RedundancyMiner
User’s Manual

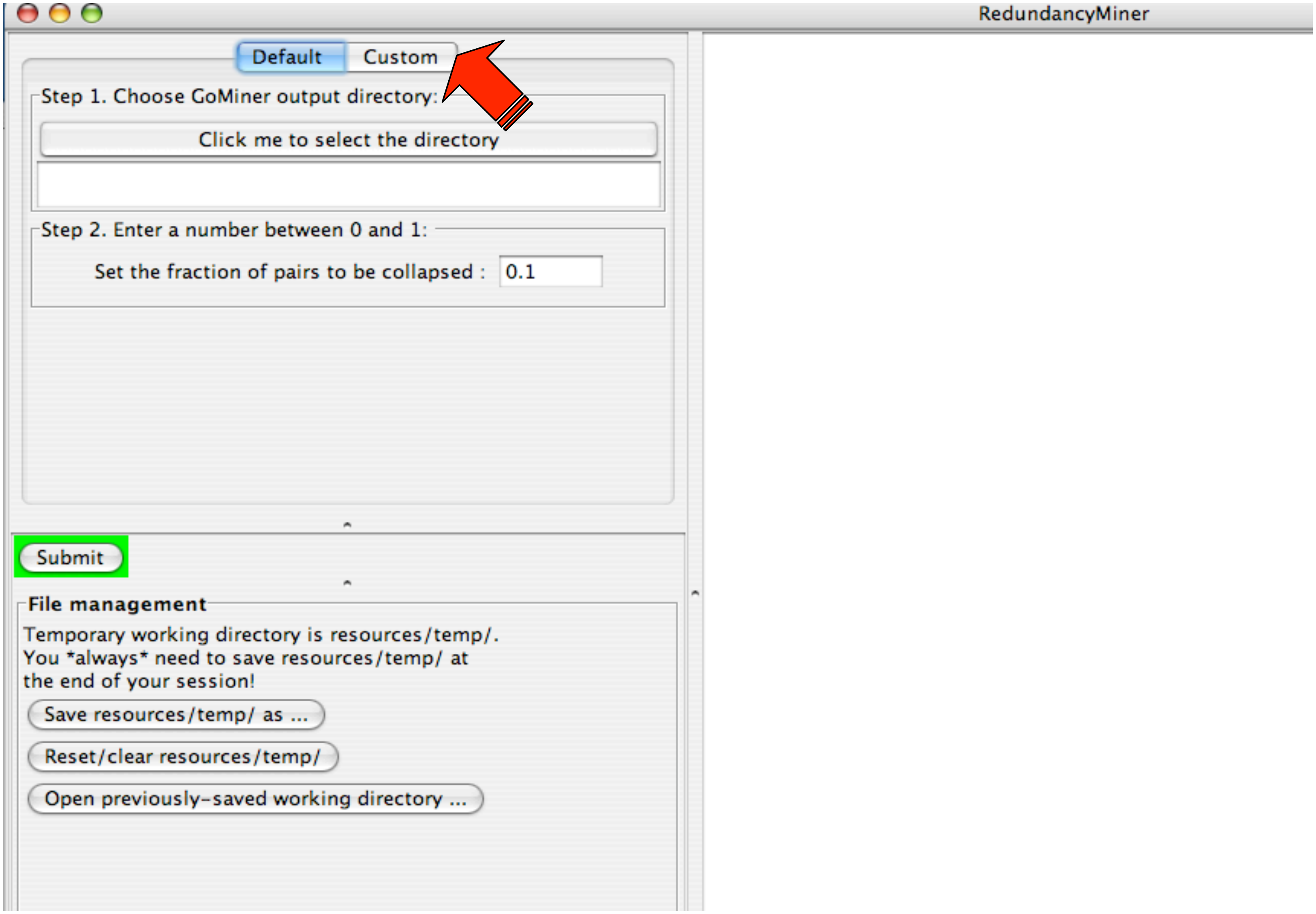
To follow along with the presentation, please download a simplified version of the HTGM result directory that is exemplified in the user's manual.

This is available from http://discover.nci.nih.gov/rm/supplementaryMaterials.html

Custom Mode

- Computing the similarity matrix
  - Select .CIM file
  - Select .gce or .tvt file
  - Submit the job
- Clustering
  - Select P-value threshold
  - Submit the job
- File management
  - Save the working directory
  - Retrieve the working directory

Custom Mode: Select Custom Mode



Step 1. Choose GoMiner output directory:

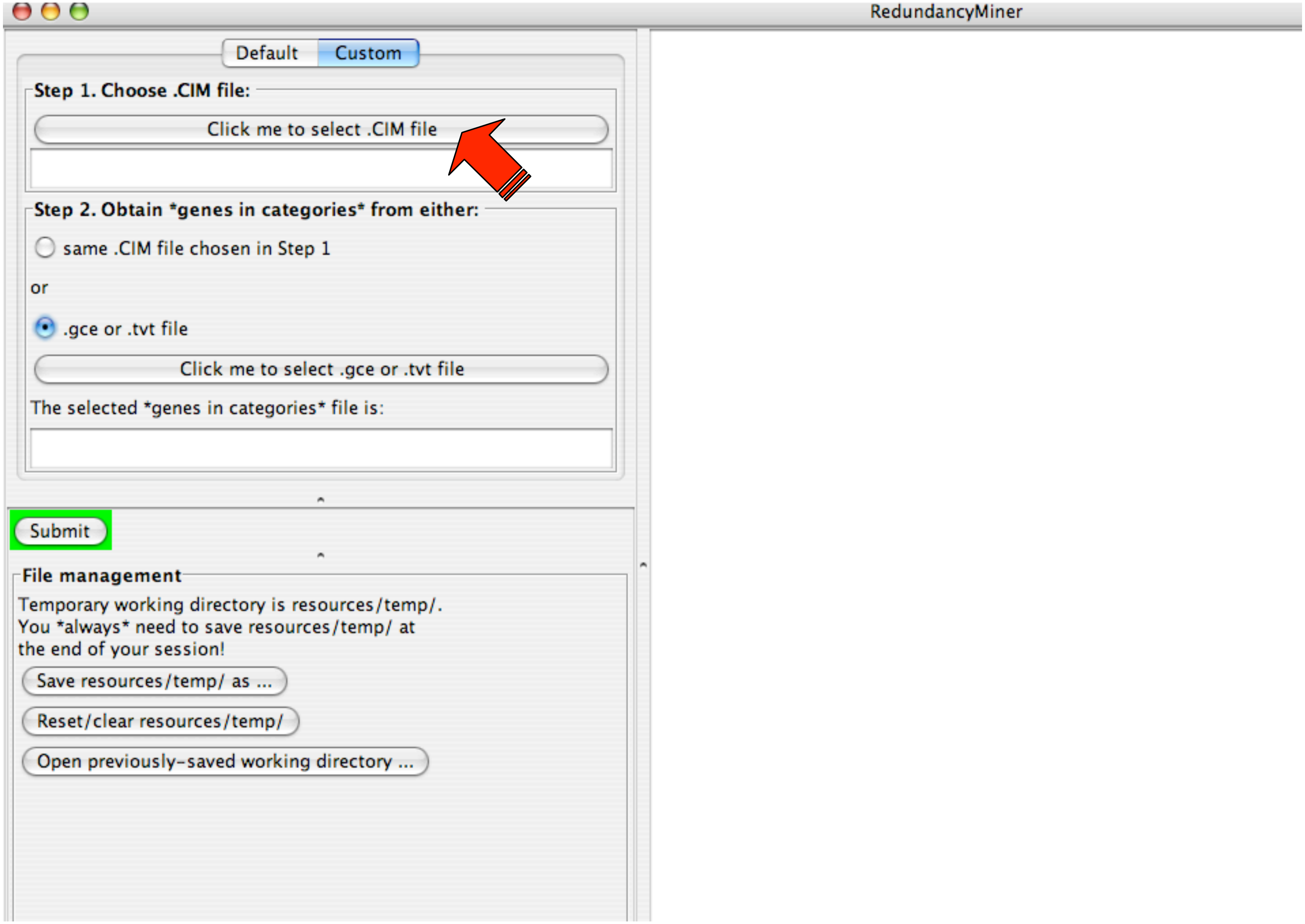
Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed : 0.1

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Compute the similarity matrix: Choose .CIM (Step 1)



Step 1. Choose .CIM file:

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

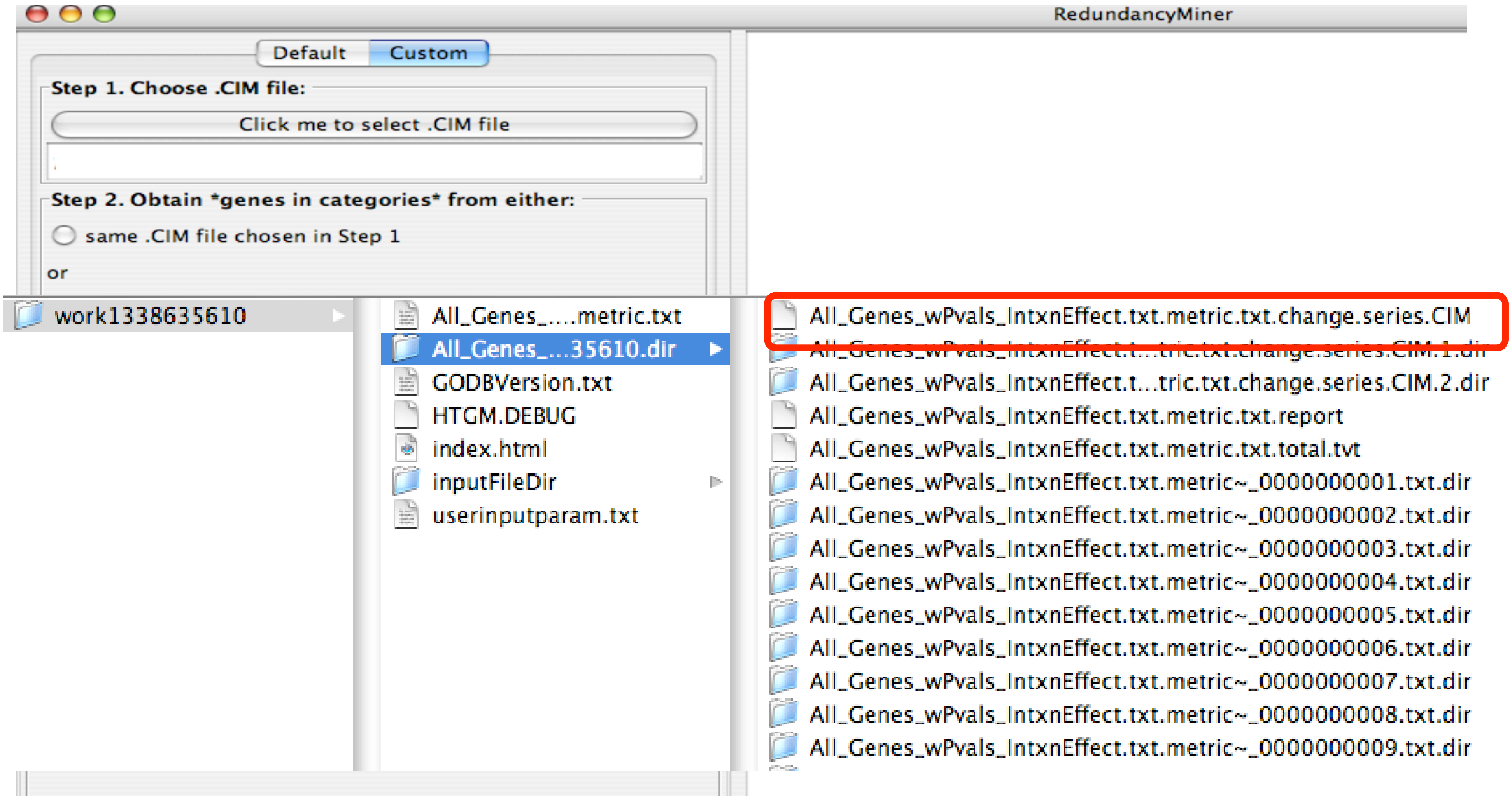
● .gce or .tvt file

The selected *genes in categories* file is:

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Compute the similarity matrix: Choose .CIM (Step 2)



Step 1. Choose .CIM file:

