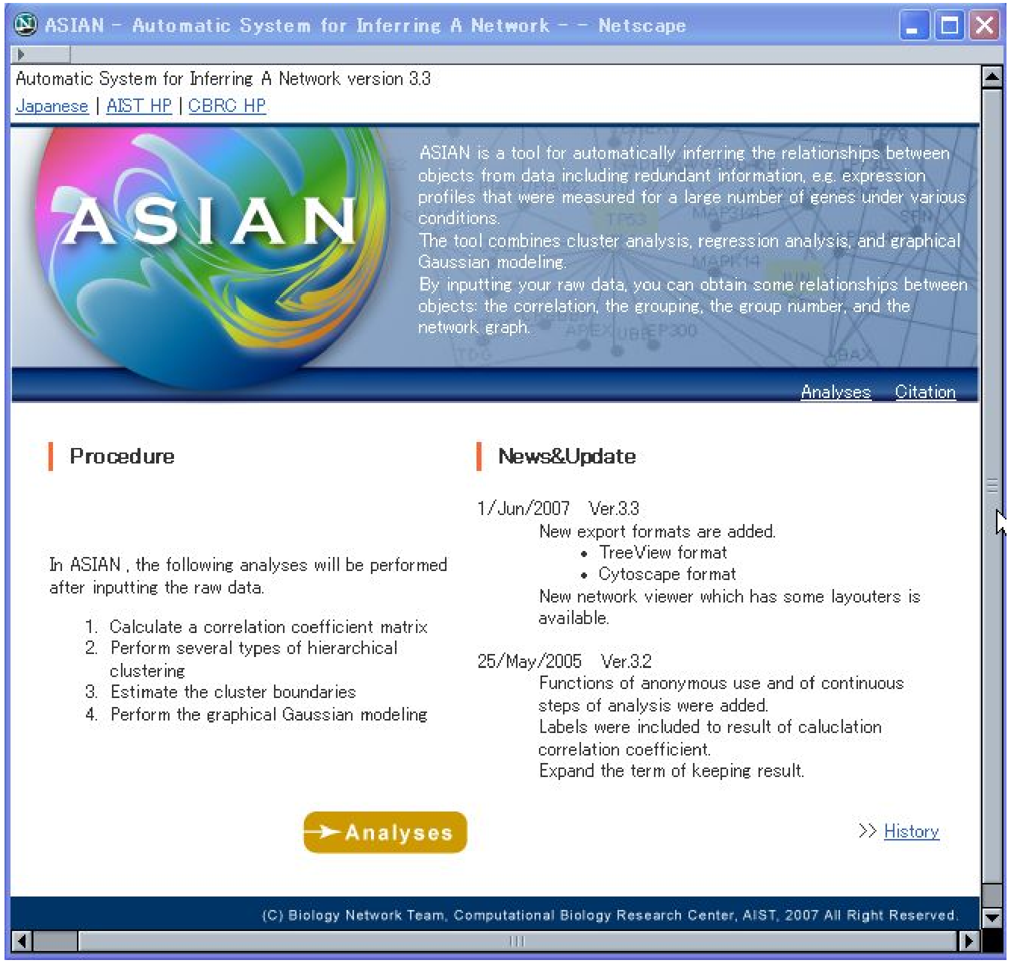
トランスクリプトーム解析基礎演習

http://eureka.cbrc.jp/asian/



Automatic System for Inferring A Network version 3.3

ASIAN is a tool for automatically inferring the relationships between objects from data including redundant information, e.g. expression profiles that were measured for a large number of genes under various conditions.
The tool combines cluster analysis, regression analysis, and graphical Gaussian modeling.
By inputting your raw data, you can obtain some relationships between objects: the correlation, the grouping, the group number, and the network graph.

Procedure

In ASIAN , the following analyses will be performed after inputting the raw data.

1. Calculate a correlation coefficient matrix
2. Perform several types of hierarchical clustering
3. Estimate the cluster boundaries
4. Perform the graphical Gaussian modeling

News&Update

1/Jun/2007 Ver.3.3
New export formats are added.
- TreeView format
- Cytoscape format

New network viewer which has some layouters is available.

25/May/2005 Ver.3.2
Functions of anonymous use and of continuous steps of analysis were added.
Labels were included to result of caluclation correlation coefficient.
Expand the term of keeping result.

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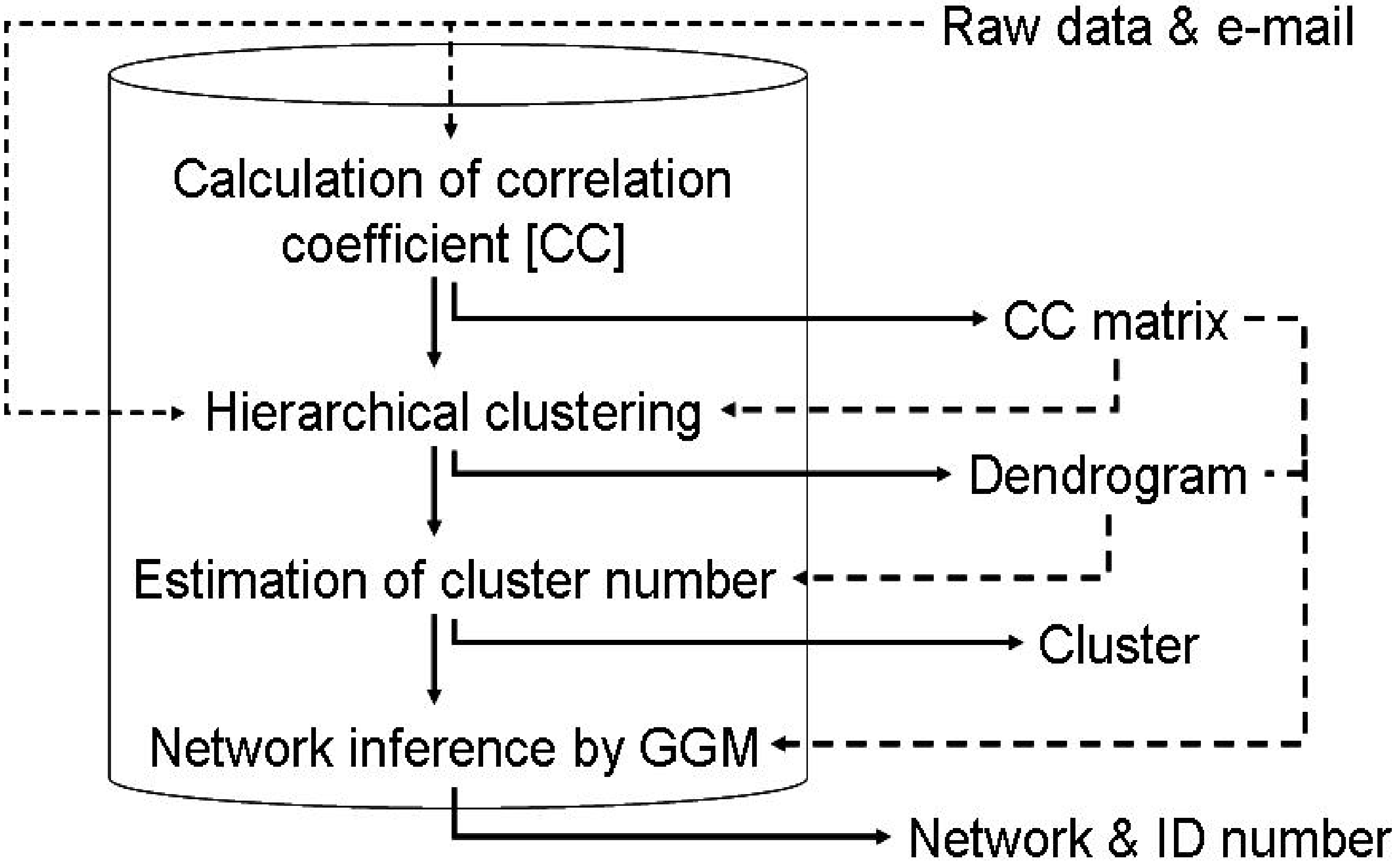
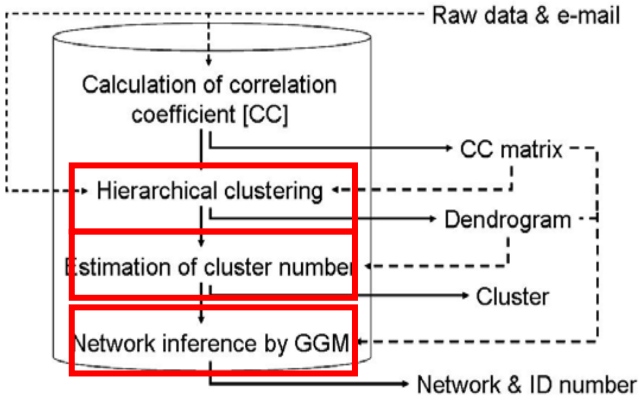
ASIAN: A Network Inference Web Server

Overview of ASIAN



The procedure of Application GGM to expression profiles



The genes are grouped into some clusters by hierarchical clustering

Estimation of the cluster boundaries

Calculation of the average expression profiles in each cluster

Calculation of the correlation coefficient matrix between the estimated clusters from average expression profiles in each cluster

Application of GGM (graphical Gaussian modeling) to the clusters

ASIAN フロントページ


Automatic System for Inferring A Network version 3.3

Japanese | AIST HP | CBRC HP

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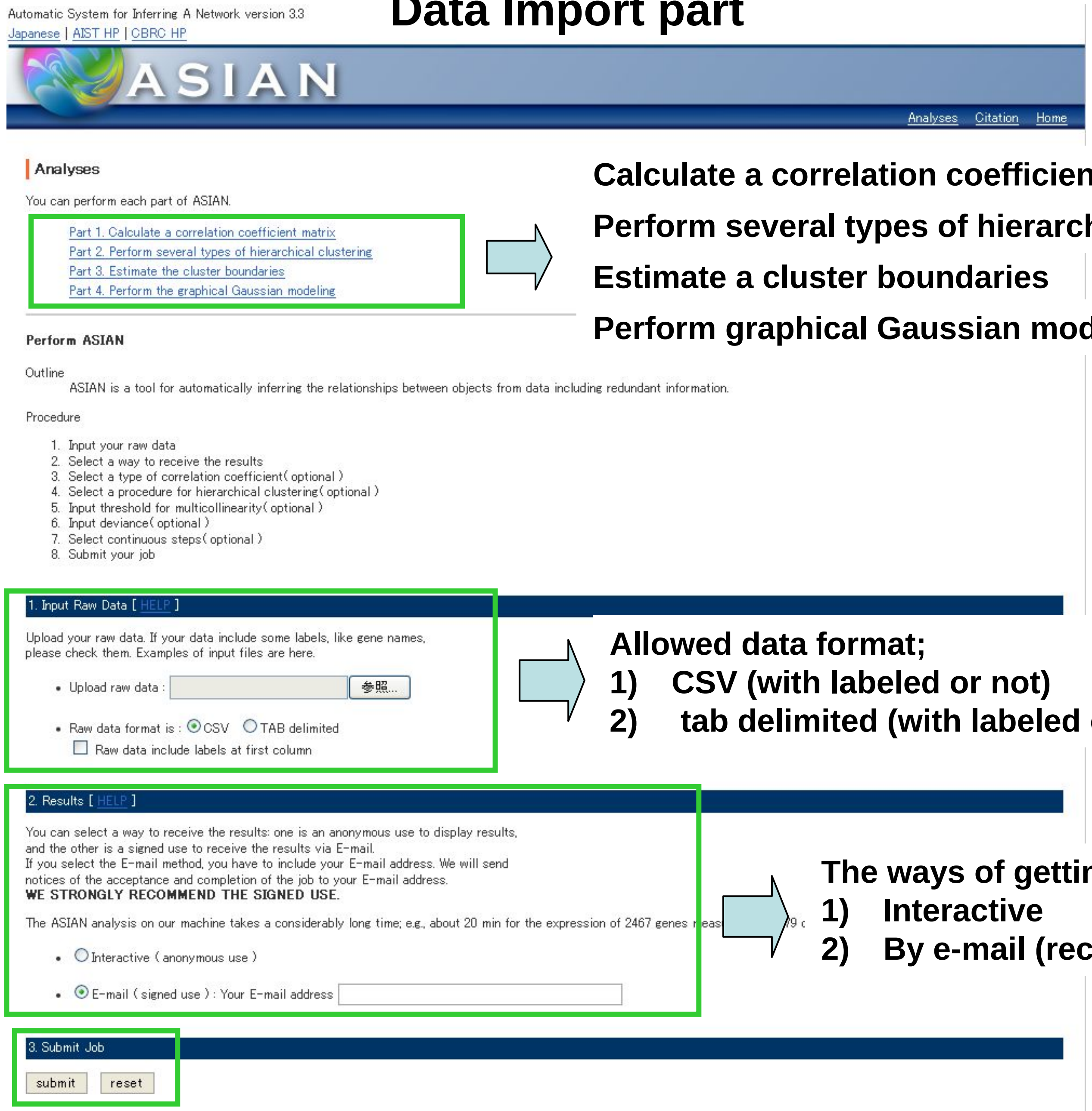
ASIANによってできる解析

お知らせ＆バージョン情報

解析ページへの実行ボタン

解析ページ(1/2)

Data Import part



Automatic System for Inferring A Network version 3.3
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Analyses

You can perform each part of ASIAN.

