular biology (genomics, large-scale systems biology) research in the life sciences is becoming increasingly data rich. The aim of this course is to provide students with a good understanding of how to use R for advanced data analyses. For this purpose participants will learn key concepts for writing advanced R code,

Upon successful completion of this course, participants will be able to more proficiently use R for data analysis in life science research by applying loops, functions, control structures and create profound plots.

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: A basic understanding of R as shown by successful completion of the course "Introduction into R for Life Science Researchers".

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

Registration: zmf-sekretariat@medunigraz.at (deadline: March, 5th 2018)

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

DFP: 7-Points

March 15th 2018 (9 am - 4 pm)

ZMF seminar room 3rd floor 03-012

Contact: zmf-sekretariat@medunigraz.at
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Core Facility Computational Bioanalytics

Introduction into Galaxy for Life Science Researchers

Galaxy is an open source, web-based platform for data intensive biomedical research. This workshop will teach participant the basics of Galaxy, introducing the Galaxy interface including a working example.

The course participant will take the first steps with Galaxy. Upon successful completion of this course, they will be familiar with:

- Galaxy interface,
- Working with histories
- Data upload, data analysis and visualization
- Using existing and creating your own workflows
- Share data with others

Teaching and learning method: Interactive hands-on training

Languages of instruction: English

Target audience: PhD students, technicians and researchers

Entrance qualifications: No

Hardware and Software: Please take a laptop with you. You can log into Galaxy with your MUG-account.

Costs: for free

Registration: zmf-sekretariat@medunigraz.at (deadline: February, 02nd 2018)

As the number of participants is limited (min. 3 and max. 10), please register early to confirm your seat!

February 7th 2018 (1 pm - 3 pm)

ZMF seminar room ground floor EG-087

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
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Core Facility Computational Bioanalytics

Introduction into R for Life Science Researchers

R is a statistical program that can be used interactively to explore data or used as a programming language to implement complex data analyses. It is extensible via *libraries* which can add both new functions for analysis and new data for reference. The course participants will take the first steps with R and learn to master the basics. In several sections, they will cover its basic syntax, making them ready to undertake their own first data analysis using R.

Upon successful completion of this course, participants will be familiar with: data structures in R, basic commands, data import/export, installation of packages, help function in R, data visualizations with basic plot functions.

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: No

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

Registration: zmf-sekretariat@medunigraz.at (deadline: February, 26th 2018)

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

DFP: 7-Points

March 8th 2018 (9 am - 4 pm)

ZMF seminar room 3rd floor 03-012

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
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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: April, 2nd 2018)

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

April 10th 2018 (9 am - 4 pm)

ZMF seminar room 3rd floor 03-012

Contact: zmf-sekretariat@medunigraz.at
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DFP: 7-Points

Core Facility Computational Bioanalytics

Statistical data analysis for qPCR

Learn how appropriate statistics are selected and applied correctly to get the most out of your qPCR data. This one-day course teaches statistical principles and tools that are used in qPCR data analysis. The course includes practical computer based exercises to help you choose the correct analysis as well as how to best design your experiment.

The hands-on workshop contains:

- Experimental design (factors, groups and sample size)
- Basic principles of statistics (statistical hypothesis testing, Gaussian statistics, central limit theorem, p-values, outlier detection)
- Descriptive statistics (mean, SD, percentiles, coefficient of variation, confidence interval)
- Statistical tests (Gaussian vs. non-Gaussian methods, one-tailed or two tailed tests, false discovery rate, Benjamini Hochberg and Bonferroni correction)
- Comparison of two groups and time points (paired and unpaired studies)
- Multivariate data analysis and data visualization
- Guideline for publication of qPCR data analysis (MIQE)
- Additionally you have the opportunity to analyze your own data.

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: SPSS basic knowledge (e.g. SPSS course day 1 and basic statistics)

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

Registration: zmf-sekretariat@medunigraz.at (deadline: April, 16th 2018)

As the number of participants is limited (min. 3 and max. 12), please register early to confirm your seat!

April 26th 2018 (9 am - 4 pm)

ZMF seminar room 3rd floor 03-012

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

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DFP: 7-Points

Core Facility Imaging & Computational Bioanalytics

How to perform and analyze cell-based assays?

A variety of cell-based assays are available to characterize physiological reactions (e.g. viability, apoptosis, necrosis, organelle function, proliferation of cells). The course introduces into selection of the right assay, correct performance, troubleshooting and appropriate statistical evaluation of the results. Practical work includes cell culturing, treatment, analysis by plate reader and practical computer based exercises for correct data analysis.