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

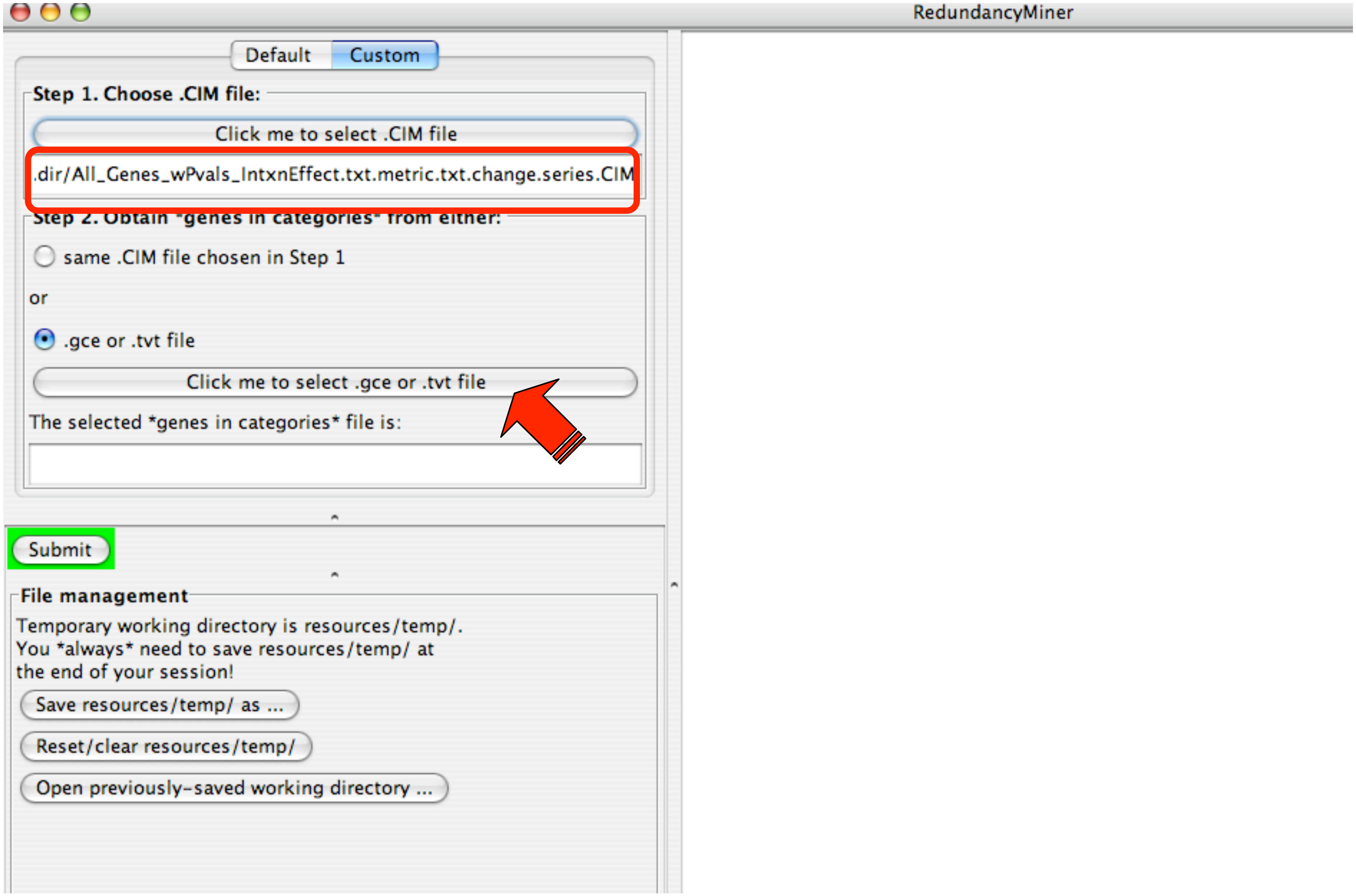
or

work1338635610

All_Genes_....metric.txt
All_Genes_...35610.dir
GODBVersion.txt
HTGM.DEBUG
index.html
inputFileDir
userinputparam.txt

All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM
All_Genes_wPvals_IntxnEffect.t...tric.txt.change.series.CIM.1.dir
All_Genes_wPvals_IntxnEffect.t...tric.txt.change.series.CIM.2.dir
All_Genes_wPvals_IntxnEffect.txt.metric.txt.report
All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000001.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000002.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000003.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000004.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000005.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000006.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000007.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000008.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000009.txt.dir

Compute the similarity matrix: Choose .gce or .tvt (Step 1)



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

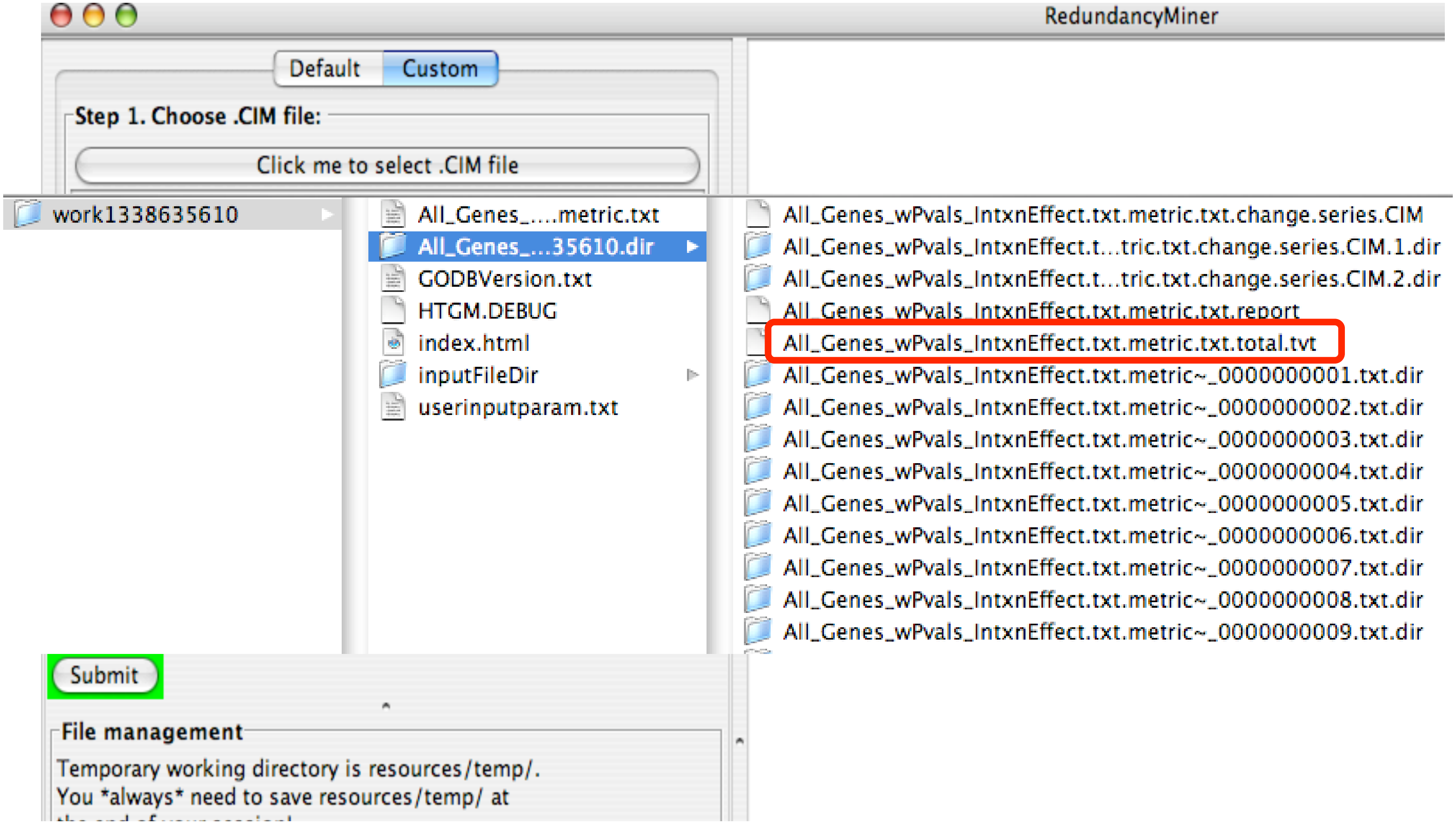
● .gce or .tvt file

The selected *genes in categories* file is:

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Compute the similarity matrix: Choose .gce or tvt (Step 2)



Step 1. Choose .CIM file:

work1338635610

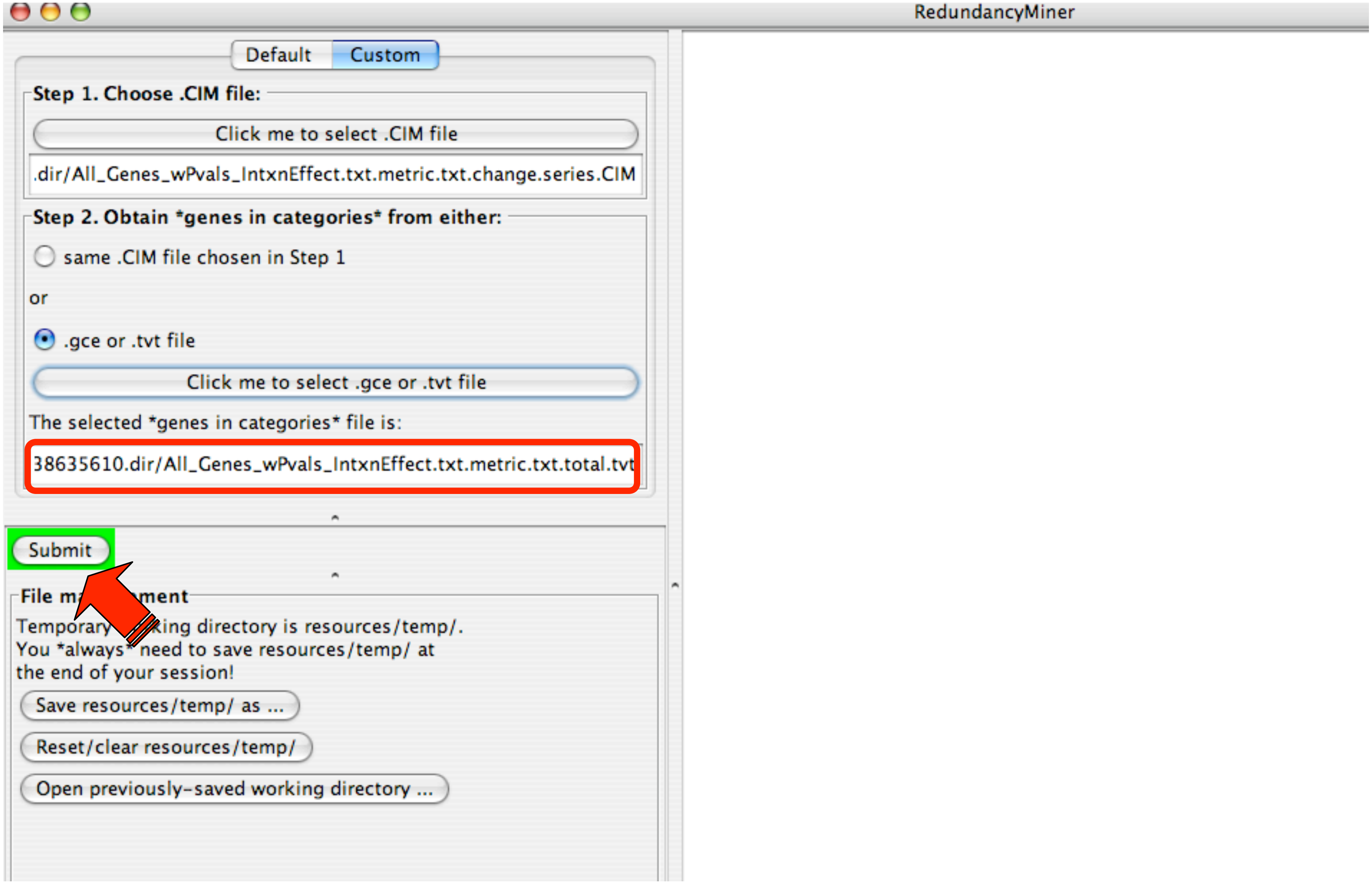
All_Genes_....metric.txt
All_Genes_...35610.dir
GODBVersion.txt
HTGM.DEBUG
index.html
inputFileDir
userinputparam.txt

All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM
All_Genes_wPvals_IntxnEffect.t...tric.txt.change.series.CIM.1.dir
All_Genes_wPvals_IntxnEffect.t...tric.txt.change.series.CIM.2.dir
All_Genes_wPvals_IntxnEffect.txt.metric.txt.report
All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000001.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000002.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000003.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000004.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000005.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000006.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000007.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000008.txt.dir
All_Genes_wPvals_IntxnEffect.txt.metric~_0000000009.txt.dir

