

Session on Computation in Biological Pathways

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The computational management and analysis of biological pathways is at the intersection of a surprisingly diverse set of disciplines, including biochemistry, chemical engineering, genomics, developmental biology, artificial intelligence, simulation, and control theory. These disciplines encompass both a range of biological pathway types, and a range of analysis techniques. A PSB session on this topic is timely for two reasons: Several new information sources on biological pathways have appeared on the WWW in the last year, resulting in a surprisingly large number of pathway-database projects^a Communication among the developers of these databases will allow them to build on each others efforts in the areas of schema design, and user-interface design, and may reduce duplicate data entry, and encourage data validation. Communication among database developers and users will inform developers of user needs, and inform users of database capabilities. In addition, the recent completion of several genomic sequencing projects, along with the imminent completion of several others, provides a driving force for the prediction of pathways from sequence data.

The papers in this session indeed encompass both pathway databases and computational tools for pathway analysis. Goto et al discuss a database of metabolic pathways for several organisms whose genomes have recently been sequenced. Okamoto et al present a toolkit for use by chemical engineers in modeling, optimizing, and visualizing pathways. Bergeron et al describe techniques for studying regulatory pathways such as those involved in transcription, translation, and signaling. Papers by Mittenthal, and by Sellers and Wagg, explore the problems of enumerating the possible pathways present in a set of reactions, in the areas of transport and protein-protein interactions.

^aFor an overview of these resources, see <http://www.ai.sri.com/~pkarp/pathways.html>.