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Efficient Graph Matching Algorithms for Querying Biological Networks and their Application to Web Service Composition

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Summary

- Dr. Hasan Jamil presented that traditional models do not support graph representation, that RDBMS is flat and XML is a whole graph. They need to find some form of unit representation that: Units can be processed one at a time in memory; Units can be stored and indexed; The global view of graphs can be recreated from the units.

Biological networks such as pathways and protein-protein interactions are naturally modeled using graphs. Searching for exact network is possible using identifiers or graph attribute match; however, a query graph is generally used to find matches that closely resemble the network. Such matching is fundamentally different from isomorphic matching of both attributed and non-attributed graphs.

- In the mathematical discipline of graph theory, a matching or independent edge set in a graph is a set of edges without common vertices. It may also be an entire graph consisting of edges without common vertices. Dr. Hasan Jamil introduced us a new approach to attributed graph matching using sub graph isomorphism with optimization opportunities.
- Their research NetQL is still ongoing. It performs well on unattributed graphs that is XML based implementation, the In-memory algorithm is being implemented, and approximate matching is ongoing. AtoM is highly scalable and parallelizable: Optimization is not currently possible but being investigated; MapReduce implementation underway.