CS2220 Introduction to Computational Biology
Student Presentations on 7/3/08 and 18/4/08

This presentation contributes 15% to the course grade

You may choose to earn up to 15% of the course grade by picking a paper below and making a presentation on 7/3/08 or 18/4/08.

You will be graded according to:

- the quality of your ppt (readability, organization, attractiveness)
- the quality of your presentation (organization, delivery, Q&A)
- the level of understanding of what your are presenting
- inputs from your fellow students

Protein Subcellular Localization Prediction (7/3/08)

[sorting1-nielsen-pe97.pdf] Nielsen et al, "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites", *Protein Eng*, 10(1):1-6, 1997

[sorting2-bannai-cabios02.pdf] Bannai et al, "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites", *Bioinformatics*, 18(2):298-305, 2002

[sorting3-andrade-jmb98.pdf] Andrade et al, "Adaptation of protein surfaces to subcellular location", *JMB*, 276:517-525, 1998

[sorting4-subloc-cabios01.pdf] Hua & Sun, "Support vector machine approach for protein subcellular localization prediction", *Bioinformatics*, 17:721—728, 2001

[sorting5-hmm-febs99.pdf] Yuan, "Prediction of protein subcellular locations using Markov chain models", *FEBS Letters*, 451:23—26, 1999

[sorting6-hwang-proteins06.pdf] Yu et al, "Prediction of protein subcellular localization", *Proteins*, 64:643-651, 2006

[sorting7-hsu-bmc07.pdf] Su et al, "Protein subcellular localization prediction based on compartment-specific features and structure conservation", *BMC Bioinformatics*, 8:330, 2007

Gene Expression Analysis (18/4/08)

[ge1-FDR1995.pdf] Benjamini & Hochberg, “Controlling the false discovery rate: A practical and powerful approach to multiple testing”, *J Roy Stat Soc B*, 57(1):289-300, 1995 [ge2-chengchurch-ismb00.pdf] Cheng & Church, "Biclustering of expression data", *Proc ISMB*, 2000

[ge3-mappfinder-gb03.pdf] Doniger et al, "MAPPFinder: Using GO and GenMAPP to create a global gene expression profile from microarray data", *Gen Biol*, 4:R7, 2003

[ge4-gominer-gb03.pdf] Zeeberg et al, "GoMiner: A resource for biological interpretation of genomic and proteomic data", *Gen Biol*, 4:R28, 2003

[ge5-weipan-cabios06.pdf] Pan "Incorporating gene functions as priors in model-based clustering of microarray gene expression data", *Bioinformatics*, 22(7):795-801, 2006

[ge6-GSEA.pdf] Subramanian et al, "Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles", *PNAS*, 102(43):15545-15550, 2005

[ge7-troyanskaya-cabios01.pdf] Troyanskaya et al, "Missing value estimation methods for DNA Microarrays", *Bioinformatics*, 17(6):520-525, 2001

[ge8-tuikkala-cabios06.pdf] Tuikkala et al, "Improving missing value estimation in microarray data with gene ontology", *Bioinformatics*, 22(5):566-572, 2006

Grading Scheme

You will be graded according to:

- the quality of your ppt (readability, organization, attractiveness)
- the quality of your presentation (organization, delivery, Q&A)
- the level of understanding of what your are presenting

Your marks for the presentation will be the average of the inputs from your classmates and myself using the distribution scheme below:

	poor	ok	super	remarks
quality of ppt	10	20	30	
quality of presentation	10	20	30	
level of understanding	10	20	30	
gone beyond the paper assigned	0	0	10	

Presentor: ____

Grader:____

	poor	ok	super	remarks
quality of ppt	10	20	30	
quality of presentation	10	20	30	
level of understanding	10	20	30	
gone beyond the paper assigned	0	0	10	

Presentor: ____

Grader: ____

	poor	ok	super	remarks
quality of ppt	10	20	30	
quality of presentation	10	20	30	
level of understanding	10	20	30	
gone beyond the paper assigned	0	0	10	

Presentor:_____________________________________

Grader:______________________________________

	poor	ok	super	remarks
quality of ppt	10	20	30	
quality of presentation	10	20	30	
level of understanding	10	20	30	
gone beyond the paper assigned	0	0	10	