

TAPESTRY (Network- centric Target Prioritization in Disease- related Signaling Networks)

USER GUIDE (Version 1.0)

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1. TAPESTRY Installation

TAPESTRY uses several other publicly available tools and software for pre-processing files and storing data. In particular, the PostgreSQL database management system is used for storing data and R is used for computing statistical test results. PostgreSQL and R (together with the listed packages) have to be installed in order for TAPESTRY to function. Please adhere to the recommended version as it has been tested. Note that TAPESTRY has been tested for installation on the Windows 7 Professional platform.

1.1 PostgreSQL 9.3

Installing PostgreSQL 9.3

Step 1: Download and install PostgreSQL v9.3.x from <http://www.postgresql.org/>.

Please refer to <http://www.postgresqltutorial.com/install-postgresql/> for additional guidance on installation using the PostgreSQL installer for Windows.

Step 2: During the setup progress, when prompted for password (Fig.1), type in “tenet”.

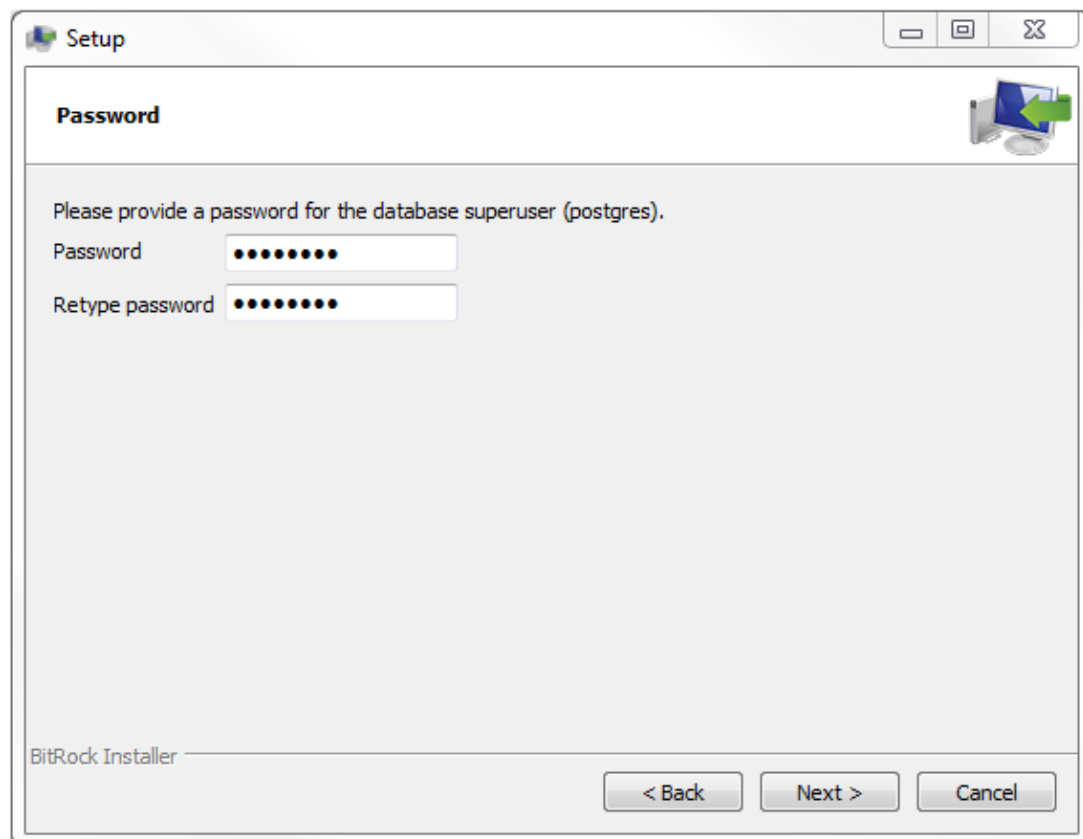


Fig. 1: Password prompt during PostgreSQL installation on Windows.

Verifying the installation

Step 3: Select “pgAdmin III” from programs to launch PostgreSQL (Fig. 2)

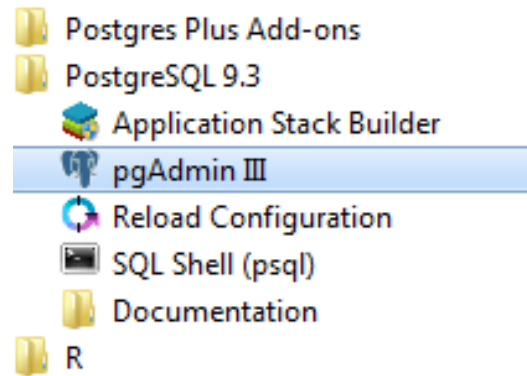


Fig. 2: Launching PostgreSQL

Step 4: Double click on PostgreSQL 9.3 on the object browser and enter “tenet” as the password when prompted (Fig. 3).