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at

Compute the similarity matrix: Submit the job



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

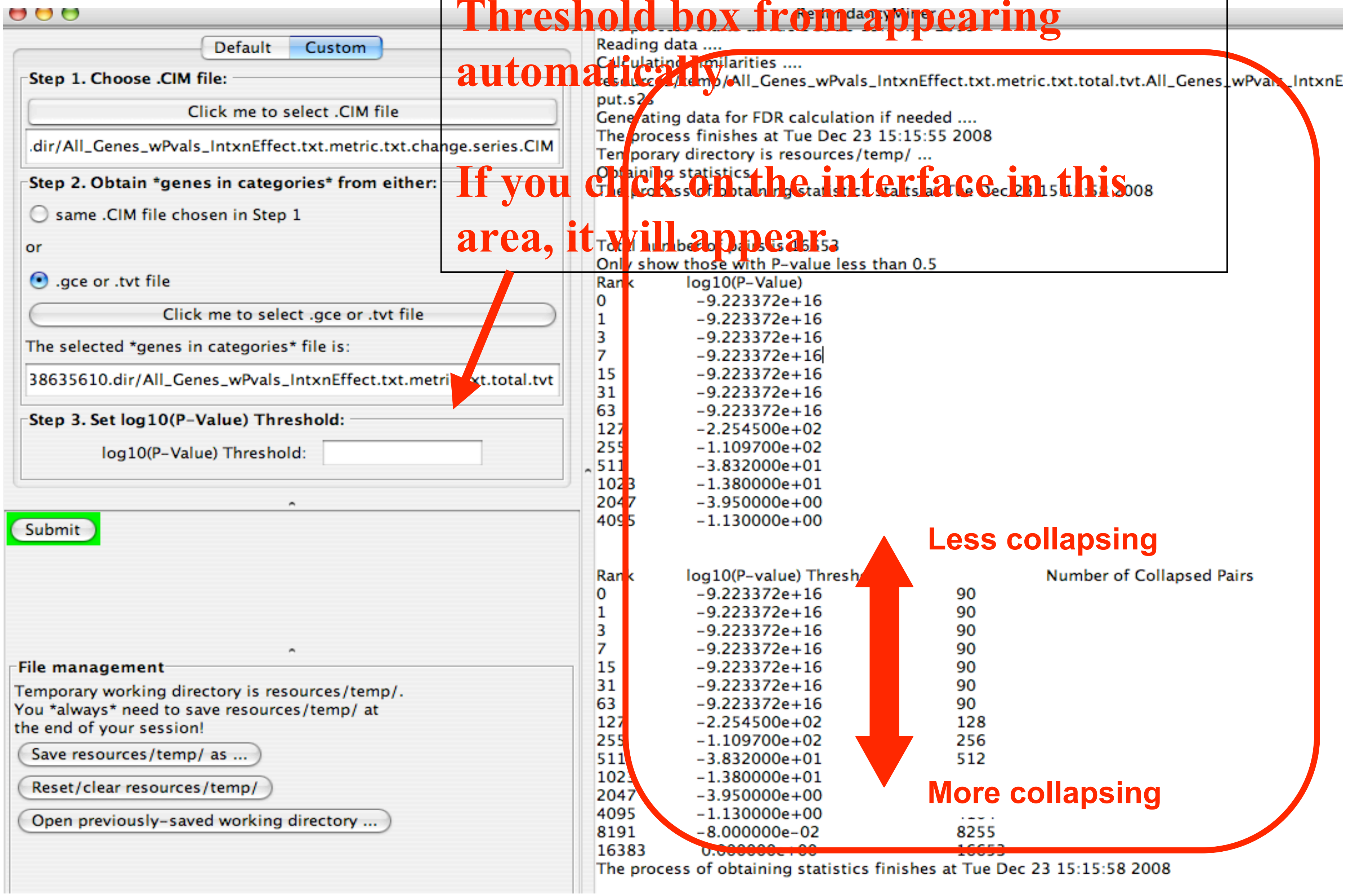
File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Cluster: Select P-value threshold (Step 1)

A glitch in the java interface keeps the Threshold box from appearing automatically.

If you click on the interface in this area, it will appear.



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

log10(P-Value) Threshold:

File management

Temporary working directory is resources/temp/. You *always* need to save resources/temp/ at the end of your session!

```
Reading data ....
Calculating similarities ....
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnE
put.s2
Generating data for FDR calculation if needed ....
The process finishes at Tue Dec 23 15:15:55 2008
Temporary directory is resources/temp/ ...
Obtaining statistics ...
The process of obtaining statistics starts at Tue Dec 23 15:1 :5 2008


Total number of pairs is 16653
Only show those with P-value less than 0.5
Rank         log10(P-Value)
0             -9.223372e+16
1             -9.223372e+16
3             -9.223372e+16
7             -9.223372e+16
15            -9.223372e+16
31            -9.223372e+16
63            -9.223372e+16
127           -2.254500e+02
255           -1.109700e+02
511           -3.832000e+01
1023          -1.380000e+01
2047          -3.950000e+00
4095          -1.130000e+00


Rank         log10(P-value) Thresh                          Number of Collapsed Pairs
0             -9.223372e+16            90
1             -9.223372e+16            90
3             -9.223372e+16            90
7             -9.223372e+16            90
15            -9.223372e+16            90
31            -9.223372e+16            90
63            -9.223372e+16            90
127           -2.254500e+02            128
255           -1.109700e+02            256
511           -3.832000e+01            512
1023          -1.380000e+01
2047          -3.950000e+00
4095          -1.130000e+00
8191          -8.000000e-02            8255
16383         0.000000e+00             16653
The process of obtaining statistics finishes at Tue Dec 23 15:15:58 2008
```

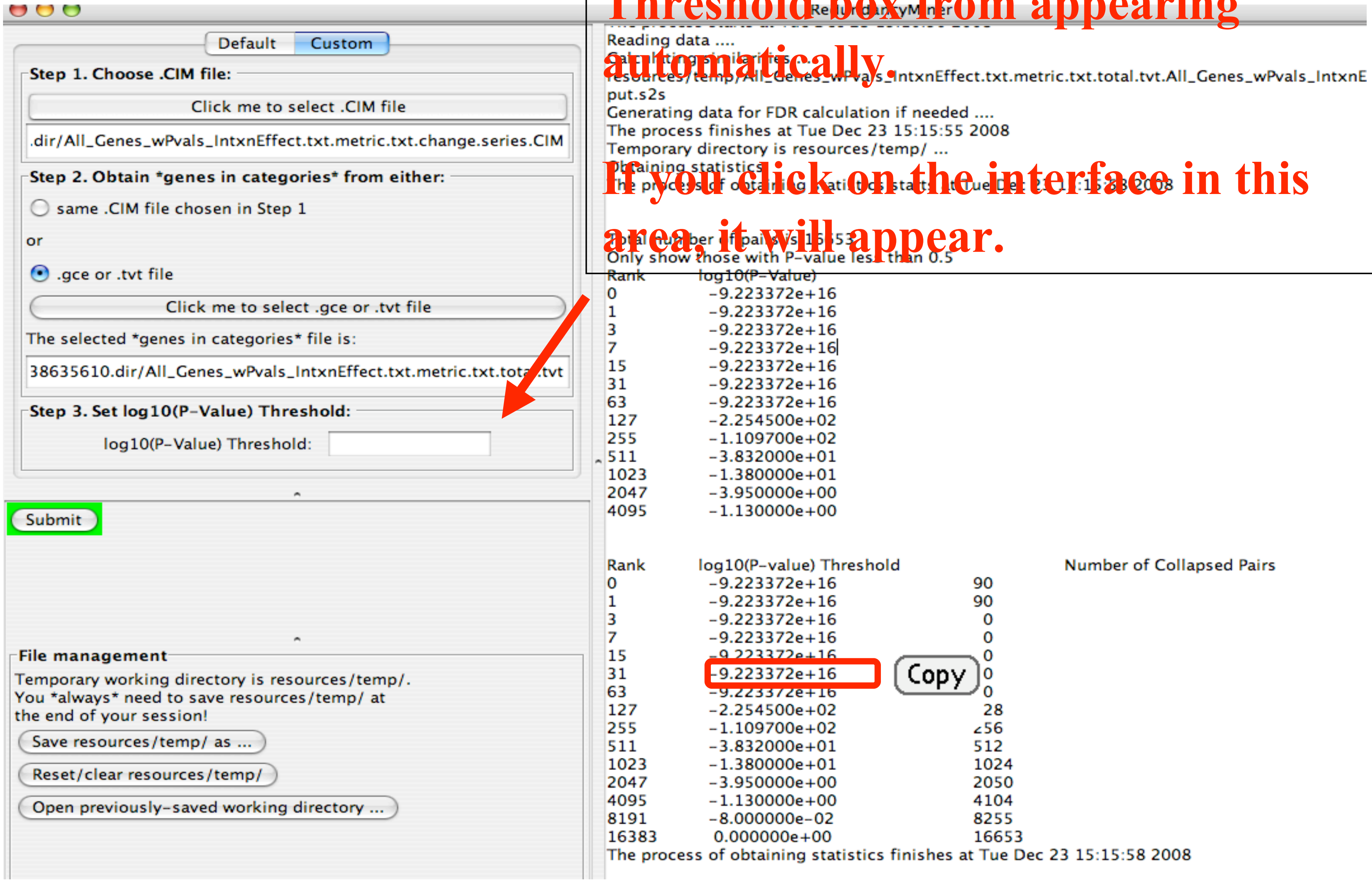
Less collapsing

More collapsing

Cluster: Select P-value threshold (Step 2)

A glitch in the java interface keeps the Threshold box from appearing automatically.

If you click on the interface in this area, it will appear.



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

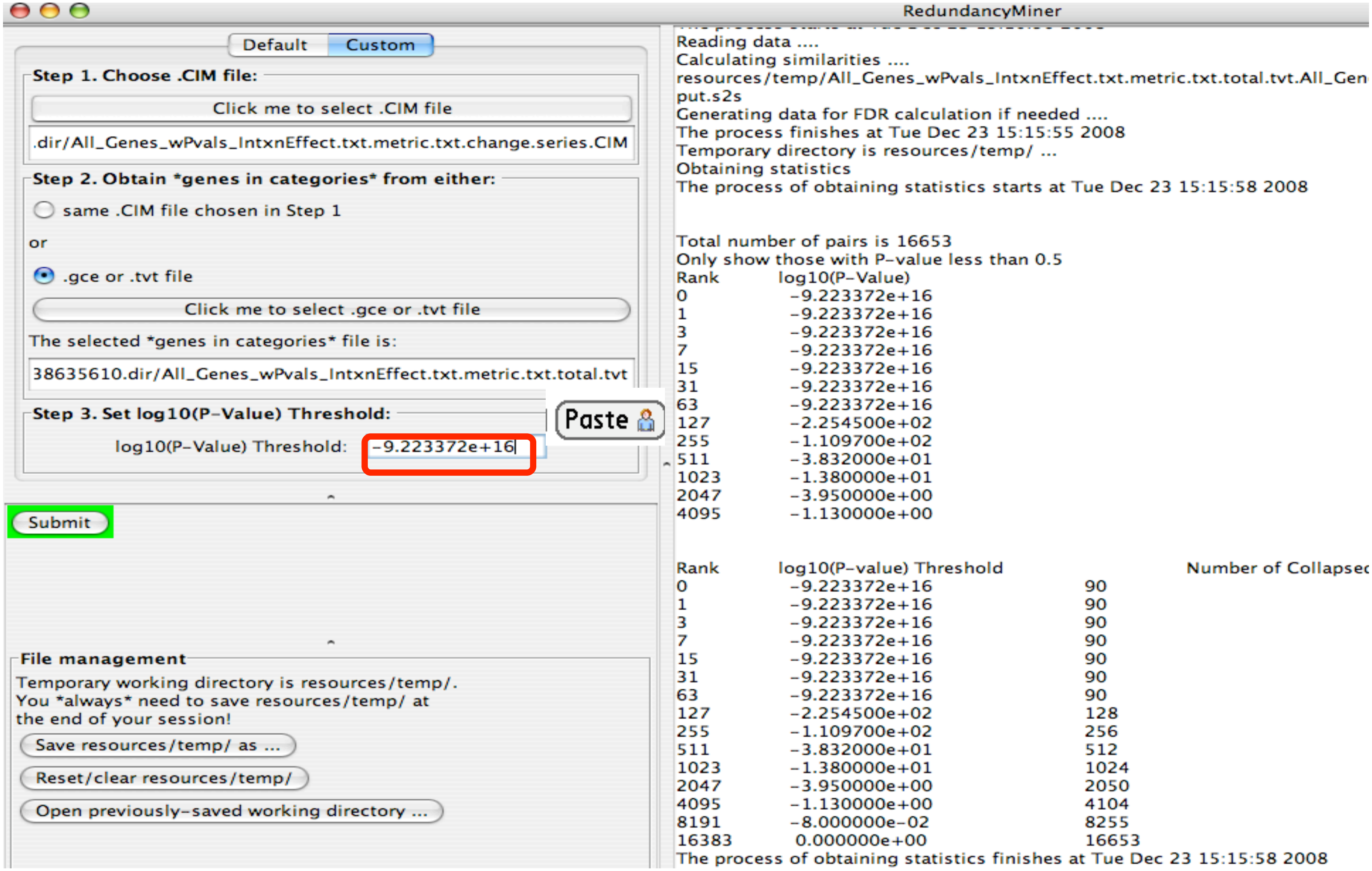
log10(P-Value) Threshold:

