

Schedule for presentation:

Name	Paper
Rajan	W. Maddison, Gene Trees in Species Trees, Systematic Biology 46(3): 523-536, 1997.
Sindhu	G. Jin, L. Nakhleh, S. Snir, T. Tuller. Inferring phylogenetic networks by the maximum parsimony criterion: a case study. MBE, Vol. 24(1):324-337, 2007. G. Jin, L. Nakhleh, S. Snir, and T. Tuller. Maximum likelihood of phylogenetic networks. Bioinformatics, Vol 22(21):2604-2611, 2006.
TD	L. Nakhleh, D. Ruths, and L-S. Wang. RIATA-HGT: a fast and accurate heuristic for reconstructing horizontal gene transfer. COCOON 2005, Vol. 3595:84-93, 2005.
Jaffrey	M. Hallet, J. Lagergren, and A. Tofigh. Simultaneous identification of duplications and lateral transfers. in RECOMB 2004, pp. 347-356.
Mahesh	L. Nakhleh, T. Warnow, C. R. Linder, and K. St. John. Reconstruction of phylogenetic networks: theory and practice. Journal Computational Biology, Vol 12(6): 796-811, 2005
Badri	
Bakhtiyar	A. Dress and D. Huson. Constructing splits graphs. TCBB Vol 1(3):109-115, 2004
Vikas	
Rezieh	B. Holland, G. Conner, K. Huber, and V. Moulton. Imputing supertrees and supernetworks from quartets. Systematic Biology, Vol. 56(1): 57-67, 2007.
John	TBD