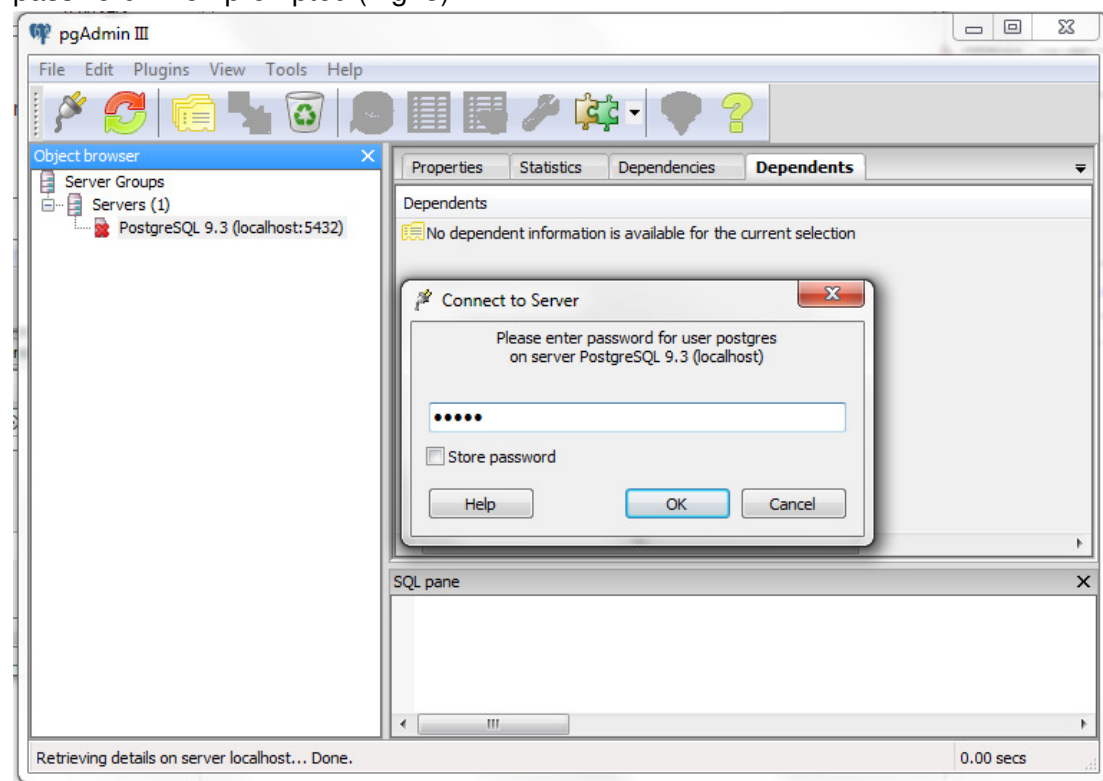


Fig. 3: Connecting to PostgreSQL server

Creating the TAPESTRY database

The TAPESTRY database is used by TAPESTRY for storing data and has to be created before running TAPESTRY. The database creation has to be done only once during the installation phase and will be available subsequently when TAPESTRY is run.

Step 5: Right-click on “Databases” on the object browser and select “New Database...” (Fig. 4)

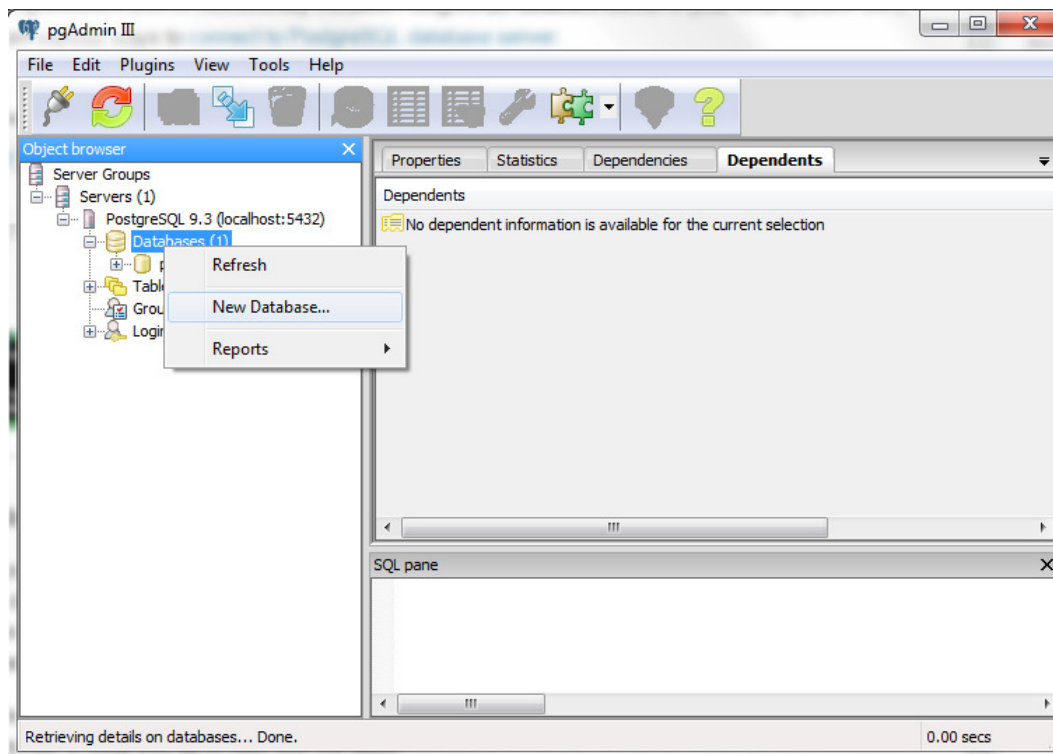


Fig. 4: Creating new database

Step 6: Type in “TAPESTRY” as the name of the database (Fig. 5) and select “OK”.

