

ABRF 2009:
Optimization and Application of Existing and Emerging Biotechnologies
February 7-10, 2009 – Memphis, Tennessee

SATELLITE EDUCATIONAL WORKSHOP PROGRAM
(sw5) Proteome Informatics
(current as of 11/28/08)

Saturday, February 7, 2009
8:00 am – 4:00 pm
Memphis Cook Convention Center.

Real-life Proteome Bioinformatics for Laboratories
Lennart Martens, EMBL-European Bioinformatics Institute, UK (organizer),
David Tabb, Vanderbilt University (co-organizer),
Brian Searle, Proteome Software, and Kathryn Lilley, Cambridge University, UK

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| 7:00 am - 12:00 pm | REGISTRATION OPEN - Lobby |
| 7:00 - 8:00 am | CONTINENTAL BREAKFAST - Ballroom Foyer |
| 8:00 - 9:00 am | MS AND MS/MS SEARCH ENGINES
<i>Brian Searle, Proteome Software</i>
A variety of different algorithms to identify mass spectra, both commercial and free, are available today. This session will review the underlying mechanisms of the search algorithms and will examine the most common ones used today. |
| 9:00 - 10:00 am | ASSESSING THE RELIABILITY OF IDENTIFICATIONS
<i>Brian Searle, Proteome Software</i>
This session will address the difficult problem of deciding whether a peptide identified from an MS/MS spectrum represents a correct identification or a false positive. We will explore how to estimate the false discovery rate from an experiment. We will discuss strategies aimed at minimizing the number of false positives in a dataset. |
| 10:00 - 10:30 am | REFRESHMENT BREAK - Ballroom Foyer |
| 10:30 - 11:00 am | SEQUENCE DATABASES AND ONLINE RESOURCES
<i>Lennart Martens, EMBL-European Bioinformatics Institute, UK</i>
In the vast majority of cases, the sequence database that is used for peptide identification or protein inference plays an extremely important role in the overall workflow. However, the sequence database is typically the most neglected component in many workflows. This session will examine the differences between different databases and explore how their variation can be exploited in various circumstances. An overview of useful online resources will be presented. |
| 11:00 am - 12:00 pm | PROTEIN INFERENCE
<i>David Tabb, Vanderbilt University</i>
Identifying peptides from MS/MS spectra represents only half the work. Since the end goal of most experiments is the identification of proteins, peptide lists need to be processed into protein lists. This session will provide detailed information on the problems underlying protein inference. Tools and approaches that can facilitate protein inference will be presented and discussed. |

12:00 - 1:00 pm	LUNCH - <i>Ballroom Foyer</i>
1:00 - 1:40 pm	QUANTITATION STRATEGIES AND DATA ANALYSIS <i>Kathryn Lilley, Cambridge University, UK</i> A variety of proteomics quantitation strategies are currently available. This session will present an overview of these techniques. Issues related to processing and interpretation of data from these techniques will be discussed in detail.
1:40 - 2:20 pm	IDENTIFYING MODIFIED OR MUTATED PROTEINS <i>David Tabb, Vanderbilt University</i> This session will explore the various ways in which peptides or proteins can be identified when they are novel, if they carry complicated or unexpected post-translational modifications, or if they contain mutations.
2:20 - 2:50 pm	REFRESHMENT BREAK - <i>Ballroom Foyer</i>
2:50 - 3:30 pm	DATA STANDARDS AND PUBLIC DATA DISSEMINATION <i>Lennart Martens, EMBL-European Bioinformatics Institute, UK</i> Funding agencies and journals are increasingly demanding that the results of funded or published experiments be readily available to the public. This session will discuss the state of standardization in the field and the means to disseminate data as easily and efficiently as possible.
3:30 - 4:00 pm	ASK THE EXPERTS SESSION Informal discussions between presenters, organizers, and attendees