

Special Session on Data Analysis for Mass Spectrometric Problems

Session Organizers

Frank-Michael Schleif
University of Leipzig, Dept. of Computational Intelligence
& Bruker Daltonik GmbH
Karl-Tauchnitz-Str. 25, D-04107 Leipzig, Germany
Tel: +49-341-24 31-480 Fax: +49-341-96252-15
E-Mail: fms@bdal.de

Thomas Villmann
University of Leipzig, Dept. of Computational Intelligence
Karl-Tauchnitz-Str. 25, D-04107 Leipzig, Germany
E-Mail: villmann@informatik.uni-leipzig.de

Jens Decker
Bruker Daltonik GmbH
Research & Development
Fahrenheitstr. 4, D-28359 Bremen, Germany
E-Mail: jde@bdal.de

This session is organized as a part of

***The 7th International FLINS Conference
on Applied Artificial Intelligence (FLINS 2006)***

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In several areas of bioinformatics like mass spectrometry (ms), genome expression, biosignal analysis a.s.o. applied artificial intelligence methods play an important role in data analysis and data processing. These methods include all kinds of machine learning approaches as well as neural networks, modern statistics, genetic algorithms etc. In this session we focus on data processing in mass spectrometry. The most relevant problems arising in this domain are due to high dimensional but sparse data, processing of structures (functional data) and fuzziness. These topics are of more general interest also in the machine learning community. Otherwise ms plays an increasing role in the field of clinical proteomics and chemometrics.

In the announced special session we focus on all kind of data analysis occurring during the processing of ms data like peak detection, feature extraction, pattern recognition, classification etc. The quality of these data analysis tools crucially influences the medical investigation results. This is especially true for the analysis of high-dimensional functional MALDI-TOF or SELDI-TOF spectra of body fluids from clinical proteomics studies.

To improve the state of the art in this field both the processing of the spectra as well as new algorithms for the supervised and unsupervised analysis of the extracted spectral features should be reconsidered in the light of new research results. The special session *Data Analysis for Mass Spectrometric Problems* on FLINS 2006 aims on collecting the state of the art activities in these fields and invites to bring researchers together working on these important topics. Therefore, we encourage the submission of contributions which aim on improvements of all kinds of data processing for MS.

Recommended topics include but are not limited to the following:

- Machine Learning approaches for ms data analysis
- Fuzzy data analysis
- Rule extraction
- Automatic reasoning
- Denoising
- Baseline correction and noise estimation
- Recalibration
- Automatically evaluation of spectra quality
- Feature extraction and selection
- Classification of ms data (e.g. within clinical proteomics)
- Statistical methods for data analysis of ms data
- Applications in Clinical Proteomics, Metabolic Profiling

Submission of papers

Authors are invited to submit a paper up to 8 pages by December 15, 2005. You can submit your paper to the session organizers by email to: fms@bdal.de or [{Schleif, villmann}@informatik.uni-leipzig.de](mailto:{Schleif,villmann}@informatik.uni-leipzig.de)

All papers submitted in this session will be peer-reviewed. Accepted papers will be published in the conference proceedings as the book "**Applied Artificial Intelligence**" by **World Scientific** (to be EI indexed). Final papers should be prepared according to the **publisher's instructions** :

http://www.worldscientific.com/style/proceedings_style.shtml

Please select the trim size: 9" x 6". Papers that are not prepared according to these guidelines will not be published.

Important dates

- Paper submissions: December 15, 2005
- Acceptance letter: February 15, 2006
- Final papers submissions: April 15, 2006