EPFL

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 2 years

Remark

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

Summary

Explorative 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.

Note

Note that while the course is open to all first year EPFL doctoral students, priority will be given to EDMS students, given that they are mandated to take three of EDMS practical modules. Note also that doctoral students from the Bucher laboratory cannot take this course. Access is limited to 4 students.

Resources

Websites

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