- Part 1. Calculate a correlation coefficient matrix
- Part 2. Perform several types of hierarchical clustering
- Part 3. Estimate the cluster boundaries
- Part 4. Perform the graphical Gaussian modeling

Perform ASIAN

Outline

ASIAN is a tool for automatically inferring the relationships between objects from data including redundant information.

Procedure

1. Input your raw data
2. Select a way to receive the results
3. Select a type of correlation coefficient(optional)
4. Select a procedure for hierarchical clustering(optional)
5. Input threshold for multicollinearity(optional)
6. Input deviance(optional)
7. Select continuous steps(optional)
8. Submit your job

1. Input Raw Data [HELP]

Upload your raw data. If your data include some labels, like gene names, please check them. Examples of input files are here.

- Upload raw data :
- Raw data format is : ● CSV ○ TAB delimited
  ☐ Raw data include labels at first column

2. Results [HELP]

You can select a way to receive the results: one is an anonymous use to display results, and the other is a signed use to receive the results via E-mail.
If you select the E-mail method, you have to include your E-mail address. We will send notices of the acceptance and completion of the job to your E-mail address.
WE STRONGLY RECOMMEND THE SIGNED USE.

The ASIAN analysis on our machine takes a considerably long time; e.g., about 20 min for the expression of 2467 genes

- ○ Interactive (anonymous use)
- ● E-mail (signed use) : Your E-mail address

3. Submit Job

Calculate a correlation coefficient matrix

Perform several types of hierarchical clustering

Estimate a cluster boundaries

Perform graphical Gaussian modeling

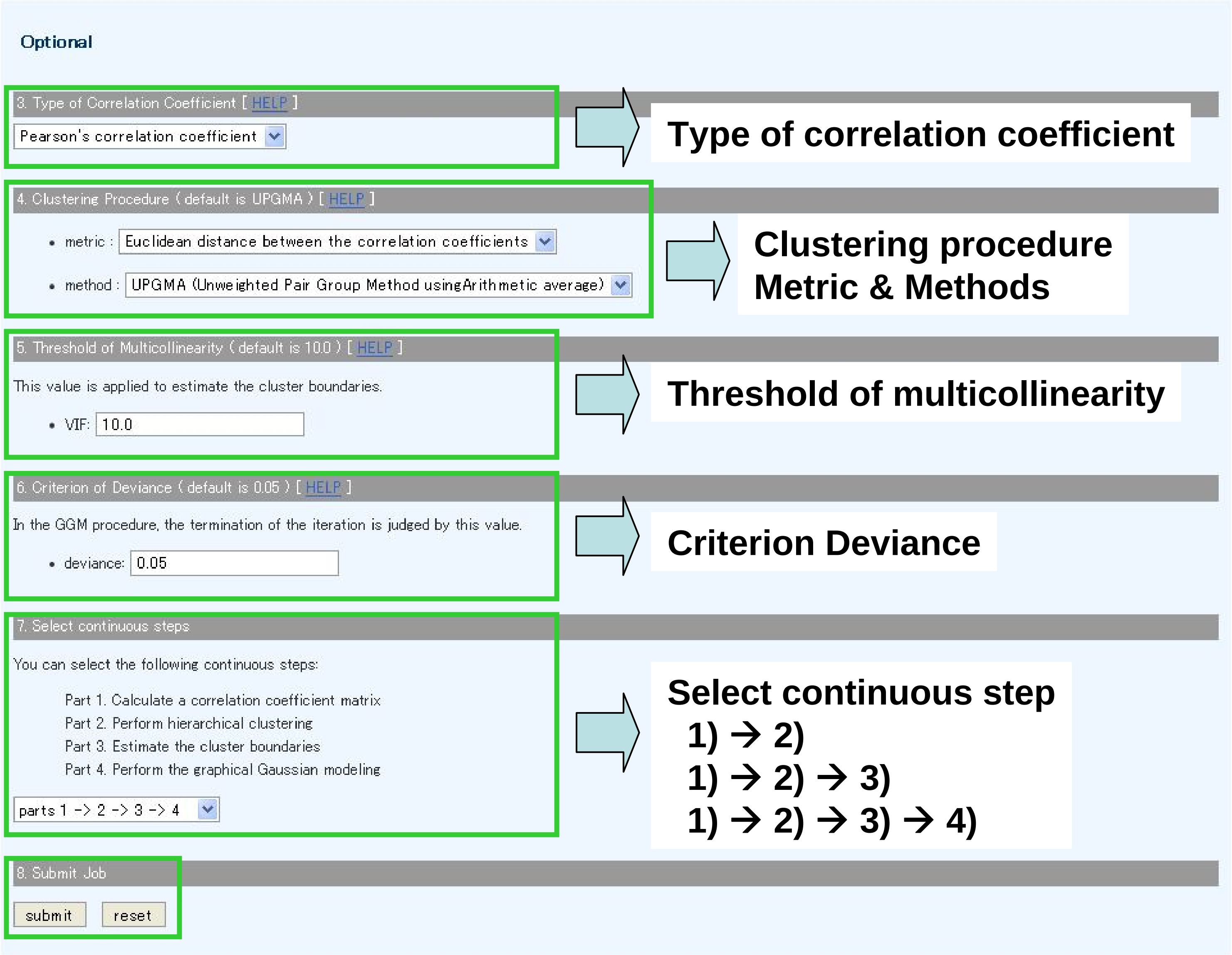
Allowed data format;

1) **CSV (with labeled or not)**
2) **tab delimited (with labeled or not)**

The ways of getting results

1) **Interactive**
2) **By e-mail (recommended)**

解析ページ(2/2)　Optional Part



Optional

3. Type of Correlation Coefficient [HELP]

Pearson's correlation coefficient

4. Clustering Procedure (default is UPGMA) [HELP]

- metric : Euclidean distance between the correlation coefficients
- method : UPGMA (Unweighted Pair Group Method usingArithmetic average)

5. Threshold of Multicollinearity (default is 10.0) [HELP]

This value is applied to estimate the cluster boundaries.

- VIF: 10.0

6. Criterion of Deviance (default is 0.05) [HELP]

In the GGM procedure, the termination of the iteration is judged by this value.

- deviance: 0.05

7. Select continuous steps

You can select the following continuous steps:

Part 1. Calculate a correlation coefficient matrix
Part 2. Perform hierarchical clustering
Part 3. Estimate the cluster boundaries
Part 4. Perform the graphical Gaussian modeling

parts 1 -> 2 -> 3 -> 4

8. Submit Job

Type of correlation coefficient

Clustering procedure
Metric & Methods

Threshold of multicollinearity

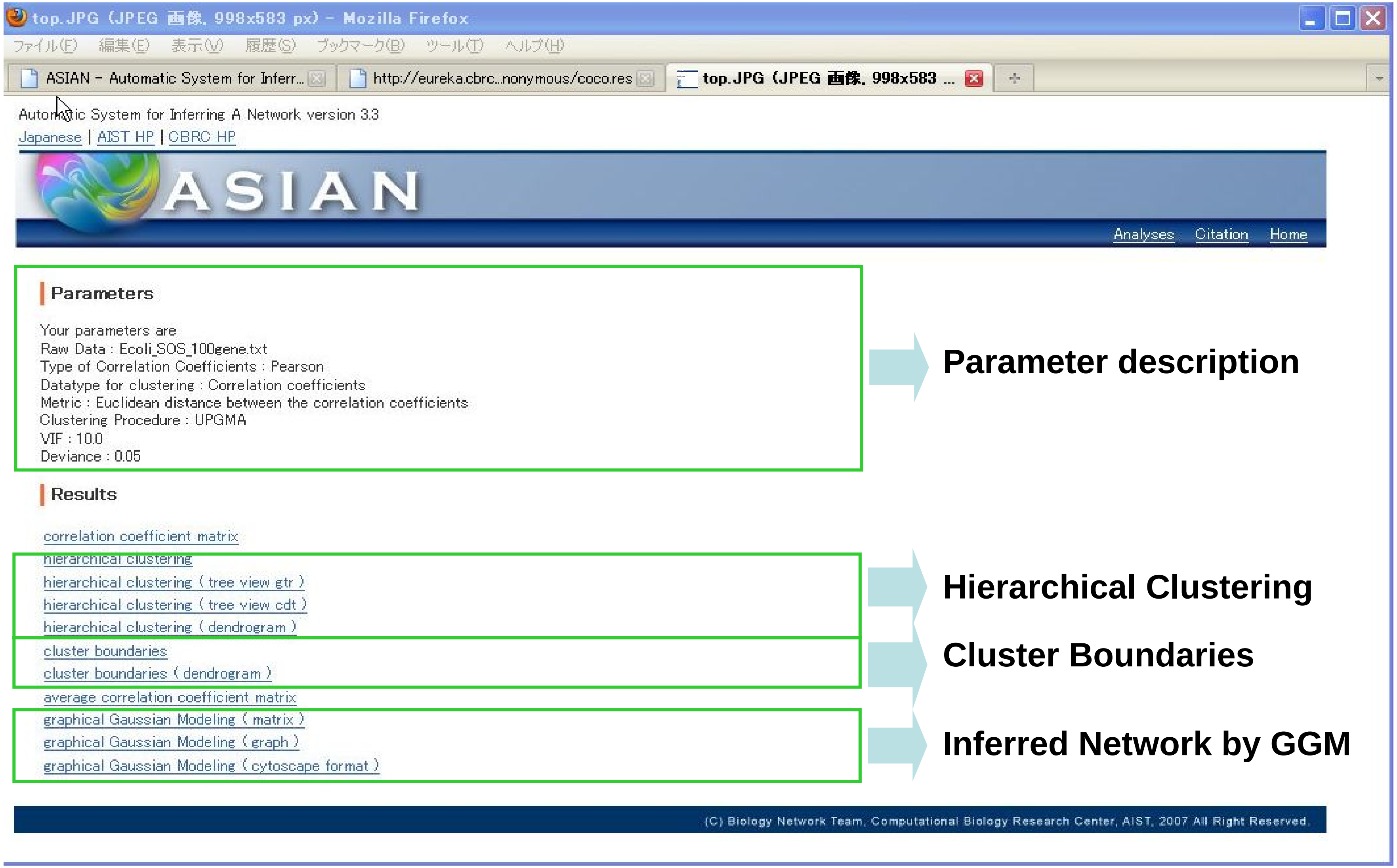
Criterion Deviance

Select continuous step
1) → 2)
1) → 2) → 3)
1) → 2) → 3) → 4)

