Bioinformatics

LAB 2 & 3

BLAST

Review chapter 1- 3.

1) Do a pairwise alignment using the tools at NCBI:
searching for "blast 2 sequences ncbi" to get the sites – note: choose different programs for nucleotides or proteins. Pay attention to the parameters and outputs -

2) Using the same set of sequences to do a pairwise alignment using tools at

http://www.ebi.ac.uk/Tools/psa/emboss_needle/

Read the following document: (if you have time -)

Chapter 16 in the NCBI handbook

http://www.ncbi.nlm.nih.gov/books/NBK21097/

If you need any help, click help at
http://blast.ncbi.nlm.nih.gov/Blast.cgi

Learn how to use BLAST to find homologous sequences and then retrieve these sequences using links in the blast output.

Try use the examples in the book or the gene of your interest as query to do different types of blast (you can search "tomato aldehyde oxidase" – a family of genes I cloned for your lab exercises. TAO1 accession number AAG22605; TAO2: AAG22606; TAO3: AAG22607)

To see the differences in the output after changing different parameters. For example, change e-value, limit the number of output, change scoring matrix, filter on/off, etc.

Manually retrieve 10 – 30 homologous sequences in FASTA format (including proteins and protein-coding DNA sequences) from at least 10 different species.
Make sure to save DNA and protein sequences in different files (text file), make sure to include species information in the definition line.