

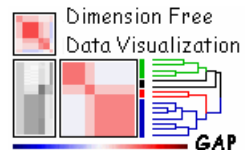
# GAP Software Tutorial

*Version 0.1.015 Build20060515*

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(吳漢銘，陳君厚)

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# Outlines

■ Download and Installation

■ Features

■ Two Demo Datasets

■ Four Steps of GAP  
Procedures

■ Other Functionalities

■ Module: Microarray Tool

GAP: Generalized Association Plots - Microsoft Internet Explorer

檔案(E) 編輯(E) 檢視(V) 我的最愛(A) 工具(T) 說明(H)

← 上一頁

網址(I) <http://gap.stat.sinica.edu.tw/Software/GAP/index.htm>

**GAP** is a java-designed software for generalized association plots (Chen, 2002) and exploratory data analysis. It is programmed for the java runtime environment 1.5 (JRE version 1.5.0\_04), which is available for most operating systems.

Last Updated: 2006/02/07

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Taipei, Taiwan, R. O. C.

**Official Website of GAP Software:**  
<http://gap.stat.sinica.edu.tw/Software/GAP>

**Current Version:**  
v0.1.014, Build 2006-02-07

**Contact:**  
[hmwu@stat.sinica.edu.tw](mailto:hmwu@stat.sinica.edu.tw)

**Features:**

- Clustering Analysis
- Various Display Conditions
- GAP with a Covariate Adjusted
- Nonlinear Association Analysis
- Missing Value Imputation
- Histogram, 2D Scatterplot, 3D Scatterplot (Rotatable)

More...

[Latest Features](#) The latest features of GAP.

[FAQ](#) Frequently asked questions.

[Bug Reports/Fixed](#) Bug reports and fixed.

The GAP Main Window [more screenshots...]

<http://gap.stat.sinica.edu.tw/Software/GAP>

<http://gap.stat.sinica.edu.tw/GAPforums>



# GAP Features

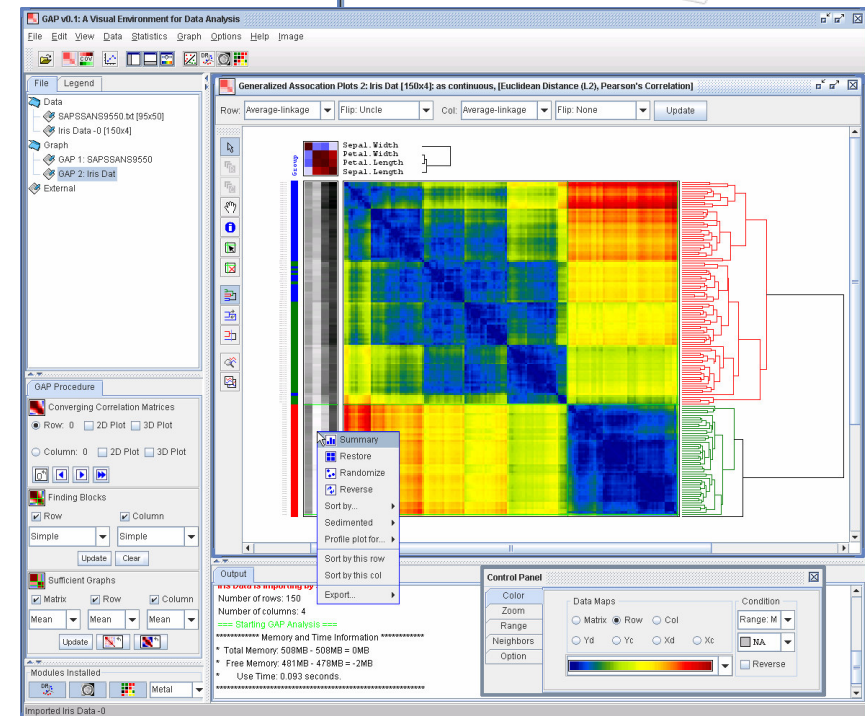
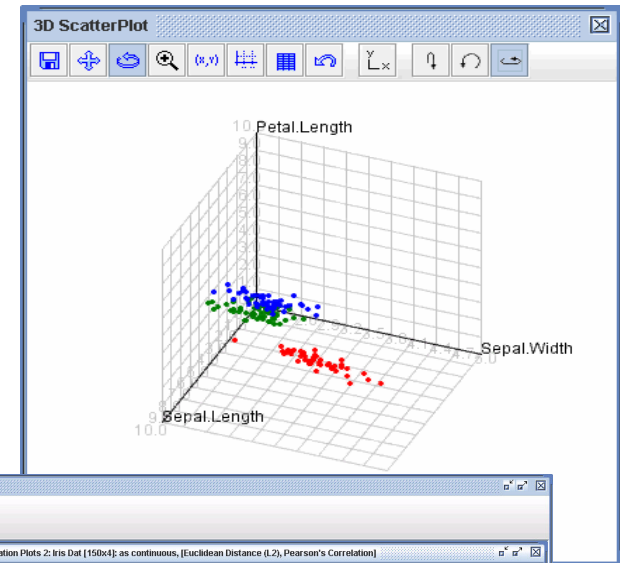


## Generalized Association Plots

- Input Data Type: continuous or binary.
- Various seriation algorithms and clustering analysis.
- Various display conditions.
- GAP with Covariate Adjusted
- GAP with Nonlinear Association Analysis
- GAP with Missing Value Imputation

## Statistical Plots

- 2D Scatterplot, 3D Scatterplot (Rotatable)

