Graph drawing algorithms for Bioinformatics

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Abstract: Graph drawing has recently received growing attention as various techniques have been developed for applications in areas ranging from software technology to business modeling, from network administration to cognitive sciences.

Recently, we have designed and realized the tool yWays to support the analysis of biochemical pathways by visualization. In the talk, we will use this tool as a example to discuss to what extend the standard layout algorithms can be used, and what the challenges are to achieve 'real' applicability.

References:

- 1. G.Di Battista, P.Eades, R.Tamassia, I.G.Tollis: Graph drawing: algorithms for the visualization of graphs, Prentice Hall, 1999.
- 2. Markus Eiglsperger, Michael Kaufmann: Visualization of Biodegradation Pathways in the UM-BBD, RECOMB 2001, poster session.
- M.Sirava, T.Schaefer, M. Eiglsperger, M.Kaufmann, O.Kohlbacher, E. Bornberg-Bauer, H.P. Lenhof: BioMiner - Modeling, Analyzing, and Visualizing Biochemical Pathways and Networks, submitted. available from the authors
- 4. M.Eiglsperger: yWays homepage: http://www-pr.informatik.uni-tuebingen.de/~eiglsper/pathways/index.html

Algorithmic Challenges in Mass Spectrometry and Systems Biology

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Abstract: Cell biology is in the middle of a paradigm change where approaches focusing on the biochemically oriented understanding of single genes are slowly replaced by the systems approach that views systems of genes and proteins in their network context [1]. In this talk we will examine a number of new computational challenges associated with this approach, from various aspects of interpreting peptide mass spectra, to the visualization and integration of heterogenous data types in the molecular network context [2-5].

References:

- 1. Ideker, T., T. Galitski, and L. Hood. 2001. A new approach to decoding life: Systems Biology. Annu. Rev. Genomics Hum. Genet. 2:343-372.
- Schwikowski, B., P. Uetz, and S. Fields. 2000. A network of protein-protein interactions in yeast. Nat Biotechnol. 18:1257-61.
- Ideker, T., V. Thorsson, J.A. Ranish, R. Christmas, J. Buhler, J.K. Eng, R. Bumgarner, D.R. Goodlett, R. Aebersold, and L. Hood. 2001. Integrated genomic and proteomic analyses of a systematically perturbed metabolic network. Science. 292:929-34.
- 4. Ideker, T., O. Ozier, B. Schwikowski, and A. Siegel. 2002. Discovering regulatory and signaling circuits in molecular interaction networks. In ISMB 2002 proceedings, Edmonton, Canada.
- Ideker, T., B. Schwikowski, P. Shannon, N. Amin, M. Johnson, O. Ozier, A. Markiel, D. Ramage, and V. Thorsson. 2002. Cytoscape - A Software Platform for Visualizing and Analyzing Molecular Interaction Networks.
 http://www.cytoscape.org.

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