ASIANのパラメータ

Parameter		Default	Option
Types of Correlation Coefficients		Pearson's CC	Eisen's CC Kendall's Rank CC
Clustering Procedure	Metric	Euclidean distance between CC	Euclidean distance between the raw values Eisen's distance
	Hierarchical Clustering procedure	UPGMA	Single Linkage WPGMA Complete Linkage WPGMC UPGMC Ward's Method
Threshold of Multicollinearity		10.0	numerical value (< Multicollinearity error)
Criterion of Deviance		0.05	numerical value (<1.0)

解析結果 トップページ



Automatic System for Inferring A Network version 3.3

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Parameters

Your parameters are
Raw Data : Ecoli_SOS_100gene.txt
Type of Correlation Coefficients : Pearson
Datatype for clustering : Correlation coefficients
Metric : Euclidean distance between the correlation coefficients
Clustering Procedure : UPGMA
VIF : 10.0
Deviance : 0.05

Results

correlation coefficient matrix
hierarchical clustering
hierarchical clustering (tree view gtr)
hierarchical clustering (tree view cdt)
hierarchical clustering (dendrogram)
cluster boundaries
cluster boundaries (dendrogram)
average correlation coefficient matrix
graphical Gaussian Modeling (matrix)
graphical Gaussian Modeling (graph)
graphical Gaussian Modeling (cytoscape format)

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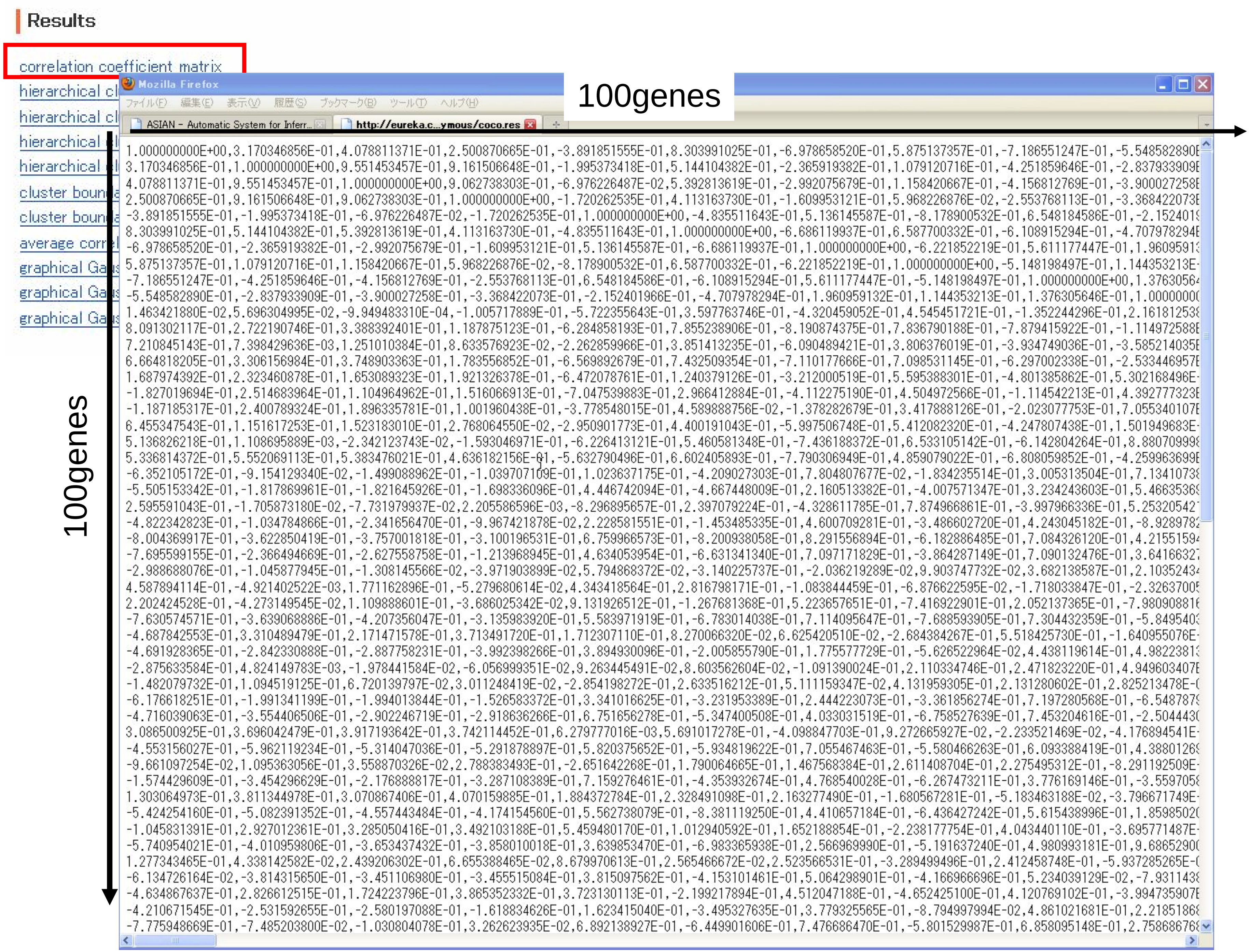
Parameter description

Hierarchical Clustering

Cluster Boundaries

Inferred Network by GGM

You are allowed to access the result page by enter your e-mail address and calculation ID number



Results

correlation coefficient matrix
hierarchical cl
hierarchical cl
hierarchical cl
hierarchical cl
cluster boun
cluster boun
average corr
graphical Ga
graphical Ga
graphical Ga

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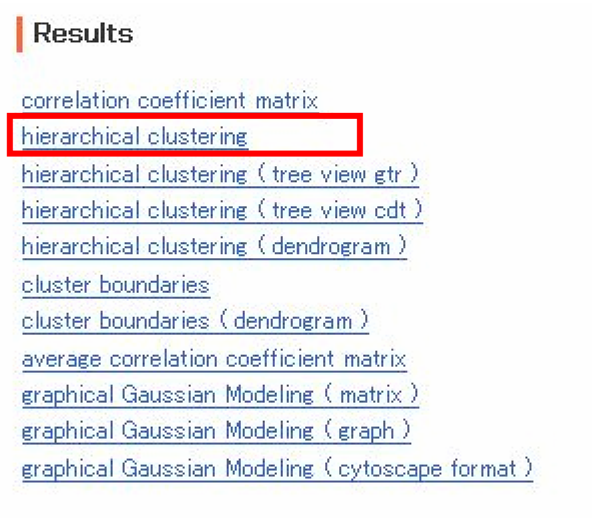
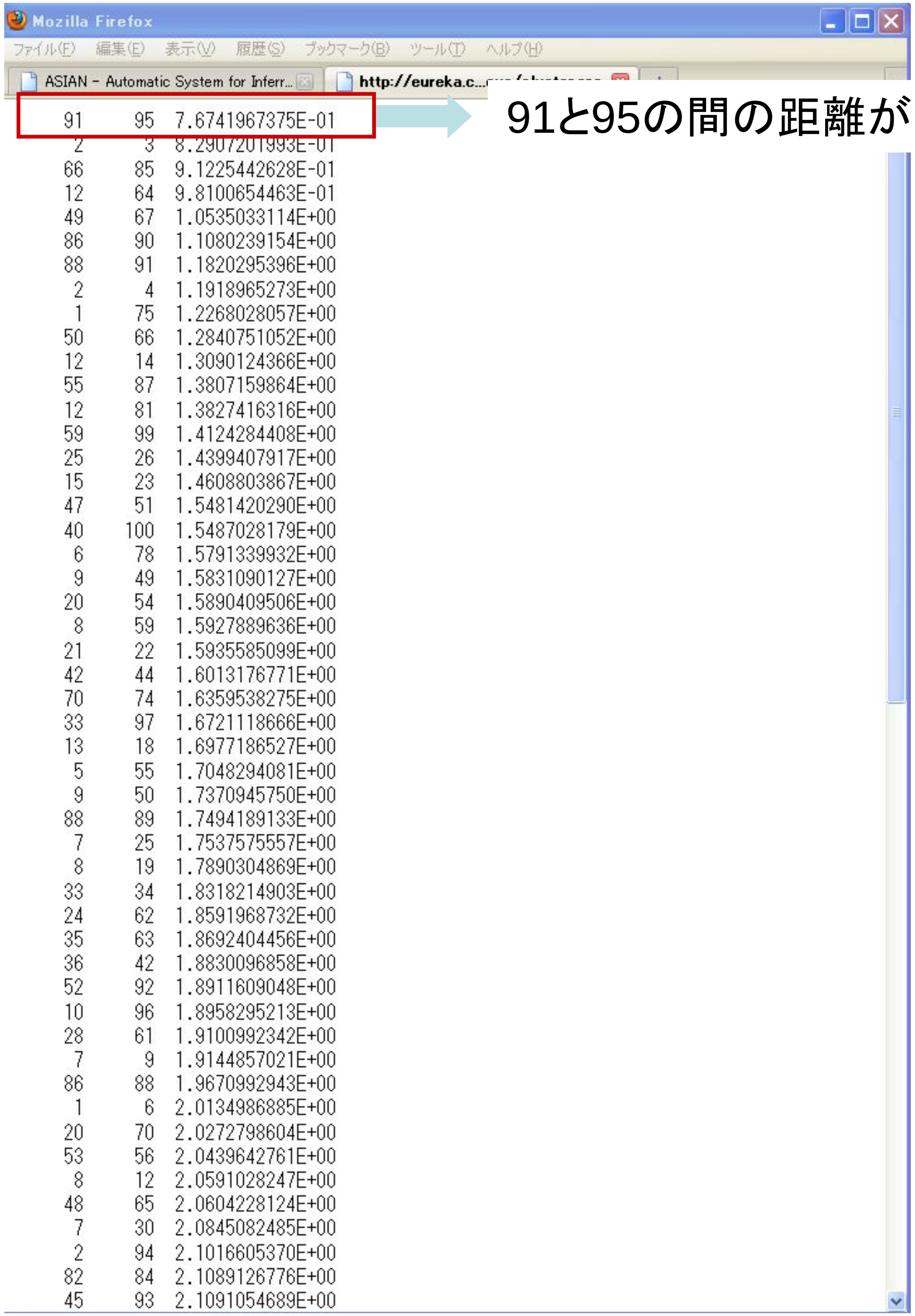


Results

- correlation coefficient matrix
- hierarchical clustering
- hierarchical clustering (tree view gtr)
- hierarchical clustering (tree view cdt)
- hierarchical clustering (dendrogram)
- cluster boundaries
- cluster boundaries (dendrogram)
- average correlation coefficient matrix
- graphical Gaussian Modeling (matrix)
- graphical Gaussian Modeling (graph)
- graphical Gaussian Modeling (cytoscape format)



