Schedule of Student Presentations in COMP 571
Fall 2008

Name	Date	Topic/Paper
Bachman, Benjamin J.	Nov 11, 2008	“Discovery of regulatory elements by a computational method for phylogenetic footprinting”. Genome Research, 12:739-748, 2002.
Barik, Rajkishore	Nov 11, 2008	“Combining statistical alignment and phylogenetic footprinting to detect regulatory elements”. Bioinformatics, 24(10):1236-1242, 2008.
Bryant, Drew H.	Nov 11, 2008	“Evolutionary predictions of binding surfaces and interactions”. Curr. Opin. Struct. Biol., 12 (1):21-27, 2002.
Crompton, Joanna E.	Nov 13, 2008	“T-Coffee: A novel method for fast and accurate multiple sequence alignment”. J. Mol. Biol., 302(1):205-217, 2000.
Inoue, Jun	Nov 13, 2008	“MAFFT: A novel method for rapid multiple sequence alignment based on fast Fourier transform”. Nucleic Acids Research, 30:3059-3066, 2002.
Jenkins, Chase A.	Nov 13, 2008	“MUSCLE: a multiple sequence alignment method with reduced time and space complexity”. BMC Boinformatics, 5:113, 2004.
Kilpatrick, Jeff	Nov 18, 2008	“Genome-wide strategies for detecting multiple loci that influence complex diseases”. Nature Genetics, 37:413-417, 2005.
Li, Biao	Nov 18, 2008	“Multilocus association mapping using variable-length Markov chains”. Am. J. Hum. Gen., 78(6):903-913, 2006.
Li, Shuwei	Nov 18, 2008	“Efficient whole-genome association mapping using local phylogenies for unphased genotype data”. Bioinformatics, 2008 (advance access).
Liao, Xiaoyun	Nov 20, 2008	“Orthologs, paralogs, and evolutionary genomics”. Annu. Rev. Genet., 39(1):309-338, 2005.

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Liu, Dajiang	Nov 20, 2008	“Stochastic models for horizontal gene transfer: taking a random walk through tree space”. Genetics, 170:419-431, 2005.
Magill, Connor L.	Nov 20, 2008	“Reconciliation problems for duplication, loss and horizontal gene transfer”. RECOMB proceedings, 316-325, 2004.
Narula, Jatin	Nov 25, 2008	“The probability of topological concordance of gene trees and species trees”. Theoretical Population Biology, 61(2):225-247, 2002.
Park, HyunJung	Nov 25, 2008	“Genomic relationships and speciation times of human, chimpanzee, and gorilla inferred from a coalescent hidden Markov model”. PLoS Genetics, 3(2): e7, 2007.
Rostami, Masoud	Nov 25, 2008	“High-resolution species tree without concatenation” (with supporting information). PNAS, 104(14):5936-5945, 2007.
Ruths, Troy	Dec 2, 2008	“Combining phylogenetic and hidden Markov models in biosequence analysis”. J. Comput. Biol., 11:413-428, 2004.
Shih, Ching-Hua	Dec 2, 2008	“Computational identification of cis-regulatory elements associated with groups of functionally related genes in Saccharomyces cerevisiae”. J. Mol. Biol., 296(5):1205-1214, 2000.
Tasirlar, Sagnak	Dec 2, 2008	“PhyloGibbs: A Gibbs sampling motif finder that incorporates phylogeny”. PLoS Computational Biology, 1(7): e67, 2005.
Tiwari, Abhinav	Dec 4, 2008	“Genome rearrangements in Mammalian evolution: Lessons from human and mouse genomes”. Genome Research, 13(1): 37-45, 2003.
Yang, Xuebei	Dec 4, 2008	“LAGAN and Multi-LAGAN: efficient tools for large-scale multiple alignment of genomic DNA”. Genome Research, 13(4): 721-731,2003.

Yudin, Natalie	Dec 4, 2008	“Mauve: multiple alignment of conserved genomic sequences with arrangements”. Genome Research, 14(7):1394-1403, 2004.