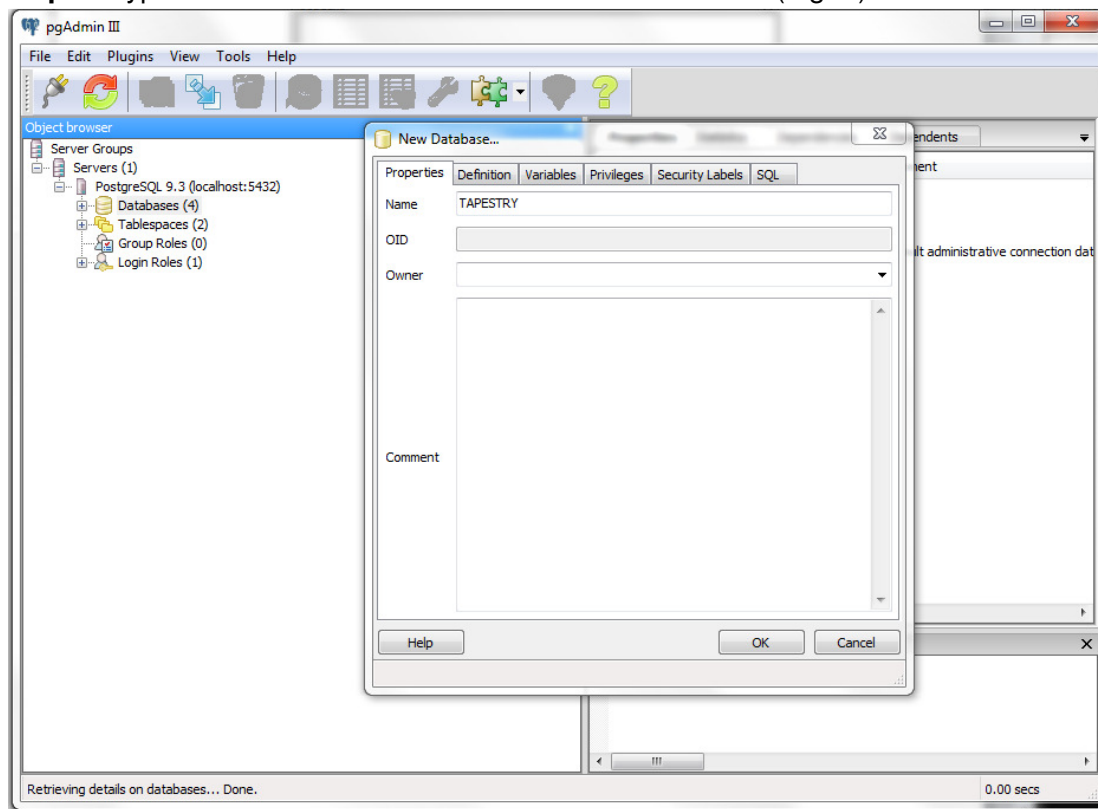


Fig. 5: Setting the name of the new database

Step 7: Verify that the “TAPESTRY” database has been created

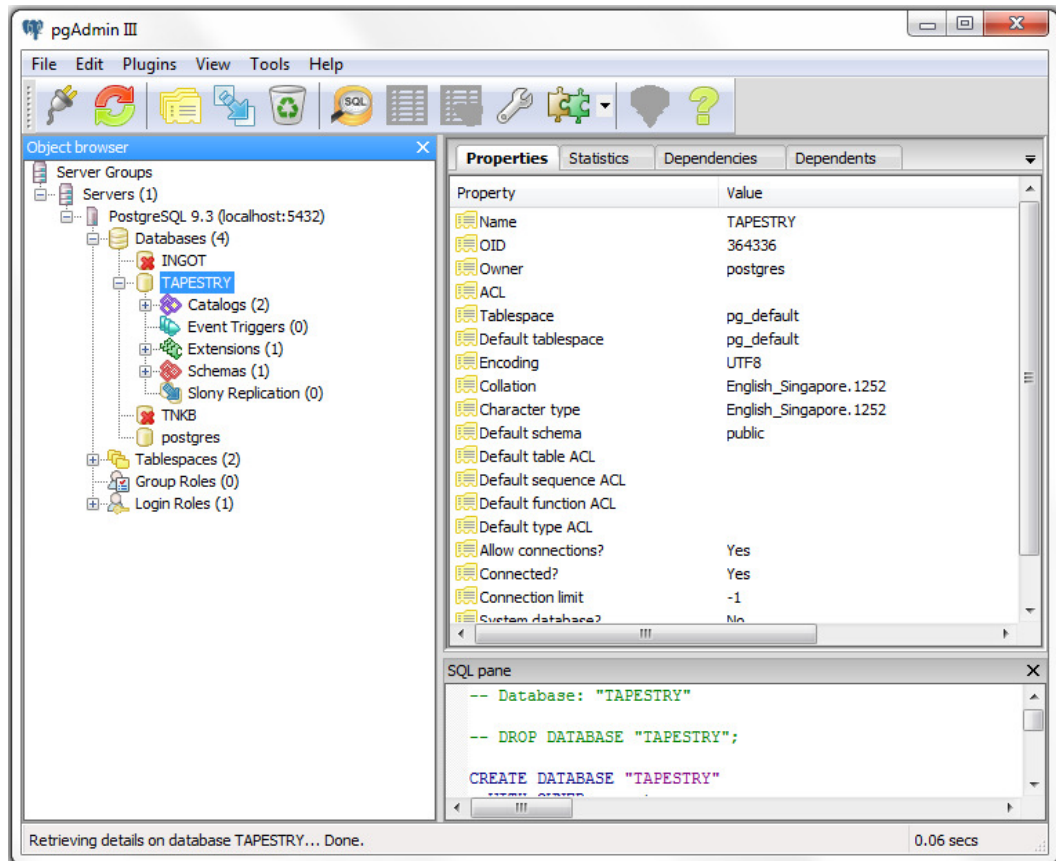


Fig. 6: Verify that the new database has been created

1.2 R 3.1.2

Step 1: Install R version 3.1.2.

