university of groningen / faculty of science and engineering / centre for data science and systems complexity

DSSC SEMINAR

You are cordially invited to the DSSC seminar on

15 May 2017, 16.00-18.00, Bernoulliborg, room 5161.0105

How recycling big data can help improve to diagnose and treat disease

Speaker: Prof. Dr. Lude Franke

Faculty of Medical Sciences, Department of Genetics

Abstract

Developing a new drug is now typically costing over 3 billion Euro's. Is it possible to save some of these enormous amounts of money? Within the UMCG we are developing new computational methods to speed up and 'de-risk' drug development. We do this by studying 10,000 genetic risk factors that have been found in the last 10 years for many different diseases, and by ascertaining whether these genetic risk factors show effects on other molecular levels, such as gene expression, methylation or protein levels, with the aim to identify the disrupted disease-causing processes for these diseases. By targeting these biological pathways and genes through drugs, it might be possible to treat patients. In this presentation I will describe how we recycle large amounts of publicly available data, what computational and statistical methods we develop to do this, and how we have now implemented this in the genetics department to better diagnose patients. Finally I will outline ongoing strategies that we are currently pursuing to also use this information to better treat patients.

Biography

Lude Franke is associate professor of systems genetics at the University Medical Center Groningen. His group focuses on the development and application of novel statistical and computational methods to better understand what key genes, pathways and cell-types are causally disrupted in disease. This is achieved through the (re)analysis of large existing (single-cell) multi-omics datasets and quantitative trait locus mapping.

Exploring the limit of mass spectrometry molecular profiling for clinical applications

Speaker: Prof. Dr. Peter Horvatovich

Groningen Research Institute of Pharmacy

Abstract

Proteins are the active molecular component of biology built from 20 amino acids and modified by more than 300 types of post-translational modifications. These building blocks result in wide chemical space of proteins, which spans 7-11 order of magnitude dynamic concentration range. Mass spectrometry coupled to liquid chromatography (LC-MS/MS) allows comprehensive profiling of peptides derived from proteins originated from complex biological samples and allows to identify protein concentration changes that occurs during disease onset, development and treatment. This talk will introduce the audience in LC-MS/MS proteomics molecular profiling and will present the bioinformatics approaches and challenges that aimed to pre-process and analyze the acquired data. The talk will highlight the main characteristics of the developed algorithms and will provides clinical application examples. These examples include results from urine profiling studies which aim to identify biomarkers for protein urea and pregnancy disorders and a proteogenomics study that integrate genomics and proteomics data to reveal the molecular mechanism of chronic obstructive pulmonary disease using human lung tissue.

Biography

The current research of Peter Horvatovich is at intersection of analytical chemistry, biomarker discovery, proteomics, statistics and computational mass spectrometry. In the past, he performed research in food analytical chemistry, drug discovery and cheminformatics. During the last ten years, his scientific interest focused mainly on quantitative aspects of LC-MS/MS and mass spectrometry imaging data processing with application in biomarker discovery and differential proteomics studies. His main scientific achievements include the development of novel LC-MS/MS time alignment algorithms and quantitative LC-MS data pre-processing pipelines such as msCompare and Threshold Avoiding Proteomics Pipeline. Peter Horvatovich is author of more than 60 peer-reviewed articles, edited one book and contributed in four book chapters.