BST281: Genomic Data Manipulation, Spring 2018

Wednesday 12: Proteins: Proteomics, Families, and Folds

**Proteomics**

* The direct detection and quantification of the proteins in a biological system
  + Can also assay protein “states” [post-translational modifications (PTMs), e.g. phosphorylation]
  + Provides high-confidence detection of proteins/validation of putative coding genes
  + Provides more accurate protein abundance estimate than inference via mRNA abundance
* Antibody arrays use protein-specific antibodies to detect and quantify proteins (~microarray)
  + Useful for small sets of specific proteins (e.g. cytokines)
* 2D gels separate a protein mixture based on two properties, typically size and pH/charge
  + Compare 2D coordinates to reference positions for identification
* Tandem mass-spectrometry (MS-MS) = shotgun sequencing for proteins
  + Protein mixture is stratified (e.g. by liquid chromatography) to reduce complexity
  + Proteins are digested (e.g. by Trypsin) into short peptide fragments
  + Peptide fragments are isolated in a first round of MS
  + Fragments are shattered into ions along peptide bonds
  + “Stepped” mass/charge (m/z) ratios reveal amino acid sequence during second round of MS

**Protein families**

* Protein sequences map to functions/folds many-to-one (genotype-phenotype mapping)
* Multiple strategies for defining protein “families” (sequences compatible with a given function)
* Global protein similarity
  + Clusters of Orthologous Groups (COGS) – Reciprocal best BLAST hit relationships
  + UniRef – Clustering of the protein universe at different levels of sequence identity
* Local protein similarity (domains/motifs)
  + Pfam (and related approaches) define local multiple sequence alignments (MSAs) for domains
  + Multiple domains can occur in a protein = domain architecture

**Protein structure determination and data**

* Methods for determining protein structure
  + X-ray crystallography (gold standard, requires protein to crystallize)
  + Nuclear Magnetic Resonance (NMR; can probe dynamic processes, but limited to small proteins)
  + *Ab initio* folding on a computer based on physical models (hard)
  + Knowledge-based folding (homology modeling, threading, fragment assembly)
* Structure data (x, y, z coordinates of atoms) are stored in the Protein Data Bank
* Structures are organized into hierarchies based on the similarity of their folds (e.g. CATH, SCOP)
  + Structures at top levels in the hierarchy may not be obviously related by descent, or at all

**Hidden Markov Models (HMMs) – part of slide “extras”**

* A Markov model is a set of states and transition probabilities
* In a HMM, we don’t observe states directly, but rather “clues” emitted in the form of symbols
  + Ex. Genomic CpG dinucleotide symbols emitted more often in “gene” state than “not gene” state
* Protein family MSAs are represented as HMMs to enable highly sensitive detection in new sequences
  + Each MSA column is a state; emission probabilities are amino acid frequencies in that column
  + Additional states allow deletions and insertions

**Suggested reading**

* Pevsner: Ch. 12, pp. 539-575 (Proteomics); Ch. 13, pp. 589-625 (Protein structure)
* Bloom, Jesse D., et al. "[Structural determinants of the rate of protein evolution in yeast](https://academic.oup.com/mbe/article/23/9/1751/1014274/Structural-Determinants-of-the-Rate-of-Protein)." *Molecular biology and evolution* 23.9 (2006): 1751-1761.