

Supplemental files used to generate and query the GGM network

1. The unzipped folder should contain the following files:
 - a. Instructions.pdf
 - b. GGM_Network_for_Arabidopsis_Significant_Interactions.txt
 - c. Script.R
2. Required software
 - a. R (<http://www.r-project.org>)
 - b. “graph” package from <http://www.bioconductor.org>, which can be installed within an R console using the following two command lines:

```
source("http://bioconductor.org/biocLite.R")
biocLite("graph")
```

(Any version of the package "graph" will be OK. The newest one is version 1.14.2. The script will install the newest version).
 - c. Graphviz Downloaded from <http://www.graphviz.org>. For Windows user, make sure the folder containing “Graphviz/bin” is in your PATH (we need fdp.exe). You may need to restart you R program after installing Graphviz.
3. Procedures to generate and query the GGM network
 - a. Start the R console, change the working directory to the one containing these three files:

```
“Instructions.pdf”,
“GGM_Network_for_Arabidopsis_Significant_Interactions.txt”, and
“Script.R”.
```

You can change the directory using “File -> Change dir...” menu in the Rgui console, or using the “setwd” command.
 - b. Run “Script.R” within the R console, by issuing the following command

```
source (“Script.R”)
```

This script will generate the graph using the significant edges, which are stored in the file.

```
“GGM_Network_for_Arabidopsis_Significant_Interactions.txt”.
```

The script also defines the functions “subnet” and “gr2dot”, which are used to query and output sub-networks.
 - c. Query the network by using the following commands:

```
sg <- subnet(“SQD2”, 2)
gr2dot (sg, filename = “graph.dot”)
system (“fdp graph.dot -T png -o graph.png”)
system (“fdp graph.dot -Tps -o graph.ps”)
```


Note: The first command will generate a sub-network centered on the “SQD2” gene, within 2 edges removed. You may replace “SQD2” with your favorite gene, and 2 with other numbers. The second command outputs the generated sub-network as a file “graph.dot”. The third command uses the fdp program within Graphviz to visualize the sub-network, and output it as “graph.png”. The fourth command will output the graph as a postscript file.

Note: It must be understood that extending the network to 3 or 4 edges will require time for calculations that may, depending on the computer take a long time, or even a crash of the computer, and the graphs may become too crowded to be interpreted. It is recommended to start by extending the network by 1 or 2 edges only.

You may also query two genes at a time:

```
sg <- subnet(c(“TOC1”, “CCA1”),2)
gr2dot (sg, filename = “circadian.dot”)
system (“fdp circadian.dot -T png -o circadian.png”)
```

- d. Query your favorite genes now. But make sure they are in the network by looking at Supplemental Table S1.

It must be realized that some genes are included in the Affymetrix chips using their AT-IDs (e.g., AT1G10200) but a number of genes are also included by their specific gene names (e.g., ABI1).

Note. When querying according to the AT-ID, all letters must be capitalized.