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
Reading data ....
Calculating similarities ....
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnE
put.s2s
Generating data for FDR calculation if needed ....
The process finishes at Tue Dec 23 15:15:55 2008
Temporary directory is resources/temp/ ...
Obtaining statistics
The process of obtaining statistics starts at Tue Dec 23 15:15:58 2008

Total number of pairs is 16653
Only show those with P-value less than 0.5
Rank        log10(P-Value)
0            -9.223372e+16
1            -9.223372e+16
3            -9.223372e+16
7            -9.223372e+16
15           -9.223372e+16
31           -9.223372e+16
63           -9.223372e+16
127          -2.254500e+02
255          -1.109700e+02
511          -3.832000e+01
1023         -1.380000e+01
2047         -3.950000e+00
4095         -1.130000e+00


Rank        log10(P-value) Threshold              Number of Collapsed Pairs
0            -9.223372e+16                90
1            -9.223372e+16                90
3            -9.223372e+16                0
7            -9.223372e+16                0
15           -9.223372e+16                0
31           -9.223372e+16                0
63           -9.223372e+16                0
127          -2.254500e+02                28
255          -1.109700e+02                256
511          -3.832000e+01                512
1023         -1.380000e+01                1024
2047         -3.950000e+00                2050
4095         -1.130000e+00                4104
8191         -8.000000e-02                8255
16383         0.000000e+00                16653
The process of obtaining statistics finishes at Tue Dec 23 15:15:58 2008
```

Cluster: Select P-value threshold (Step 3)



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P–Value) Threshold:

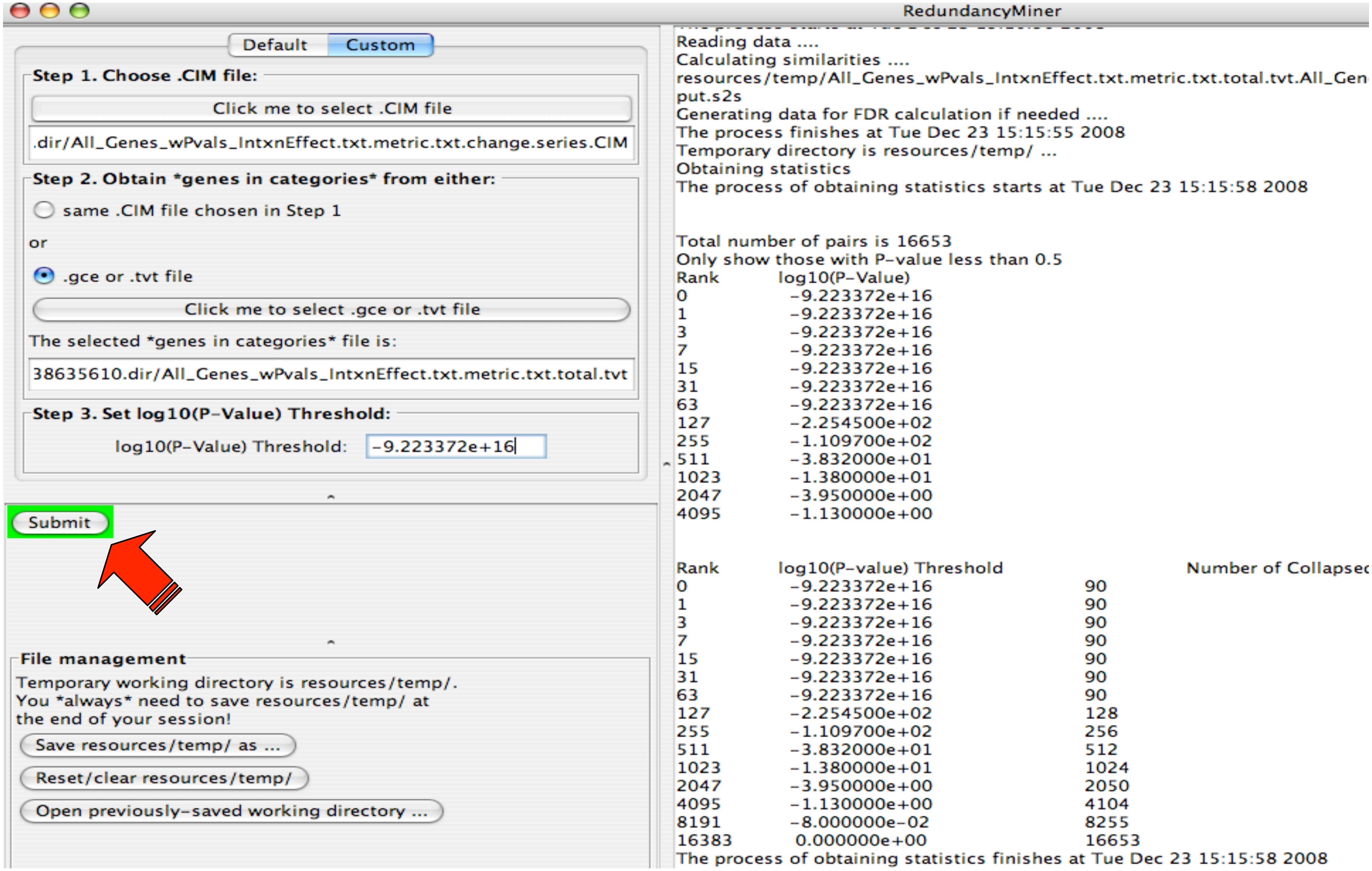
log10(P–Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
Reading data ....
Calculating similarities ....
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Gen
put.s2s
Generating data for FDR calculation if needed ....
The process finishes at Tue Dec 23 15:15:55 2008
Temporary directory is resources/temp/ ...
Obtaining statistics
The process of obtaining statistics starts at Tue Dec 23 15:15:58 2008


Total number of pairs is 16653
Only show those with P-value less than 0.5
Rank          log10(P-Value)
0               -9.223372e+16
1               -9.223372e+16
3               -9.223372e+16
7               -9.223372e+16
15              -9.223372e+16
31              -9.223372e+16
63              -9.223372e+16
127             -2.254500e+02
255             -1.109700e+02
511             -3.832000e+01
1023            -1.380000e+01
2047            -3.950000e+00
4095            -1.130000e+00


Rank          log10(P-value) Threshold                    Number of Collapsec
0               -9.223372e+16            90
1               -9.223372e+16            90
3               -9.223372e+16            90
7               -9.223372e+16            90
15              -9.223372e+16            90
31              -9.223372e+16            90
63              -9.223372e+16            90
127             -2.254500e+02            128
255             -1.109700e+02            256
511             -3.832000e+01            512
1023            -1.380000e+01            1024
2047            -3.950000e+00            2050
4095            -1.130000e+00            4104
8191            -8.000000e-02            8255
16383            0.000000e+00            16653
The process of obtaining statistics finishes at Tue Dec 23 15:15:58 2008
```

Cluster: Submit the job



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

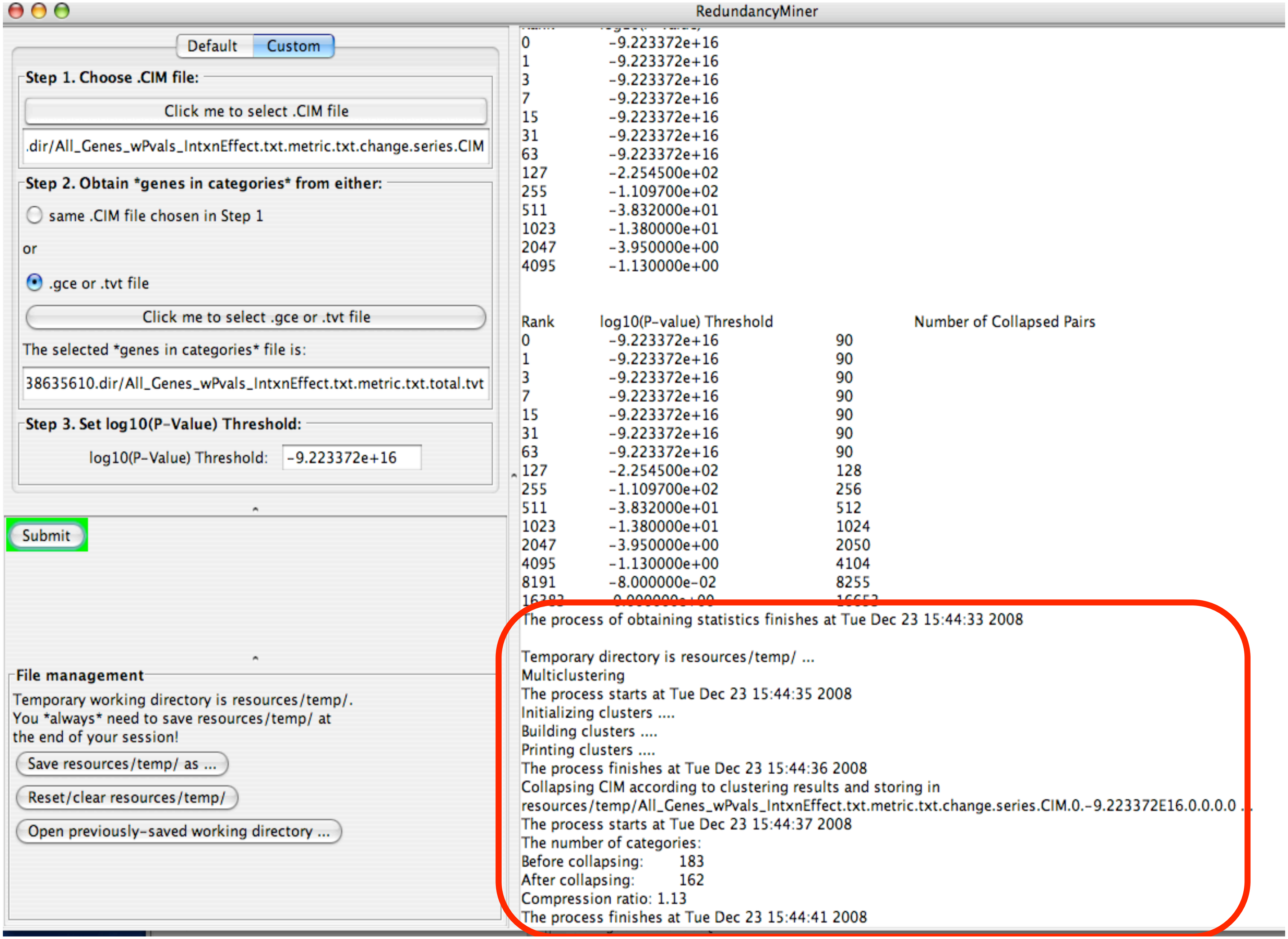
log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
Reading data ....
Calculating similarities ....
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Gen
put.s2s
Generating data for FDR calculation if needed ....
The process finishes at Tue Dec 23 15:15:55 2008
Temporary directory is resources/temp/ ...
Obtaining statistics
The process of obtaining statistics starts at Tue Dec 23 15:15:58 2008


Total number of pairs is 16653
Only show those with P-value less than 0.5
Rank        log10(P-Value)
0            -9.223372e+16
1            -9.223372e+16
3            -9.223372e+16
7            -9.223372e+16
15           -9.223372e+16
31           -9.223372e+16
63           -9.223372e+16
127          -2.254500e+02
255          -1.109700e+02
511          -3.832000e+01
1023         -1.380000e+01
2047         -3.950000e+00
4095         -1.130000e+00


