Institute of
Molecular Biology

IMB TechTalk

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“Computational biology for large-scale omics data analysis”

2 May 2017, 13:30 (*s.t.*)

Venue: IMB Seminar Room, 2nd Floor
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend.

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Abstract:

Computational biology for large-scale omics data analysis

Currently, a main bottleneck in proteomics is the downstream biological analysis of highly multivariate quantitative protein abundance data. It will be shown how the Perseus software supports researchers in interpreting protein quantification, interaction and posttranslational modification data. A comprehensive portfolio of statistical tools for high-dimensional omics data analysis is contained covering normalization, pattern recognition, time series analysis, cross-omics comparisons and multiple hypothesis testing. A machine learning module supports classification and validation of patient groups for diagnosis and prognosis, also detecting predictive protein signatures. Central to Perseus is a user-friendly, interactive workflow environment providing complete documentation of computational methods used in a publication. All activities in Perseus are realized as plugins and users can extend the software by programming their own, which can be shared through a plugin store. Perseus combines a powerful arsenal of algorithms with intuitive usability by biomedical domain experts, making it suitable for interdisciplinary analysis of complex large datasets.