

CS2220 Introduction to Computational Biology

Student Presentations on 20/2/09 and 3/4/09

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-Protein Interaction Reliability Assessment (20/2/09)

[[p01-skng-jbcb04.pdf](#)] Ng & Tan, “Discovering protein-protein interactions”, *JBCB*, 1(4):711-741, 2004.

[[p02-sprinzak-jmb03.pdf](#)] Sprinzak et al, “How reliable are experimental protein-protein interaction data?”, *JMB*, 327:919-923, 2003.

[[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.

[[p04-marcotte-gb05.pdf](#)] Ramani et al, “Consolidating the set of known human protein-protein interactions in preparation for large-scale mapping of the human interactome”, *Genome Biology*, 6:R40, 2005.

[[p05-gerstein-bmc04.pdf](#)] Lin et al, “Information assessment on predicting protein-protein interactions”, *BMC Bioinformatics*, 5 :154, 2004.

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

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

[[p08-chenjin-kdd06.pdf](#)] Chen et al, “NeMoFinder: Dissecting genome-wide protein-protein interactions with meso-scale network motifs”, *Proc. KDD 2006*.

[[p09-limsoon-giw06.pdf](#)] Chen et al, “Increasing confidence of protein-protein interactomes”, *Proc. GIW 2006*. [Please focus on sections 2 and 4.]

[[p10-guimei-giw08.pdf](#)] Liu et al, “Assessing and predicting protein interactions using both local and global network topological metrics”, *Proc. GIW 2008*.

Protein Interaction and Protein Complex Prediction (3/4/09)

[[q01-shoemaker-plos07.pdf](#)] Shoemaker & Panchenko, “Deciphering protein-protein interactions. Part II”, *PLOS Computational Biology*, 3(4):595-601, 2007.

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

[[q03-persico-bmc05.pdf](#)] Persico et al, “HomoMINT : An inferred human network based on orthology mapping of protein interactions discovered in model organisms”, *BMC Bioinformatics*, 6(S4):S21, 2005.

[[q04-sprinzak-jmb01.pdf](#)] Sprinzak & Margalit, “Correlated sequence-signatures as markers of protein-protein interaction”, *JMB*, 311:681-692, 2001.

[[q05-han-nar04.pdf](#)] Han et al, “PreSPI: A domain combination based prediction system for protein-protein interaction”, *NAR*, 32(21):6312-6320, 2004.

[[q06-haiyuan-cabios06.pdf](#)] Yu et al, “Predicting interactions in protein networks by completing defective cliques”, *Bioinformatics*, 22(7):823-829, 2006.

[[q07-valencia-jmb97.pdf](#)] Pazos et al, “Correlated mutations contain information about protein-protein interaction”, *JMB*, 271 :511-523, 1997.

[[q08-valencia-pe01.pdf](#)] Pazos & Valencia, “Similarity of phylogenetic trees as indicator of protein-protein interaction”, *Protein Engineering*, 14(9):609-614, 2001.

[[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.

[[r01-bader-bmc03.pdf](#)] Bader & Hogue, “An automated method for finding molecular complexes in large protein interaction networks”, *BMC Bioinformatics*, 4:2, 2003.

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

[[r03-kenny-jbcb08.pdf](#)] Chua et al, “Using indirect protein-protein interactions for protein complex prediction”, *JBCB*, 6(3):435-466, 2008.

[[r04-guimei-draft08.pdf](#)] Liu et al, “Complex discovery from weighted PPI networks”, unpublished manuscript, 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

Presenter: _____

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	

Presenter: _____

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	

Presenter: _____

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	