BIOE C144L First Lecture: introduction information

January 21, 2014

Make sure to print out lecture slides before each of the lectures. Consider using some digital note taking strategy.

Office Hours: to be discussed

Homology-based annotation transfer

Start with a protein of unknown function

- Run BLAST on it to find homologs.

- If the homolog at the top hit has a resaonable E-value, then transfer the annotation to the protein of interest.

Sources of annotation error

- neofunctionalization: ortholog instead of paralog

- Domain shuffling: comes from multiple domain architecture of proteins Some domains are promiscuous, and therefore the domain can be found in many different combinations.

Reading

Start by reading the Sjolander review article. Brown & Sjolander, "Functional Classification using Phylogenomic Inference." PLoS Computational Biology, 2006

The Wild West of tool development. There are many opportunities in this field for making tools more functinal. So many of the available tools today are error prone.