

Visualization of Protein-Protein Interactions

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Visualizing protein-protein interaction data is challenging because it yields a complicated, nonplanar graph with large number of edge crossings and because it produces a disconnected graph consisting of many connected components with nodes of a wide range of degrees. We have developed a new algorithm for drawing large-scale protein interaction networks in three-dimensional space. Unique features of the algorithm include: (1) it is much faster than other drawing algorithms, (2) it can be used not only for drawing protein-protein interaction networks but also for comparing them, and (3) it provides an integrated framework for dynamically querying protein-protein interaction databases and directly visualizing the query results, making the visualization and analysis of large amounts of updated data easy. Experimental results showed that our algorithm efficiently generates clear and aesthetically pleasing drawings of large-scale protein-protein interaction networks and that it is an order of magnitude faster than other drawing algorithms.