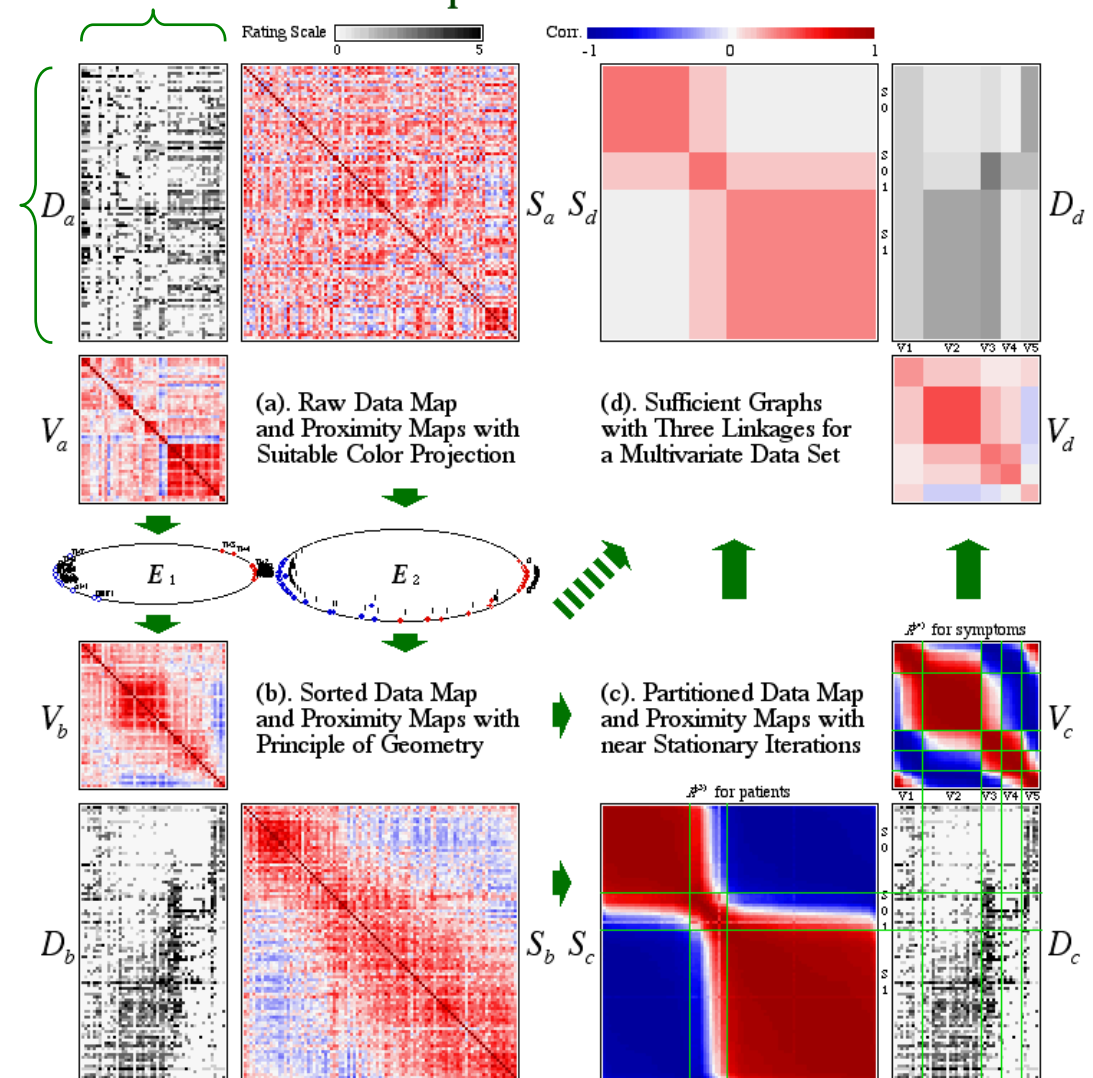




# Demo Data 1: Schizo Data

- The data set consists of the Andreasen's positive and negative symptom scales (Andreasen (1983, 1984)) for **95** first-time hospitalized psychosis disorder patients. 95 patients: **69** schizophrenic and **26** bipolar disorders.
- Scale for Assessment of Positive Symptoms (**SAPS**): **30 items**, four subgroups: Hallucinations (AH1-6), Delusions (DL1-12), Behavior (BE1-4) Thought disorder (TH1-8).
- Scale for Assessment of Negative Symptoms (**SANS**): **20 items**, five subgroups: Expression (NA1-7), Speech (NB1-4), Hygiene (NC1-3), Activity (ND1-4) and Inattentiveness (NE1-2).
- The available data set has **95** subjects (patients) with **50** variables (symptoms).
- All the symptoms are recorded on a six point scale (**0-5**).

## A Complete GAP Procedure





# Demo Data 2: Iris Data

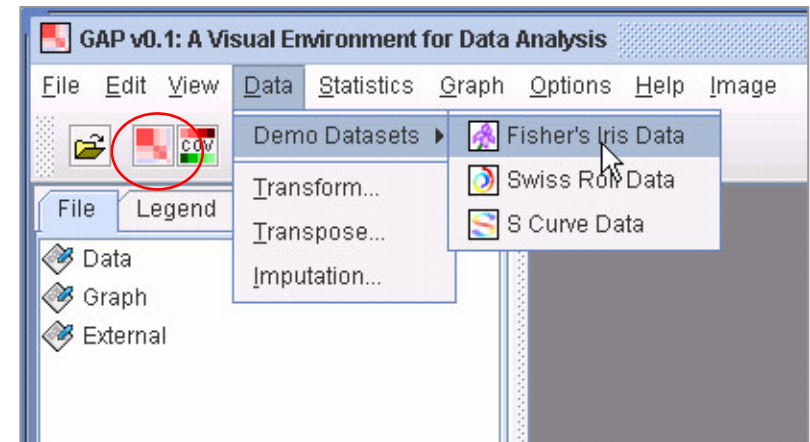
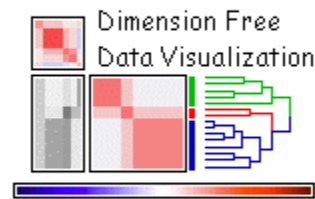
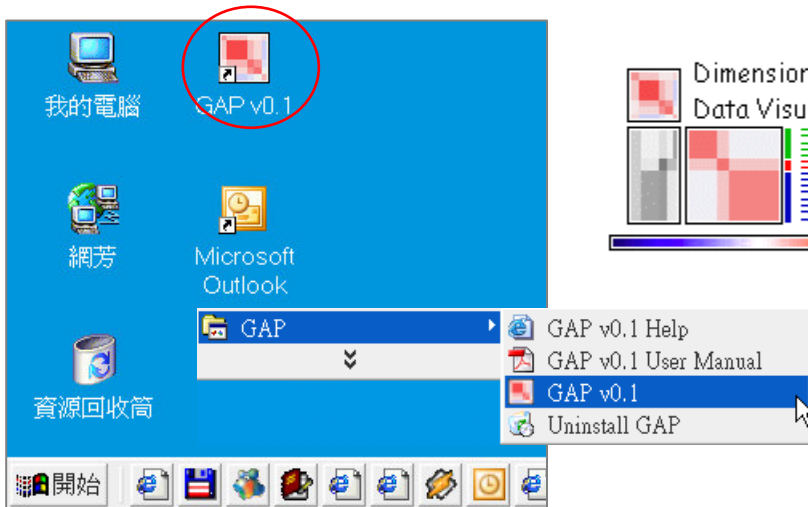
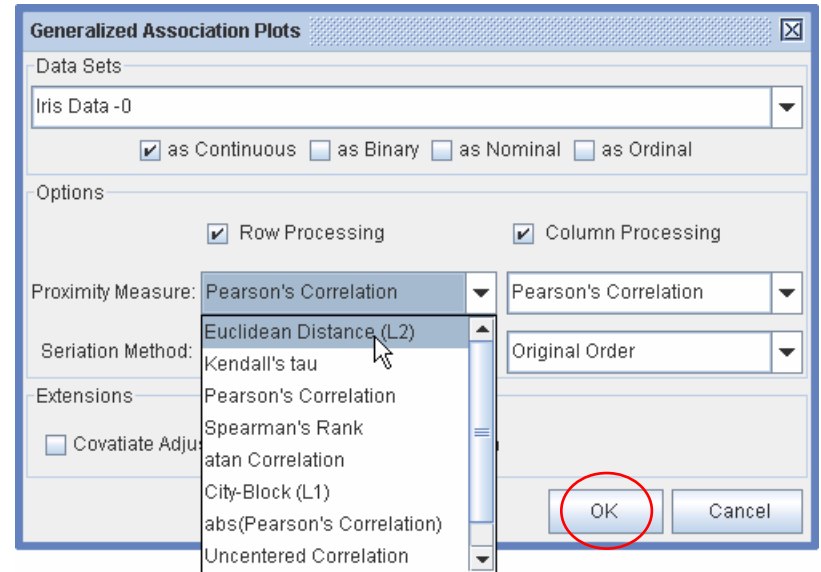
no.	Species	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	setosa	5.1	3.5	1.4	0.2
2	setosa	4.9	3.0	1.4	0.2
3	setosa	4.7	3.2	1.3	0.2
4	setosa	4.6	3.1	1.5	0.2
5	setosa	5.0	3.6	1.4	0.2
...					
76	versicolor	6.6	3.0	4.4	1.4
...					
150	virginica	5.9	3.0	5.1	1.8

