MCB5472 Computer Methods in Molecular Evolution
Preliminary Outline

Date   topic

1/22   lect/lab: Overview; projects; Intro to Unix, connecting to cluster, intro to perl
1/27   lect: Jill Wegrzyn (Bioinformatics specialist, UConn Biotech center): cluster etiquette, how to submit jobs; intro to NCBI and other data resources
1/29   lab: downloading data from NCBI; into to perl part #2
2/3   lect: Primer on genome sequencing and assembly
2/5   lab: basic genome statistics; determining genome quality
2/10   lect: Types of homology; BLAST
2/12   lab: command line BLAST to compare genomes #1; parsing tabular data
2/17   lect: Homology continued; PSI-BLAST; HMMs
2/19   lab: command line BLAST to compare genomes #2; parsing tabular data
2/24   lect: Gene prediction, structure, annotation; orthology databases (COG, KEGG, Pfam, GO)
2/26   lab: genome annotation using public resources
3/3   lect: Sequence alignment (needle, clustalw, muscle, mafft, sate)
3/5   lab: Sequence alignment
3/10   lect: Review session
3/12   lab: midterm
SPRING BREAK
3/24   lect: approaches to phylogenetic reconstruction
3/26   lab: strand bias, oligo nucleotide frequencies
3/31   lect: Bayesian approaches, bipartition paradox, spectral decomposition
4/2   lab: comparing genomes: gene plot, mummer, average nucleotide identities (ANI) and
        tetramer usage using J-species
4/7   lect: Types of selection (dN/dS)
4/9   lab: phylogenetic trees, phylip, phyml, raxml, MrBayes
4/14   lect: supertrees/supermatrix, gene families, in and out paralogs
4/16   lab: AU-test using consel, quartet decomposition, PyMOL and sequence conservation
4/21   lect: Student Presentations 1
4/23   lab: Extracting data from repetitive tasks
4/28   lect: Student Presentations 2
4/30   lab: Student Presentations 3 & 4

Grade: 30% midterm, 30% student project, 20% in class participation, 20% homework assignments