Lecture 14: Suggested reading and Home assignment

Please read following two highly recommended article:

1. Stephen J Fey and Peter Mose Larsen 2D or not 2D. Opinion in Chemical Biology 2001, 5:26–33

   **Abstract of the article (Opinion in Chemical Biology 2001, 5:26–33)**

   2D gel electrophoresis is the technology that everyone loves to hate — it requires manual dexterity and precision to reproduce precisely and is thus not well-suited as a high-throughput technology. Although almost everyone would like to replace it, the resolution and sensitivity it offers are exquisite and unsurpassed if one wants a global view of cellular activity. There have been several recent developments, for example, the detection of low abundance proteins, and the resolution possible with narrow-range IPG gels.


   **Abstract of the article (In Silico Biol. 2002;2:507-10.)**

   2-D Gel Technology has had profound impact on proteomic research over the years. Informatics support brought a new dimension to 2D gels and associated technologies. But with advent of new and emerging technologies, it will be interesting to observe the trends of 2D gel technology in the years to come. Here we review 2D gel technology and its applications besides looking at the future scope of 2D gels in the post genome era.


   **Abstract of the article (Nucleic Acids Research, 2004, 32, D582-D585.)**

   GELBANK is a publicly available database of two-dimensional gel electrophoresis (2DE) gel patterns of proteomes from organisms with known genome information (available at http://gelbank.anl.gov and ftp://bioinformatics.anl.gov/gelbank/). Currently it includes 131 completed, mostly microbial proteomes available from the National Center for Biotechnology Information. A web interface allows the upload of 2D gel patterns and their annotation for registered users. The images are organized by species, tissue type, separation method, sample type and staining method. The database can be queried based on
protein or 2DE-pattern attributes. A web interface allows registered users to assign molecular weight and pH gradient profiles to their own 2D gel patterns as well as to link protein identifications to a given spot on the pattern. The website presents all of the submitted 2D gel patterns where the end-user can dynamically display the images or parts of images along with molecular weight, pH profile information and linked protein identification. A collection of images can be selected for the creation of animations from which the user can select sub-regions of interest and unlimited 2D gel patterns for visualization. The website currently presents 233 identifications for 81 gel patterns for Homo sapiens, Methanococcus jannaschii, Pyrococcus furiosus, Shewanella oneidensis, Escherichia coli and Deinococcus radiodurans.

**Home assignment**

Please visit the webpage [http://www.jvirgel.de/index.html](http://www.jvirgel.de/index.html)

JVirGel is a software for the simulation and analysis of proteomics data. This determines the theoretical isoelectric points and the molecular weights of proteins of an organism (with known genome sequence) from sequence data and visualizes these as a virtual two-dimensional (2D) protein map. Several similar online resources are available. Please do a survey

*Submit your assignment to course developer by e-mail; you will get an e-mail reply with grading and feedback in a week time.*