CS2220 Introduction to Computational Biology
Student Presentations on 25/2/10 and 1/4/10
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 25/2/10 or 1/4/10.

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-Protein Interaction Reliability Assessment (25/2/10)

[p01-skng-jbcb04.pdf] Ng & Tan, "Discovering protein-protein interactions", *JBCB*, 1(4):711-741, 2004. **[Er Huai Der Benjamin]**

[p02-sprinzak-jmb03.pdf] Sprinzak et al, "How reliable are experimental protein-protein interaction data?", *JMB*, 327:919-923, 2003. **[Koh Lee Heng Keith]**

[p03-saito-nar02.pdf] Saito et al, "Interaction generality, a measurement to assess the reliability of a protein-protein interaction", *NAR*, 30(5):1163-1168, 2002. **[Zeng Zhanpeng]**

[p06-myers-cabios07.pdf] Myers & Troyanskaya, "Context-sensitive data integration and prediction of biological networks", *Bioinformatics*, 23(17):2322-2330, 2007. **[Tomithy Too]**

[p07-chenjin-cabios06.pdf] Chen et al, "Increasing confidence of protein interactomes using network topological metrics", *Bioinformatics*, 22(16):1998-2004, 2006. **[Chai Haoqiang]**

[p09-limsoon-giw06.pdf] Chen et al, "Increasing confidence of protein-protein interactomes", *Proc. GIW 2006*. [Please focus on sections 2 and 4.] **[Cao Fun]**

[p10-guimei-giw08.pdf] Liu et al, "Assessing and predicting protein interactions using both local and global network topological metrics", *Proc. GIW 2008*. **[Mao Ning]**

Protein Interaction and Protein Complex Prediction (1/4/10)

[q02-michaut-cabios08.pdf] Michaut et al, "InteroPORC : Automated inference of highly conserved protein interaction networks", *Bioinformatics*, 24(14) :1625-1631, 2008. **[Dharshini Soundarajoo]**

[q04-sprinzak-jmb01.pdf] Sprinzak & Margalit, "Correlated sequence-signatures as markers of protein-protein interaction", *JMB*, 311:681-692, 2001. **[Goh Shiying Melissa]**

[q07-valencia-jmb97.pdf] Pazos et al, "Correlated mutations contain information about protein-protein interaction", *JMB*, 271 :511-523, 1997**. [Bong Xiu Feng]**

[q08-valencia-pe01.pdf] Pazos & Valencia, "Similarity of phylogenetic trees as indicator of protein-protein interaction", *Protein Engineering*, 14(9):609-614, 2001. **[Joanna Tan Hui Juan]**

[q09-valencia-pnas08.pdf] Juan et al, "High-confidence prediction of global interactomes based on genome-wide coevolution networks", *PNAS*, 105(3):934-939, 2008. **[Su Lingtong]**

[r02-king-cabios04.pdf] King et al, "Protein complex prediction via cost-based clustering", *Bioinformatics*, 20(17):3013-3020, 2004. **[Tran Binh Ngoc]**

[r04-guimei-draft08.pdf] Liu et al, "Complex discovery from weighted PPI networks", unpublished manuscript, 2008. **[Nash Tan Weilong?]**

Host-Pathogen Protein Interactions (8/4/10)

[h01-dyer-cabios07.pdf] Dyer et al. "Computational prediction of host-pathogen protein-protein interactions", *Bioinformatics*, 23(ISMB/ECCB2007):i159-166, 2007. **[Lu Vinh Thinh]**

[h02-davis-proteinsci07.pdf] Davis et al. "Host-pathogen protein interactions predicted by comparative modeling", *Protein Science*, 16:2585-2596, 2007. **[Zhou Kangxiang]**

[h03-evans-bmc09.pdf] Evans et al. "Prediction of HIV-I virus-host protein interactions using virus and host sequence motifs", *BMC Medical Genomics*, 2:27, 2009.

[h04-krishna-insilico08.pdf] Krishnadev et al. "A data integration approach to predict host-pathogen protein-protein interactions: Application to recognize protein interactions between human and a malaria parasite", *In silico Biology*, 8:0020, 2008.

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	

A computational biologist often has to communicate with biologists or computer scientists who either do not have sufficient background in computing, mathematics, or biology. The inputs from your classmates are especially important for assessing whether your presentation is sufficiently clear and easily understood by such non-experts.

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	