Step 2: Install and load the following packages

- Rserve
- survcomp (installation instruction for survcomp can be found at <http://www.bioconductor.org/packages/release/bioc/html/survcomp.html>)

1.3 network_lib_TAPESTRY folder

This folder contains the example files for running TAPESTRY. TAPESTRY uses SVM to perform target prioritization and intermediate files generated while running the SVM are stored in the “svmTraining” folder within the “network_lib_TAPESTRY” folder.

TAPESTRY requires several files from this folder for proper execution:

1. featureLib_list.txt
 - contains the list of files (e.g., hatakeyama2003_MAPK_features.xlsx) containing the feature values of the training networks used by TAPESTRY for target prioritization.

- contains the list of files (e.g., hatakeyama2003_MAPK_model.dat) containing the SVM regression model of the training networks (generated by TENET).
 - contains the list of predictive topological features of the training networks.
2. <trainingNetwork>_timeseries.dat
 - contains the time series data for computing the PSSD feature. The data in this folder are generated by Copasi using the .sbml file of the training network as inputs.
 3. <signalingNetwork>.xml
 - contains the signalling network model that is described in SBML format. An example is Hatakeyama2003_MAPK.xml. The BioModels repository (<http://www.ebi.ac.uk/biomodels-main/>) provides signalling networks that are described in the SBML format.

Step 8: Copy the “network_lib_TAPESTRY” folder to the C directory “C:\” (Fig. 7)

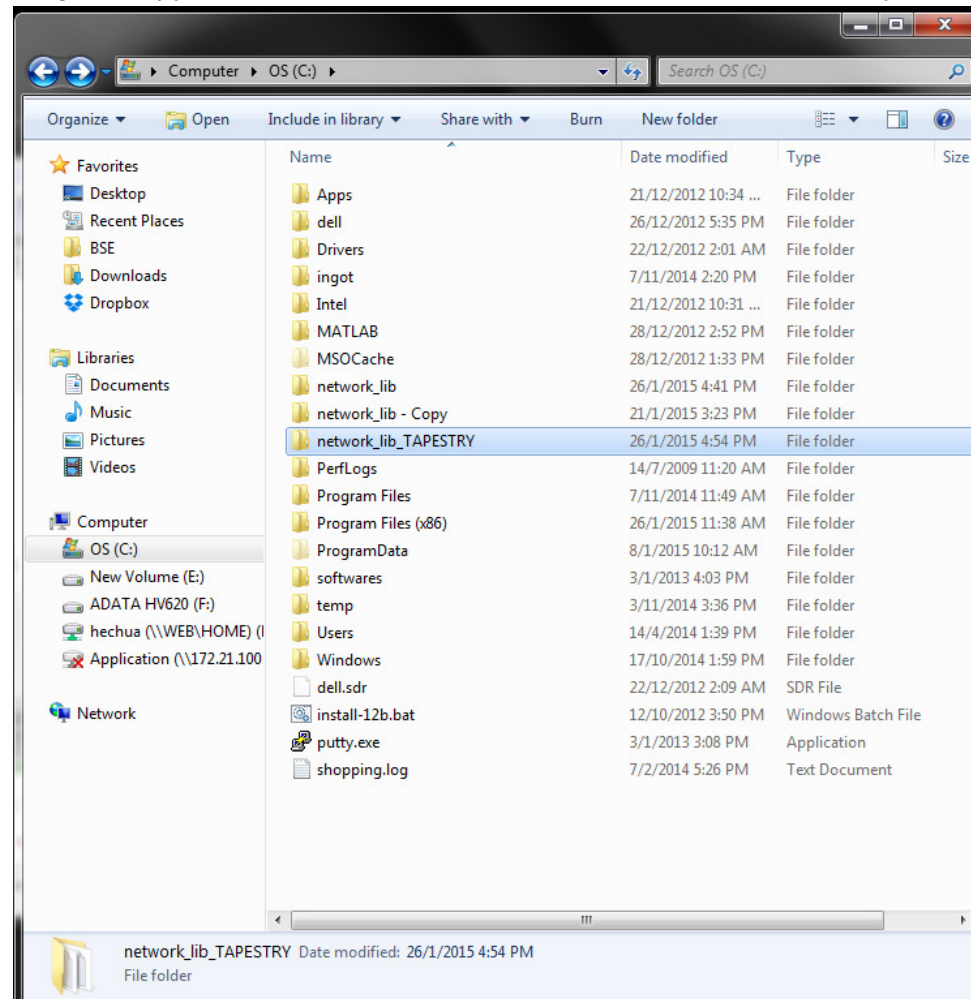


Fig. 7: Copy “network_lib_TAPESTRY” folder to C directory

1.4 TAPESTRY_wrapper.jar

Step 9: Copy TAPESTRY_wrapper.jar to a desired location (e.g., “C:\Desktop”).

2. Launching TAPESTRY

Step 1: Start Rserve from R (Fig. 8).

