# **GRAPES** v 2.9.mp.vf2 User's Guide

# developed by

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## **GRAPES - Version 2.9**

**GRAPES** is a querying system for parallel searching in databases of graphs, and single target graph, using symmetric multiprocessing (SMP) architectures. It implements a parallel version of well established graph searching algorithms providing efficient solutions for graphs indexing and matching.

**GRAPES** is developed in C++ under GNU\Linux using POSIX Threads programming and no further dependencies out of standard GNU C++ library. It can also be compiled to run under Windows and MAC OSx systems.

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# **Usage**

**GRAPES** is developed in C++ under GNU\Linux using POSIX Threads programming and no further dependencies out of standard GNU C++ library. It works on Unix and Mac OS X systems with G++ installed, and it can be compiled under Windows using Gygwin.

### **Build Source Code**

Executables are available only after building source code on your system.

```
cd GRAPES-2.9.mp.vf2
make clean
make -B
```

At the end of the build process, the command grapes is available.

#### **Database Index Construction**

Build the index of the given database of graphs.

```
./grapes NTHREADS -b -[gfu|gfd] db_file [-lp lp]
```

#### Command parameters:

NTHREADS number of parallel threads

-[gfu|gfd] input file format

-gfu undirected graphs file format-gfd directed graphs file format

db\_file textual graphs database file. All database graphs are stored into the same file.

[-lp lp] OPTIONAL, specify feature paths length, namely the depth of the DFS which extract

paths. 1p must be greater than 1, eg -1p 3. Default value -1p 4.

The indexing phase ever produces the db file.index.grapes file in which the database index is stored.

## Querying

Querying operations are available by the command grapes that allow to search a single pattern graph (query) inside the database of graphs.

#### Restrictions:

- the system allows to search only for sub-isomorphisms between the query (pattern graph) and the database
- one query per time can be processed, thus the input query file cannot contains more than one graph
- before run a query, the database index must have been computed by the command <code>grapes -b</code> and the resultant <code>.index.grapes</code> file must be maintained in the same directory of the database textual file.

Search by coarse-grained matching phase.

```
./grapes NTHREADS -f -[gfu|gfd] db file query file -[no|console|file] [-lp lp]
```

#### Parameters:

NTHREADS number of parallel threads

-[gfu|gfd] input file format

-gfu undirected graphs file format-gfd directed graphs file format

db\_file textual graphs database file

query file textual guery graph file. It must contain just one graph.

-[no|console|file] print found matches (sub-isomorphisms)

-no do not print

-console print matches on screen

-file print matches on files. Each thread prints found matches in a

different file

[-lp lp] OPTIONAL ONLY IF the database index was built with a lp value different from 4,

specify feature paths length, namely the depth of the DFS which extract paths.

lp must be greater than 1, eg -lp 3. Default value -lp 4.

# **Input Formats**

Graphs are stored in text files containing one or more items. The current input format allows the description of undirected -gfu or directed -gfd graphs with labels on nodes.

Graph description language format:

```
#[graph_name]
[number of nodes]
[label_of_first_node]
[label_of_second_node]
...
[label_of_last_node]
[number of edges]
[node id] [node id]
[node id] [node id]
...
```

GRAPES assigns IDs to nodes following the order in which they are written in the input file, starting from 0.

#### Restrictions:

- multigraphs and hypergraphs are not allowed
- attributes (labels) can be assigned only to the nodes (vertices) of the graph
- · labels are case-sensitive
- [graph\_name] and labels can not contain blank characters (space, tabs and so on)
- duplicated edges are ignored