

Bioinformatics

Lab 8 Proteomics

1) Read the following paper:

Using UniProtKB to find the protein you are interested in:

<http://www.uniprot.org/help/uniprotkb>

You can use BLAST or IDmapping or other functionalities. Look at the detailed annotation of your proteins: including related function, subcellular location, GO, related literature, etc.

2) Using your proteins or organisms of your interests, visit Gene Ontology website

<http://geneontology.org/>

3) Visit the following website to see tools related to protein analysis

<http://www.expasy.ch/tools/>

then try to practice with your own protein sequences or sequences for some of the tools, including MW, secondary structure analysis, domain/motif/pattern, etc

http://web.expasy.org/compute_pi/

<http://www.ebi.ac.uk/interpro/search/sequence-search>

<http://prosite.expasy.org/scanprosite/>

<http://crdd.osdd.net/raghava/apssp/>

4) Protein Subcellular Location Prediction (**will be done in next lab**)

Read this paper first:

Lum G and Min XJ. (2013) Bioinformatic Protocols and the Knowledge-Base for Secretomes in Fungi. In: Laboratory Protocols in Fungal Biology: Current Methods in Fungal Biology.

http://proteomics.yzu.edu/courses/BIOL4800_6900/ExtraReadings/FungalProtocol_chapter54.pdf

Then test some these tools:

SignalP – signal peptide prediction

<http://www.cbs.dtu.dk/services/SignalP/>

(Human insulin P01308 to retrieve it from UniProtKB at <http://www.uniprot.org/>)

WoLFPSORT –

<http://www.genscript.com/wolf-psort.html>

TMHMM – transmembrane domains

<http://www.cbs.dtu.dk/services/TMHMM-2.0/>

(Human cox1 protein Q5S9T0 to retrieve it from UniProtKB).

Please visit the secretome databases developed in Dr. Min's lab at
<http://bioinformatics.ysu.edu/tools/index.html>

Read one of the following papers to understand more on the databases we developed:

Lum G, Min XJ. (2011) FunSecKB: the Fungal Secretome KnowledgeBase. Database - the Journal of Biological Databases and Curation. Vol. 2011. doi: 10.1093/database/bar001.

Meinken J, Asch DK, Neizer-Ashun KA, Chang GH, Cooper JR CR, Min XJ. (2014) FunSecKB2: a fungal protein subcellular location knowledgebase. Computational Molecular Biology. 4(7): 1-17.

Powell B, Amerishetty V, Meinken J, Knott G, Yu F, Cooper C, Min XJ (2016) ProtSecKB: The Protist Secretome and Subcellular Proteome Knowledgebase. Computational Molecular Biology 6(4):1-12. (Doi:10.5376/cmb.2016.06.0004).

Lum G, Meinken J, Orr J, Frazier S, Min XJ. (2014) PlantSecKB: the plant secretome and subcellular proteome knowledgebase. Computational Molecular Biology. 4(1): 1-17 (doi:10.5376/cmb.2014.04.0001).

Meinken J, Walker G, Cooper CR, Min XJ (2015) MetazSecKB: the human and animal secretome and subcellular proteome knowledgebase. Database, bav077.

Min XJ. (2010) Evaluation of computational methods for secreted protein prediction in different eukaryotes. J. Proteomics Bioinform. 3:143-147.

Meinken J, Min XJ. (2012) Computational prediction of protein subcellular locations in eukaryotes: an experience report. Computational Molecular Biology. 2(1): 1-7 (doi: 10.5376/cmb.2012.02.0001).

More tools at:

<http://bioinformatics.ysu.edu/tools/subcell.html>