PRG, Turku Centre for Biotechnology, BioCity Turku, Finland

MS IMAGING BIOINFORMATICS COURSE

30 November-4 December 2009

Turku Proteomics Facility, Finland

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Label free imaging of tissues by MS uses an intrinsic molecular parameter, the molecular mass, to determine and visualise the distribution of a wide variety of biomolecules at and on surfaces. The field, known as Imaging MS (IMS), is an emerging technology however. Important developments and novel applications performed in the field of IMS still occur at a high-rate, underscoring the emerging status of this new application in mass spectrometry.

IMS and MS-based profiling of tissue sections has demonstrated how biomolecular signatures from different regions of tissues can be used to classify pathological states. The biomolecular markers used in these classifications are based on the interplay of multiple biomarker proteins that show the potential of multiplexed analysis. This course is therefore devoted to discuss and convey best practices in processing and validating imaging mass spectrometry data.

Contents

In this course the following elements of computational IMS analysis will be covered:

- *Integration of MS imaging into biological & biomedical investigations*
- *Basic MS processing & imaging fundamentals: How to qualify raw data; How to generate images; Good IMS practice*
- *Metadata, information management system*
- *Principal component analysis and how to use PCA – grouping/classification; PCA can do's & can't do's*
- *Hierarchical clustering and how to use hierarchical clustering – grouping/classification*
- *Standardisation and sharing: iMZML & available tools*
- *Quantitation of pharmaceutical compounds*
- *Using software:*
  - *Biomap practical*
  - *ClinProTools - unsupervised analysis of single datasets and patient cohorts*
  - *ClinProTools - supervised analysis and classification*

The course is from Monday 30 November until Friday 4 December at the Turku Centre for Biotechnology, BioCity Turku, Finland. The course will incorporate lectures and practical training. To ensure all participants get hands-on training the number of places is limited.
The course is in the first instance open to PhD participants from Nordic countries (Finland, Denmark, Iceland, Norway, Sweden). Transport and accommodation will be provided to PhD participants from the Nordic countries, and course fees will be waived. Several places will be made available to other European participants, however in this case transport and accommodation costs cannot be provided and must be met in full by the participant. A fee of 1000€ exists for other participants.

Registration

Register to the course by sending a short application to Susanne Nees. In the application which is no longer than one A4 page you should provide the following information:

- *Your name*
- *Graduate school*
- *Short description of your project (0,5 A4 max.)*
- *Institution*
- *Your supervisor*
- *How bioinformatics would benefit your project*

Trainers

Garry Corthals
Anni Vehmas
Turku Centre for Biotechnology, Turku

Ron Heeren
FOM AMOLF, Amsterdam

Liam Mcdonnell
Leiden University Medical Centre

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Anna Nilsson
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Andreas Römpp
Justus Liebig University Giessen

More information available at proteomics .btk.fi