Iris Flowers

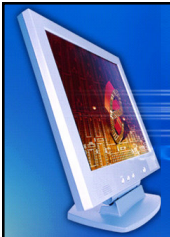


○ Iris Setosa    ○ Iris Versicolor    ○ Iris Virginica

The sepal length, sepal width, petal length, and petal width are measured in centimeters on fifty iris specimens from each of three species, *Iris setosa*, *I. versicolor*, and *I. virginica*. Fisher (1936)



# GAP Main Window

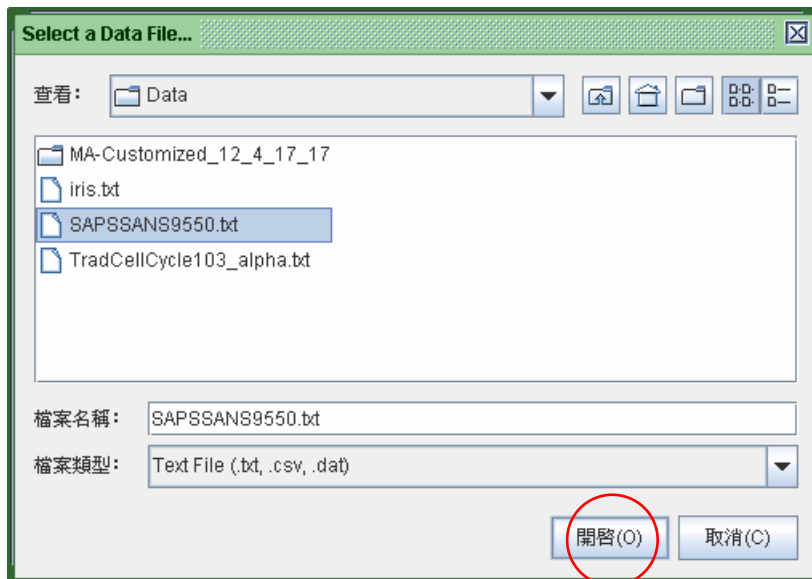
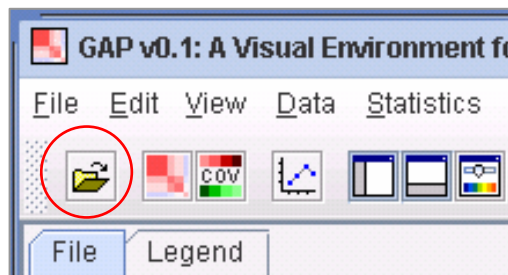


The screenshot shows the GAP v0.1 main window with the following components labeled:

- Menu Bar:** Located at the top, containing File, Edit, View, Data, Statistics, Graph, Options, Help, and Image.
- Tool Bar:** Located below the menu bar, containing icons for file operations and analysis.
- File/Data View:** A tree view on the left showing the project structure, including 'Iris Data -0 [150x4]' and 'GAP 1: Iris Dat'.
- Color Legend:** A legend box on the left side of the main window, currently empty.
- GAP Procedure:** A control panel on the left for configuring analysis parameters, including 'Converging Correlation Matrices', 'Finding Blocks', and 'Sufficient Graphs'.
- Mouse Tools:** A set of icons on the left side of the main window for interacting with the data.
- Variables/Subjects:** A table in the center-left showing the data structure with columns 'id' and 'col', and rows listing variables like 'Sepal.Width' and subjects like 'virginica'.
- Heatmap:** A large heatmap in the center-right showing the results of the analysis, with a color scale from blue (low) to red (high).
- Serialiation and Tree Flip:** A control panel on the right side of the heatmap for adjusting the dendrogram.
- GAP Maps Window:** A window on the right side of the heatmap showing the dendrogram structure.
- Output Window:** A window at the bottom showing the results of the analysis, including '#rows: 97', '#columns: 52', and memory usage information.
- Control Panel:** A window at the bottom right for configuring the visualization, including 'Data Maps' (Matrix, Row, Col) and 'Condition' (Range, NA, Reverse).
- Modules Installed:** A list of installed modules at the bottom left, including 'Metal'.

# Open/Import Data

**Data Format:** plain text with tab separator



Row/Column Name

Number of Y Discrete/Continuous Covariates

Number of X Discrete/Continuous Covariates

Open Data

Data Information

File: C:\Program Files\GAP\Data\SAPSSANS9550.bt

No. Row: 95

No. Col: 50

Missing Value: NA

Row name

Col name

Ydiscr.: 1

Yconti.: 0

Xdiscr.: 0

Xconti.: 0

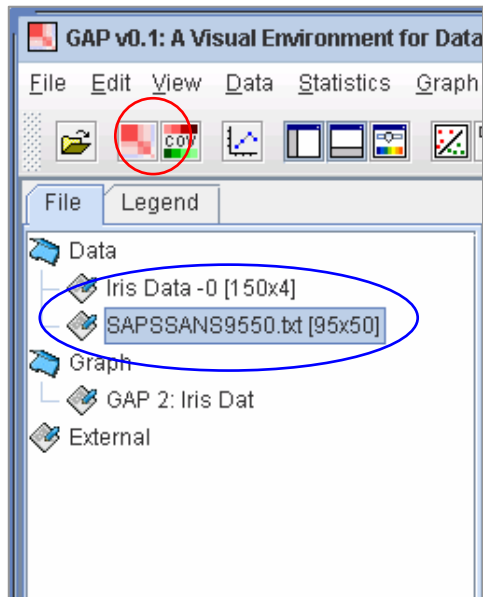
var0	var1	var2	var3	var4	var5	var6
UNIQID	AH1	AH2	AH3	AH4	AH5	AH6
1	Xd	Yd	Ye	0	0	0
1	Xc	5	5	5	0	0
1	5	5	5	5	4	5
0	0	0	0	0	0	0
1	2	0	2	0	0	2
0	0	0	0	0	0	0
1	3	1	1	0	0	0
1	5	5	1	0	0	4
0	0	0	0	0	0	0
1	2	0	2	0	0	0
1	5	0	1	0	0	0
1	0	0	0	5	0	0
0	0	0	0	0	0	0
1	5	5	5	0	0	0
0	0	0	0	0	0	0

