

BIO-609

Practical - Bucher Lab

Bucher Philipp

Cursus	Sem.	Type
Molecular Life Sciences		Obl.

Language of teaching	English
Credits	1
Session	
Exam	Project report
Workload	30h
Hours	24
Courses	3
TP	21
Number of positions	2

Frequency

Every year

Remark

3-day Block course, every year in January. To register, contact EDMS Administration

SummaryExplorative analysis of *in vivo* transcription factor binding sites using public ChIP-seq data and web-based analysis tools.**Content**

The ChIP-seq server is a web-based bioinformatics analysis platform developed and maintained by the Bucher group. It offers access to a large database of public data. At the beginning of the course, each student will select a ChIP-seq data sample from the ChIP-seq server menu. The subsequent analysis of the data sample will focus on the following tasks:

- Data quality control
- Generation of "peak lists" corresponding to *in vivo* transcription factor binding sites
- Motif mining and motif enrichment analysis in peak regions
- Statistics about peak location relative to gene bodies and gene set enrichment analysis
- Genomic context analysis: histone modifications, DNase I hypersensitive regions, sequence conservation and SNP density in the neighborhood of peaks

During the work, students will familiarize themselves with a number of in-house developed and external bioinformatics resources: ChIP-seq server, Signal Search analysis (SSA), PWMTools, MEME-ChIP, GREAT and Nebula. At the end of the course, each student will summarize the results obtained in a research paper-like format.

Resources**Websites**

- <http://bucher-lab.epfl.ch/>
- <http://ccg.vital-it.ch>