

Proteomics

10.5.09

Objective: To give a presentation of about 40-90 minutes at the end of the week covering the key aspects of proteomics.

The questions and contents below are meant as motivators and need not be followed,

The Big Questions Are:

- What are the key classes of data (OMICS)?
- What is the inherent variation in proteomics?
- What was the first proteomics investigation?
- Which omics classes are often combined in analysis?
- What are the largest proteomics studies to date?
- Which models are used to analyze data?
- How quantitative can proteomics be?
- Are there examples of pQTLs?
- How can you use proteomics to elucidate function?
- Are there examples of clear disease associations?
- What are the dimensions of data?
- What are the methodological differences between metabolomics and proteomics?

Recommended literature is only meant to get you started. You might very well be able to find papers more suited for your purpose.

Davies, Rafnar, Hellenthal and Hein (2009) "Integrative Genomics and Functional Explanation" downloadable from <http://www.stats.ox.ac.uk/research/genome/publications>

Cox and Mann, (2007) "Is Proteomics the New Genomics?" *Cell* 130, 395-8

Haoudi et al. (2007) Bioinformatics and data mining in proteomics *Exp. Rev. Proteo.* 33.3.333-43.

Godoy et al. (2008) Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast *Nature* 455.1251-55

Kang et al. (2008) Neural palmitoyl-proteomics reveals dynamic synaptic palmitoylation *Nature* Vol 456.904-09

Hoog and Mann (2004) PROTEOMICS *Annu. Rev. Genomics Hum. Genet.* 5:267-93

Foss et al. (2007) Genetic basis of proteome variation in yeast *NATURE GENETICS* 39 .11.1369-74

Taylor et al. (2007) The minimum information about a proteomics experiment (MIAPE) *NATURE BIOTECHNOLOGY* 25 .8 .887-93

Gupta et al. (2007) Applications of mass-spectrometry for proteogenomic annotation Whole proteome analysis of post-translational modifications *GenRes* 17: 1362-1377;

Veltri (2007) Algorithms and tools for analysis and management of mass spectrometry data *BRIEFINGS IN BIOINFORMATICS*. 1-12

Simpson et al. (2008) Proteomics-driven cancer biomarker discovery: looking to the future *Curr.Opin.Chem.Biol.* 12:72-77

Vermeulen et al. (2008) High confidence determination of specific protein-protein interactions using quantitative mass spectrometry *Curr Opin Biotech* 19:331-337

Wolff et al. (2007) Towards the entire proteome of the model bacterium *Bacillus subtilis* by gel-based and gel-free approaches *Journal of Chromatography B*, 849 (2007) 129-140

Bandeira et al. (2007) Protein identification by spectral networks analysis *PNAS*. vol. 104 no. 15 6140-6145