OK

Cancel



# GAP Analysis Dialog

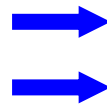


- Euclidean Distance (L2)
- Kendall's tau
- Pearson's Correlation
- Spearman's Rank
- atan Correlation
- City-Block (L1)
- abs(Pearson's Correlation)
- Uncentered Correlation
- abs(Uncentered Correlation)

- Hamman:  $a/(b+c)$
- Jaccard:  $a/(a+b+c)$
- Phi:  $(ad-bc)/\sqrt{(a+b)(a+c)}$
- Rao:  $a/(a+b+c+d)$
- Rogers:  $(a+d)/(a+2b+2c+d)$
- Simple Match:  $(a+d)/(a+b+c+d)$
- Sneath:  $a/(a+2b+2c)$
- Yule:  $(ad-bc)/(ad+bc)$

Not implemented Yet!

- (x) 2x2 Correlation
- (x) Cramer's V
- (x) Cohen's kappa
- (x) Goodman-Kruskal tau
- (x) Goodman-Kruskal's gamma
- (x) Kendall's tau\_b
- (x) Somers's d
- (x) Stuart's tau\_c
- (x) Wilson's e



**Generalized Association Plots**

Data Sets: SAPSSANS9550.txt

as Continuous  as Binary  as Nominal  as Ordinal

Options:  Row Processing  Column Processing

Proximity Measure: Pearson's Correlation

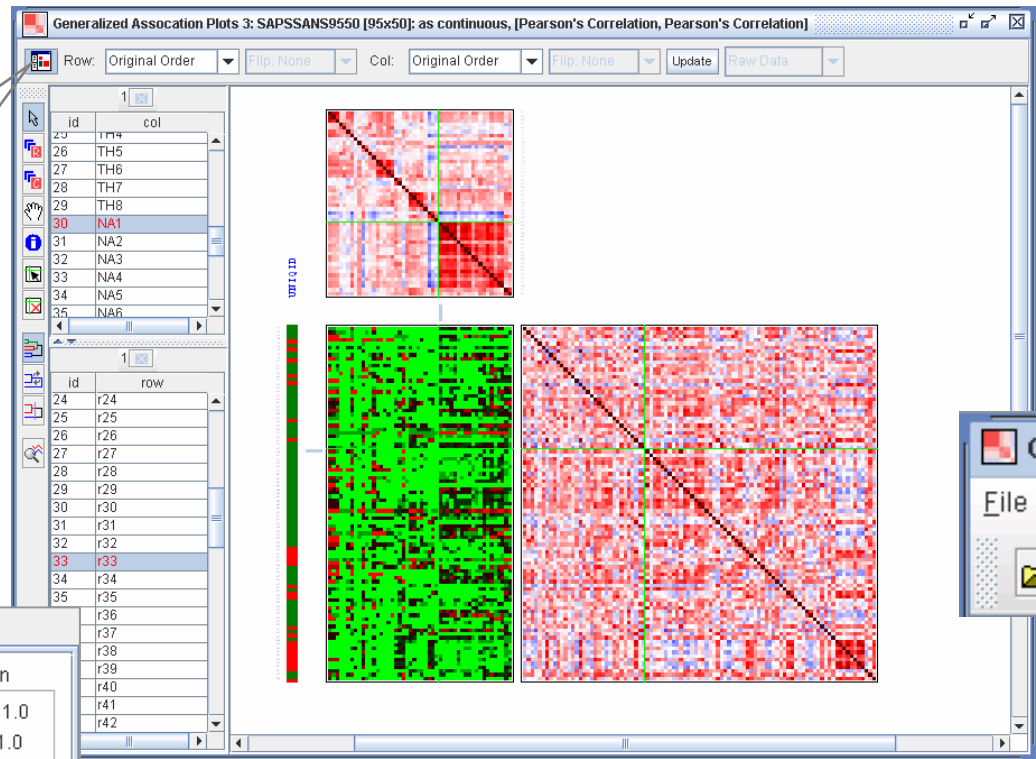
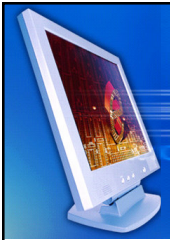
Seriation Method: Original Order

Extensions:  Covariate Adjustment  Nonlinear Association

OK Cancel

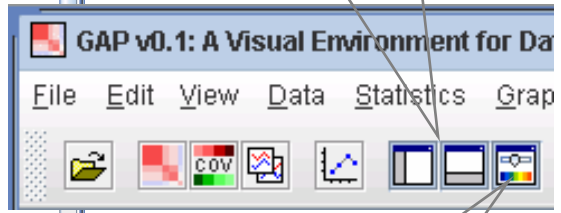


# GAP Step 1: Presentation of Raw Data Matrix

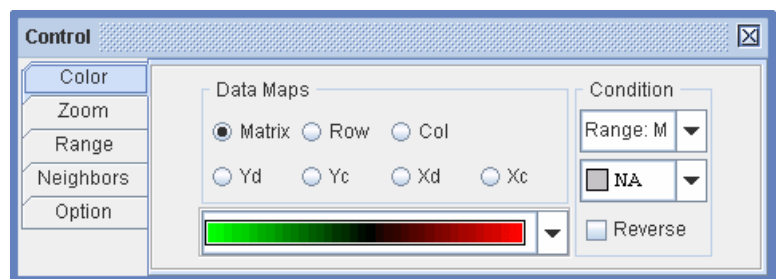
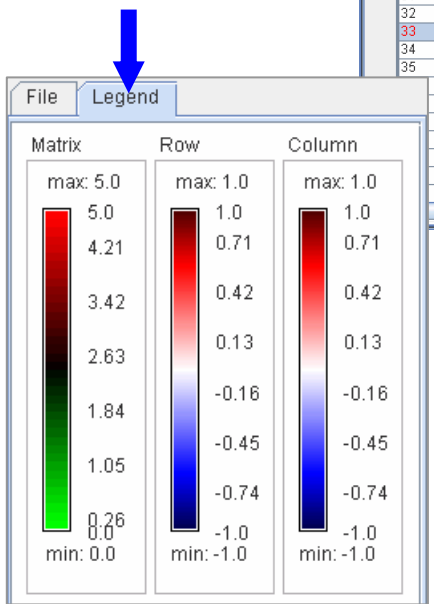


