References


Haiyan Hu, Xifeng Yan, Yu Huang, Jiawei Han, and Xianghong Jasmine Zhou. Mining coherent dense subgraphs across massive biological networks for functional discovery. In *ISMB2005*, pages 213–221, 2005.


[119] Magesh Jayapandian, Adriane Chapman, V. Glenn Tarcea, Cong Yu, 
Aaron Elkiss, Angela Ianni, Bin Liu, Arnab Nandi, Carlos Santos, Philip 
Andrews, Brian Athey, David States, and H. V. Jagadish. Michigan Molecular 

[120] Lars Juhl Jensen, Jasmin Saric, and Peer Bork. Literature mining for 

[121] H. Jeong, S.P. Mason, A.L. Barabási, and Z.N. Oltvai. Lethality and 

654, October 2000.


[124] Raja Jothi, Maricel G. Kann, and Teresa M. Przytycka. Predicting 
protein-protein interaction by searching evolutionary tree automorphism 

[125] V. Kandiah and D. L. Shepelyansky. Google matrix analysis of DNA 

[126] Noam Kaplan and Michal Linial. False annotations of proteins: Automatic 

[127] Peter D. Karp. An ontology for biological function based on molecular 

[128] S. Katrenko and et al. Learning biological interactions from Medline ab-

[129] Sophia Katrenko and Pieter Adriaans. Learning relations from biomedical 

[130] Sophia Katrenko and Pieter Adriaans. Learning relations from biomedical 

[131] Mehmet Kayaalp, Alan R. Aronson, Susanne M. Humphrey, Nicholas C. 
Ide, Lorraine K. Tanabe, Lawrence H. Smith, Dina Demner-Fushman, 
Russell R. Loane, James G. Mork, and Olivier Bodenreider. Methods 


[38] B. P. Suomela and M. A. Andrade. Ranking the whole MEDLINE database according to a large training set using text indexing. BMC Bioinformatics, 6(75), March 24, 2005.


20


