



de.NBI Summer School 2016

From Big Data to Big Insights

Computational methods for the analysis and interpretation of mass-spectrometric high-throughput data

Date: 26th-30th September 2016

Location: Castle Dagstuhl, Wadern

Website: <https://goo.gl/ZRgxuV>

Keynote Speakers

Oliver Serang

(Institute of Computer Science Metagenomics, FU Berlin)

Protein Identification, FIDO

Lennart Martens

(Department of Biochemistry, Ghent University)

Proteomics Data Analysis, PeptideShaker

Jürgen Cox

(Max Planck Institute of Biochemistry, Martinsried)

Protein Quantification, MaxQuant

Samuel Payne

(Pacific Northwest National Laboratory, Richland)

Pan-Omics, Active Data Biology

Juan Antonio Vizcaino

(EMBL-EBI, Hinxton)

PRIDE and ProteomeXchange

George Rosenberger

(Institute of Molecular Systems Biology, ETH Zürich)

Protein Quantification, OpenSwath

Sebastian Böcker

(Chair of Bioinformatics, Friedrich-Schiller-Universität Jena)

Metabolomics, CSI:FingerID

de.NBI Speakers

Stefan Albaum

(Center for Biotechnology - CeBiTec, Universität Bielefeld)

Martin Eisenacher

(Medizinisches Proteom-Center, Ruhr-Universität Bochum)

Oliver Kohlbacher

(Applied Bioinformatics Group, Eberhard Karls Universität Tübingen)

Robert Ahrends

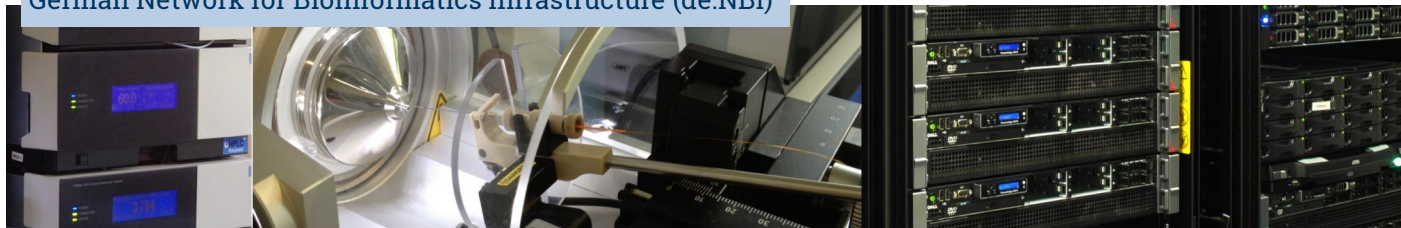
(Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V.)

Michael Berthold

(Bioinformatics and Information Mining, Universität Konstanz)

Topics

To a large extent, proteomics and metabolomics are based on experimental data, for which mass spectra of a sample are assigned to specific biomolecules. Questions arising from basic and applied research can be answered, for example the differentiation of the protein composition between healthy and diseased persons or the early detection of diseases. As the omics technologies are rather wide-spread today, developed algorithms should be usable also by non-computer science experts and sustainably utilizable by them, e.g. as combinable modules in workflow systems.



Aims and Requirements

The summer school has the aim to give PhD students and postdocs from life sciences / bioinformatics / computer science as well as developers of bioinformatics algorithms and analysis software deeper insights in the details of existing algorithms or software systems, which are frequently used in proteomics and metabolomics. Participants will use - instructed by keynote and de.NBI speakers - existing tools to analyse and visualize real-world datasets (data prepared for the tutorials specifically as well as the participants' own data). Beyond that, they will be put into a position to be able to combine their own existing and future algorithms or tools with other solutions as well as to integrate them into a sustainable software system. To this end the summer school will also contain hackathons to quickly prototype novel tools.

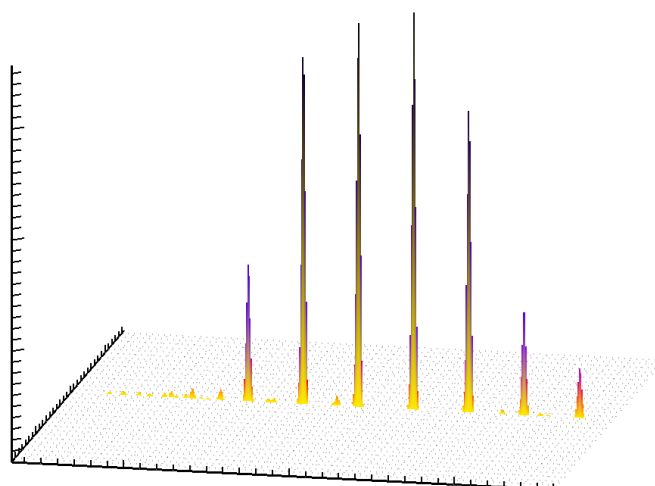
Application and Deadlines

In total, 20 participants (advanced PhD students / postdocs from life sciences / bioinformatics / computer science coming from Germany, Europe, world-wide) will be selected based on short applications. Please provide the following documents:

- CV (e.g. topic of PhD thesis / research focus)
- Motivation letter
- Description of bioinformatics skills (e.g. "experience in applying bioinformatics tools", "knowledge about scripting / command line usage", "tool developer / programmer")
- Description of own data sets (if any)

Send your application via email to PD Dr. Martin Eisenacher (full contact details below). There will be no participation fee. Accommodation will be supplied by the de.NBI consortium. Travel expenses have to be paid by the participants.

Application Deadline:	1 st June 2016
Selection of Participants:	20 th June 2016



Contact Details:

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D-44801 Bochum
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e-mail: martin.eisenacher@rub.de

Organizers:

de.NBI service centers BioInfra.Prot, CiBi and BiGi:
Martin Eisenacher (Bochum) Jens Stoye (Bielefeld)
Oliver Kohlbacher (Tübingen) Stefan Albaum (Bielefeld)
Knut Reinert (Berlin) Robert Ahrends (Dortmund)
Michael Berthold (Konstanz)

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