Show or Hide variables/subjects

Show or Hide File/Data View, Output Panel


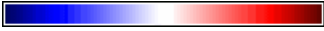







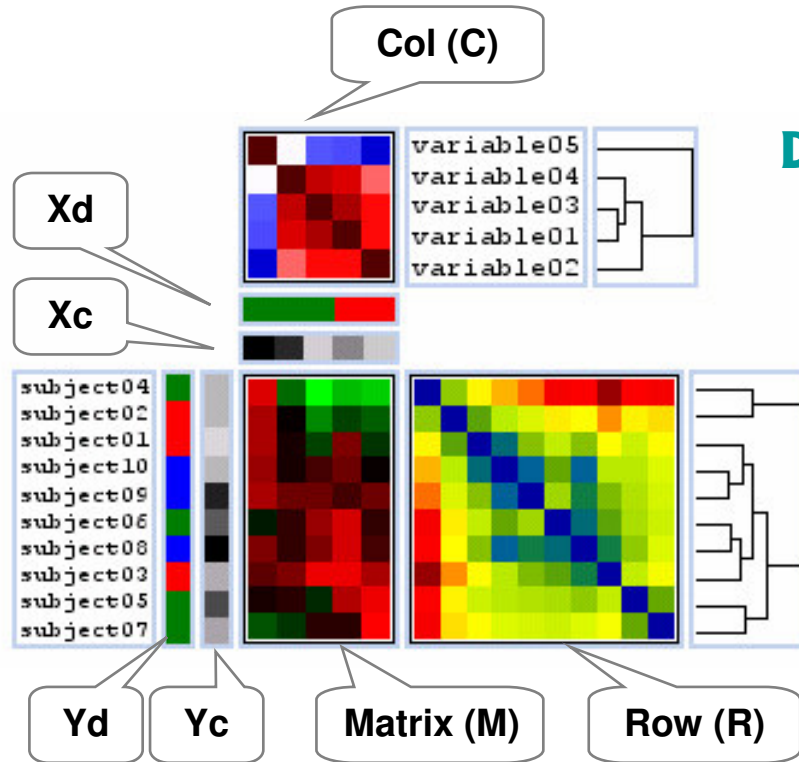
Show or Hide Control Panel



# Control Panel: Color

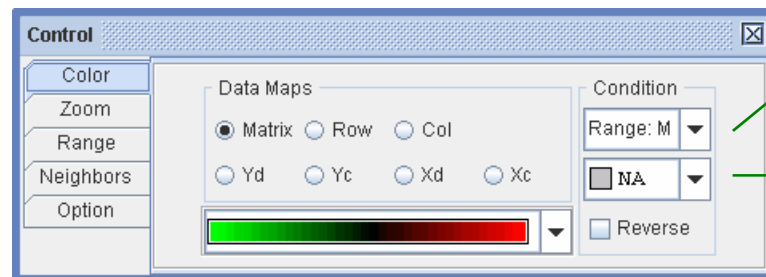


- Rainbow 130**  
 Distance
- Blue-white-Red 200**  
 Correlation
- Green-Black-Red 38**  
 Gene Expression
- Grey 256**  
 Range
- Discrete 16**  

- Biallel Marker**  

- ACGT**  







**Display Conditions**  
(only for Matrix)

- Range: M
- Range: R
- Range: C
- Center: M
- Center: R
- Center: C
- Std: M (x)
- Std: R (x)
- Std: C (x)
- Rank: M
- Rank: R
- Rank: C



**Missing Value**

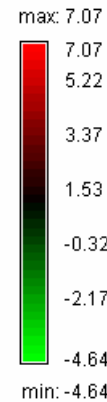
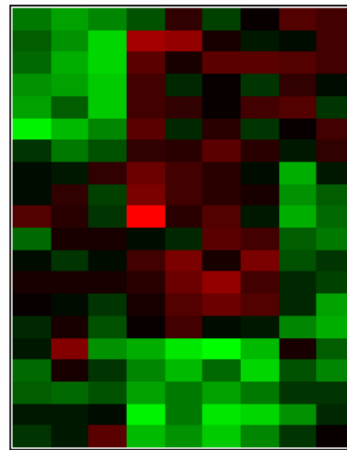
-  NA
-  NA
-  NA



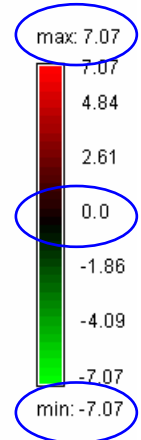
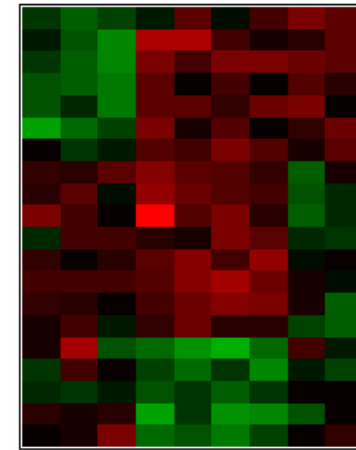


# Display Conditions

	A	B	C	D	E	F	G	H	I
1	-1.37	-2.30	-1.80	-0.55	2.45	-0.13	1.49	3.03	2.48
2	-0.68	-2.11	-3.42	4.67	4.57	1.75	0.61	0.92	2.52
3	-1.19	-2.49	-3.66	3.14	1.70	3.29	3.33	2.92	2.48
4	-1.93	-2.28	-3.16	2.51	0.32	1.49	0.21	2.20	1.03
5	-2.21	-0.79	-3.29	2.55	2.44	1.45	2.68	3.03	0.19
6	-4.14	-2.91	-1.64	3.21	0.37	1.93	0.14	1.27	2.67
7	0.21	-1.36	-0.44	2.22	1.85	3.11	2.03	0.67	2.40
8	1.13	0.79	2.25	3.65	2.52	2.09	1.13	-2.59	0.67
9	0.95	2.33	-0.07	3.89	2.72	2.13	1.75	-2.17	-0.90
10	3.04	1.85	0.21	7.07	2.01	3.05	0.76	-2.58	-1.04
11	-1.02	1.65	1.53	0.95	0.60	3.12	2.52	-0.77	-1.40
12	1.21	0.24	1.04	2.50	3.69	1.81	3.98	-0.33	0.11
13	1.74	1.60	1.70	2.02	3.45	4.46	2.69	0.41	-0.09
14	1.34	1.06	0.06	1.81	2.90	3.64	3.04	0.49	-2.33
15	0.57	1.81	-0.47	1.40	2.70	0.99	0.82	-1.61	-2.56
16	0.61	4.22	-2.03	-2.61	-4.00	-4.64	-2.92	1.55	-0.71
17	-1.13	1.64	0.01	-1.77	-2.85	-1.24	-3.41	-0.59	-1.64
18	-0.86	-1.17	-0.41	-2.20	-1.30	-2.37	-1.41	0.08	0.25
19	0.75	0.66	1.04	-4.26	-1.41	-3.99	-3.53	-2.17	0.34
20	0.15	0.68	3.18	-2.86	-2.01	-3.18	-1.58	0.10	1.28