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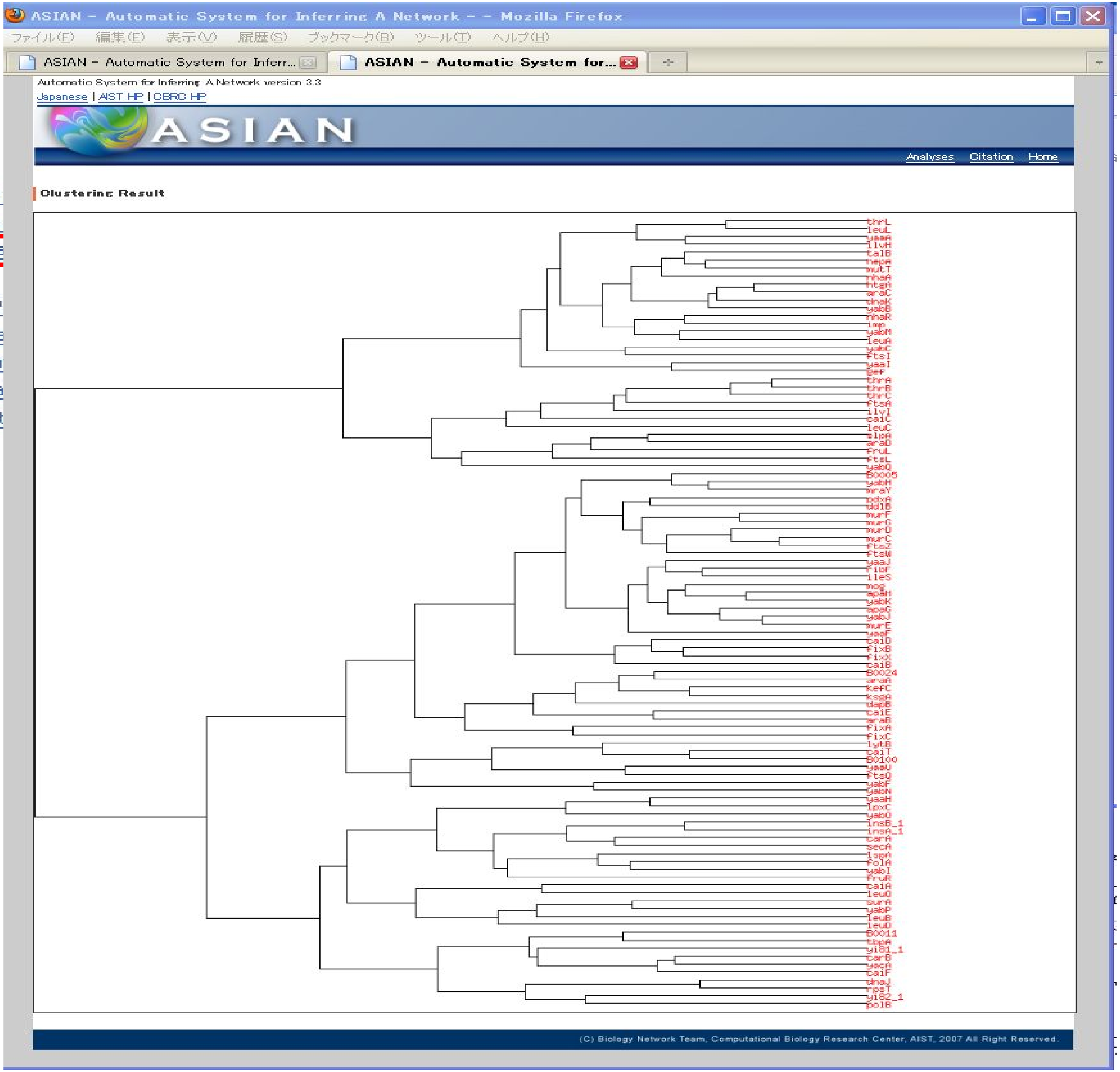
  55    87   1.3807159864E+00
  12    81   1.3827416316E+00
  59    99   1.4124284408E+00
  25    26   1.4399407917E+00
  15    23   1.4608803867E+00
  47    51   1.5481420290E+00
  40   100   1.5487028179E+00
   6    78   1.5791339932E+00
   9    49   1.5831090127E+00
  20    54   1.5890409506E+00
   8    59   1.5927889636E+00
  21    22   1.5935585099E+00
  42    44   1.6013176771E+00
  70    74   1.6359538275E+00
  33    97   1.6721118666E+00
  13    18   1.6977186527E+00
   5    55   1.7048294081E+00
   9    50   1.7370945750E+00
  88    89   1.7494189133E+00
   7    25   1.7537575557E+00
   8    19   1.7890304869E+00
  33    34   1.8318214903E+00
  24    62   1.8591968732E+00
  35    63   1.8692404456E+00
  36    42   1.8830096858E+00
  52    92   1.8911609048E+00
  10    96   1.8958295213E+00
  28    61   1.9100992342E+00
   7     9   1.9144857021E+00
  86    88   1.9670992943E+00
   1     6   2.0134986885E+00
  20    70   2.0272798604E+00
  53    56   2.0439642761E+00
   8    12   2.0591028247E+00
  48    65   2.0604228124E+00
   7    30   2.0845082485E+00
   2    94   2.1016605370E+00
  82    84   2.1089126776E+00
  45    93   2.1091054689E+00
```

91と95の間の距離が一番小さい

Results

correlation coefficient matrix
hierarchical clustering
hierarchical clustering (tree view
hierarchical clustering (tree view
hierarchical clustering (dendrogra
cluster boundaries
cluster boundaries (dendrogram)
average correlation coefficient ma
graphical Gaussian Modeling (ma
graphical Gaussian Modeling (gra
graphical Gaussian Modeling (cyt



Automatic System for Inferring A Network version 3.3

Clustering Result

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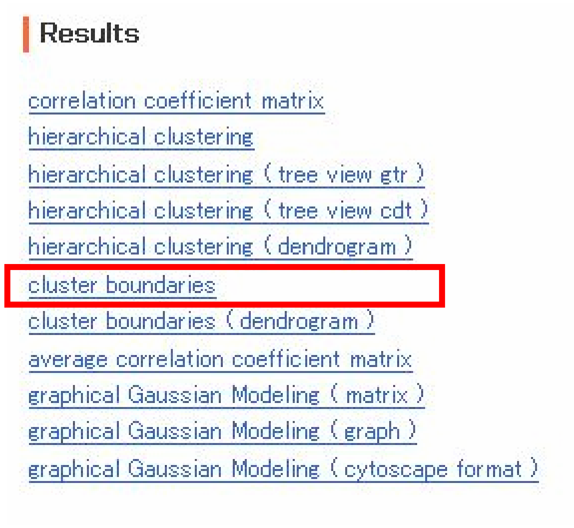
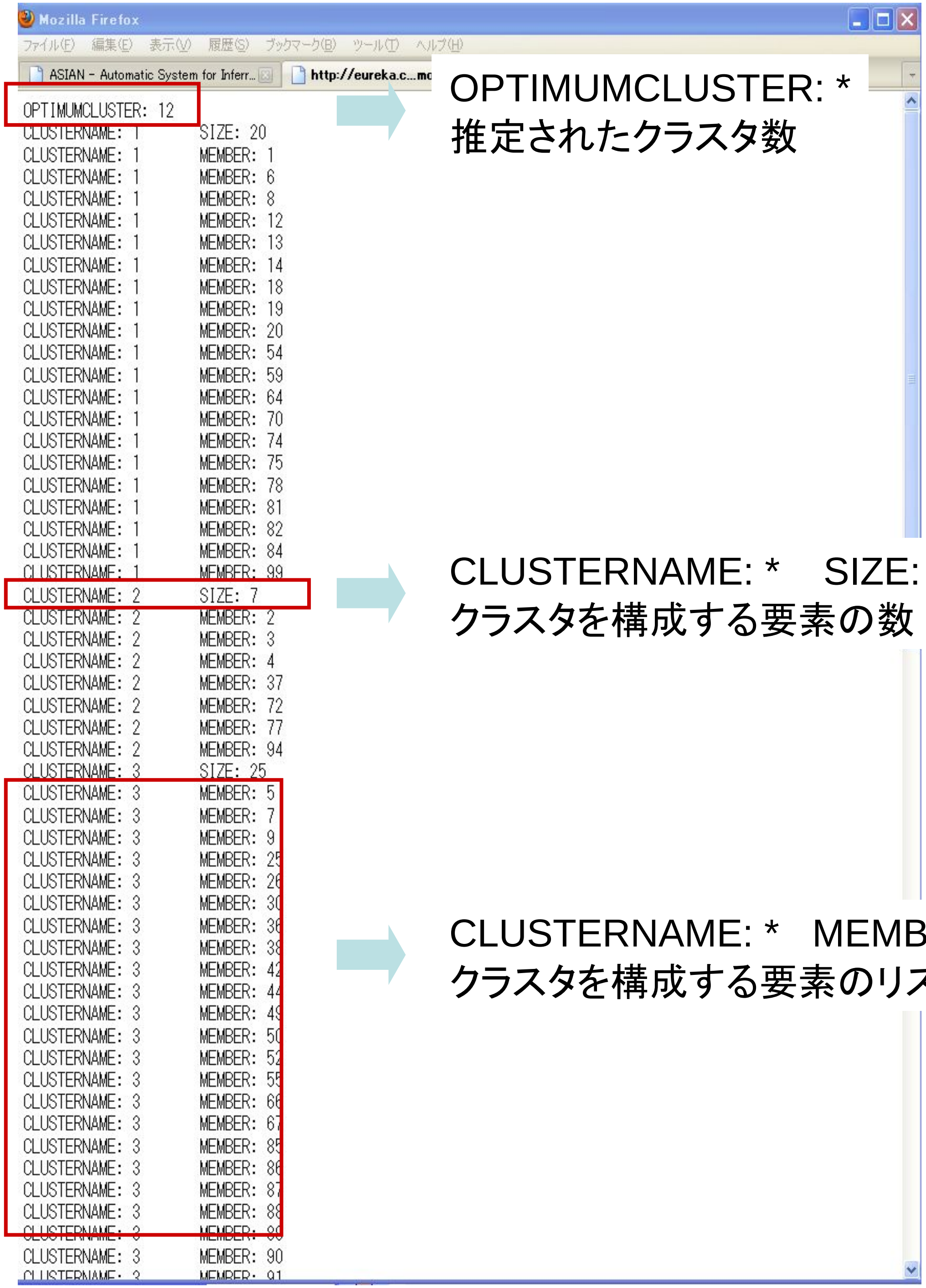


Results

- correlation coefficient matrix
- hierarchical clustering
- hierarchical clustering (tree view gtr)
- hierarchical clustering (tree view cdt)
- hierarchical clustering (dendrogram)
- cluster boundaries
- cluster boundaries (dendrogram)
- average correlation coefficient matrix
- graphical Gaussian Modeling (matrix)
- graphical Gaussian Modeling (graph)
- graphical Gaussian Modeling (cytoscape format)

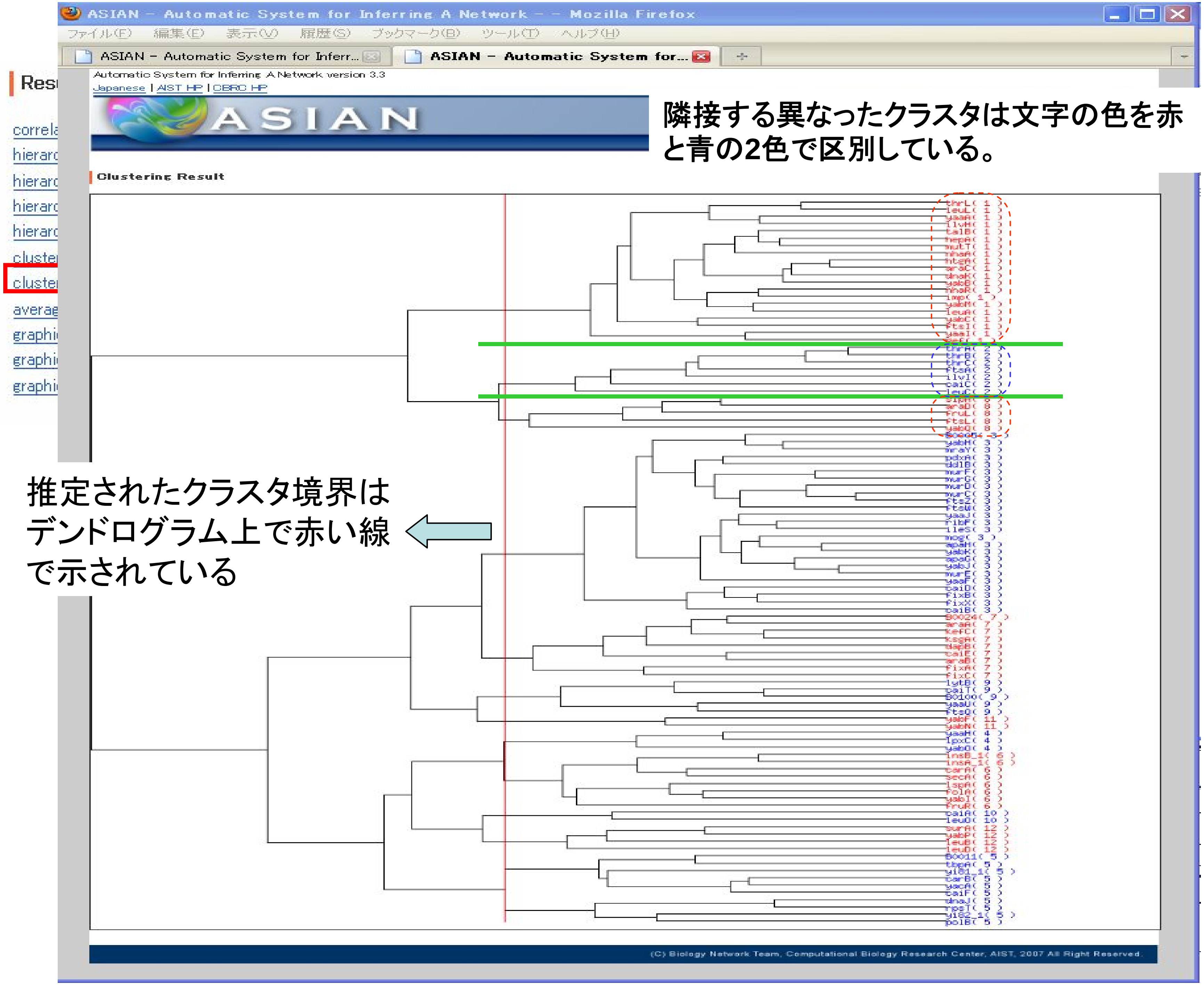