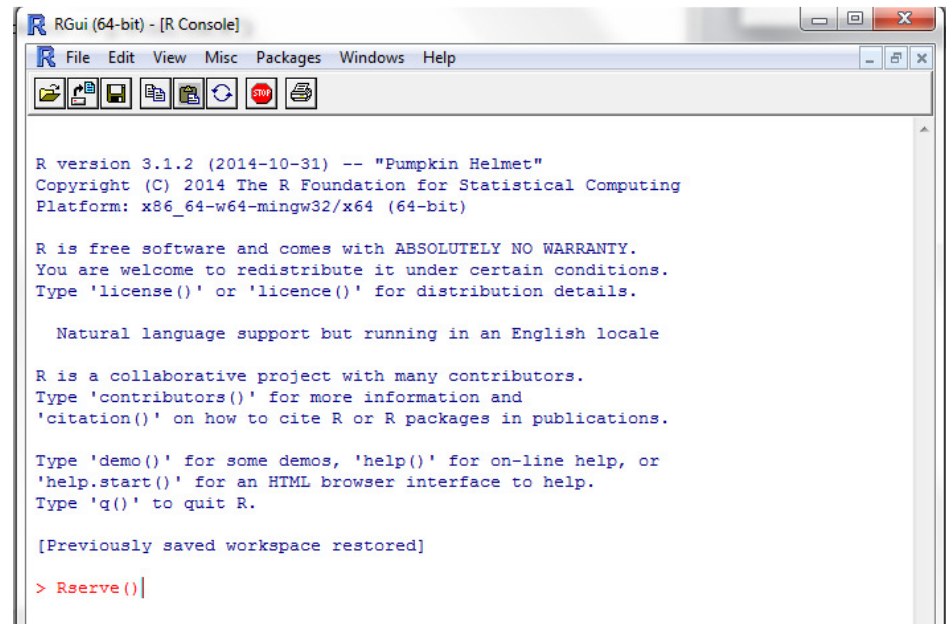


Fig. 8: Start Rserve

Step 2: Launch command prompt dialog (cmd.exe) (Fig. 9).

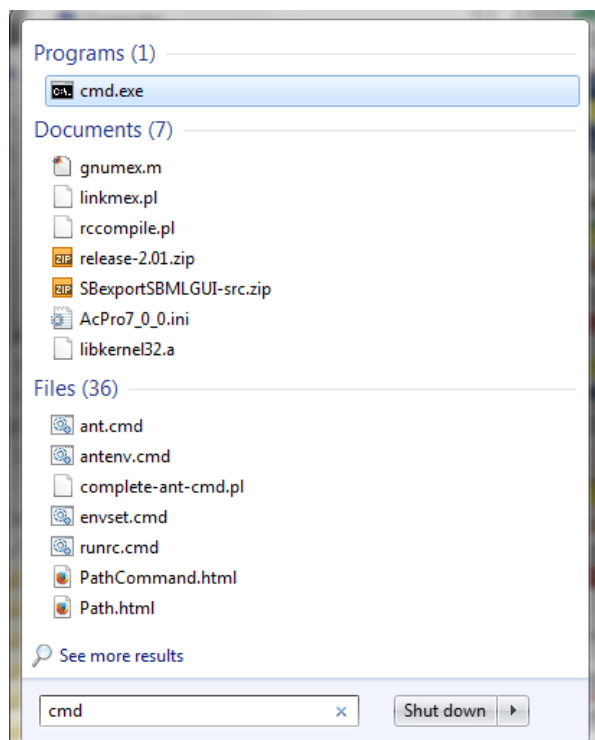
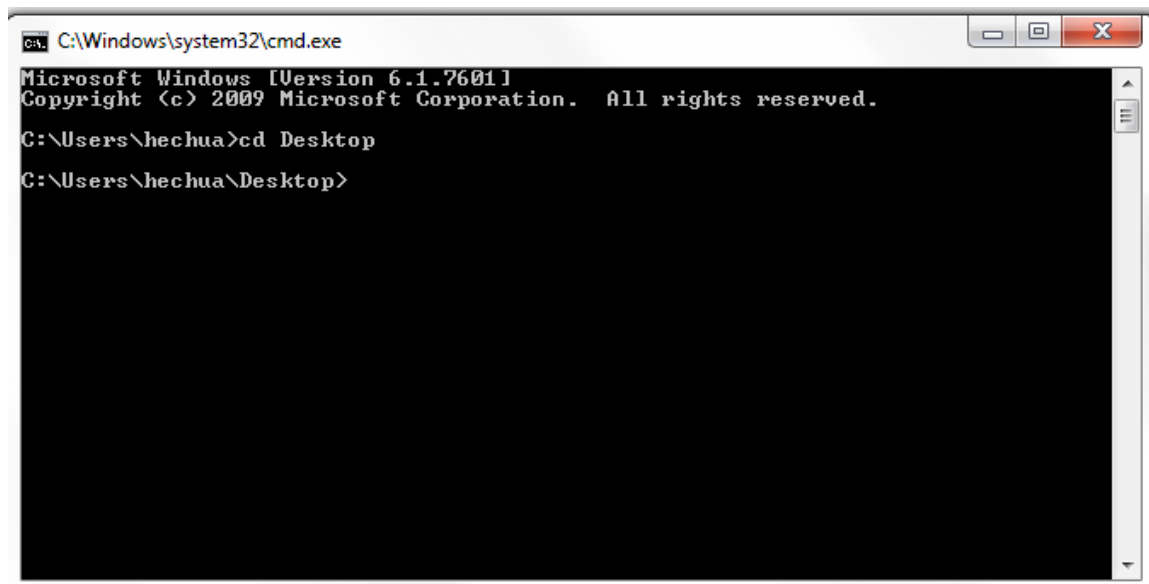


Fig. 9: Launch cmd.exe

Step 3: Change the directory to the one that contains TAPESTRY_wrapper.jar (Fig. 10).

