REMODISCOVERY

ReMoDiscovery is free to use for academic purposes only. If used in your academic work, please include all relevant references by its authors. For any non-academic purpose, please contact its authors.
In addition, ReMoDiscovery can be distributed freely for academic purposes, as long as this file and all other files mentioned in this file are distributed along with the code.

ReMoDiscovery makes use of JFreeChart and JCommon (http://www.jfree.org/), the original jar files of which are also included in this distribution. They should always be distributed along with ReMoDiscovery, as well as this reference to JFreeChart and JCommon. By using ReMoDiscovery you agree to adhere to the terms of the GNU Lesser General Public License (LGPL) to which JFreeChart and JCommon are subject. The GNU Lesser General Public License (LGPL) is included in this distribution, and should remain so, if further distributed: LGPL-license.txt.

Please direct comments and questions related to the software to: tijl.debie@gmail.com or Kathleen.marchal@biw.kuleuven.be

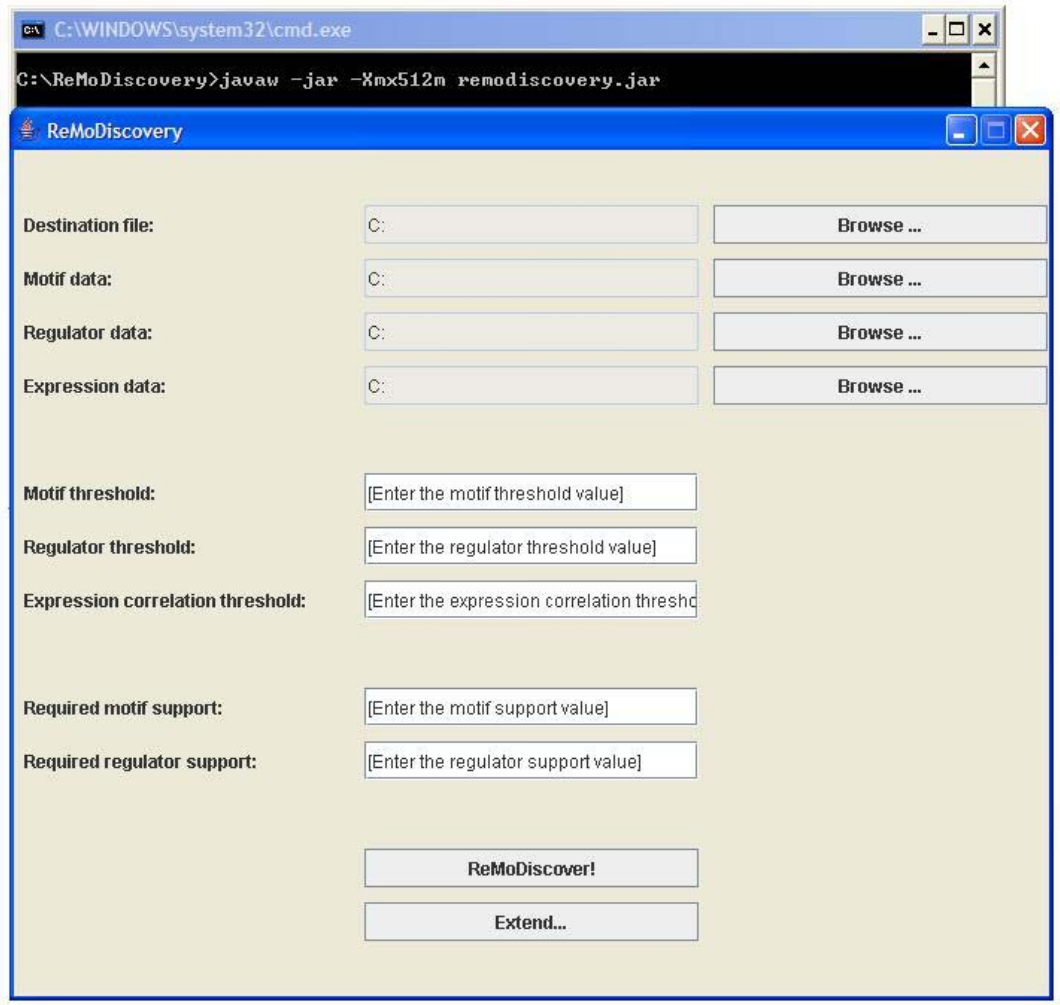
Also check the accompanying website for recent updates (http://homes.esat.kuleuven.be/~kmarchal/Supplementary_Information_Lemmens_2006/Index.html)