```
OPTIMUMCLUSTER: 12
CLUSTERNAME: 1        SIZE: 20
CLUSTERNAME: 1        MEMBER: 1
CLUSTERNAME: 1        MEMBER: 6
CLUSTERNAME: 1        MEMBER: 8
CLUSTERNAME: 1        MEMBER: 12
CLUSTERNAME: 1        MEMBER: 13
CLUSTERNAME: 1        MEMBER: 14
CLUSTERNAME: 1        MEMBER: 18
CLUSTERNAME: 1        MEMBER: 19
CLUSTERNAME: 1        MEMBER: 20
CLUSTERNAME: 1        MEMBER: 54
CLUSTERNAME: 1        MEMBER: 59
CLUSTERNAME: 1        MEMBER: 64
CLUSTERNAME: 1        MEMBER: 70
CLUSTERNAME: 1        MEMBER: 74
CLUSTERNAME: 1        MEMBER: 75
CLUSTERNAME: 1        MEMBER: 78
CLUSTERNAME: 1        MEMBER: 81
CLUSTERNAME: 1        MEMBER: 82
CLUSTERNAME: 1        MEMBER: 84
CLUSTERNAME: 1        MEMBER: 99
CLUSTERNAME: 2        SIZE: 7
CLUSTERNAME: 2        MEMBER: 2
CLUSTERNAME: 2        MEMBER: 3
CLUSTERNAME: 2        MEMBER: 4
CLUSTERNAME: 2        MEMBER: 37
CLUSTERNAME: 2        MEMBER: 72
CLUSTERNAME: 2        MEMBER: 77
CLUSTERNAME: 2        MEMBER: 94
CLUSTERNAME: 3        SIZE: 25
CLUSTERNAME: 3        MEMBER: 5
CLUSTERNAME: 3        MEMBER: 7
CLUSTERNAME: 3        MEMBER: 9
CLUSTERNAME: 3        MEMBER: 25
CLUSTERNAME: 3        MEMBER: 26
CLUSTERNAME: 3        MEMBER: 30
CLUSTERNAME: 3        MEMBER: 36
CLUSTERNAME: 3        MEMBER: 38
CLUSTERNAME: 3        MEMBER: 42
CLUSTERNAME: 3        MEMBER: 44
CLUSTERNAME: 3        MEMBER: 49
CLUSTERNAME: 3        MEMBER: 50
CLUSTERNAME: 3        MEMBER: 52
CLUSTERNAME: 3        MEMBER: 55
CLUSTERNAME: 3        MEMBER: 66
CLUSTERNAME: 3        MEMBER: 67
CLUSTERNAME: 3        MEMBER: 85
CLUSTERNAME: 3        MEMBER: 86
CLUSTERNAME: 3        MEMBER: 87
CLUSTERNAME: 3        MEMBER: 88
CLUSTERNAME: 3        MEMBER: 89
CLUSTERNAME: 3        MEMBER: 90
CLUSTERNAME: 3        MEMBER: 91
```

OPTIMUMCLUSTER: *
推定されたクラスタ数

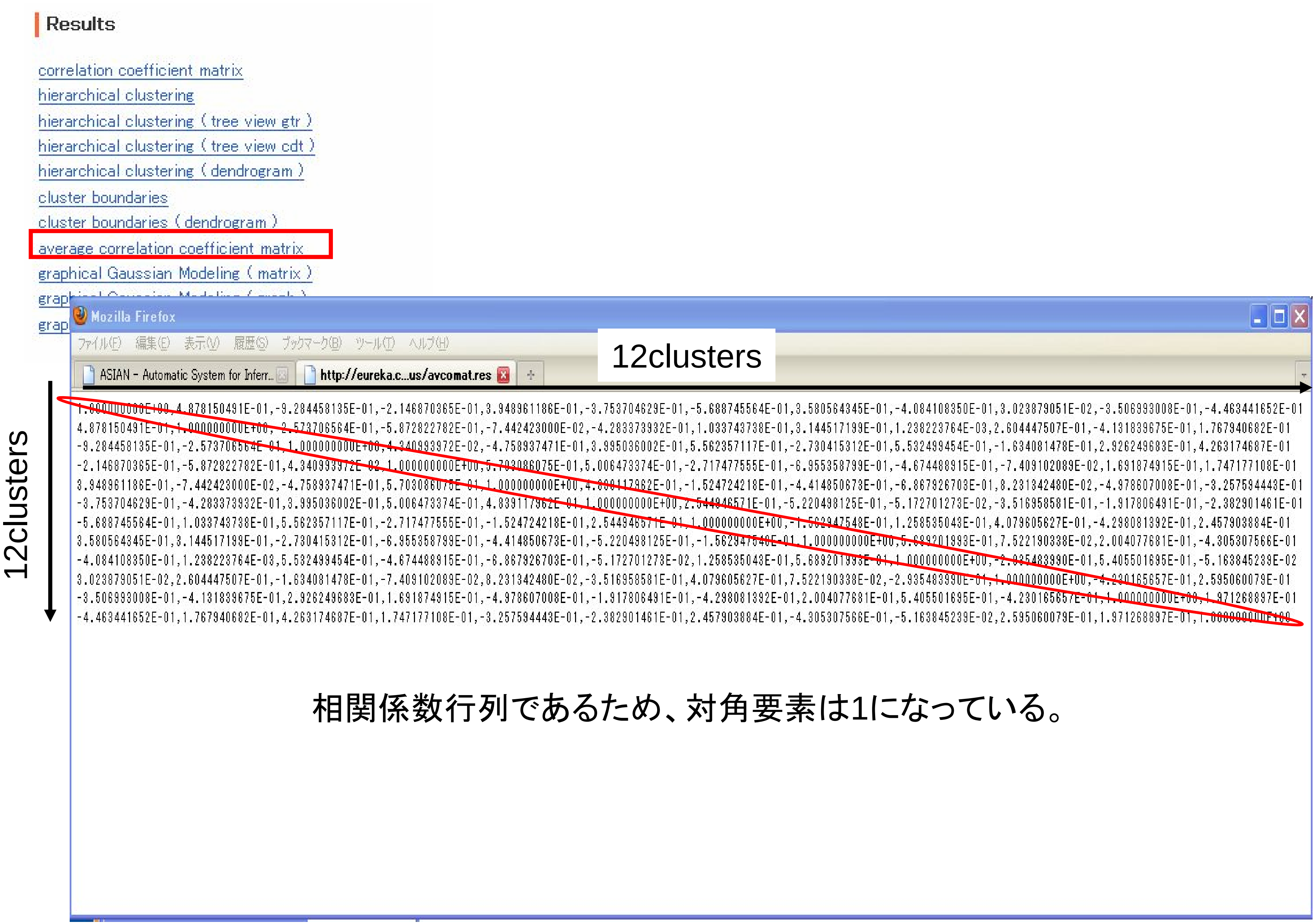
CLUSTERNAME: *　SIZE: **
クラスタを構成する要素の数

CLUSTERNAME: *　MEMBER: **
クラスタを構成する要素のリスト



隣接する異なったクラスタは文字の色を赤と青の2色で区別している。

推定されたクラスタ境界はデンドログラム上で赤い線で示されている

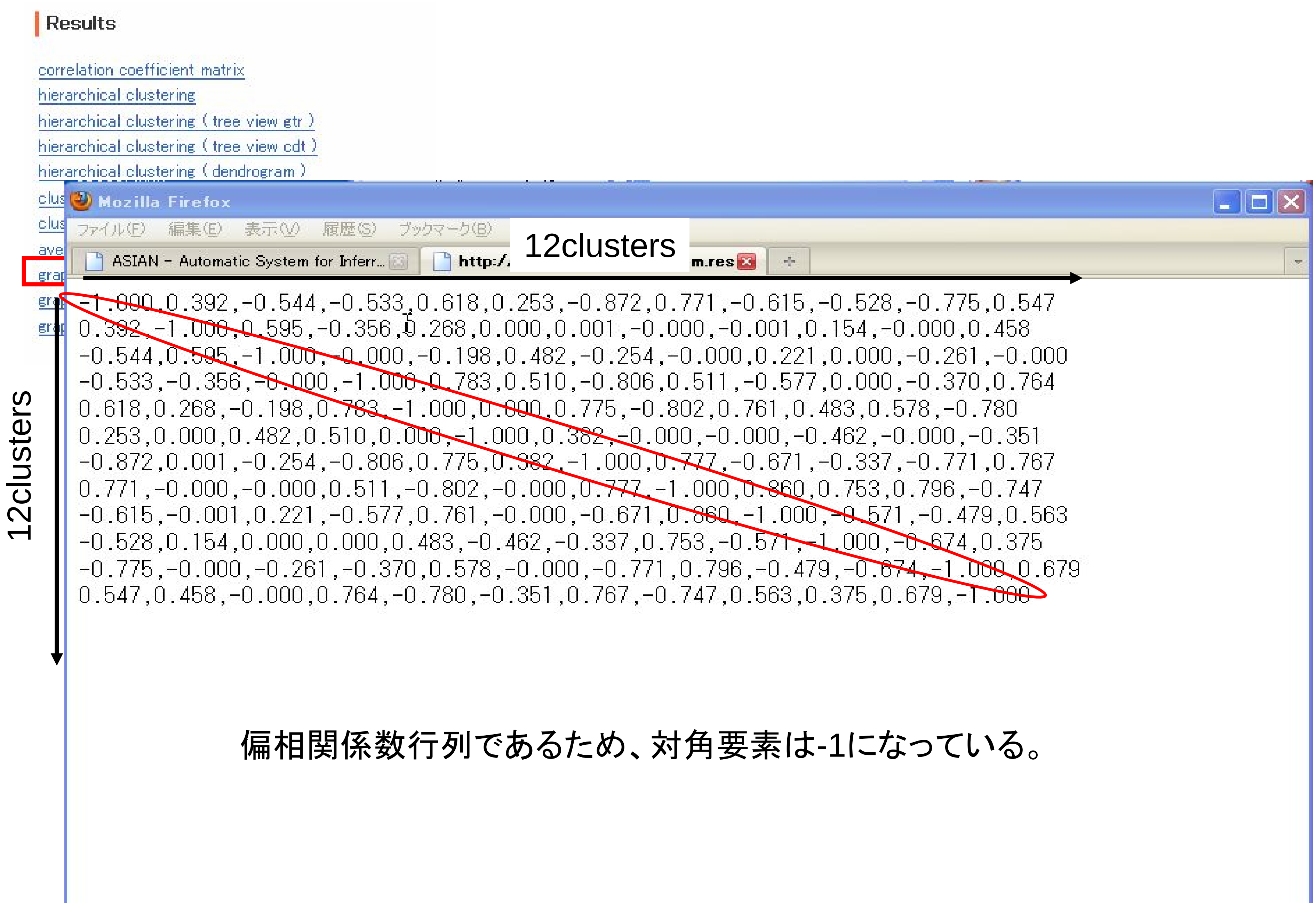


Results

- correlation coefficient matrix
- hierarchical clustering
- hierarchical clustering (tree view gtr)
- hierarchical clustering (tree view cdt)
- hierarchical clustering (dendrogram)
- cluster boundaries
- cluster boundaries (dendrogram)
- average correlation coefficient matrix
- graphical Gaussian Modeling (matrix)
- grap
- grap

