

Basic statistics and analysis of small and large data sets made easy:
A practical paradigm for solving common problems in the wet lab

Description	As scientists, we are frequently faced with very similar questions regarding statistics in the lab. Typically, we are interested in comparing two or more experimental conditions/parameters and would like to understand if the data obtained represent real differences. We therefore are in need of strategies on how to analyze (or fit) the data and present these differences. With the increase of high-throughput technologies there is an increase in publicly available data that can be exploited. Another objective of the course is therefore to provide an overview of the wide variety of publicly available data sources as well as an outline of strategies on how to use them.
Eligibility	PhD students and post-doctoral fellows with an interest in data analysis. Minimum requirement: Master's degree in life sciences or its equivalent.
Course Structure	It will be a two-day course. In the morning various lectures will be given to provide the students with the necessary theoretical background. In the afternoons, the students will be asked to do basic data analysis themselves. Each student should bring a portable computer to the course.
Assessment	At end of the course, the students will be asked to briefly present possible ways to analyze their own data.
Dates	Monday, April 22 & Tuesday, April 23, 2013
Credits	1.0 ECTS
Facilitators	Pascale Anderle (University of Bern/Swiss Institute of Bioinformatics), Benjamin Clemençon (University of Bern), Matthias Hediger (University of Bern), Nicolas Montalbetti (University of Bern), Fred Schütz (Swiss Institute of Bioinformatics)
Location	University of Bern, Institute of Anatomy, Bülhlstrasse 26, room A263
Registration	send an email to Carsten.KniggeSalis@ibmm.unibe.ch
No. of spots	The maximum capacity of the course is 30 students. Priority will be given to members (PhD students & postdoctoral fellows) from NCCR & IFP TransCure.

Programm

Time	Speaker	Topic
Monday 22nd April 2013		
8.15-8.30	M. Hediger	Welcome
8.30-8.45	P. Anderle	Introduction: Goals of the course, bioinformatics facility, presentation of typical "statistical questions in the lab"
8.45-9.30	JL. Reymond	Data mining and visualization in chemical space
9.30-10.15	F. Schütz	Brush up in statistics: Difference between median and mean, SD, quartiles, normal distribution (easy way to check), data presentation, confidence interval
10.15-10.45	Coffee break	
10.45-12.00	F. Schütz	How to statistically compare two and three groups
12.00-13.00	Lunch break	
13.00-15.00	P. Anderle F. Schütz B. Clemençon	Introduction into R: Set up, various exercises: Reading data, calculating mean, median, SD, generating boxplots, mean +/- SD, log transformation: Impact of data presentation
15.00-16.00	P. Anderle F. Schütz B. Clemençon	Comparing two and three groups (including interaction) of normally distributed and not normally distributed data
16.00-17.00	P. Anderle F. Schütz	Overview of different programs used for data analysis
Tuesday 23rd April 2013		
8.30-9.15	T. Hegedus	Bioinformatics of the chemoimmune system with focus on ABC transporters
9.15-9.45	P. Anderle	Genomics data: GEO depository and importance of data structures
9.45-10.30	N. Montalbetti	Transport assays and kinetics
10.30-11.00	Coffee break	
11.00-11.45	F. Schütz	Curve fitting: Important aspects
12.00-13.00	Lunch break	
13.00-14.00	Various	Exercises for curve fitting in R and other software
14.00-15.00	Groups	Discussion of examples from attendees
15.00-16.00	Groups	Presentation of solutions and strategies

Green = Lecture / Blue = Practical Part / Pink = Discussion