References


[96] 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.


14


17


[192] Carlos Santos, Daniela Eggle, and David J. States. Wnt pathway cura-
tion using automated natural language processing: Combining statistical methods with partial and full parse for knowledge extraction. *Bioinfor-


[218] 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.


[257] Golan Yona, Nathan Linial, Naftali Tishby, and Michal Linial. A map of
the protein space: An automatic hierarchical classification of all protein

[258] Hong Yu and Eugene Agichtein. Extracting synonymous gene and protein

[259] Hong Yu, Won Kim, Vasileios Hatzivassiloglou, and John Wilbur. A large
scale, corpus-based approach for automatically disambiguating biomedical

BIOKDD04: Workshop on data mining in Bioinformatics. *SIGKDD-EN*,

[261] Andreas Zanzoni, Luisa Montecchi-Palazzi, Michele Quondam, Gabriele
Ausiello, Manuela Helmer-Citterich, and Gianni Cesareni. MINT: A
20, 2002.

names in biomedical texts: A machine learning approach. *Bioinformatics*,