The hands-on workshop contains:

- Part 1
 - Seeding of cells, planning of plate layout, positive and negative controls, treatment of adherent and suspension cells
 - Performance of lactate dehydrogenase detection, cellular dehydrogenase measurement and ATP content assays
 - Readout by absorbance, fluorescence and luminescence reader dependent on the assay
- Part 2
 - Introduction and analysis of the generated data including: basic principles of statistics (outlier detection, statistical hypothesis testing, Gaussian statistics, Statistical key concepts including p-values)
 - Descriptive statistics (mean, SD, percentiles, coefficient of variation, confidence interval)
 - Statistical tests (Gaussian vs. non-Gaussian methods, one-tailed or two tailed tests)
 - Group comparisons and repeated measurements (paired and unpaired studies), multivariate data analysis and data visualization
 - Calculation of IC-50 or/and EC-50

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: experience in cell culture

Costs: 350 Euro (University)/ 500 Euro (Company)

Registration: zmf-sekretariat@medunigraz.at (deadline: May, 18th 2018)

As the number of participants is limited (min. 4 and max. 12), please register early to confirm your seat!

June 5th & 6th 2018 (9 am - 5 pm)

ZMF seminar room 3rd floor 03-012

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

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Stiftingtalstrasse 24, A-8010 Graz
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Core Facility Computational Bioanalytics

Introduction to Linux and command line data analysis

Most tasks of bioinformatics are processed using the Linux operating system (OS). Therefore, familiarity with and understanding of basic Linux command lines is essential for bioinformatics analysis. This course will provide you an introduction to the Linux OS and its basic command line tools. Material will cover logging into remote machines, filesystem organization and file manipulation, and installing and using software.

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

- Basic Linux commands (including grep, sort, awk, sed, etc.)
- Basic regular expressions - useful syntax for matching and substituting string and sequence data
- Conda package manager and sourcing different environments
- Running tools over SLURM (cluster management and job scheduling system)

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: April, 13th 2018)

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

April 18th 2018 (9 am - 4 pm)

ZMF seminar room EG 086

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
<https://zmf.medunigraz.at>

DFP: 7-Points

Core Facility Computational Bioanalytics

Microbiome data analysis with R

The advent of next-generation sequencing (NGS) enabled the study of microbial communities to reach a new level. Examining large number of ecology samples has become common routine. On the other hand researches have to cope with analysis of large and very complex datasets.

Using standard data analysis pipelines in QIIME or Mothur it is very fast and convenient to generate abundancies tables and phylogenetic trees of the microbial communities found in the samples. Further analysis, like alpha and beta diversity for example is very well supported and often used in the popular statistical programming language R. During this course we will present different procedures to analyze the data and generate publication ready graphics.

Upon successful completion of this course, participants will be able to understand and analyse Microbiome data with R.

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: March, 19th 2018)

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

DFP: 7-Points

March 28th 2018 (9 am - 4 pm)

ZMF seminar room ground floor EG-086

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
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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

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
<https://zmf.medunigraz.at>

DFP: 7-Points



Core Facility Computational Bioanalytics

**Statistical data analysis with SPSS for Life
Science Researchers**

SPSS basics and Group comparisons

This course is an introduction to statistical methods and statistical software. On the basis of various practical examples, the participants learn to analyse and visualize data using the software SPSS and get insight how to interpret statistical results. A main goal is to show participants the importance of quality control, assessing assumptions and ensuring adequate sample size. Upon successful completion of this course, participants will be familiar with basic statistical methods and will be able to interpret statistical analysis. The participants will have the ability to choose the suitable statistical analysis method for different data sets.

SPSS basics (Day 1) : Getting started with SPSS, data management, exploratory data analysis, outlier diagnostics, common plots, analysis of categorical data, scientific presentation of results

Group comparisons (Day 2) : Hypothesis testing, type I and II errors, sample size, effect size, power calculation, confounding factors, Comparing means: t-test, multiple testing, one-factor-ANOVA, Mann-Whitney, Wilcoxon, Kruskal-Wallis, Friedman analysis of ranks, scientific presentation of results

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications for day 2: SPSS basics course

Costs: 150 Euro (University)/ 300 Euro (Company) per day; Each day can be booked separately.