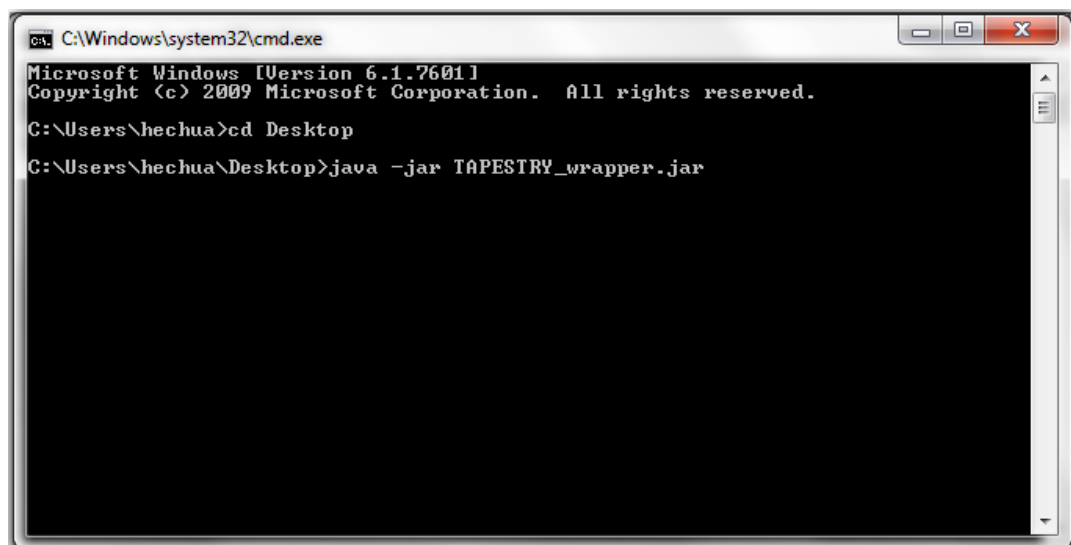


```
C:\Windows\system32\cmd.exe
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation. All rights reserved.

C:\Users\hechua>cd Desktop
C:\Users\hechua\Desktop>
```

Fig. 10: Set to the directory containing TAPESTRY_wrapper.jar

Step 4: Run TAPESTRY by using the command “java -jar TAPESTRY_wrapper.jar” (Fig. 11).



```
C:\Windows\system32\cmd.exe
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation. All rights reserved.

C:\Users\hechua>cd Desktop
C:\Users\hechua\Desktop>java -jar TAPESTRY_wrapper.jar
```

Fig. 11: Run TAPESTRY

3. Using TAPESTRY

Step 1: Select the signalling network whose nodes are to be prioritized (Fig. 12).

