

Good Practice in DNA Microarray Analysis 2005

2005 May 13-14 in Munich

This course focuses on problems emerging in projects related to the classification of high-dimensional data and the functional annotation of gene expression data.

Registration is open.

The course is restricted to members of the NGFN

To apply for this course, please send

- a short description of the project (3 pages - design, principle questions, data generating procedures, analysis, interpretation)
- a list of main problems and needs
- a description of your data
- a short description of your statistical background
- a short description of your computational experiences (data bases, statistical software, ...)

to mansmann@ibe.med.uni-muenchen.de. Additionally, please tell us your *NGFN Förderkennziffer*(FKZ).

Preliminary Course schedule Friday, May 13 - Formulating goals and specific questions

Providing needed background information

09.00-11.15	Introducing the projects and project specific questions	Short presentations and monitored discussion
11.30-13.00	Strategies for successful classification tasks in high dimensional data	Rainer Spang, Axel Benner
14.00-15.30	Strategies for functional annotation	Joerg Rahnenführer, Benedikt Brors
16.00-17.30	Strategies for reproducible computations	Wolfgang Huber, Markus Ruschhaupt
18.00-20.00	Making your data ready for computation	Group work on computer

**Preliminary Course schedule Friday, May 13 - Formulating goals and specific questions
Providing needed background information**

**Saturday, May 14 - Performing an appropriate analysis
correct interpretation of your results**

09.00-10.00	Problem specific software compendia	
10.30-13.00	Performing your analysis	Mentored group work on the computer
14.00-16.00	Performing your analysis	Mentored group work on the computer
16.30-18.00	Drawing appropriate conclusions	Mentored group work

Background Knowledge

Ideally, you are preparing or conducting your project and are highly interested to apply state of the art methods for the analysis of your data. Furthermore, you are preparing a publication and aim at an appropriate presentation and interpretation of your results. This course focuses on problems emerging in projects related to the classification of high-dimensional data and the functional annotation of gene expression data.

We strongly recommend you to refresh your mathematical and programming skills before attending the course.

Please use the [links to software and literature](#) to prepare yourself before the course begins.

R and Bioconductor

In the afternoon exercises you will learn how to analyze data using the statistical computing environment *R* [<http://www.r-project.org>] and *BioConductor* [<http://www.bioconductor.org>], an open source software for bioinformatics. *R* sources and package sources can be downloaded from *The Comprehensive R Archive Network* at <http://cran.r-project.org>.

This is a course in microarray analysis -- not an introduction to *R*. Please read the [Introduction to R](#) before the course begins.

Bring your own data

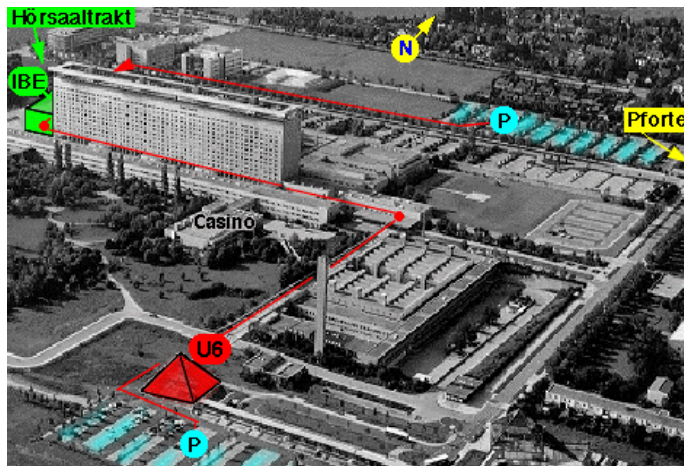
You are encouraged to bring some of your own data to the course (e.g. genepix files or CEL/CDF). We will work with your data to derive relevant results. If you expect to have own data only later in the year, it may in fact be advantageous also to register for one of the [later courses](#).

How to find us

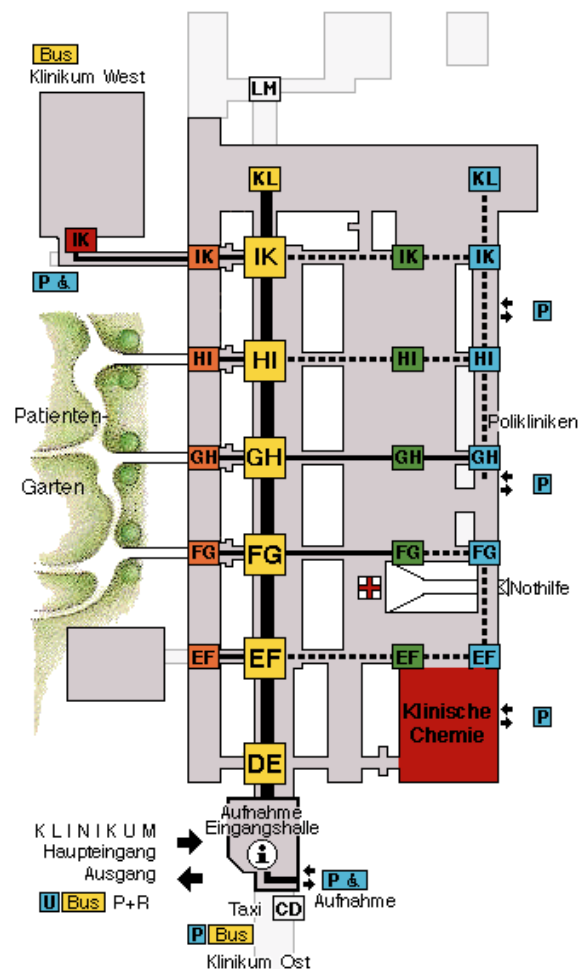
We meet at the *Klinikum Großhadern, Hörsaaltrakt, Floor K O2, Seminarroom 5, Marchioninistraße 15, 81377 München.*

Großhadern lies in the south-west of Munich ([map](#)). A detailed how-to-get-there is found [here](#) (in german only). For navigating, you might also find the [roadmap](#) and the following directions helpful:

- If you arrive in Munich by plane, take the S-bahn S8 ("Airport line") to *Marienplatz*.
- If you arrive by train, take any S-bahn or U-bahn to *Marienplatz*.
- From *Marienplatz* take U6 to final stop *Klinikum Großhadern*.
- Leaving the platform, you stand inside a glass pyramid (marked in red in the left figure below).



The red pyramid is the U-bahn-station at which you arrive using U6. The building marked in green is your destination.



This is the inside of the clinical center. The seminarrooms are on the upper right next to the letters "KL".

Accommodation

You will need to make your own accommodation arrangements. We recommend rooms at the [Hotel Neumayr](#), which lies in *Großhadern* close

to the clinical center. If you want to stay closer to the center of Munich, we recommend hotels in *Schwabing*, which is 15min by U-bahn from *Großhadern*. Have a look at [Hotel Hauser](#), [Hotel Lettl](#), or [Renner Hotel Savoy](#).

Further information

Please contact Ulrich Mansmann: mansmann@ibe.med.uni-muenchen.de.