```
1.000000000E+00,4.878150491E-01,-9.284458135E-01,-2.146870365E-01,3.948961186E-01,-3.753704629E-01,-5.688745564E-01,3.580564345E-01,-4.084108350E-01,3.023879051E-02,-3.506993008E-01,-4.463441652E-01
4.878150491E-01,1.000000000E+00,-2.573706564E-01,-5.872822782E-01,-7.442423000E-02,-4.283373932E-01,1.033743738E-01,3.144517199E-01,1.238223764E-03,2.604447507E-01,-4.131839675E-01,1.767940682E-01
-9.284458135E-01,-2.573706564E-01,1.000000000E+00,4.340993972E-02,-4.758937471E-01,3.995036002E-01,5.562357117E-01,-2.730415312E-01,5.532499454E-01,-1.634081478E-01,2.926249683E-01,4.263174687E-01
-2.146870365E-01,-5.872822782E-01,4.340993972E-02,1.000000000E+00,5.703086075E-01,5.006473374E-01,-2.717477555E-01,-6.955358799E-01,-4.674488915E-01,-7.409102089E-02,1.691874915E-01,1.747177108E-01
3.948961186E-01,-7.442423000E-02,-4.758937471E-01,5.703086075E-01,1.000000000E+00,4.839117962E-01,-1.524724218E-01,-4.414850673E-01,-6.867926703E-01,8.231342480E-02,-4.978607008E-01,-3.257594443E-01
-3.753704629E-01,-4.283373932E-01,3.995036002E-01,5.006473374E-01,4.839117962E-01,1.000000000E+00,2.544946571E-01,-5.220498125E-01,-5.172701273E-02,-3.516958581E-01,-1.917806491E-01,-2.382901461E-01
-5.688745564E-01,1.033743738E-01,5.562357117E-01,-2.717477555E-01,-1.524724218E-01,2.544946571E-01,1.000000000E+00,-1.562947548E-01,1.258535043E-01,4.079605627E-01,-4.298081392E-01,2.457903884E-01
3.580564345E-01,3.144517199E-01,-2.730415312E-01,-6.955358799E-01,-4.414850673E-01,-5.220498125E-01,-1.562947548E-01,1.000000000E+00,5.689201993E-01,7.522190338E-02,2.004077681E-01,-4.305307566E-01
-4.084108350E-01,1.238223764E-03,5.532499454E-01,-4.674488915E-01,-6.867926703E-01,-5.172701273E-02,1.258535043E-01,5.689201993E-01,1.000000000E+00,-2.935483990E-01,5.405501695E-01,-5.163845239E-02
3.023879051E-02,2.604447507E-01,-1.634081478E-01,-7.409102089E-02,8.231342480E-02,-3.516958581E-01,4.079605627E-01,7.522190338E-02,-2.935483990E-01,1.000000000E+00,-4.230165657E-01,2.595060079E-01
-3.506993008E-01,-4.131839675E-01,2.926249683E-01,1.691874915E-01,-4.978607008E-01,-1.917806491E-01,-4.298081392E-01,2.004077681E-01,5.405501695E-01,-4.230165657E-01,1.000000000E+00,1.971268897E-01
-4.463441652E-01,1.767940682E-01,4.263174687E-01,1.747177108E-01,-3.257594443E-01,-2.382901461E-01,2.457903884E-01,-4.305307566E-01,-5.163845239E-02,2.595060079E-01,1.971268897E-01,1.000000000E+00
```

相関係数行列であるため、対角要素は1になっている。

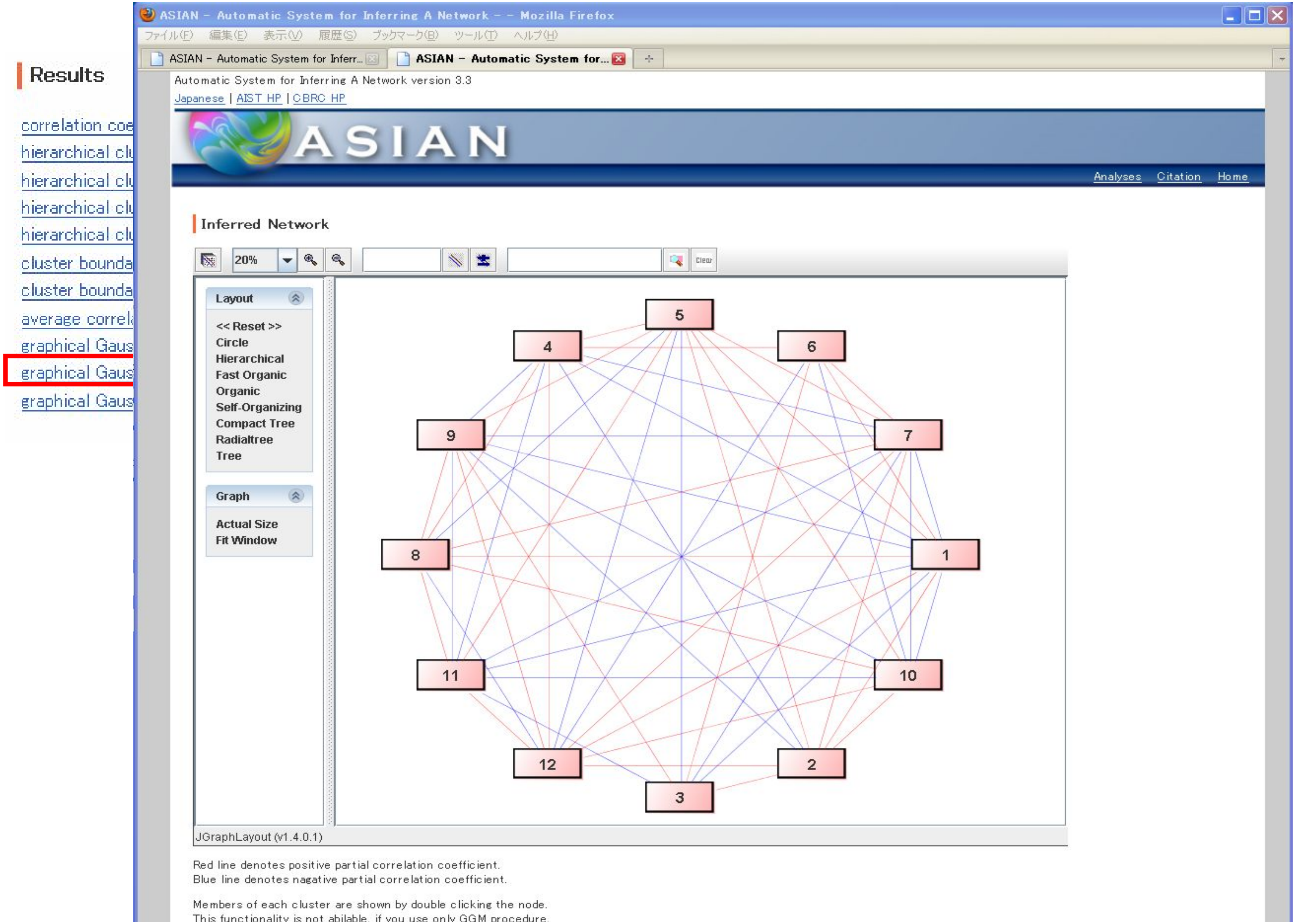


Results

correlation coefficient matrix
hierarchical clustering
hierarchical clustering (tree view gtr)
hierarchical clustering (tree view cdt)
hierarchical clustering (dendrogram)