Range Matrix Condition



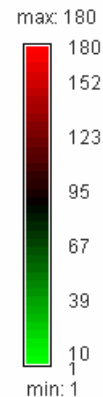
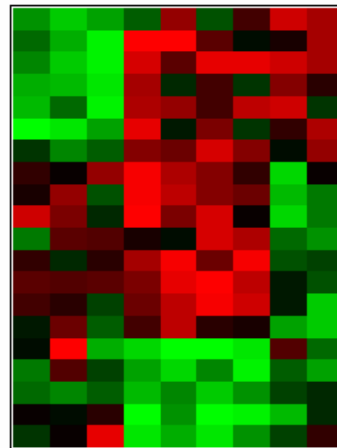
Center Matrix Condition

## Bidirectional Color Spectrum

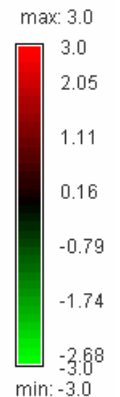
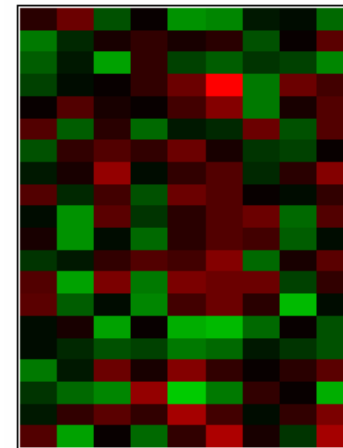
Blue-white-Red 200



Green-Black-Red 38

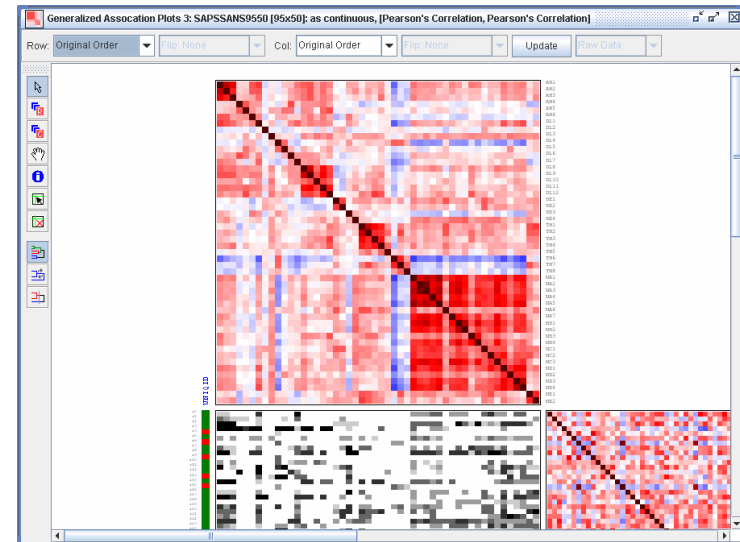


Rank Matrix Condition



Standardize Matrix Condition

# Control Panel: Zoom



**Actual Size**

**Fit Window**

**Fit Width**

**Control**

Color

Zoom

Range

Neighbors

Option

100%

100%

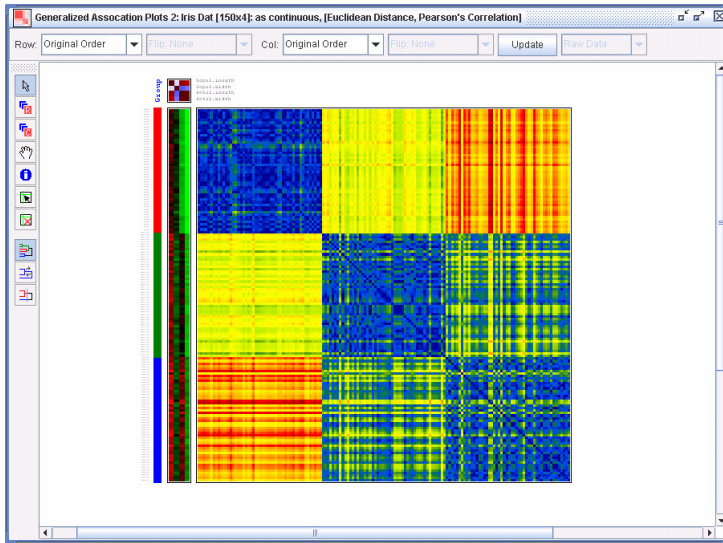
76%

The Control panel includes a 'Zoom' section with three rows of controls. Each row has a magnifying glass icon, a slider, and a percentage value. The top row is set to 100%, the middle row to 100%, and the bottom row to 76%. A blue circle highlights the sliders, and blue arrows point from the 'Actual Size' and 'Fit Window' labels to the top and middle rows respectively. The 'Fit Width' label points to the bottom row.

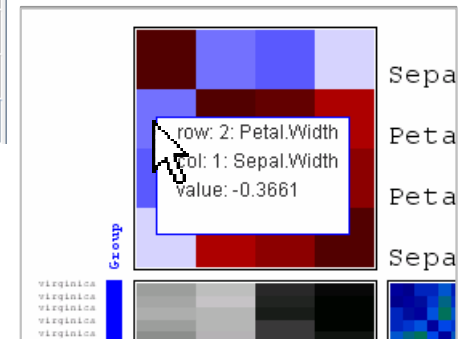
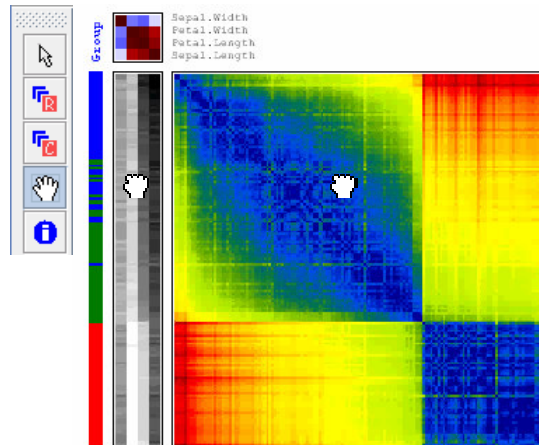
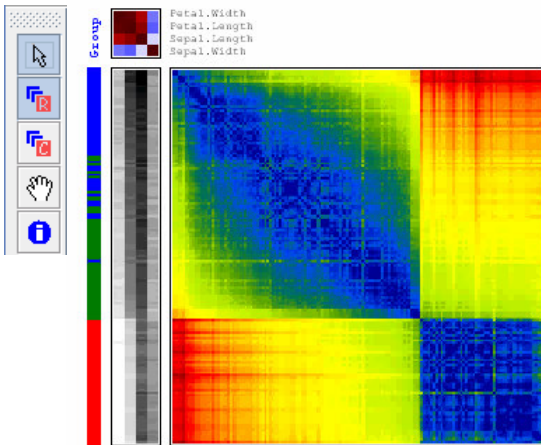
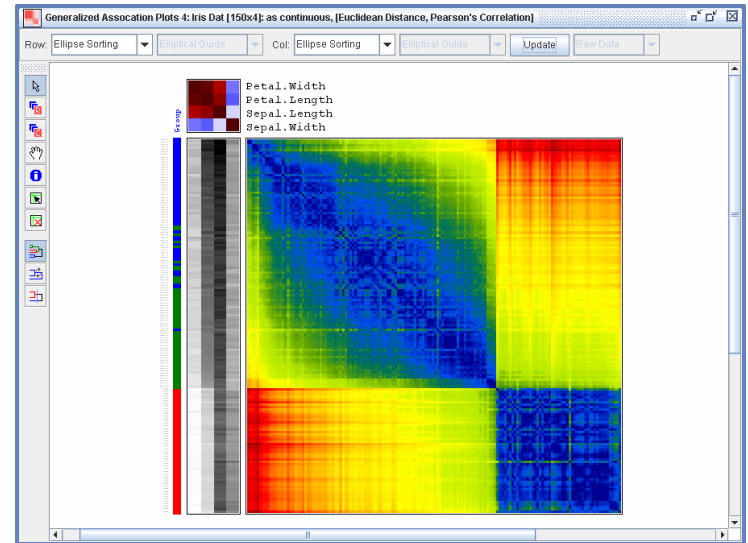
# GAP Step 2-1: Ellipse Seriation