INSTRUCTIONS

Unpack the zip-file ReMoDiscovery.zip and store all files in the same folder.
Make sure java 1.5 is installed.

Then:
- In windows: double-click on 'ReMoDiscovery.bat'.
- Otherwise: execute the command 'java -jar -Xmx512m remodiscovery.jar' in a terminal, in the folder in which the files are stored.

The following window appears:



Output file (e.g. output.txt):

- Destination file: this file will contain the genes, regulators and motifs that are present in the seed modules.

Input files (Motif data (e.g. M.tx), Regulator data (e.g. C.tx), Expression data (e.g. A.txt)):

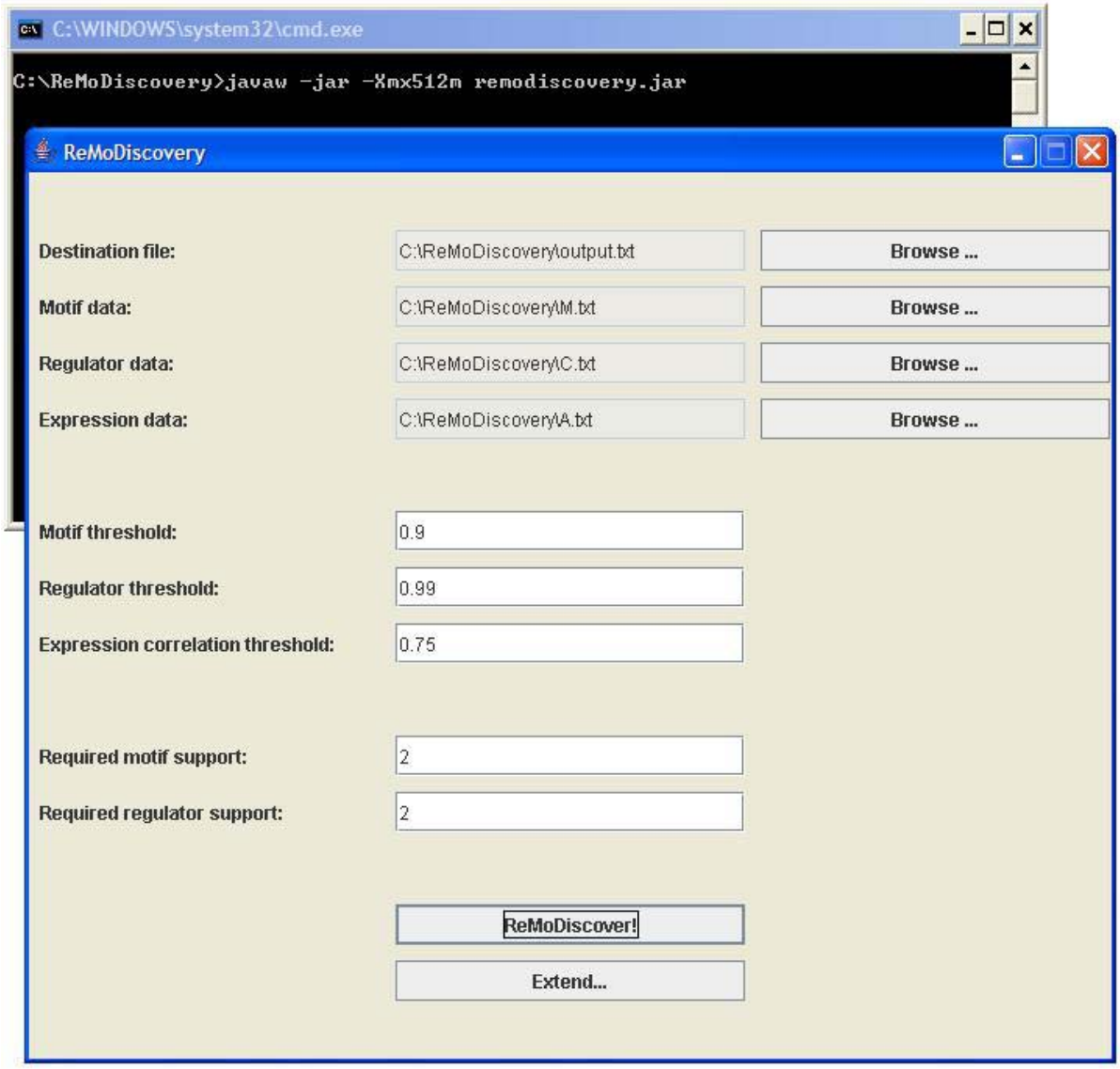
The input files should be of the following format: the rows represent the genes, and for each of the respective input files the columns represent the motifs (motif data), the regulators (ChIP-chip data) or the experiments (expression data). Each input file should contain the same number of genes, ordered in the same way. Both the rows and the columns should be numbered in the input file. For example files see the accompanying website .