Rank        log10(P-value) Threshold                  Number of Collapse
0            -9.223372e+16             90
1            -9.223372e+16             90
3            -9.223372e+16             90
7            -9.223372e+16             90
15           -9.223372e+16             90
31           -9.223372e+16             90
63           -9.223372e+16             90
127          -2.254500e+02             128
255          -1.109700e+02             256
511          -3.832000e+01             512
1023         -1.380000e+01             1024
2047         -3.950000e+00             2050
4095         -1.130000e+00             4104
8191         -8.000000e-02             8255
16383         0.000000e+00             16653
The process of obtaining statistics finishes at Tue Dec 23 15:15:58 2008
```

Cluster: Completed



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

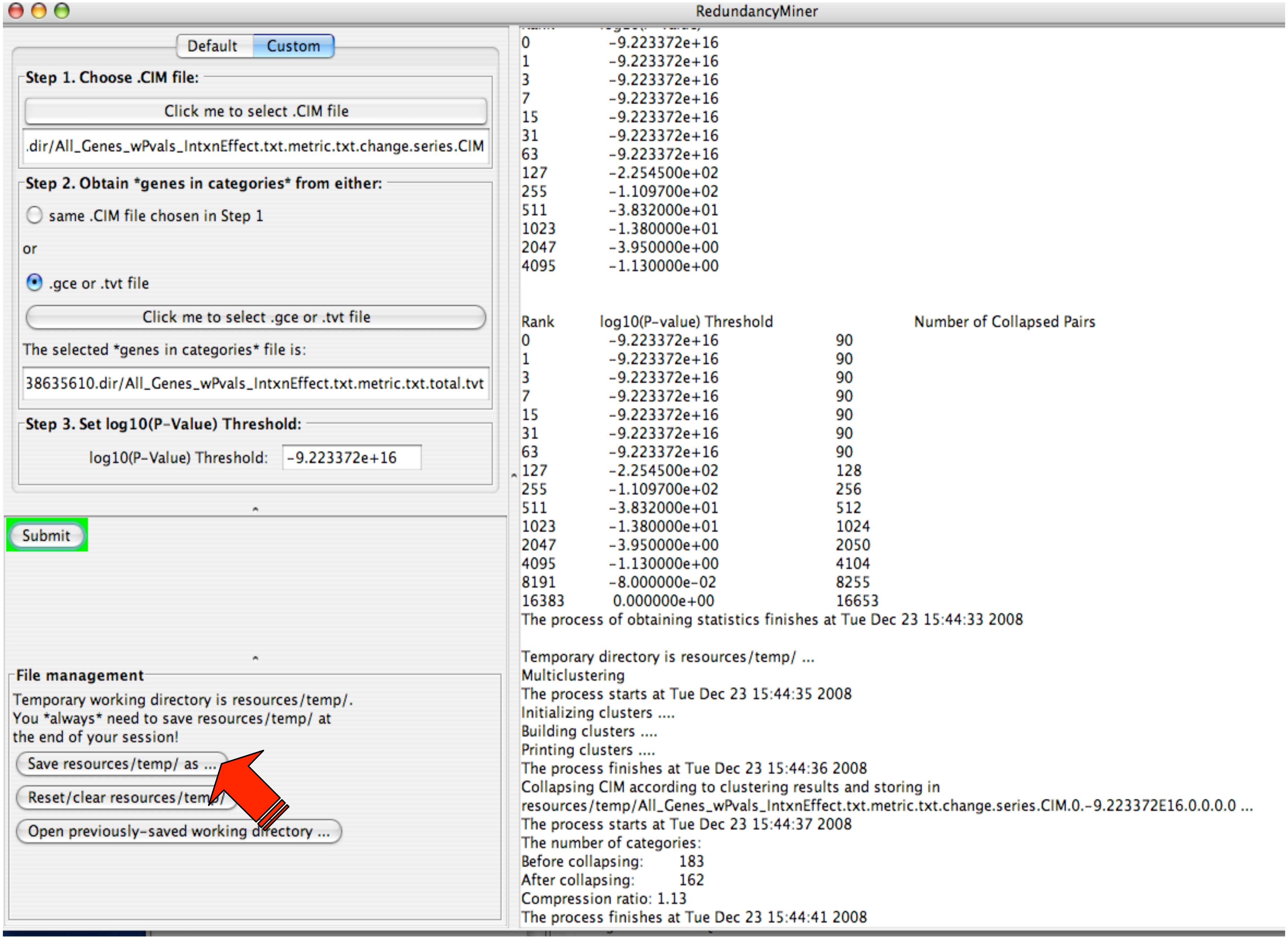
log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
0           -9.223372e+16
1           -9.223372e+16
3           -9.223372e+16
7           -9.223372e+16
15          -9.223372e+16
31          -9.223372e+16
63          -9.223372e+16
127         -2.254500e+02
255         -1.109700e+02
511         -3.832000e+01
1023        -1.380000e+01
2047        -3.950000e+00
4095        -1.130000e+00


Rank        log10(P-value) Threshold                Number of Collapsed Pairs
0           -9.223372e+16           90
1           -9.223372e+16           90
3           -9.223372e+16           90
7           -9.223372e+16           90
15          -9.223372e+16           90
31          -9.223372e+16           90
63          -9.223372e+16           90
127         -2.254500e+02           128
255         -1.109700e+02           256
511         -3.832000e+01           512
1023        -1.380000e+01           1024
2047        -3.950000e+00           2050
4095        -1.130000e+00           4104
8191        -8.000000e-02           8255
16383       0.000000e+00            16653
The process of obtaining statistics finishes at Tue Dec 23 15:44:33 2008

Temporary directory is resources/temp/ ...
Multiclustering
The process starts at Tue Dec 23 15:44:35 2008
Initializing clusters ....
Building clusters ....
Printing clusters ....
The process finishes at Tue Dec 23 15:44:36 2008
Collapsing CIM according to clustering results and storing in
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 ...
The process starts at Tue Dec 23 15:44:37 2008
The number of categories:
Before collapsing:      183
After collapsing:       162
Compression ratio: 1.13
The process finishes at Tue Dec 23 15:44:41 2008
```

File management: Save the working directory (Step 1)



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

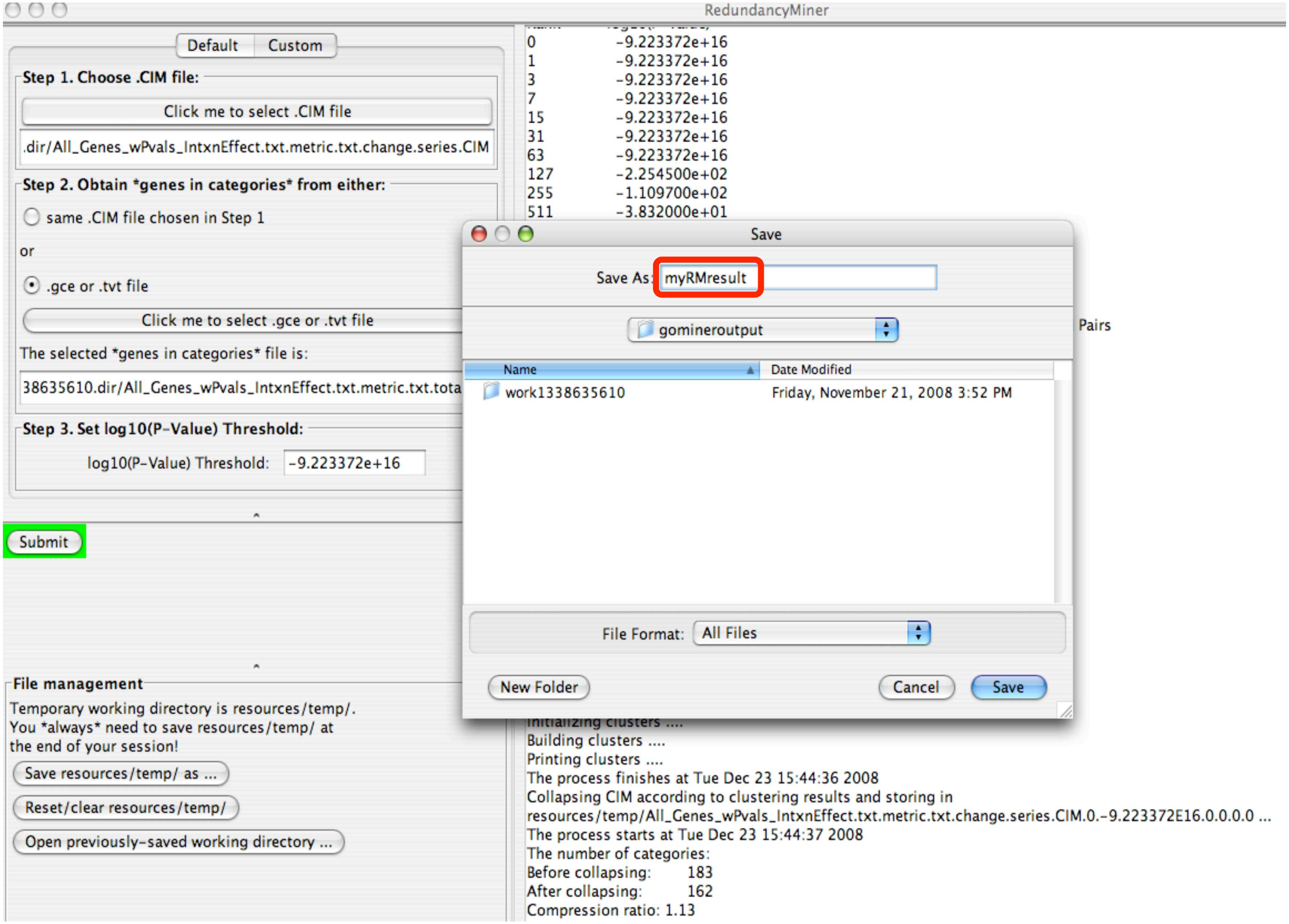
log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
0           -9.223372e+16
1           -9.223372e+16
3           -9.223372e+16
7           -9.223372e+16
15          -9.223372e+16
31          -9.223372e+16
63          -9.223372e+16
127         -2.254500e+02
255         -1.109700e+02
511         -3.832000e+01
1023        -1.380000e+01
2047        -3.950000e+00
4095        -1.130000e+00


Rank        log10(P-value) Threshold                Number of Collapsed Pairs
0           -9.223372e+16               90
1           -9.223372e+16               90
3           -9.223372e+16               90
7           -9.223372e+16               90
15          -9.223372e+16               90
31          -9.223372e+16               90
63          -9.223372e+16               90
127         -2.254500e+02               128
255         -1.109700e+02               256
511         -3.832000e+01               512
1023        -1.380000e+01               1024
2047        -3.950000e+00               2050
4095        -1.130000e+00               4104
8191        -8.000000e-02               8255
16383        0.000000e+00               16653
The process of obtaining statistics finishes at Tue Dec 23 15:44:33 2008

Temporary directory is resources/temp/ ...
Multiclustering
The process starts at Tue Dec 23 15:44:35 2008
Initializing clusters ....
Building clusters ....
Printing clusters ....
The process finishes at Tue Dec 23 15:44:36 2008
Collapsing CIM according to clustering results and storing in
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 ...
The process starts at Tue Dec 23 15:44:37 2008
The number of categories:
Before collapsing:      183
After collapsing:       162
Compression ratio: 1.13
The process finishes at Tue Dec 23 15:44:41 2008
```

File management: Save the working directory (Step 2)



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.tota

Step 3. Set log10(P-Value) Threshold:

log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Save As: myRMresult

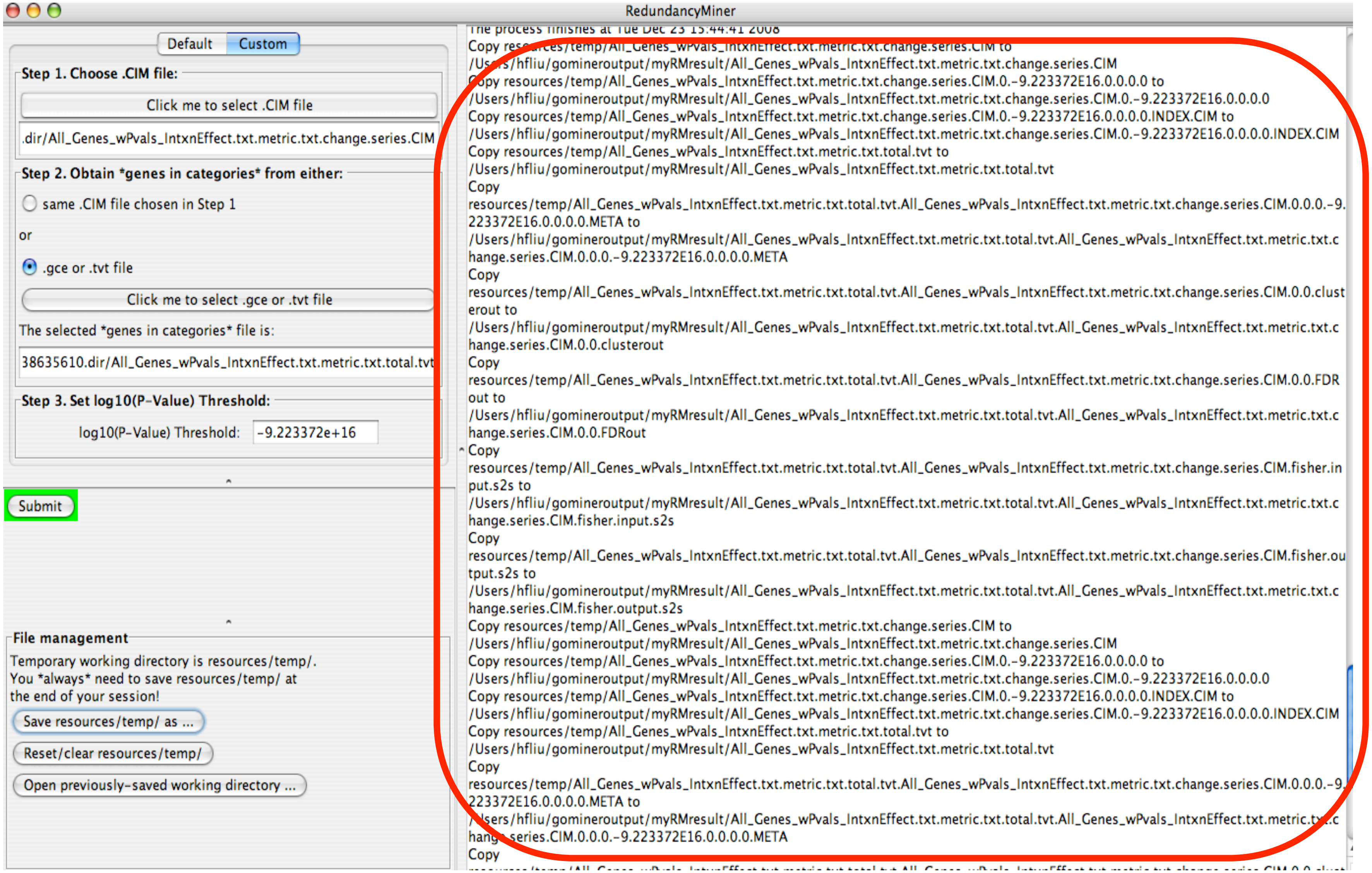
work1338635610 Friday, November 21, 2008 3:52 PM

File Format: All Files

