



EuBIC Winter School 2019

15th – 18th January 2019, Hotel Mercure Kasprowy, Zakopane, Poland



Programme



<https://www.proteomics-academy.org/eubic-winter-school-2019>

Day 1 – 15. January 2019

Educational Day

Time	Title		
09:30 - 10:00	Welcome coffee & Registration		
10:00 - 10:30	Opening Session		
10:30 - 12:00	Introduction to computational mass spectrometry using OpenMS, Part I	Computational introduction into DIA	Label-free quantification: concepts and algorithms
12:00 - 13:00	Lunch Break		
13:00 - 14:30	Introduction to computational mass spectrometry using OpenMS, Part I (continued)	Computational introduction into DIA (continued)	Quantitative proteomics: statistics, clustering and complexes
14:30 - 14:45	Coffee Break		
14:45 - 16:15	Introduction to computational mass spectrometry using OpenMS, Part II	Computational introduction into DIA (continued)	Quantitative proteomics: statistics, clustering and complexes (continued)
16:15 - 16:30	Coffee Break		
16:30 - 18:00	Introduction to computational mass spectrometry using OpenMS, Part II (continued)	Computational introduction into DIA (continued)	Quantitative proteomics: statistics, clustering and complexes (continued)

For further information on the workshops, please see the electronic version of the programme or the winter school's webpage.

Day 2 – 16. January 2019

DIA and Standards

Time	Title	Speaker(s)
08:35 - 08:40	Morning Welcome and Announcements	
08:40 - 09:25	XCorDIA: a new database search engine to detect geentic variants from DIA data	Brian Searle
09:25 - 10:10	Developing the tools for the personalized medicine revolution: Using mass spectrometry for longitudinal molecular profiling	Hannes Röst
10:10 - 10:30	Coffee Break	
10:30 - 11:15	Label-free Quantification of Complex Proteomes using Ion-Mobility-based DIA	Stefan Tenzer
11:15 - 12:00	Bioinformatics for Proteomics - any open questions?	Martin Eisenacher
12:00 - 13:00	Lunch Break	
13:00 - 13:50	Poster flash talks	
13:50 - 14:20	Sponsor talk	SVA
14:20 - 18:20	Workshop Session (Coffee break at 15:30-15:50)	see workshop descriptions
18:20 - open end	Poster Session & Come Together	

Parallel Workshops

Stefan Tenzer	Quality Control and Benchmarking of Label-Free Quantification Workflows with LFQBench
Martin Eisenacher	The essentials before and after spectrum identification: Selecting the appropriate database and inference strategy
ProFI	Discovering the open-source Proline software suite, a new efficient and user friendly solution for label-free quantification
Thermo	Proteome Discoverer 2.3 Workshop

Day 3 – 17. January 2019

Result Interpretation

Time	Title	Speaker(s)
08:35 - 08:40	Morning Welcome and Announcements	
08:40 - 09:25	STRING – Large-scale integration of data and text	Lars Juhl Jensen
09:25 - 10:10	Prosit: Proteome-wide prediction of peptide tandem mass spectra by deep learning	Mathias Wilhelm
10:10 - 10:30	Coffee Break	
10:30 - 11:15	Using phosphoproteomics data to study context-specific signalling	Evangelia Petsalaki
11:15 - 12:00	Insights into the multi-functioning proteome	Kathryn Lilley
12:00 - 13:00	Lunch Break	
13:00 - 13:30	Sponsor Talk: Novel DIA Data Analysis Workflow: Integration of De Novo Sequencing and Database Search	BSI
13:30 - 17:30	Workshop Session (Coffee break at 15:30-15:50)	see workshop descriptions
17:30 - 18:00	EuBIC Meeting	All new members are welcome
19:00 - open end	Social Event	

Parallel Workshops

Lars Juhl Jensen	Network visualization with Cytoscape and stringApp
Evangelia Petsalaki	SELPHI: using data-driven approaches for analysis of phosphoproteomics datasets
Florian Meier	Advanced data acquisition methods with MaxQuant.Live
Matthias Wilhelm	Validation of peptide identifications

Day 4 – 18. January 2019

Innovative methods

Time	Title	Speaker(s)
09:00 - 09:05	Morning Welcome and Announcements	
09:05 - 09:50	lonbot: a novel, fully data-driven search engine for open modification and mutation searches	Sven Degroeve
09:50 - 10:20	YPIC - Young Proteomics Investigators Club	
10:20 - 10:50	Coffee Break	
10:50 - 11:35	Trapped ion mobility spectrometry: a new dimension for mass spectrometry-based proteomics	Florian Meier
11:35 - 12:00	Announcement: Best Flash Talk, Best Poster Award, Closing Remarks	
12:00 - 12:45	Lunch	
13:00	Shuttle Buses leaving	

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