Generalized Association Plots 4: Iris Dat [150x4]: as continuous, [Euclidean Distance, Pearson's Correlation]

Row: Ellipse Sorting | Elliptical Guide | Col: Ellipse Sorting | Elliptical Guide | Update | Raw Data

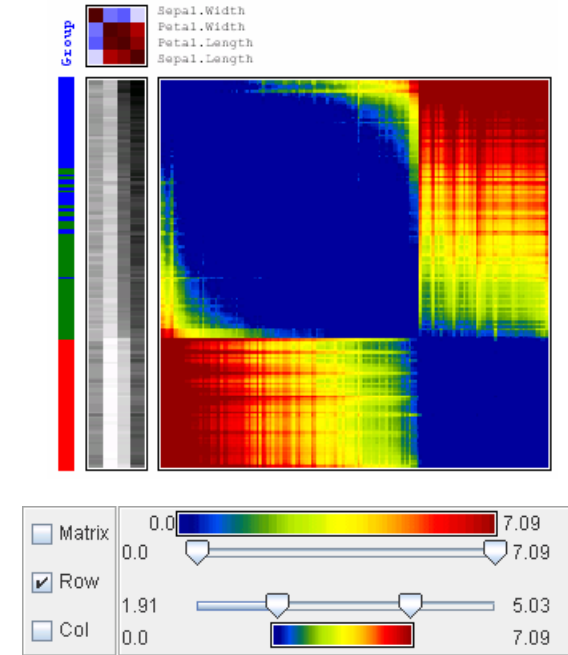
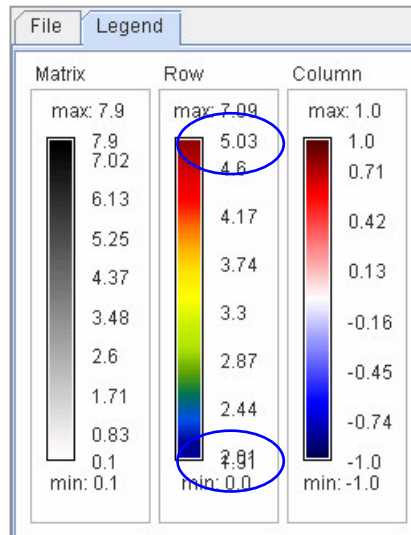
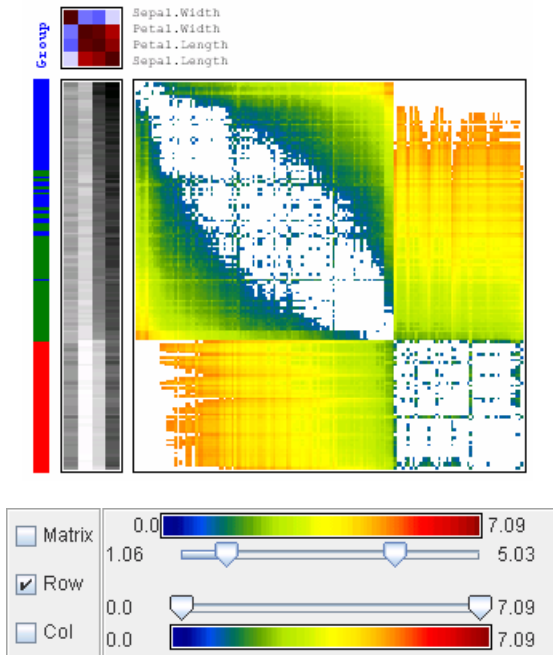


- Average-linkage
- Centroid-linkage
- Complete-linkage
- Ellipse Sorting
- Original Order
- Single-linkage
- External
- Customized

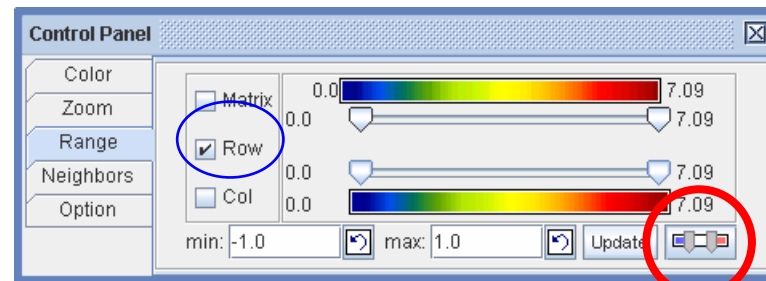
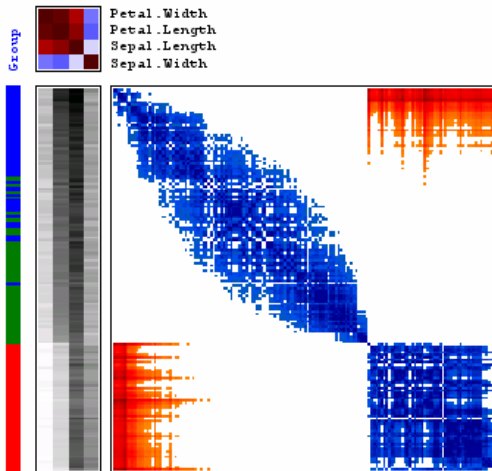