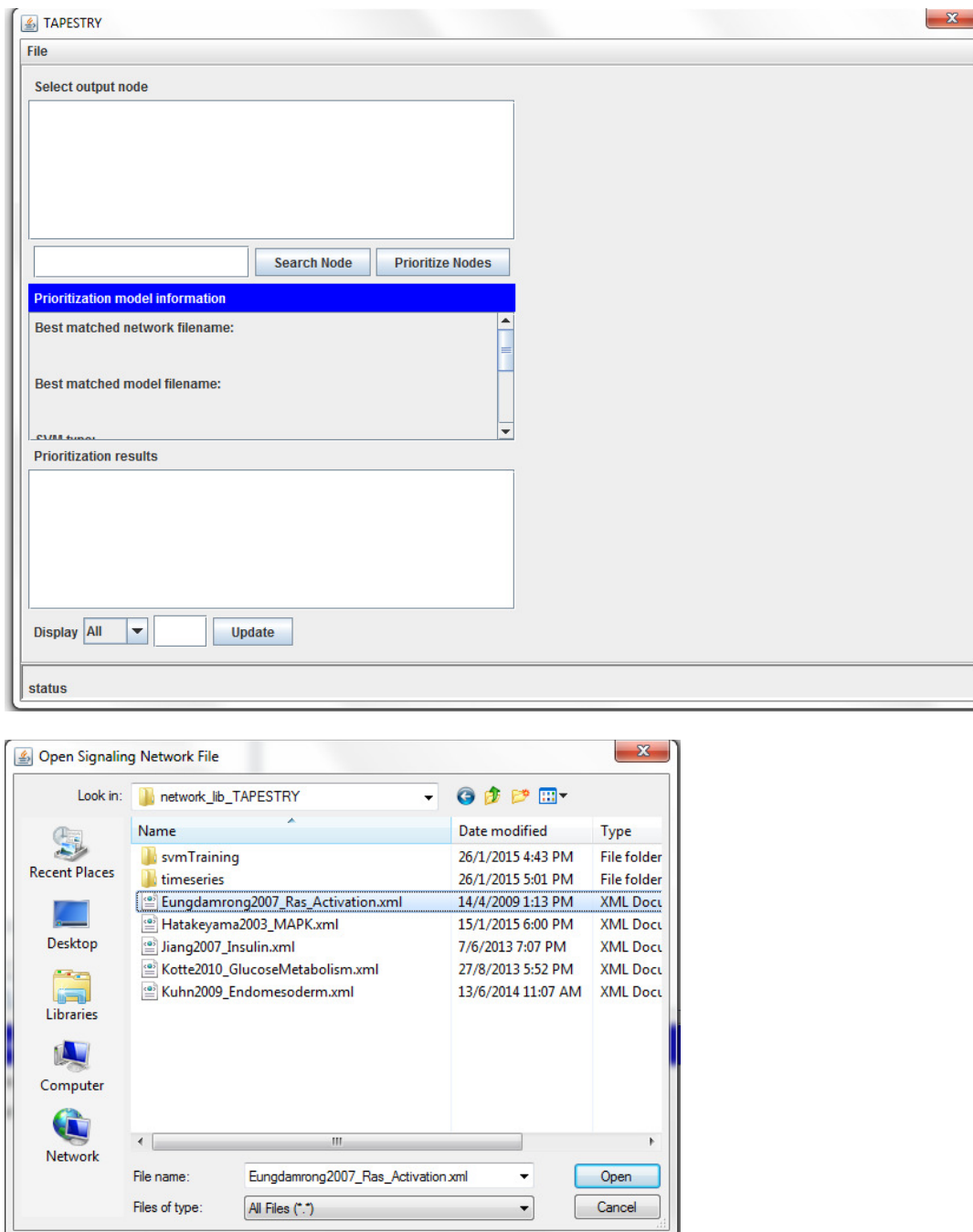


Fig. 12: Select signalling network

Step 2: Select the output node of the input signalling network (Fig. 13).

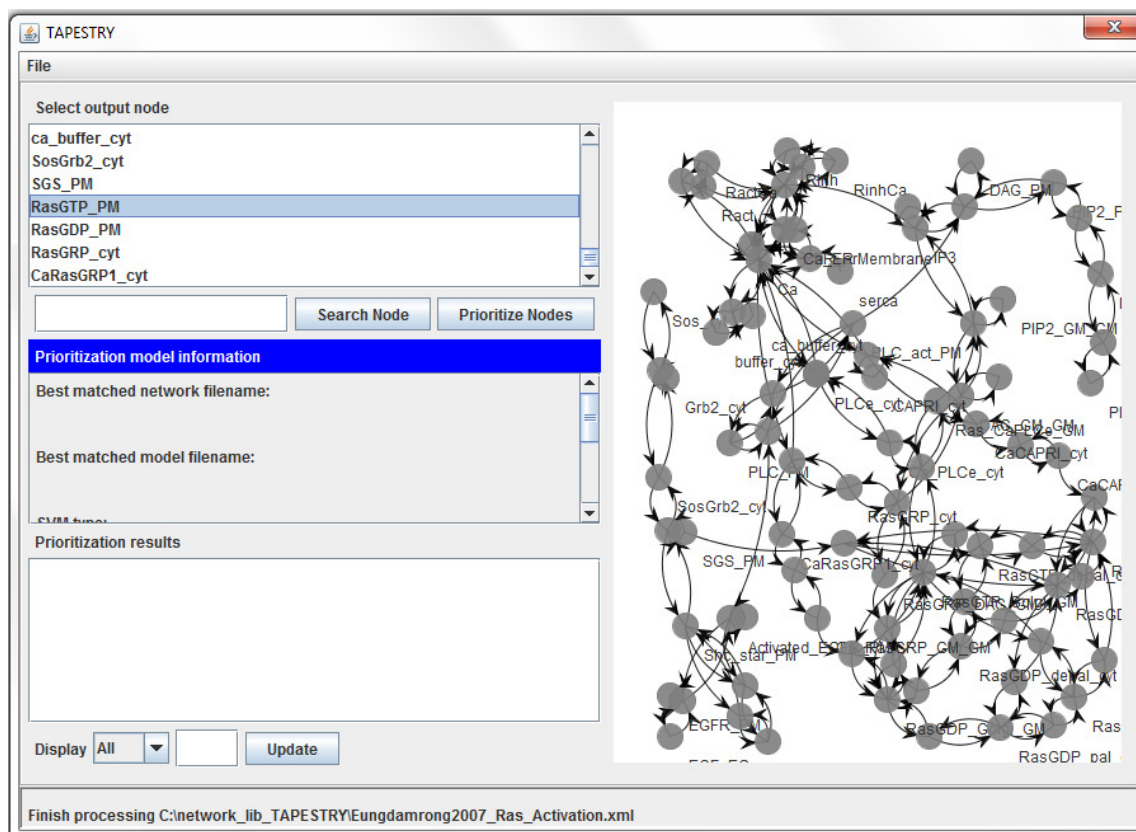


Fig. 13: Select output node for the signalling network

Step 3: Configure prioritization task by clicking on “Prioritize Nodes” button and prioritize targets by clicking on “Prioritize” button in “Configure Prioritization Task” dialog (Fig. 14).