Registration: zmf-sekretariat@medunigraz.at (deadline: February 2nd 2018)

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

Day 1: February 12th 2018 (9 am - 4 pm)

Day 2: February 13th 2018 (9 am - 4 pm)

ZMF seminar room ground floor (day1) and 3rd floor O3-012 (day2)

Contact: zmf-sekretariat@medunigraz.at

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**DFP: 7-Points per day
Total: 14-Points**



Core Facility Computational Bioanalytics

Statistical data analysis with SPSS for Life Science Researchers

Survival analysis and Analysing Categorical data

The aim of the **first day** course is to describe the various methods used for modeling and evaluating survival data, also called time-to-event data. General statistical concepts and methods discussed in this course include survival and hazard functions, Kaplan-Meier graphs, log-rank and related tests, Cox proportional hazards model, and the extended Cox model for time-varying covariates.

The **second day** course will focus on logistic regression models for the analysis of contingency table data, where the cell entries represent counts that are cross-tabulated using categorical variables. Tests for (conditional) independence are discussed in the context of odds-ratios, relative risks and simple Chi²-tests.

Upon successful completion of this courses, participants will be able to check test specific assumptions and will be familiar with common statistical methods in survival and categorical data analysis. The participants will have the ability to choose the suitable statistical analysis method for different data sets and will have insight how to interpret statistical results.

Survival analysis (Day 1): Overview of different Survival models, focussed on Kaplan Meier and Log Rank test, Cox Regression (time-dependent/independent), scientific presentation of results

Analyzing categorical data (Day 2): Odds Ratio, Relative-Risk, Chi², McNemar, Logistic Regression, estimation of cut-offs, ROC/AUC analysis, sensitivity and specificity, scientific presentation of results;

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: SPSS basics course

Costs: 150 Euro (University)/ 300 Euro (Company) per day Each day can be booked separately.

Registration: zmf-sekretariat@medunigraz.at (deadline: June 1st 2018)

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

Day 1: June 11th 2018 (9 am - 4 pm)

Day 2: June 12th 2018 (9 am - 4 pm)

ZMF seminar room ground floor EG-086

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

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DFP: 7-Points per day
Total: 14-Points

Core Facility Computational Bioanalytics

Statistical data analysis with SPSS for Life Science Researchers

Analysis of Variance and Regression analysis

This course is an introduction to statistical methods and statistical software in the field of Analysis of Variance and Regression analysis. On the basis of various practical examples, the participants learn to analyse and visualize data and how to interpret results. A main goal is to show participants the importance of quality control, assessing assumptions and ensuring adequate sample size. Upon successful completion of this course, participants will be familiar with the statistical methods covered in this two days and will be able to interpret statistical results. The participants will have the ability to choose the suitable statistical analysis method for different data sets.

Analysis of Variance (Day 1) : one-way ANOVA, factorial ANOVA, repeated measures ANOVA, MANOVA, ANCOVA, scientific presentation of results

Regression analysis (Day 2) : Pearson, Spearman, Partial correlations, simple linear regression, multiple linear regression, binary logistic regression, scientific presentation of results

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

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: SPSS basics course

Costs: 150 Euro (University)/ 300 Euro (Company) per day; Each day can be booked separately.

Registration: zmf-sekretariat@medunigraz.at (deadline: February 16th 2018)

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

DFP: 7-Points per day
Total: 14-Points

Day 1: February 26th 2018 (9 am - 4 pm)

Day 2: February 27th 2018 (9 am - 4 pm)

ZMF seminar room ground floor EG-086 (day1)
and 3rd floor O3-012 (day2)

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Core Facility Computational Bioanalytics

Statistical errors in medical research

This course is an introduction to the most common errors and pitfalls in statistics. Errors and pitfalls relating to study design and planning, data analysis, data interpretation and data presentation and even obvious data manipulations are discussed on the basis of several examples from scientific journals.

After successful completion of the course, the course participant will have the ability to read scientific papers in a critical manner and to question the methods and statistics used in publications. The course participant will have the knowledge to detect obvious errors in simple statistical models and will understand simple statistical results.

Teaching and learning method: 50% lecture and 50% interactive

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: no

Costs: 100 Euro (University)/ 200 Euro (Company)

Registration: zmf-sekretariat@medunigraz.at (deadline: March, 9th 2018)

As the number of participants is limited (min. 3 and max. 12), please register early to confirm your seat!

DFP: 5-Points

March 16th 2018 (9 am - 1 pm)

ZMF seminar room ground floor EG086

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