



4th EuPA MEETING
6th ProCura MEETING

2010
PROTEOMICS
ODYSSEY
TOWARDS NEXT DECADES

EuPA course day “Experimental design in proteomics”

10:00 am – 5:30 pm, 23 October 2010, Hotel Estoril Edén, Estoril Portugal

Chairs: Peter James & Garry Corthals

The course is designed to give a clear overview of the new guidelines regarding experimental design that the Proteomics journals have all laid down. The talks will cover practical approaches to defining the types of error sources and how this defines the number and type of replicates that are needed to be able to reach a valid conclusion (Power analysis of a pilot experiment). An overview will be given on which type of statistical tools are appropriate to handling a particular data set and how to define a data analysis flow. The day finishes with a practical demonstration of how to manage large datasets and how they may be validated. Finally a guide will be given on how to fulfil the publication requirements of Journals in submitting data to data repositories.

Saturday, October 23, 2010	
EuPA Education Workshop (Local: Hotel Estoril Eden)	
Experimental Design in Proteomics	
Organizers: Peter James & Garry Corthals, EuPA-Education Committee	
10:00 am	Introduction to Experimental Design (Peter James)
11:00 am	Introduction to statistical data analysis (Marianne Sandin)
12:00 am	Lunch
1:00 pm	Creating a data analysis workflow (Marianne Sandin)
2:00 pm	Data management and validation (Frederick Levander)
3:00 pm	Coffee Break
3:30 pm	Data management – How to handle all the data in an open source database (Frederick Levander)
4:30 pm	Handling false discovery rates (Eugene Kolker)
5:30 pm	Course Adjourns

Teachers Biography



Peter James

Graduated from Oxford University and completed his PhD at the ETH in Zurich in 1990. After a two year post-doc in USCF, San Francisco and in ThermoFinnigan, San Jose he returned to the ETH. He moved to take the chair in Proteomics at Lund University in 2001. He was a member of Founding Board of the Human Proteome Organisation, HUPO and was chairman of the education committee and is on the editorial Boards of the four leading Proteomics journals. P James is currently the SWEGENE Director of Proteomics. He has published over 100 peer reviewed articles and reviews in the field of protein chemistry and proteomics and holds 7 patents in proteomics methodologies. His research field is protein analysis with a focus on protein-protein interaction, membrane proteins and methods development for clinical proteomics. The main focus currently is on biomarker discovery for diagnosis and therapy outcome prediction for clinical use and on defining plasma membrane protein targets for directed antibody therapy.



Garry Corthals

Corthals received his Phd in 1997 and has since worked for 10 years in the field of biomedical proteomics and held positions at the Medical School, Uni Washington, Seattle (97-98), the Garvan Institute for Medical Res, Sydney (99-01), and Geneva University Hospital and Medical Faculty (02-05). Currently he is a Group Leader in Translational Proteomics at the Turku Centre for Biotechnology (www.btk.fi). In addition to research activities, he is the Director of the Turku Proteomics Facility (proteomics.btk.fi). Further tasks include coordination of the national "Proteomics and Metabolomics infrastructure" (www.ProtMet.net) of Biocenter Finland, and coordination of the Nordic Quantitative Proteomics (www.nordic-qp.net) network of research schools, Nordic Signals research network and the Nordic imaging network. He is also chair of the Education Committee of the EuPA (www.eupa.org), and serves on the HUPO (www.hupo.org) education committee. He is also an editor of the Biochemistry, Genetics and Molecular Biology section of SciTopics (www.scitopics.com).

Now in his fourth year in Finland, his research group focuses on prostate cancer, epilepsy and endometriosis which all involve the molecular spatial and temporal analysis of tissues and body fluids from patients or animal models using a collection of methods ranging from MS imaging to HTP methods for molecular definition of tissues. Additionally they are developing bioinformatics approaches to quantitation of proteins in tissues, and efficient retrieval and validation phosphorylated proteins.



Marianne Sandin

Ph.D. student at the Department of Immunotechnology, Lund University, Sweden. Received M.Sc. in Engineering Mathematics in 2009 from Lund University. Teaching experience includes statistics and bioinformatics. Research interests are applied mathematics and data analysis as well as algorithms in the field of label-free quantitative proteomics.



Fredrik Levander

Associate Professor at the Protein Technology Division of the Department of Immunotechnology, Lund University. After obtaining his PhD in Applied Microbiology in 2001 he entered the field of computational proteomics via a bioinformatics company before joining the proteomics group of Peter James at Lund University. In this high-throughput environment he has since then been addressing the needs for automated data integration and data analysis, and he has been active in the development of the Proteios platform for proteomics data management and analysis. He is also involved in the Proteomics Standards Initiative (PSI). Currently he is working on setting up a nation-wide bioinformatics infrastructure for proteomics data handling in Sweden.



Eugene Kolker

Head, Bioinformatics & High-throughput Analysis Laboratory, *Seattle Childrens Research Institute*, Biomedical & Health Informatics Division, Medical Education and Biomedical Informatics Department, School of Medicine, *University of Washington, Seattle*. Director, High-throughput Analysis Core, SCRI <http://kolkerlab.proteinspire.org/HACore.html>. Editor-in-Chief, *OMICS: A Journal of Integrative Biology*.
