

Microarrays:

An overview from wetlab to data analysis and interpretation

Description	DNA Microarrays have become important tools in life science as they allow to measure expression of thousands of genes simultaneously. Consequently, there has also been an increase in publicly available genomics data that can be exploited. The objective of the course is therefore to provide an overview of microarray technologies, to discuss their usefulness and limitations and teach basic data analysis skills necessary to analyze such data.
Eligibility	Participants must have a Master's Degree in life sciences or similar background with an interest in data analysis.
Course Structure	It will be a one-day course. In the morning various lectures will be given to provide the students with the necessary theoretical background. In the afternoon, the students will be asked to do basic data analysis themselves. Each student should bring a portable computer to the course.
Assessment	This course is making part of the newly created program "Master of Science in Bioinformatics and Computational Biology". In order for TransCure PhD students to get 0.5 ECTS points, the students will be asked to answer a few questions regarding the content of the course and to perform an easy analysis at home within one week following the course.
Dates	Wednesday, December 18, 2013
Credits	0.5 ECTS points
Facilitators	Pascale Anderle (University of Bern/ Swiss Institute of Bioinformatics)
Location	University of Bern, Institute of Cell Biology, room C159, Baltzerstrasse 4
Registration	Send an email to Carsten.KniggeSalis@ibmm.unibe.ch
No. of spots	The maximum capacity of the course is 6 students.

Program

Morning

8-9 am

Introduction into microarray technology
Wetlab and chip design

9-10 am

Basic concept in data analysis
Normalization of data
Non-supervised clustering
Supervised clustering
Identification of significant differences

10-11 am

Role of microarray data in life science in the past, present and future

Afternoon

1-2 pm

Exercises in R I
Finding chip set of interest
Normalization of chips
Quality assessment of chips

2-3 pm

Exercises in R II
Non-supervised clustering
Heatmaps
Identification of significant differences

3-4 pm

Exercises in R III
Follow-up analyses
Functional classifications