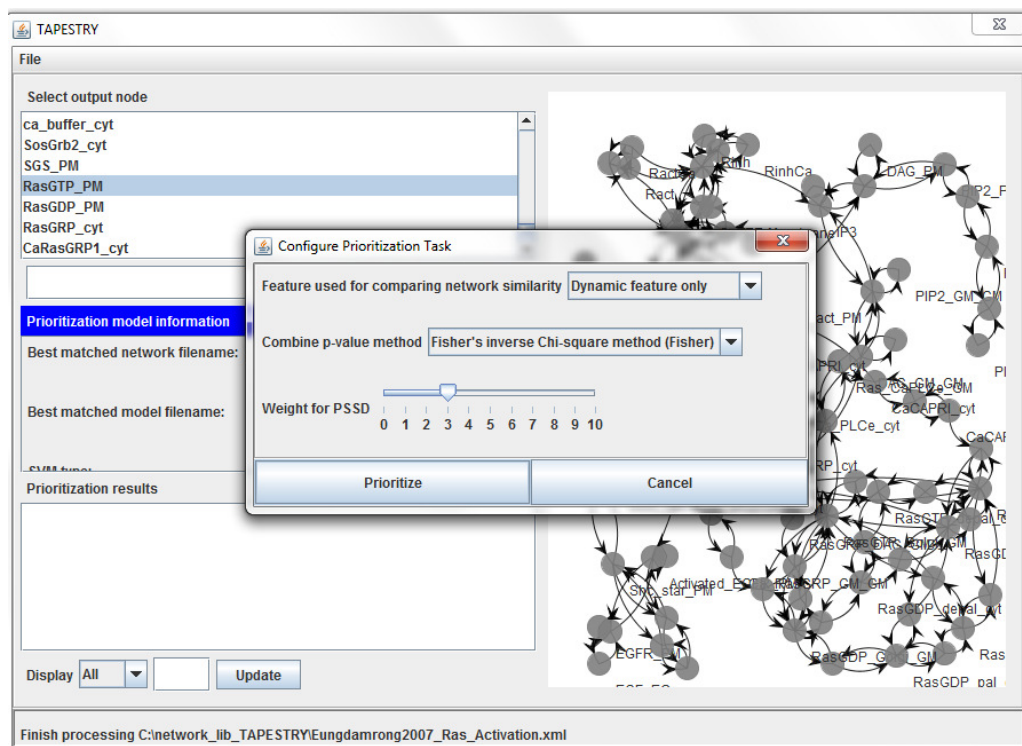


Fig. 14: Perform target prioritization for the signalling network

Step 4: View prioritization results (Fig. 15).

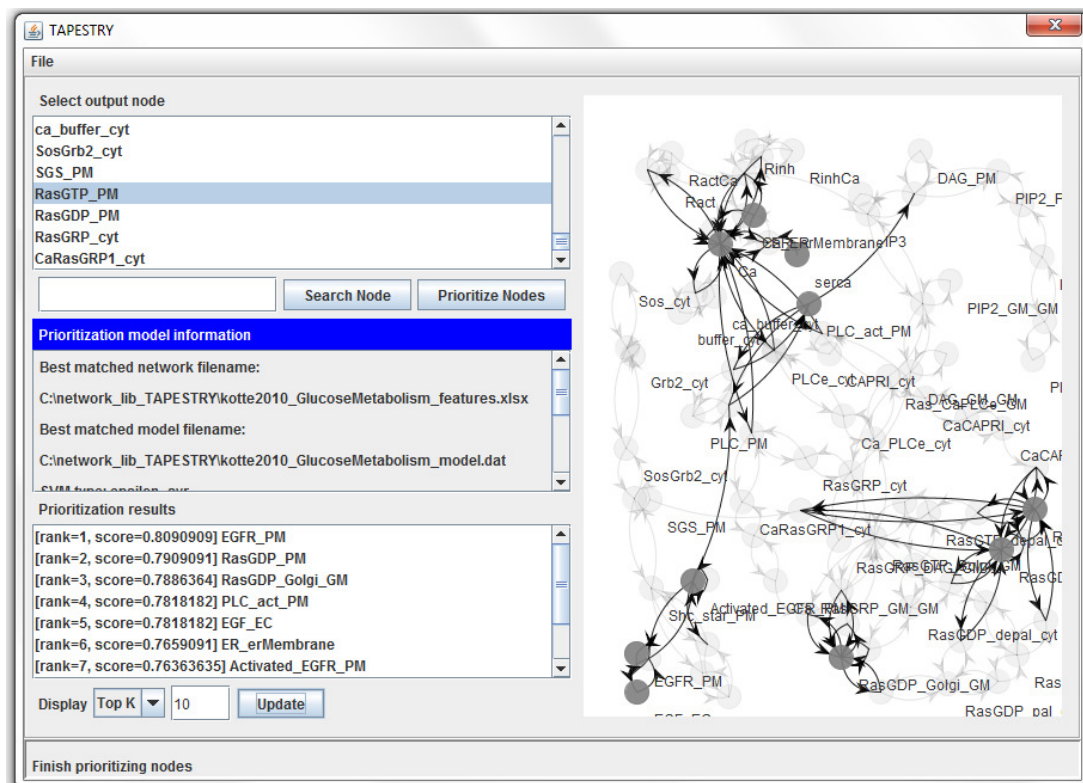


Fig. 15: Displaying top-10 prioritization results.

The “Prioritization model information” panel (middle of left panel, in blue) displays the prioritization of the best matched network in the training network library (featureLib_list.txt). The “Prioritization results” panel (bottom of left panel) displays the prioritized nodes (in decreasing putative target score). The number in front of the node (enclosed in square brackets) is the rank assigned to that node based on the putative target score ranking. Note that ranking ties are allowed (i.e., when nodes have the same putative target scores). The result displayed can be configured to display all results or top-k results. If top-k is selected, the graphical visualization of the network (right panel) will only show the top-k nodes.