

ABSTRACT

The use of graph model in a structure which complicated this time is growing rapidly especially in the model structure such as the order of molecules , a network of protein , and social network .The implementation of graph database to handle a type of data graph that have complex relationships is considered more effective than the use of relational database.

In accelerate processing query databases on graph needed a method that can be called graph indexing to be more rapid and efficient . Gindex is one of the methods graph indexing that supports query processing are the type subgraph query.

On the GIndex method applying some techniques such as size-increasing support constraint to build a database feature set and selection discriminative fragments in building index. Then compare the data in index with feature set query to get candidate set of which will be done subgraph matching event use algorithms ullman to get answer set.

This final project work on data that will serve as the dataset is the arrangement of the molecules. Based on the final project that has been done was obtained the result that from implementation of the algorithms gindex, when using the value of maximal frequent fragment large enough then it will take longer time and allow the number of candidate sets obtained will be less, as opposed to the use of minimal value discriminative fragments. A large number of candidate sets obtained will affect the time required for subgraph matching.

Keywords: *graph, graph database, GIndex, subgraph query, size-increasing support constraint, discriminative fragments, index, subgraph matching*