How to use and interpret large datasets from emerging –omics based technologies

October 20 – 23, 2014
Forskningens Hus, Room 405

This PhD course is offered by the Doctoral School in Medicine, Biomedical Science, and Technology at Aalborg University and the Clinical Cancer Research Center, Aalborg University Hospital

Organisers: Martin Bøgsted (m_boegsted@dcm.aau.dk) and Søren Risom Kristensen (srk@rn.dk)

Evaluation: Attendance at lessons and participation in exercises

ECTS: 3,2

Registration: If you want to sign up for the course, please register and login to Aalborg University's Moodle at: https://phd.moodle.aau.dk/login/index.php

Preliminary programme for the course:

October 20, 2014

Introduction to molecular biology

09:00 – 09:45 Introduction to the Central Dogma of Molecular Biology – with a view towards high throughput technologies, Suzette Sørensen, Center for Clinical Research, Aalborg University.

09:45 – 10:00 Break

Next generation sequencing

10:00 – 10:45 Sequencing technologies – an overview, Mette Sondrup Andersen, Department of Biotechnology, Chemistry, and Environmental Engineering, Aalborg University

10:45 – 11:00 Break

11:00 – 11:45 Genomics, transcriptomics, and meta-genomics, Kacper Kaminski, Department of Biotechnology, Chemistry, and Environmental Engineering, Aalborg University

11:45 – 13:00 Lunch Break

13:00 – 13:45 Basic bioinformatics for sequencing technologies – challenges and pitfals, Mads Sønderkær, Department of Biotechnology, Chemistry, and Environmental Engineering, Aalborg University

13:45 – 14:00 Break

14:00 – 14:45 Genome-wide methylation analysis, Inge Søkilde and Vang Le Quy, Department of Clinical Biochemistry, Aalborg University Hospital

14:45 – 15:00 Break

15:00 – 15:45 Clinical examples: Gene panels versus whole exome sequencing for mutations screening and non-invasive prenatal diagnostics, Inge Søkilde and Vang Le Quy, Department of Clinical Biochemistry, Aalborg University Hospital

October 21, 2014

Clinical bioinformatics and statistics I

09:00 – 09:45 Design and analysis of biomarker experiments, Martin Bøgsted, Department of Haematology, Aalborg University Hospital and Department of Clinical Medicine, Aalborg University

09:45 – 10:00 Break

10:00 – 10:45 Reproducible statistical workflows for high dimensional data analysis by R/Bioconductor R-studio, Vang Le Quy

10:45 – 11:00 Break

11:00 – 12:00 Exercises, Vang Le Quy, Steffen Falgreen, and Martin Bøgsted

12:00 – 13:00 Lunch Break

Proteomics

13:00 – 13:45 Introduction to clinical mass spectrometry based analysis, Allan Stensballe, Department of Health Science and Technology, Aalborg University

13:45 – 14:00 Break

14:00 – 14:45 Proteomics strategies in clinical proteome analysis, Allan Stensballe

14:45 – 15:00 Break

15:00 – 15:45 Clinical proteomic case studies, Allan Stensballe

October 22, 2014

Clinical bioinformatics and statistics II

09:00 – 09:45 Principal component analysis, cluster analysis, and heat maps, Steffen Falgreen, Department of Haematology, Aalborg University Hospital and Martin Bøgsted

09:45 – 10:00 Break

10:00 – 10:45 Differentially expressed features and multiple test correction, Steffen Falgreen and Martin Bøgsted

10:45 – 11:00 Break

11:00 – 12:00 Exercises, Steffen Falgreen and Martin Bøgsted

12:00 – 13:00 Lunch break

Clinical bioinformatics and statistics III

13:00 – 13:45 Feature enrichment, Steffen Falgreen and Martin Bøgsted

13:45 – 14:00 Break

14:00 – 14:45 Prediction and classification techniques, Steffen Falgreen and Martin Bøgsted

14:45 – 15:00 Break

15:00 – 16:00 Exercises, Steffen Falgreen and Martin Bøgsted

October 23, 2014

Metabolomics and NMR

09:00 – 09:45 Background of NMR: What is measured and what can be detected, Reinhard Wimmer, Department of Biotechnology, Chemistry and Environmental Engineering, Aalborg University

09:45 – 10:00 Break

10:00 – 10:45 Metabolites and metabolomics – the place in the omcis-suite. NMR and other techniques for metabolomics and applications of metabolomics, Reinhard Wimmer

10:45 – 11:00 Break

11:00 – 11:45 Restricted regression techniques, Steffen Falgreen and Martin Bøgsted

11:45 – 13:00 Lunch Break

Clinical bioinformatics and statistics IV

13:00 – 13:45 Exercises

13:45 – 14:00 Break

14:00 – 14:45 Course evaluation, organizers and lecturers