

Graduate Program in Molecular Cell Biology:

Methods Seminar - Course in: Bioinformatics I

Lecturer: Hubert Hackl

Number: 041035

Type: VU Semester hours: 1,5 ECTS

Character: Lecture with integrated computer exercises

Time/Date: 11. - 14. December 2017

Location: Computer room Schöpfstrasse 24 (U107-U108)

Limited number of 5-20 places, registration necessary YES

For registration or questions please contact: hubert.hackl@i-med.ac.at

Aim:

To handle common bioinformatics methods in particular for gene expression profiling and cancer immunology

Description/contents:

<p>Predictive methods on protein sequences (Protein domains, Signal P, NetMHCPan)</p> <p>Sequence alignment and databases (BLAST, NCBI, TCGA, Firebrowse, TCIA, GEO, IntOgen, cBioPortal)</p> <p>Differentially expressed genes (microarrays, RNAseq) (R/Bioconductor software packages <i>rma</i>, <i>limma</i>, DEseq2)</p> <p>Expression profiling and clustering (Genesis)</p> <p>Network analysis (Cytoscape)</p> <p>Gene ontology, Pathway analysis (DAVID, KEGG, Reactome, ConsensusPathDB, ClueGO)</p> <p>Gene set enrichment analysis (GSEA)</p> <p>Predictive and prognostic marker (signatures) (logistic regression, survival analysis)</p>