```
-1.000,0.392,-0.544,-0.533,0.618,0.253,-0.872,0.771,-0.615,-0.528,-0.775,0.547
0.392,-1.000,0.595,-0.356,0.268,0.000,0.001,-0.000,-0.001,0.154,-0.000,0.458
-0.544,0.595,-1.000,-0.000,-0.198,0.482,-0.254,-0.000,0.221,0.000,-0.261,-0.000
-0.533,-0.356,-0.000,-1.000,0.783,0.510,-0.806,0.511,-0.577,0.000,-0.370,0.764
0.618,0.268,-0.198,0.783,-1.000,0.000,0.775,-0.802,0.761,0.483,0.578,-0.780
0.253,0.000,0.482,0.510,0.000,-1.000,0.382,-0.000,-0.000,-0.462,-0.000,-0.351
-0.872,0.001,-0.254,-0.806,0.775,0.382,-1.000,0.777,-0.671,-0.337,-0.771,0.767
0.771,-0.000,-0.000,0.511,-0.802,-0.000,0.777,-1.000,0.860,0.753,0.796,-0.747
-0.615,-0.001,0.221,-0.577,0.761,-0.000,-0.671,0.860,-1.000,-0.571,-0.479,0.563
-0.528,0.154,0.000,0.000,0.483,-0.462,-0.337,0.753,-0.571,-1.000,-0.674,0.375
-0.775,-0.000,-0.261,-0.370,0.578,-0.000,-0.771,0.796,-0.479,-0.674,-1.000,0.679
0.547,0.458,-0.000,0.764,-0.780,-0.351,0.767,-0.747,0.563,0.375,0.679,-1.000
```

偏相関係数行列であるため、対角要素は-1になっている。



Automatic System for Inferring A Network version 3.3

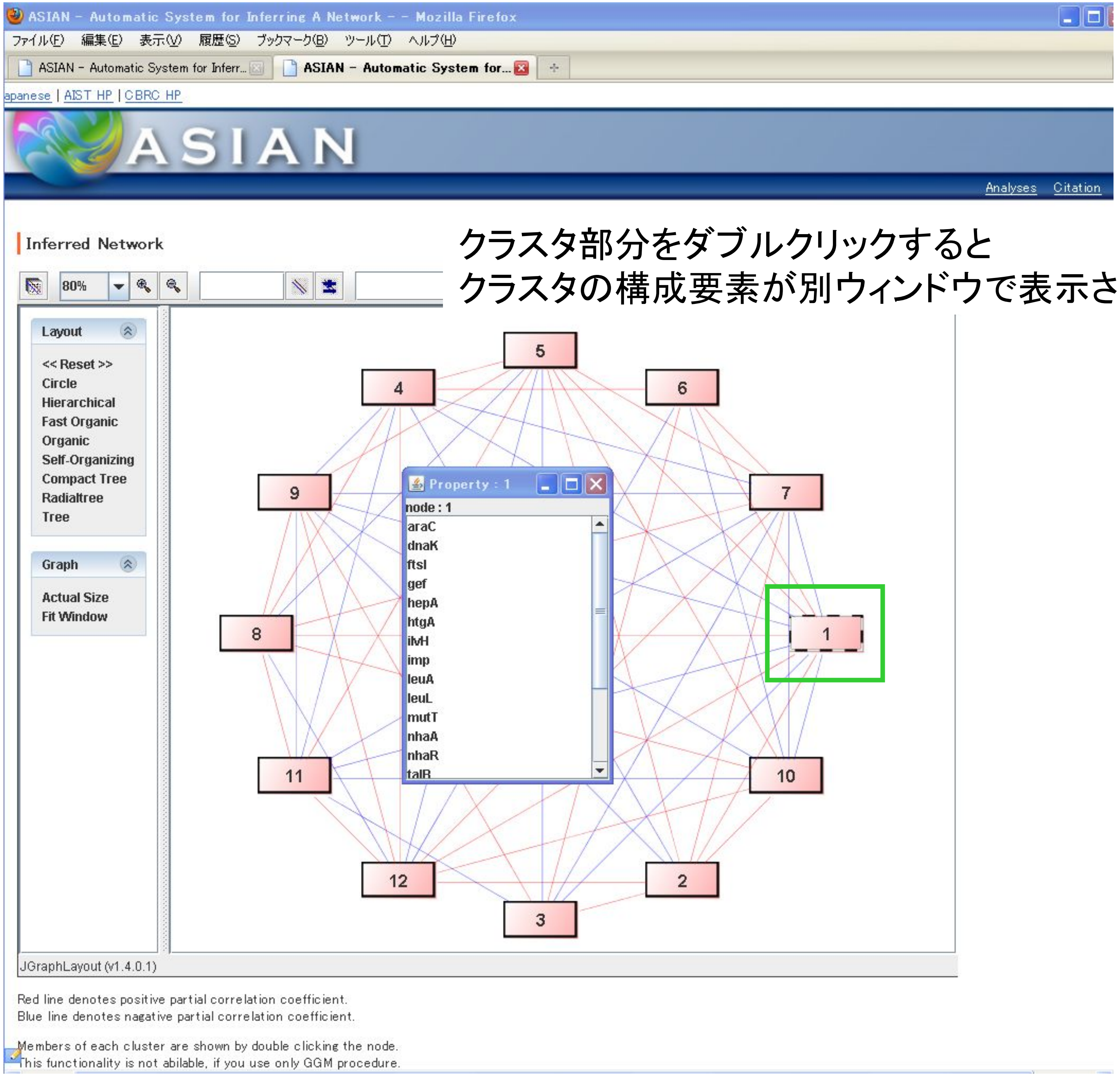
Inferred Network

Red line denotes positive partial correlation coefficient.
Blue line denotes nagative partial correlation coefficient.

Members of each cluster are shown by double clicking the node.
This functionality is not abilable, if you use only GGM procedure.

GGMによって偏相関係数の値が0になっていないクラスタ間にはエッジひかれている。
