

Summary of discussion for
A query language for biological networks
by Ulf Leser
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In this article Ulf Leser presents his concept of a special query language for use in biological networks, often organized into directed acyclical graphs (DAGs). Using his Pathway Query Language (PQL), he presents a method for asking questions about how a biological object (molecule or interaction) reacts with other biological objects. The PQL query itself returns a graph, so that nested sub-querying is also possible. The main reason for creating such a language is so that a standard abstraction layer can be created so new but consistent can be asked of how a biological network operates. Leser then presents various queries that might be answered using PQL, with varying degrees of success: some questions are very easily answered with PQL, others cannot be. Finally he discusses his actual implementation of the PQL server, using an Oracle 9.2 server with precompiled PQL queries.

This article represents a noble goal in trying to offer a standard method for biological scientists to ask questions about how molecules interact. In fact, the possible discoveries that might come from giving such a system certain parameters and “letting it loose” are compelling and exciting.

We did recognize that the data set that was used for the system discussed in the article was rather small (200,000 paths between 16,000 nodes and 23,000 edges). As the number of biological objects in the database increases, so will the amount of storage necessary for the objects and the time it takes to run more complex queries. And, of course, convincing people to adopt an entirely new query language is very difficult, if not impossible. Otherwise, we felt that the proposition of PQL, while facing a natural difficulty in being adopted, has the potential to discover new and interesting interactions as well as clarify others.