Parameters:

- Motif threshold: the minimum score that a motif should have.
- Regulator threshold: the minimum score that a regulator should have.
- Expression correlation threshold: the minimum correlation between the expression profiles of two genes.

- Required motif support: the minimum number of motifs that should be shared by the genes in a module.
- Required regulator support: the minimum number of regulators that should be shared by the genes in a module.

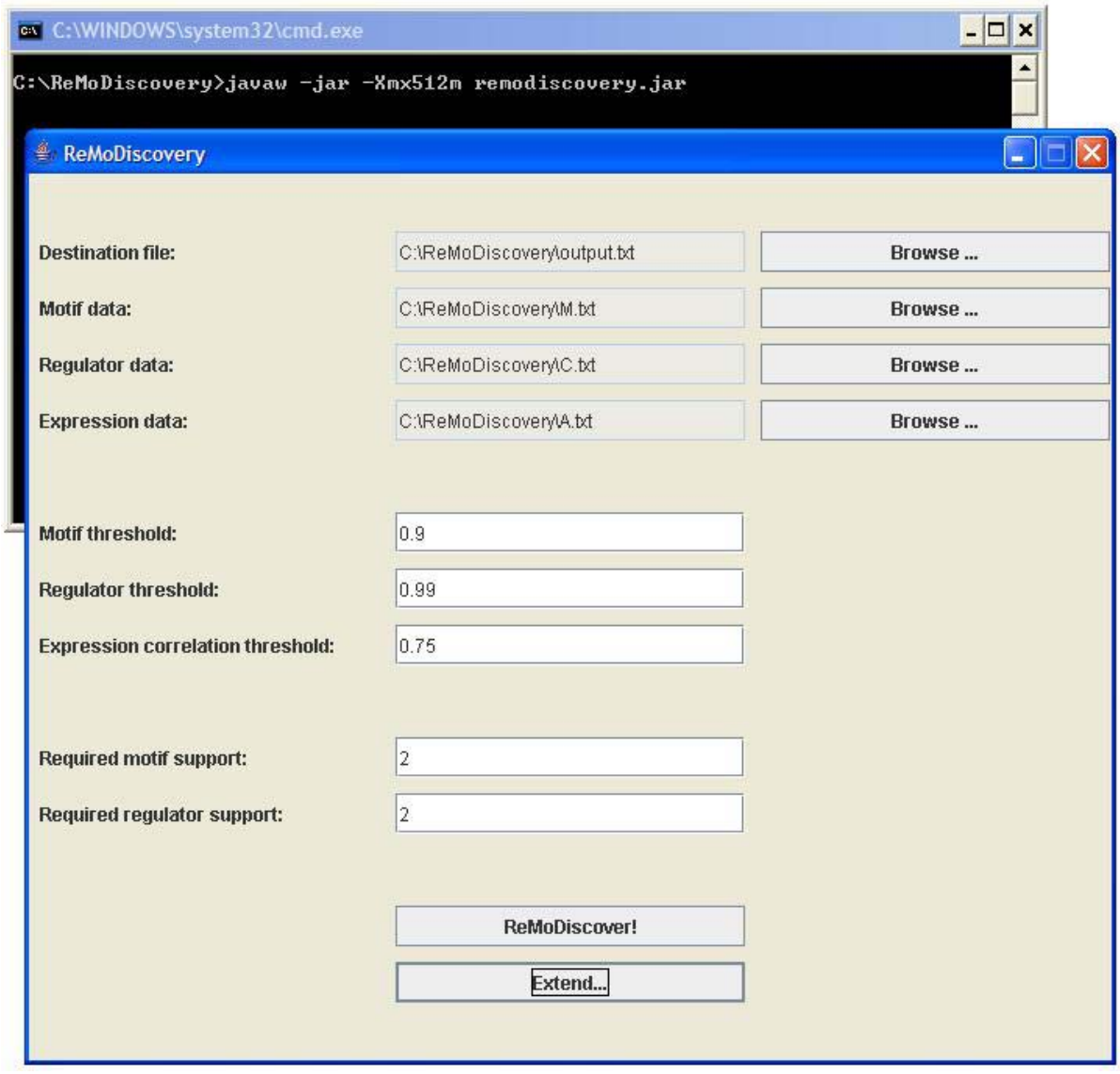
Upload the correct input files and set the parameters. Subsequently click “ReMoDiscover!”. This will perform the first step of the algorithm, i.e. the seed discovery step.



