‘System-Wide Mass Spectrometry: Proteomics and Metabolomics in Biology and the Clinic’

FALL Quarter, 2013
SPPS 268/Phar 299, 2 units
Thursdays 1-3 pm, PSB 1186
+ 20 hours contact time (2 hrs/week) for a hands-on project in the SSPPS metabolomics or proteomics laboratory, from mass spectrometry data acquisition to data analysis and conclusions.

Part I. Basics of Mass Spectrometry: Methods, Instruments, Applications and Bioinformatics

Sept. 26 Basics of Mass Spectrometry– Pieter Dorrestein

Oct. 3 Introduction of mass spectrometry applications in the clinic, diagnostics biology and research– Pieter Dorrestein
Start lab work-Small scale hands-on metabolomics/proteomics project

Oct. 10 Computational and bioinformatic analyses of mass spectrometry data
Nuno Bandeira

Part II. Biomedical and Biological Applications of Mass Spectrometry and Proteomics

Oct. 17 Spatial systems biology; imaging mass spectrometry. Shannon Cornett
Bruker Daltonics

Oct. 24 Measuring changes in metabolites; clinical metabolomics. 50 min Mohit Jain Metabolomics fundamentals, 50 min Kumar Sharma clinical applications.

Oct. 31 MS based quantitative systems biology; proteomics and PTMs. Shen Zhouxin proteomics introduction, Dorrestein/Bandeira hands-on Inspect PTM analysis.

Nov. 7 Lipids in biology; lipidomics. 50 min Oswald Quehenberger Introduction of the Fundamentals, 50 min, Marcos Milla, Janssen, clinical/drug discovery applications of lipidomics.

Nov. 14 Network analysis: Biological information from large mass spectrometry data-sets. Class will be instructed to download Cytoscape for this lecture. Dorrestein lab is covering molecular networking and Brian Demchak, Ideker lab covering mechanics of Cytoscape (proposed)

Nov. 21 Student presentation. Nuno Bandeira/Vivian Hook

Dec. 5 Student presentation. Nuno Bandeira/Vivian Hook
Course Description: see next page

Course Description for ‘System-Wide Mass Spectrometry: Proteomics and Metabolomics in biology and the clinic’ CMM 264/SPPS 268/PHAR 299
Spring Quarter 2011

Thursdays, 1-3 pm, Location PSB 1186 + lab work for completion of a hands on project (2 hours of lab contact time per week, for 20 hours total during the quarter) Location: Bruker therapeutic discovery mass spectrometry center, Basement of PSB

Course Directors:
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Introduction: Mass spectrometry is a widely used tool in the clinic to understand health and disease, diagnostics and for studying the molecular details of biological applications. Recent advances in high mass resolution and rapid scanning MS instruments have further stimulated its applications in both targeted biological applications and large-scale proteomic explorations. Further, quantitative analysis of proteins using mass spectrometry has become a widely used strategy. In this course, we will provide an overview of this rapidly evolving field by first introducing basic concept and techniques, then focusing on selected topics to stimulate exchanges of ideas and expertise among faculty and participating students towards addressing specific applications in biology.

Summary: This course contains three parts. In the first part, basics of mass spectrometry and data analysis methods will be introduced. An overview of different mass spectrometry instruments, their specific applications and available resources in UCSD and San Diego area are provided. This will be followed by critical evaluations of computational methods to analyze mass spectrometry data. Second, several schemes on the applications of mass spectrometry in biological research are planned. The topics tentatively includes quantitative mass spectrometry to characterize protein complexes, analysis of protein phosphorylation and post-translational modifications using mass spectrometry, hydrogen/deuterium exchange mass spectrometry to study protein structures, and the use of mass spectrometry with activity based probes to study protease activities that lead to drug discovery, discussion on large scale proteomics and phosphoproteomics, and selected topics based on the interests of the attending graduate students/post-docs. Thirdly there is a hands-on component to the course. Here we will carry out a metabolomics/proteomic experiment and carry this through from processing to analysis of the data.

Format of Course: The format for the first part will be 2-3 lectures with classroom discussion and questioning to follow. The format for the second part will consist of, 1) 45-60 min lectures from faculty and leaders in the mass spectrometry community, 2) mass spectrometry laboratory project (20 hours lab during the quarter, which is ~2 hrs/week), and 3) specific research proposals from students on how mass spectrometry can be used to address their specific problem of interest.
The objective is to train students to acquire expertise on how mass spectrometry could and should be used to address specific research topics on which participating students are expected to provide significant inputs.

**Grading:** Pass or fail grades, based on participation in discussion, and presentation of the results obtained in your project or small research proposal relevant to your research. Any questions regarding the course please contact Pieter Dorrestein at pdorrest@ucsd.edu or Vivian Hook at vhook@ucsd.edu.