```
0       -9.223372e+16
1       -9.223372e+16
3       -9.223372e+16
7       -9.223372e+16
15      -9.223372e+16
31      -9.223372e+16
63      -9.223372e+16
127     -2.254500e+02
255     -1.109700e+02
511     -3.832000e+01
```

```
Initializing clusters ....
Building clusters ....
Printing clusters ....
The process finishes at Tue Dec 23 15:44:36 2008
Collapsing CIM according to clustering results and storing in
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 ...
The process starts at Tue Dec 23 15:44:37 2008
The number of categories:
Before collapsing:      183
After collapsing:       162
Compression ratio: 1.13
```

File management: Save completed



Step 1. Choose .CIM file:

.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

● .gce or .tvt file

The selected *genes in categories* file is:

38635610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

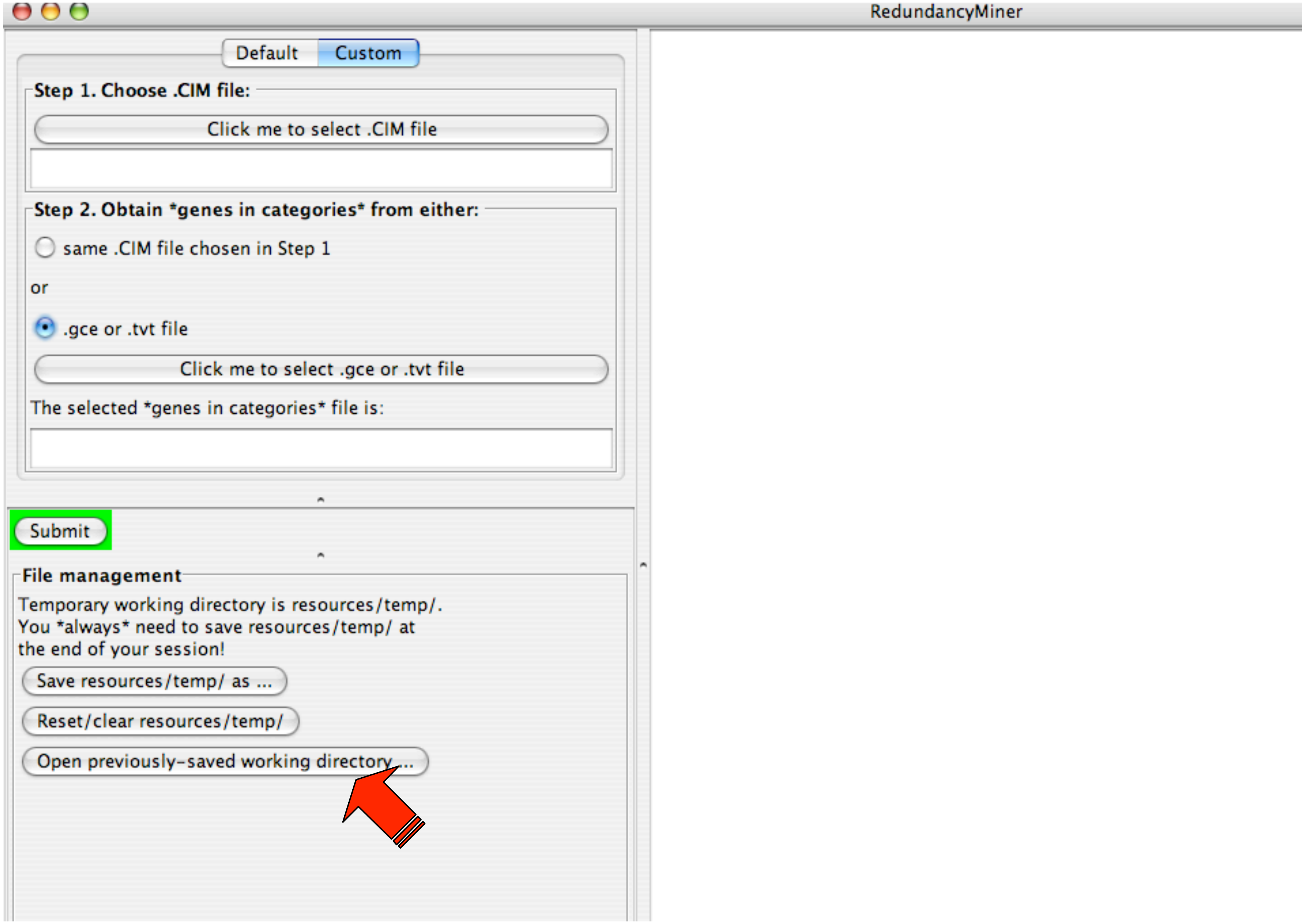
log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
The process finishes at Tue Dec 23 15:44:41 2008
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.0.-9.
223372E16.0.0.0.0.META to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.0.0.0.-9.223372E16.0.0.0.0.META
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.clust
erout to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.0.0.clusterout
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.FDR
out to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.0.0.FDRout
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.fisher.in
put.s2s to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.fisher.input.s2s
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.fisher.ou
tput.s2s to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.fisher.output.s2s
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM
Copy resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt
Copy
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.0.-9.
223372E16.0.0.0.0.META to
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.c
hange.series.CIM.0.0.0.-9.223372E16.0.0.0.0.META
Copy
```

File management: Retrieve the working directory (Step 1)



Step 1. Choose .CIM file:

Step 2. Obtain *genes in categories* from either:

○ same .CIM file chosen in Step 1

or

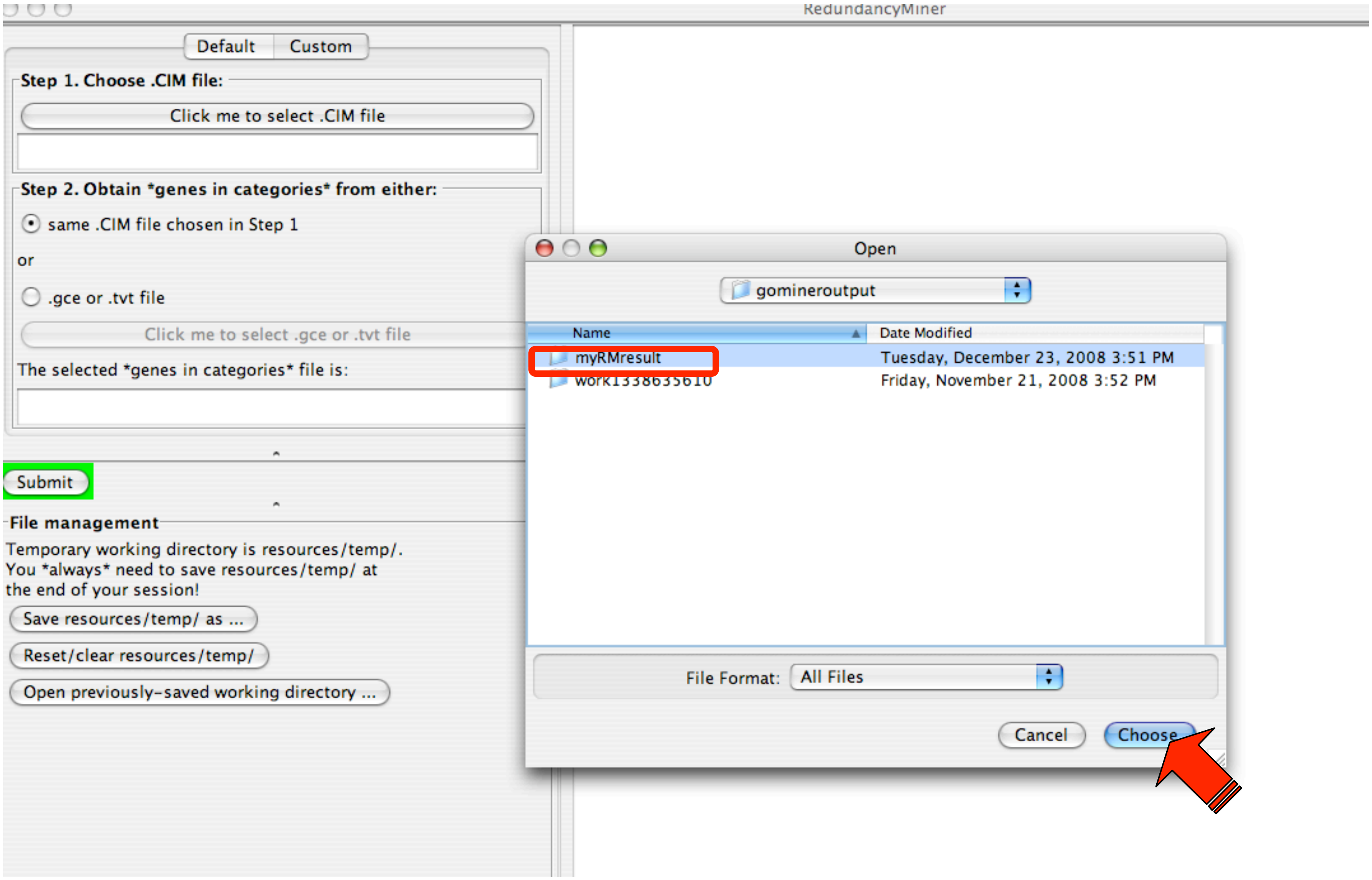
● .gce or .tvt file

The selected *genes in categories* file is:

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

File management: Retrieve the working directory (Step 2)



RedundancyMiner

Default | Custom

Step 1. Choose .CIM file:

Click me to select .CIM file

Step 2. Obtain *genes in categories* from either:

● same .CIM file chosen in Step 1

or

○ .gce or .tvt file

Click me to select .gce or .tvt file

The selected *genes in categories* file is:

Submit

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Save resources/temp/ as ...

Reset/clear resources/temp/

Open previously-saved working directory ...