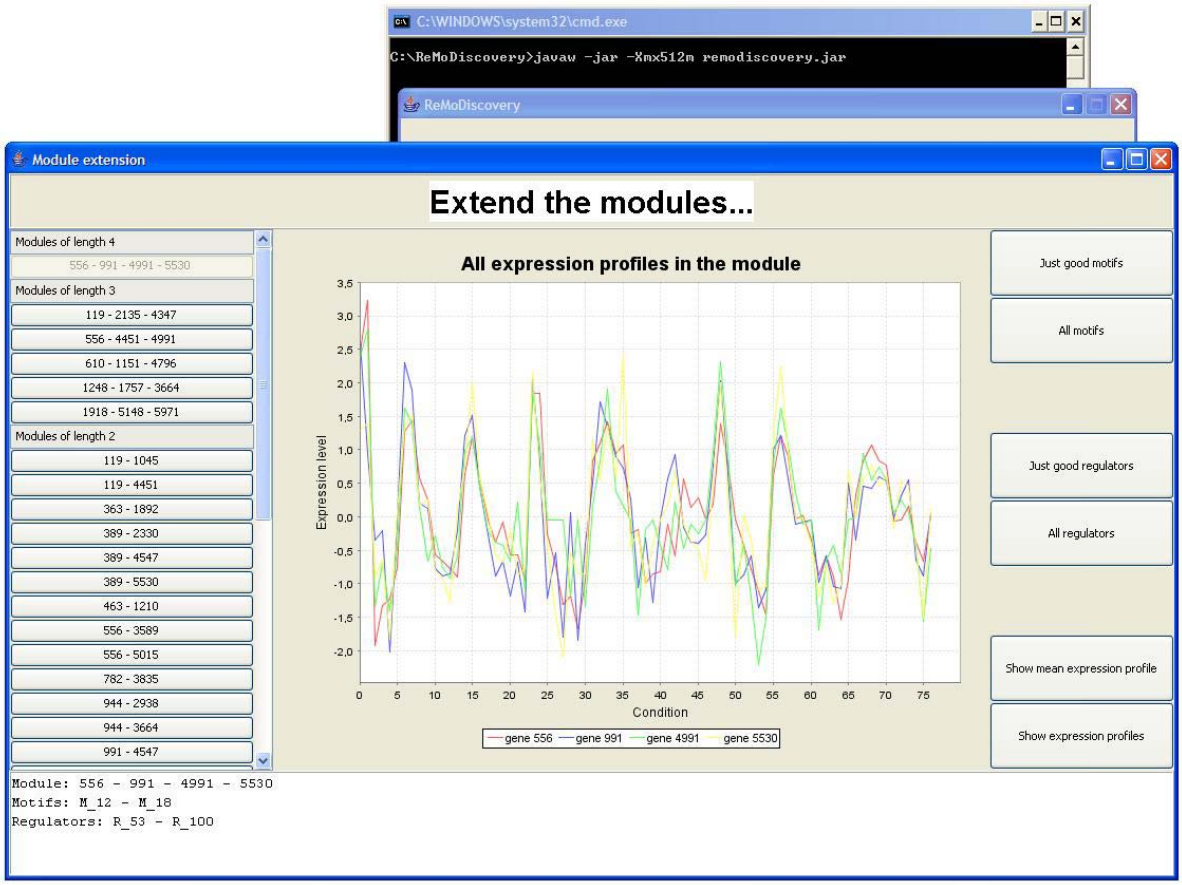
The algorithm will find sets of genes (seed modules) that satisfy the constraints. The identified seed modules can be found in the "Destination file". An example of a "Destination file" is given below: each row in the file represents an identified seed module which is characterised by the indices of the genes belonging to the module e.g. the first module is a singleton containing gene 10, motifs M_5 and M_66 and regulators R_11 and R_46.

```
Genes:    10
Motifs:   M_5     M_66
Regulators:       R_11    R_46

Genes:    11
Motifs:   M_29    M_30    M_36    M_38    M_43    M_61    M_71
Regulators:       R_57    R_62    R_86

Genes:    13
Motifs:   M_1     M_29
Regulators:       R_1     R_87

Genes:    23
Motifs:   M_1     M_5     M_15    M_29
Regulators:       R_1     R_11    R_22

Genes:    28
Motifs:   M_1     M_10    M_14    M_21    M_22    M_31    M_51    M_57
Regulators:       R_1     R_97

…

Genes:    4451    6018
Motifs:   M_2     M_18
Regulators:       R_53    R_100

Genes:    4860    5855
Motifs:   M_10    M_47
Regulators:       R_13    R_107

Genes:    5545    5855
Motifs:   M_7     M_37
Regulators:       R_78    R_79    R_107

Genes:    119     2135    4347
Motifs:   M_11    M_12    M_21
Regulators:       R_93    R_98

Genes:    556     4451    4991
Motifs:   M_11    M_18
Regulators:       R_53    R_100

Genes:    610     1151    4796
Motifs:   M_16    M_30    M_59
Regulators:       R_23    R_54    R_64

Genes:    1248    1757    3664
Motifs:   M_14    M_16
Regulators:       R_2     R_23

Genes:    1918    5148    5971
Motifs:   M_8     M_11
Regulators:       R_23    R_98


Genes:    556     991     4991    5530
Motifs:   M_12    M_18
Regulators:       R_53    R_100
```

Once the first step of the algorithm is completed, the second step, i.e. the seed extension step, can be performed by clicking “Extend…”.



The following window appears:



On the left side of the window the identified seed modules are shown. Modules are characterized by the genes contained within the module (indicated by their index), and by the motifs and regulators responsible for the corresponding regulatory program (indicated by their indices). The user can select the seed module of his interest. On the bottom of the window, the genes that are in the seed module and the regulators and the motifs of the seed regulatory program are shown. On the right side of the window you can ask to see the (mean) expression profile of the genes in the seed module, the *module enrichment p-value* plot for all regulators or for the regulators in the seed regulatory program and the *module enrichment p-value* plot for all motifs or for the motifs in the seed regulatory program.