偏相関係数の値が正の場合は赤いエッジ、負の場合は青いエッジで表示される。

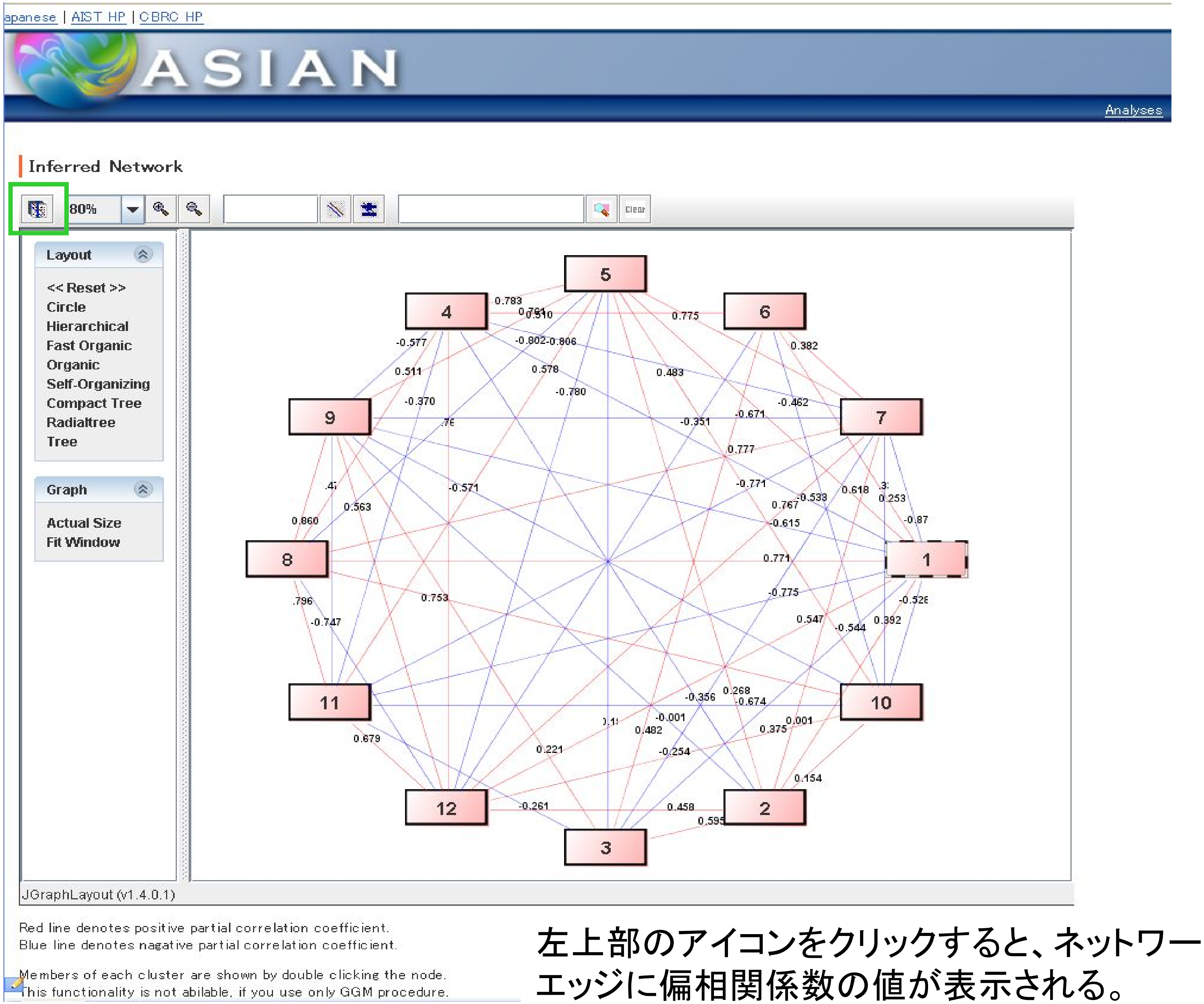
クラスタ部分をダブルクリックすると
クラスタの構成要素が別ウィンドウで表示される。



node : 1
araC
dnaK
ftsI
gef
hepA
htgA
ilvH
imp
leuA
leuL
mutT
nhaA
nhaR
talB

Red line denotes positive partial correlation coefficient.
Blue line denotes nagative partial correlation coefficient.

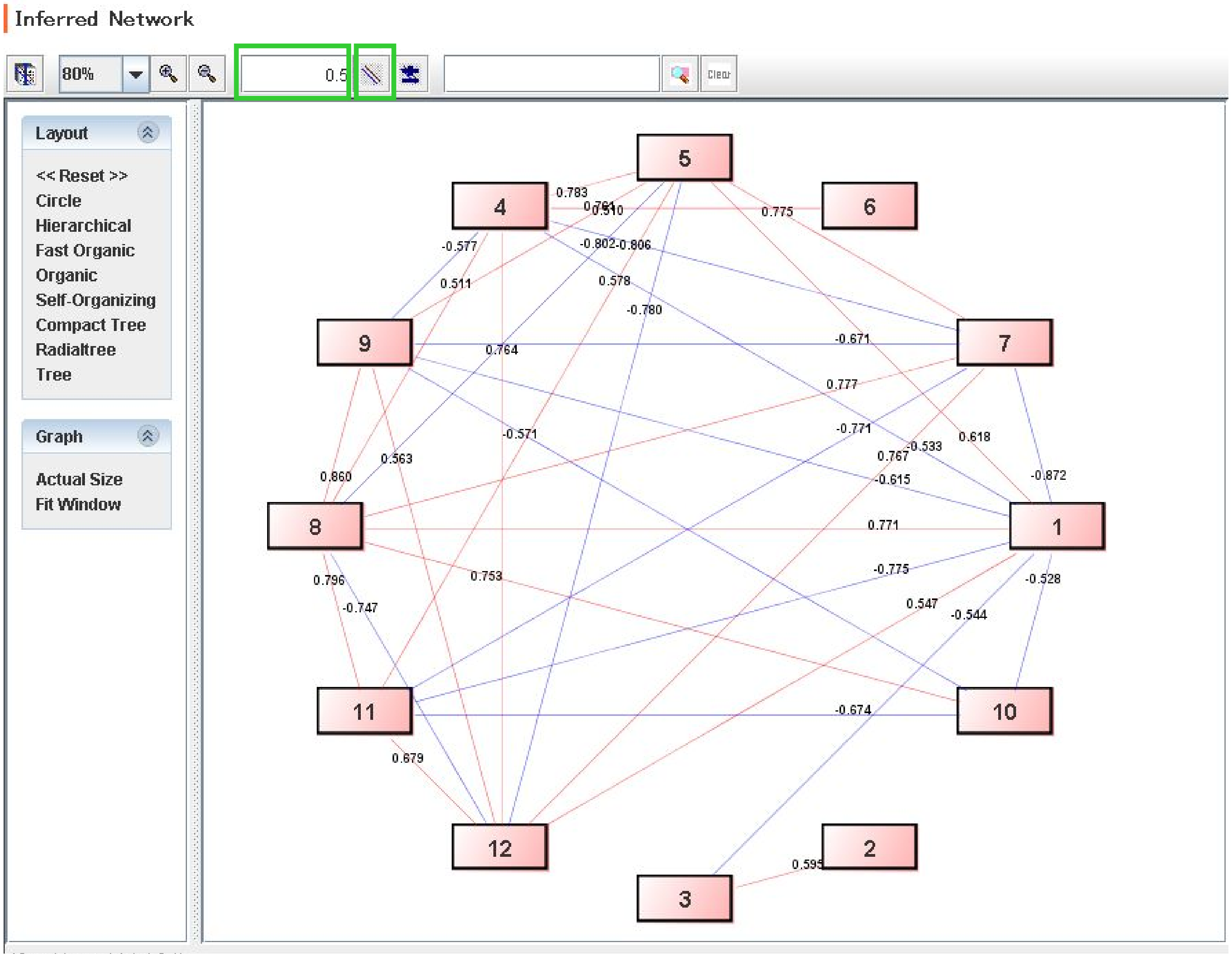
Members of each cluster are shown by double clicking the node.
This functionality is not abilable, if you use only GGM procedure.



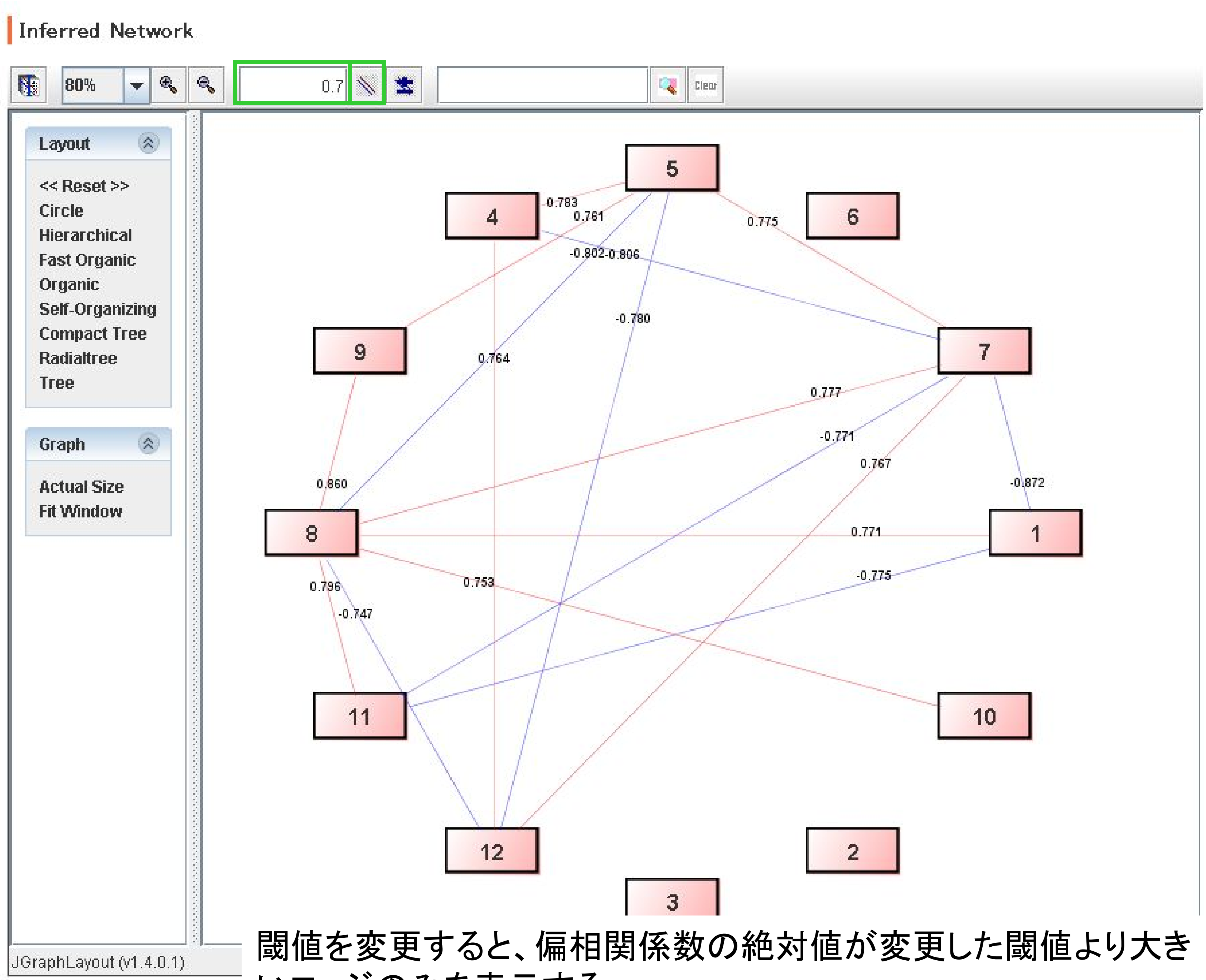
Red line denotes positive partial correlation coefficient.
Blue line denotes nagative partial correlation coefficient.

Members of each cluster are shown by double clicking the node.
This functionality is not abilable, if you use only GGM procedure.

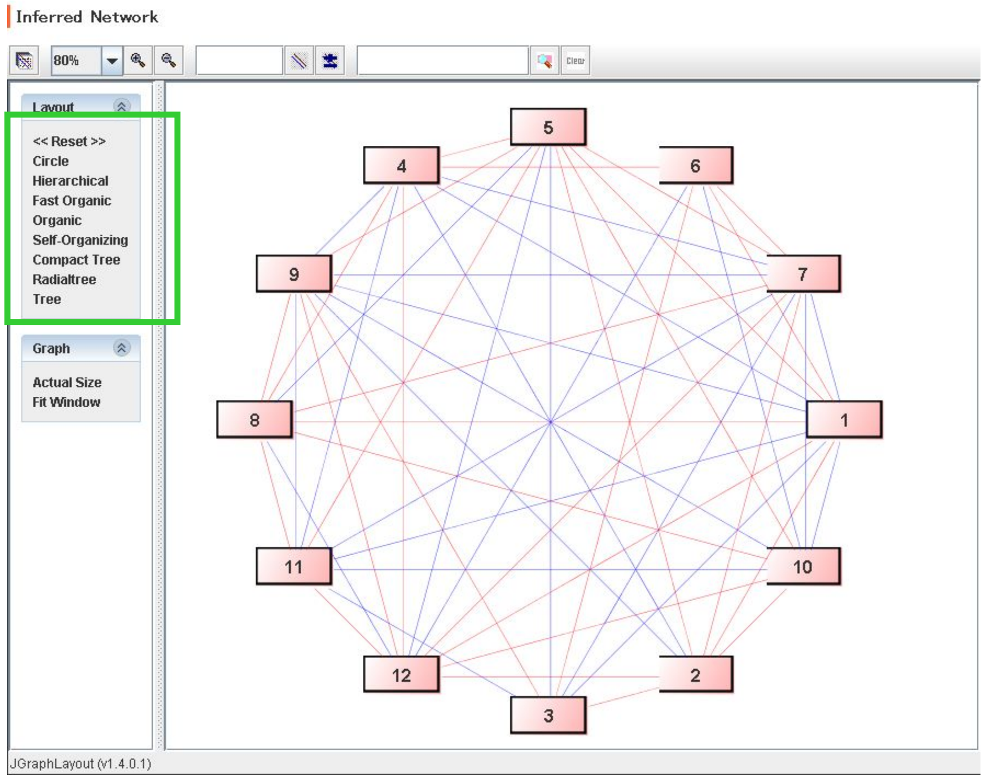
左上部のアイコンをクリックすると、ネットワーク上のエッジに偏相関係数の値が表示される。



ネットワーク上でエッジの偏相関係数の値を表示した後、ボックス内に数値を記載し、アイコンをクリックすると・・・記載した数値を閾値として、偏相関係数の絶対値が閾値より大きいエッジのみを表示する。

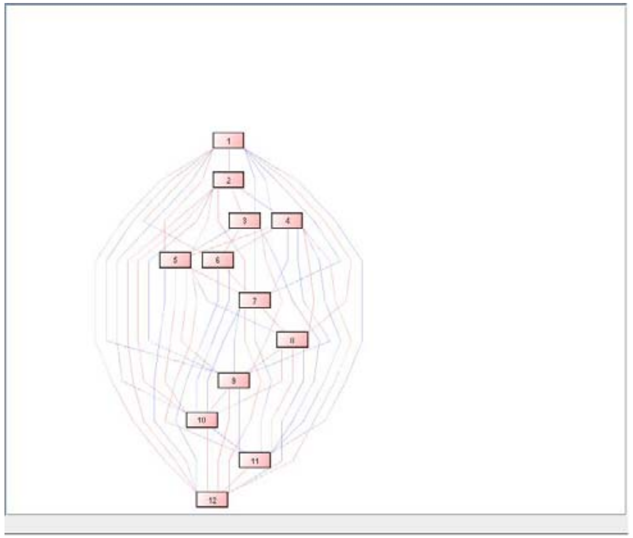


閾値を変更すると、偏相関係数の絶対値が変更した閾値より大きいエッジのみを表示する。

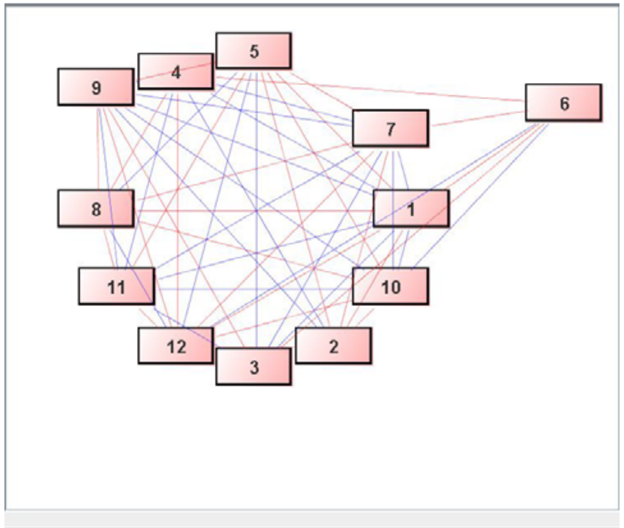


Graphic options
- **Hierarchical**
- **Fast Organic**
- **Organic**
- **Self-Organizing**
- **Compact Tree**
- **Redialtree**
- **Tree**

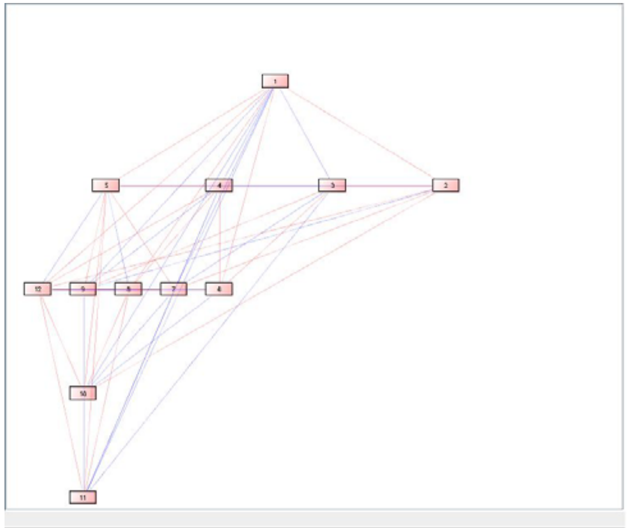
Hierarchical

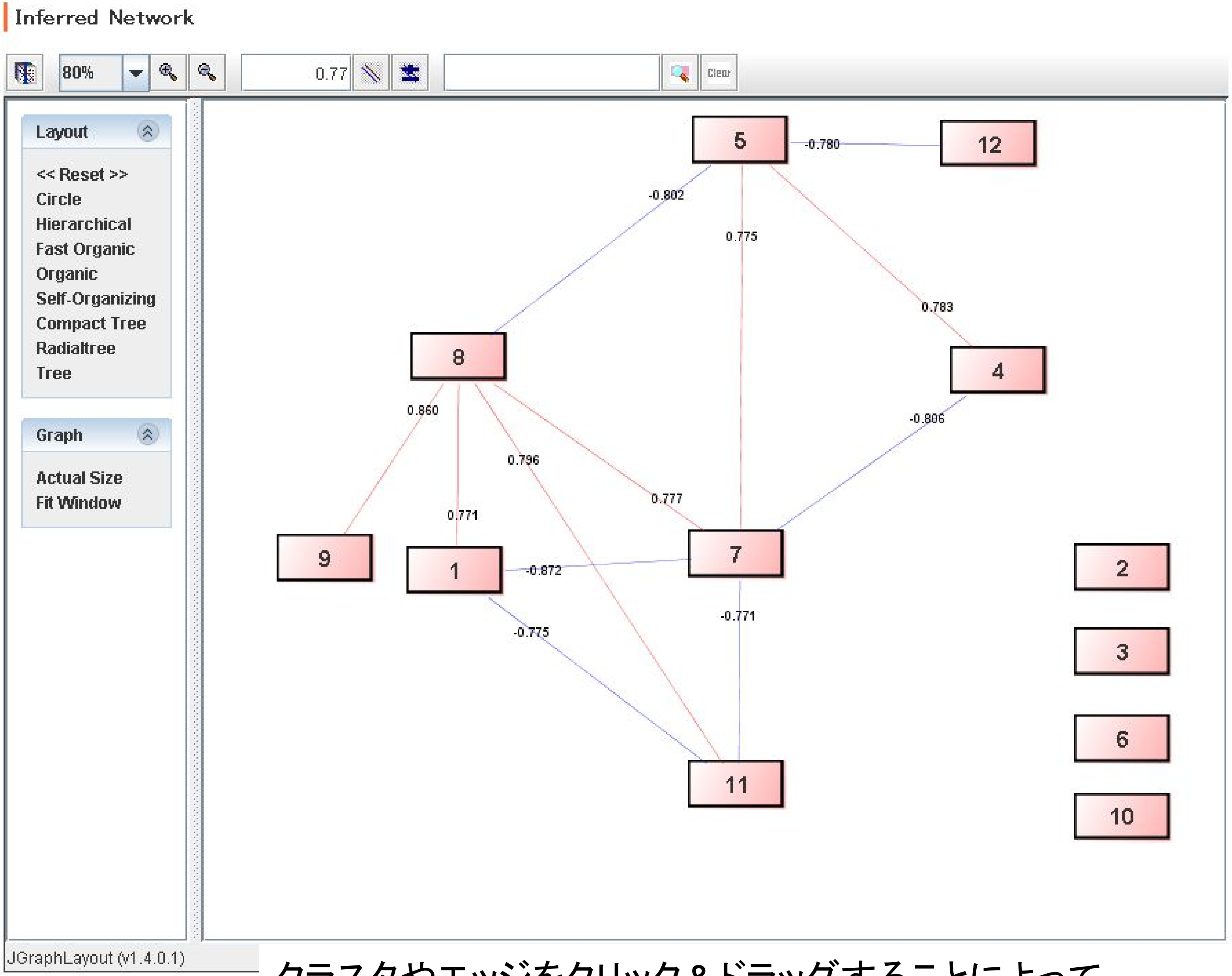


Self-Organizing



Tree





クラスタやエッジをクリック＆ドラッグすることによって
ウェブ上でネットワーク図をカスタマイズすることができる。