

WiPer

Identification of significantly inter-connected genes in co-expression networks based on a statistical permutation test.

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USER GUIDELINES

Version 1.0

1. Usage license

WiPer is available as a platform-independent Java application, and is released [under the terms of the GNU General Public License](#) (GPL).

If you use WiPer please refer to:

Azuaje F. Gene centrality analysis in co-expression networks, 2013. Manuscript under review.

2. Running the program

WiPer is available as an executable java file: “wiper.jar”. Ensure that input files are stored in the same directory.

From the command line, the program is run with:

```
java -jar wiper.jar
```

3. Constraints

The current version of the executable program can handle networks consisting of no more than 1000 nodes (genes) and 30000 edges (co-expression values). Typically, more than 1000 permutations are required for estimating P values. Depending on the size of the network and the number of permutations, an analysis can be completed in times ranging from seconds to hours. During execution the current state of the processing is indicated on the screen, and it can be aborted with the Ctrl+C command.

4. Inputs and outputs

The program requires two input files, stored in tab-separated text files.

The network file: This is a three-column file, in which each row represents a gene-gene association and its corresponding strength value (e.g., correlation):

[Gene1] [Gene2] [Co-expressionValue]

The query gene (node) file: This is a single column file that specifies the genes to be analyzed. Query genes must be included in the network file. Typically, the query file includes all the genes represented in the network.

When providing these inputs to the program, file name and extension (e.g., network_file.txt) must be written.

Apart from these files, the only parameter required from the user is the number of permutations to estimate the statistical significance of the *WNC* scores measured.

When the analysis is completed, the results are automatically stored in “output.txt”.