Open

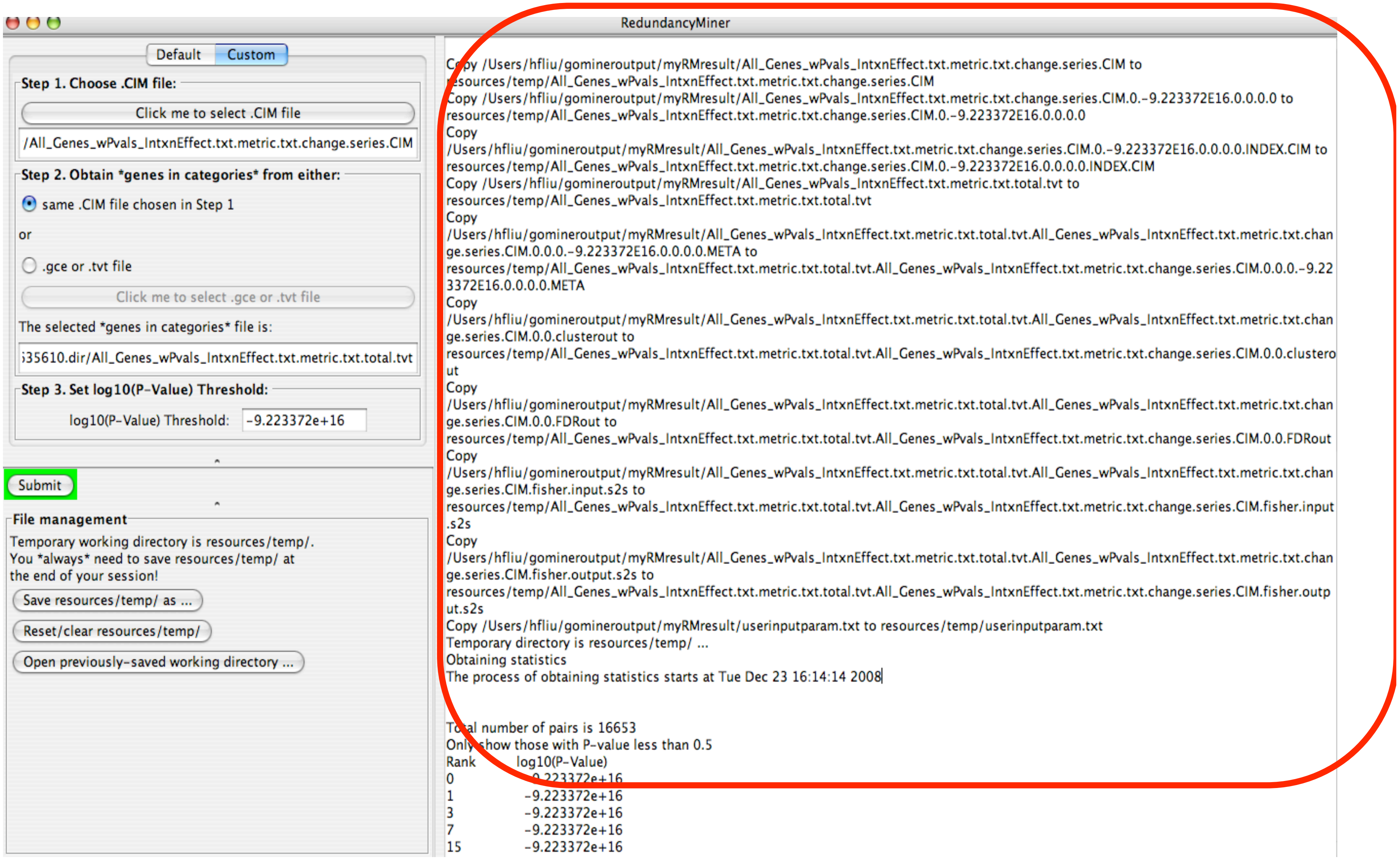
gomineroutput

Name	Date Modified
myRMresult	Tuesday, December 23, 2008 3:51 PM
work1338635610	Friday, November 21, 2008 3:52 PM

File Format: All Files

Cancel | Choose

File management: Retrieval completed



Step 1. Choose .CIM file:

/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM

Step 2. Obtain *genes in categories* from either:

● same .CIM file chosen in Step 1

or

○ .gce or .tvt file

The selected *genes in categories* file is:

535610.dir/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt

Step 3. Set log10(P-Value) Threshold:

log10(P-Value) Threshold: -9.223372e+16

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

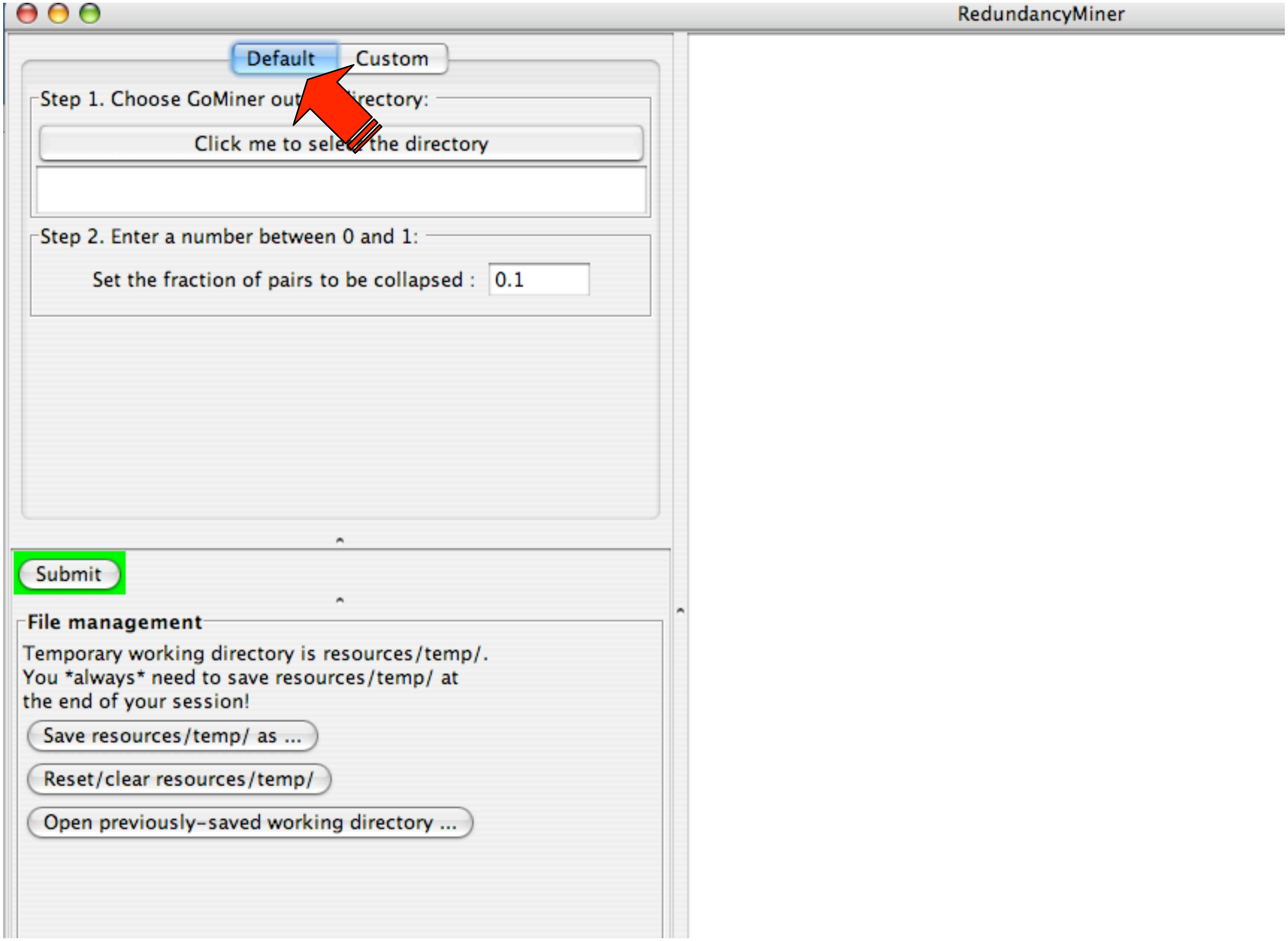
```
Copy /Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM
Copy /Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0 to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.-9.223372E16.0.0.0.0.INDEX.CIM
Copy /Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.chan
ge.series.CIM.0.0.0.-9.223372E16.0.0.0.0.META to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.0.-9.22
3372E16.0.0.0.0.META
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.chan
ge.series.CIM.0.0.clusterout to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.clustero
ut
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.chan
ge.series.CIM.0.0.FDRout to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.0.0.FDRout
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.chan
ge.series.CIM.fisher.input.s2s to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.fisher.input
.s2s
Copy
/Users/hfliu/gomineroutput/myRMresult/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.chan
ge.series.CIM.fisher.output.s2s to
resources/temp/All_Genes_wPvals_IntxnEffect.txt.metric.txt.total.tvt.All_Genes_wPvals_IntxnEffect.txt.metric.txt.change.series.CIM.fisher.outp
ut.s2s
Copy /Users/hfliu/gomineroutput/myRMresult/userinputparam.txt to resources/temp/userinputparam.txt
Temporary directory is resources/temp/ ...
Obtaining statistics
The process of obtaining statistics starts at Tue Dec 23 16:14:14 2008


Total number of pairs is 16653
Only show those with P-value less than 0.5
Rank        log10(P-Value)
0           -9.223372e+16
1           -9.223372e+16
3           -9.223372e+16
7           -9.223372e+16
15          -9.223372e+16
```

Default Mode

The default mode will generate results on the selected HTGM output directory.

- Select HTGM output directory
- Submit the job

Select Default mode



Step 1. Choose GoMiner out irectory:

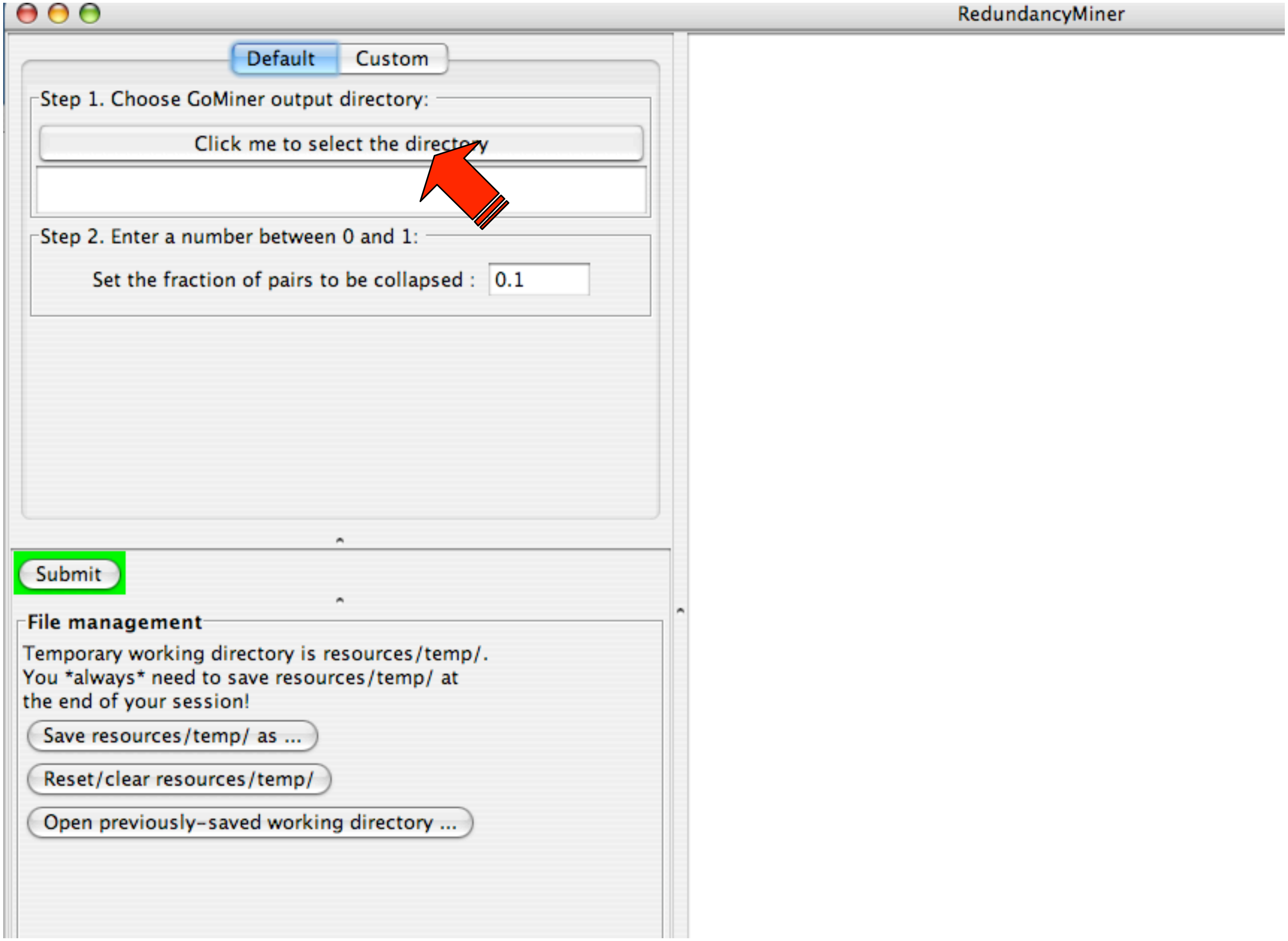
Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed : 0.1

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Select HTGM output directory (Step 1)



Step 1. Choose GoMiner output directory:

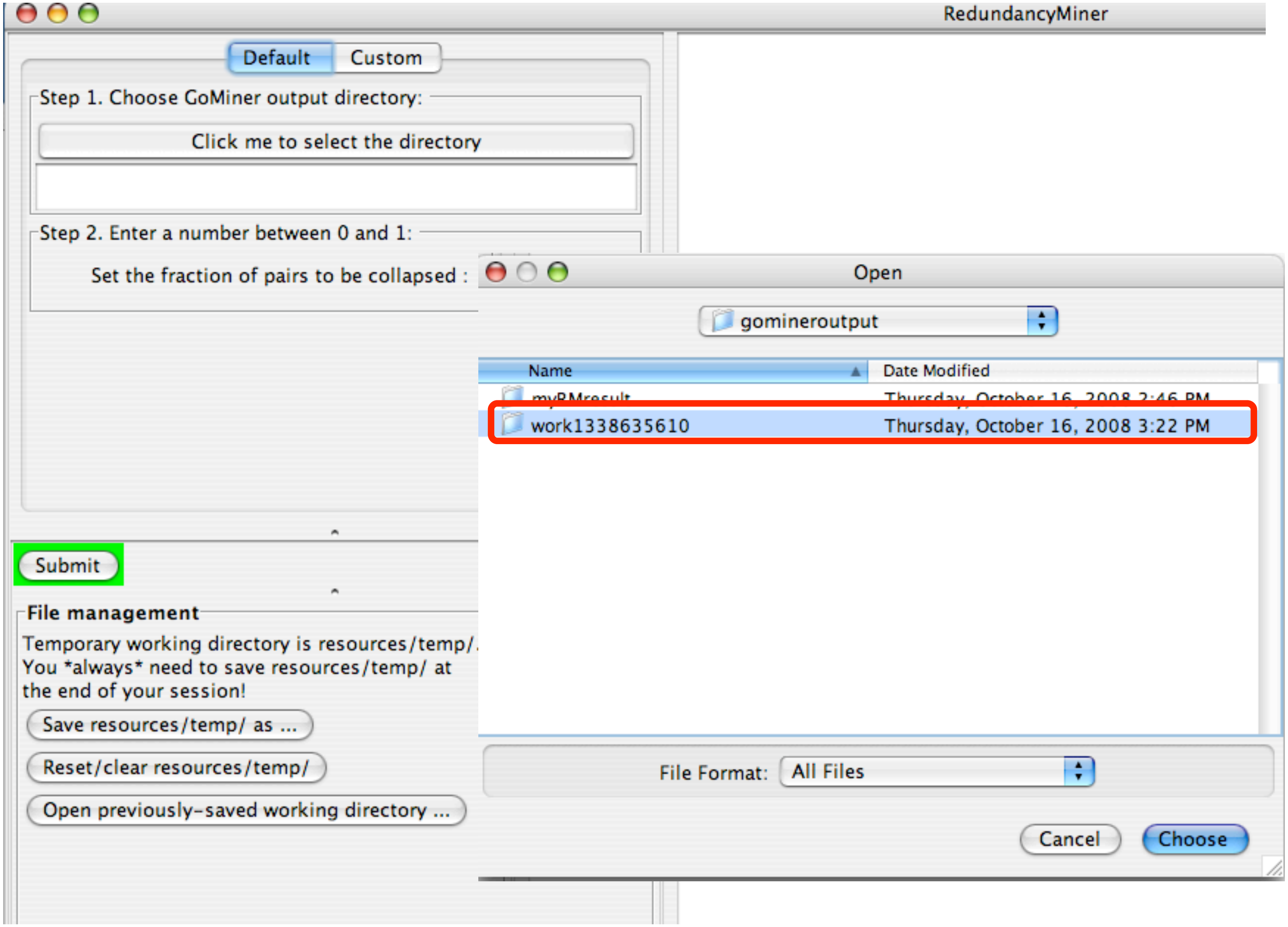
Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed : 0.1

File management

Temporary working directory is resources/temp/. You *always* need to save resources/temp/ at the end of your session!

Select HTGM output directory (Step 2)



Step 1. Choose GoMiner output directory:

Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed :

File management

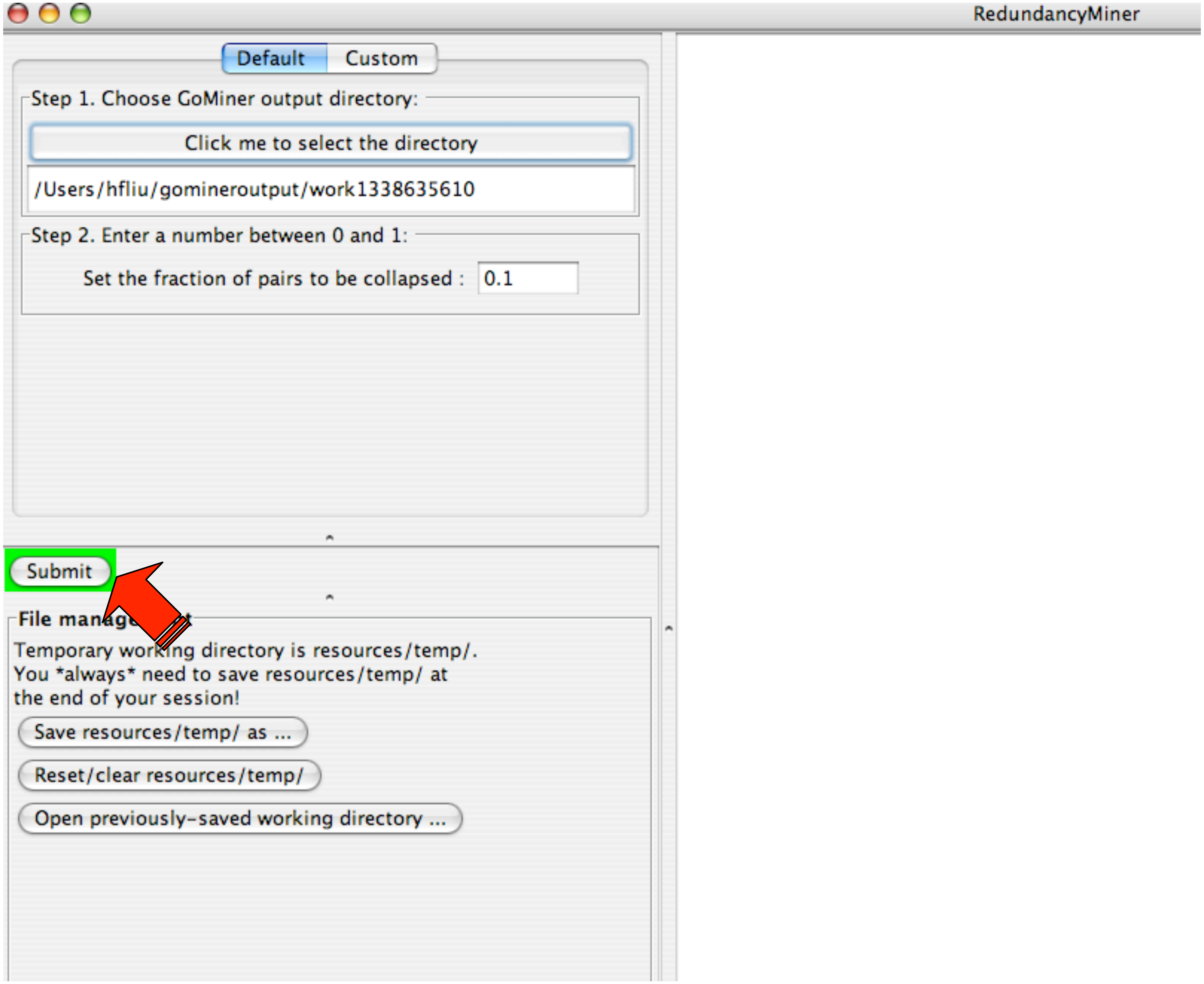
Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at the end of your session!

gomineroutput

Name	Date Modified
myRMresult	Thursday, October 16, 2008 2:46 PM
work1338635610	Thursday, October 16, 2008 3:22 PM

File Format: All Files

Submit the job (Step 3)



Step 1. Choose GoMiner output directory:

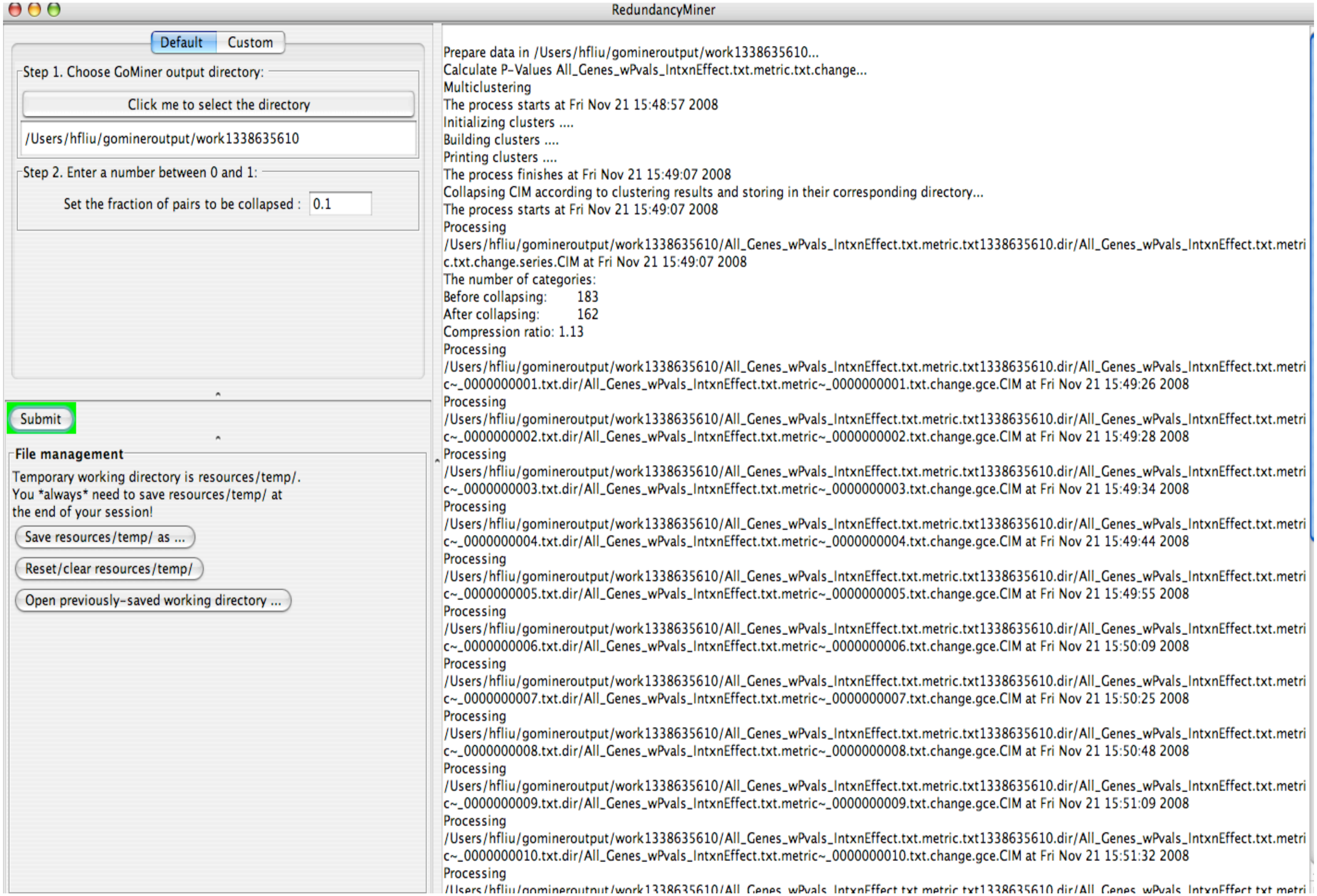
/Users/hfliu/gomineroutput/work1338635610

Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed : 0.1

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

Default mode completed



Step 1. Choose GoMiner output directory:

/Users/hfliu/gomineroutput/work1338635610

Step 2. Enter a number between 0 and 1:

Set the fraction of pairs to be collapsed : 0.1

File management

Temporary working directory is resources/temp/.
You *always* need to save resources/temp/ at
the end of your session!

```
Prepare data in /Users/hfliu/gomineroutput/work1338635610...
Calculate P-Values All_Genes_wPvals_IntxnEffect.txt.metric.txt.change...
Multiclustering
The process starts at Fri Nov 21 15:48:57 2008
Initializing clusters ....
Building clusters ....
Printing clusters ....
The process finishes at Fri Nov 21 15:49:07 2008
Collapsing CIM according to clustering results and storing in their corresponding directory...
The process starts at Fri Nov 21 15:49:07 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c.txt.change.series.CIM at Fri Nov 21 15:49:07 2008
The number of categories:
Before collapsing:      183
After collapsing:       162
Compression ratio: 1.13
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000001.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000001.txt.change.gce.CIM at Fri Nov 21 15:49:26 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000002.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000002.txt.change.gce.CIM at Fri Nov 21 15:49:28 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000003.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000003.txt.change.gce.CIM at Fri Nov 21 15:49:34 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000004.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000004.txt.change.gce.CIM at Fri Nov 21 15:49:44 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000005.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000005.txt.change.gce.CIM at Fri Nov 21 15:49:55 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000006.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000006.txt.change.gce.CIM at Fri Nov 21 15:50:09 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000007.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000007.txt.change.gce.CIM at Fri Nov 21 15:50:25 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000008.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000008.txt.change.gce.CIM at Fri Nov 21 15:50:48 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000009.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000009.txt.change.gce.CIM at Fri Nov 21 15:51:09 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
c~_0000000010.txt.dir/All_Genes_wPvals_IntxnEffect.txt.metric~_0000000010.txt.change.gce.CIM at Fri Nov 21 15:51:32 2008
Processing
/Users/hfliu/gomineroutput/work1338635610/All_Genes_wPvals_IntxnEffect.txt.metric.txt1338635610.dir/All_Genes_wPvals_IntxnEffect.txt.metri
```