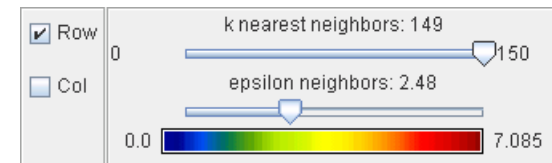
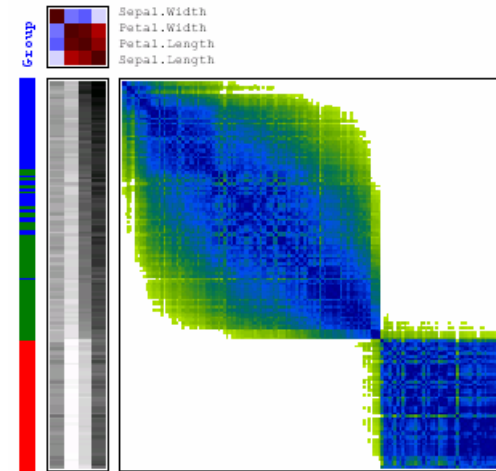
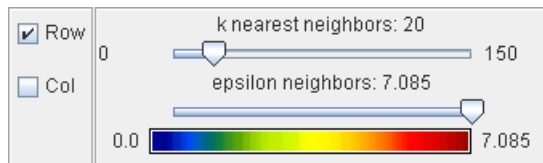
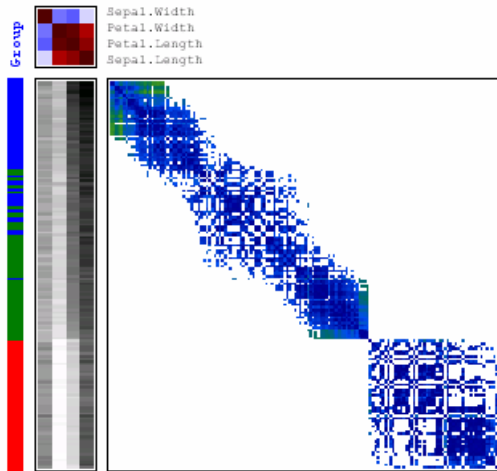
# Control Panel: Range



## “Resolution” of a Statistical Graph



# Control Panel: Neighbors



**Control Panel** [X]

Color

Zoom

Range

**Neighbors**

Option

Row

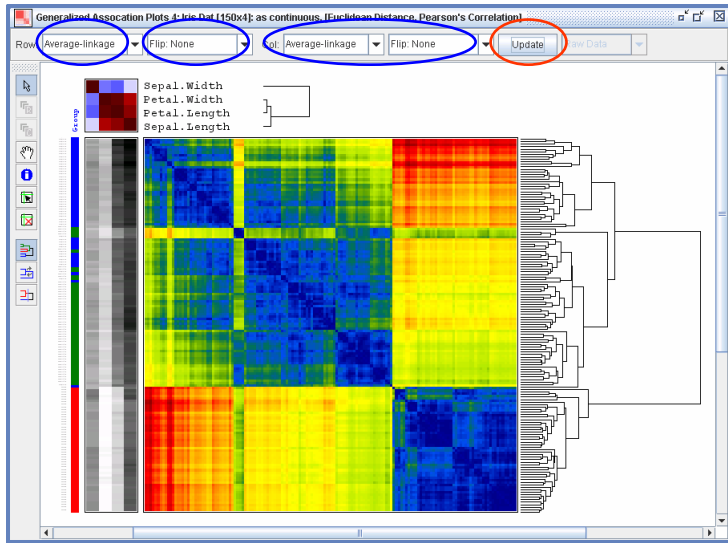
Col

k nearest neighbors: 149

epsilon neighbors: 7.085

0.0 7.085

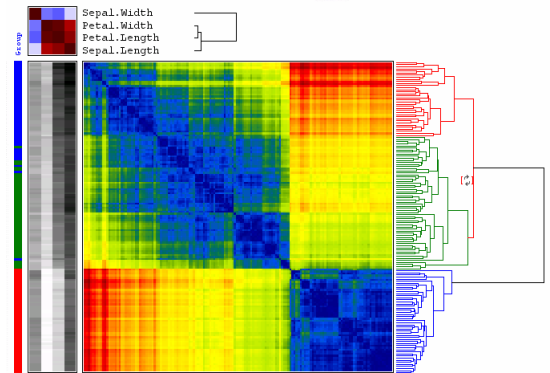
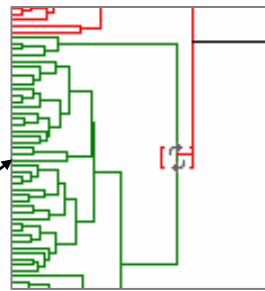
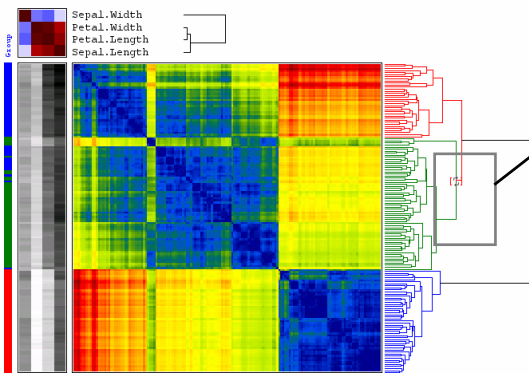
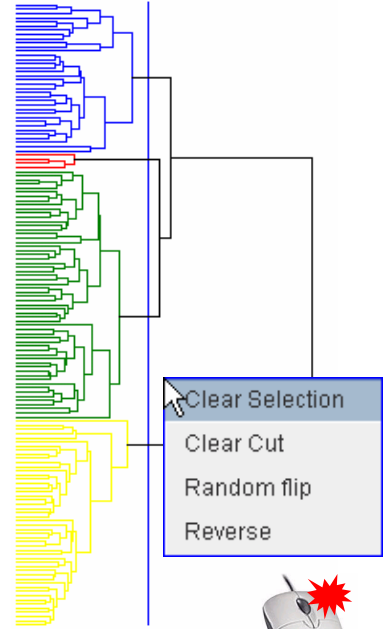
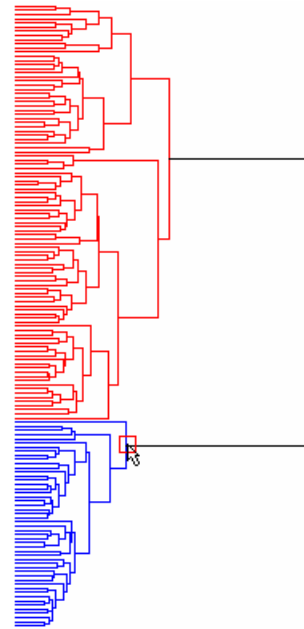
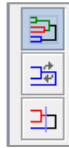
# GAP Step 2-2: Tree Seriation/Flip



- Average-linkage
- Centroid-linkage
- Complete-linkage
- Ellipse Sorting
- Original Order
- Single-linkage
- External
- Customized

- Flip: None
- Flip: Uncle
- Flip: GrandPa
- External Reference
- Elliptical Guide

Update





# Pop-Up Menu: Sort by...

Generalized Association Plots 1: SAPSSANS9550 [95x50]: as continuous, [Pearson's Correlation, Pearson's Correlation]

Row: **Ellipse Sorting** Elliptical Guide Col: **Ellipse Sorting** Elliptical Guide **Update** Raw Data

Sort  
Export data  
Export image

- Summary
- Restore
- Randomize
- Reverse
- Sort by...
  - Means
  - Medians
  - Std's
  - CV's
- Sedimented
- Profile plot for...
- Sort by this row
- Sort by this col
- Export...

Restore

Randomize

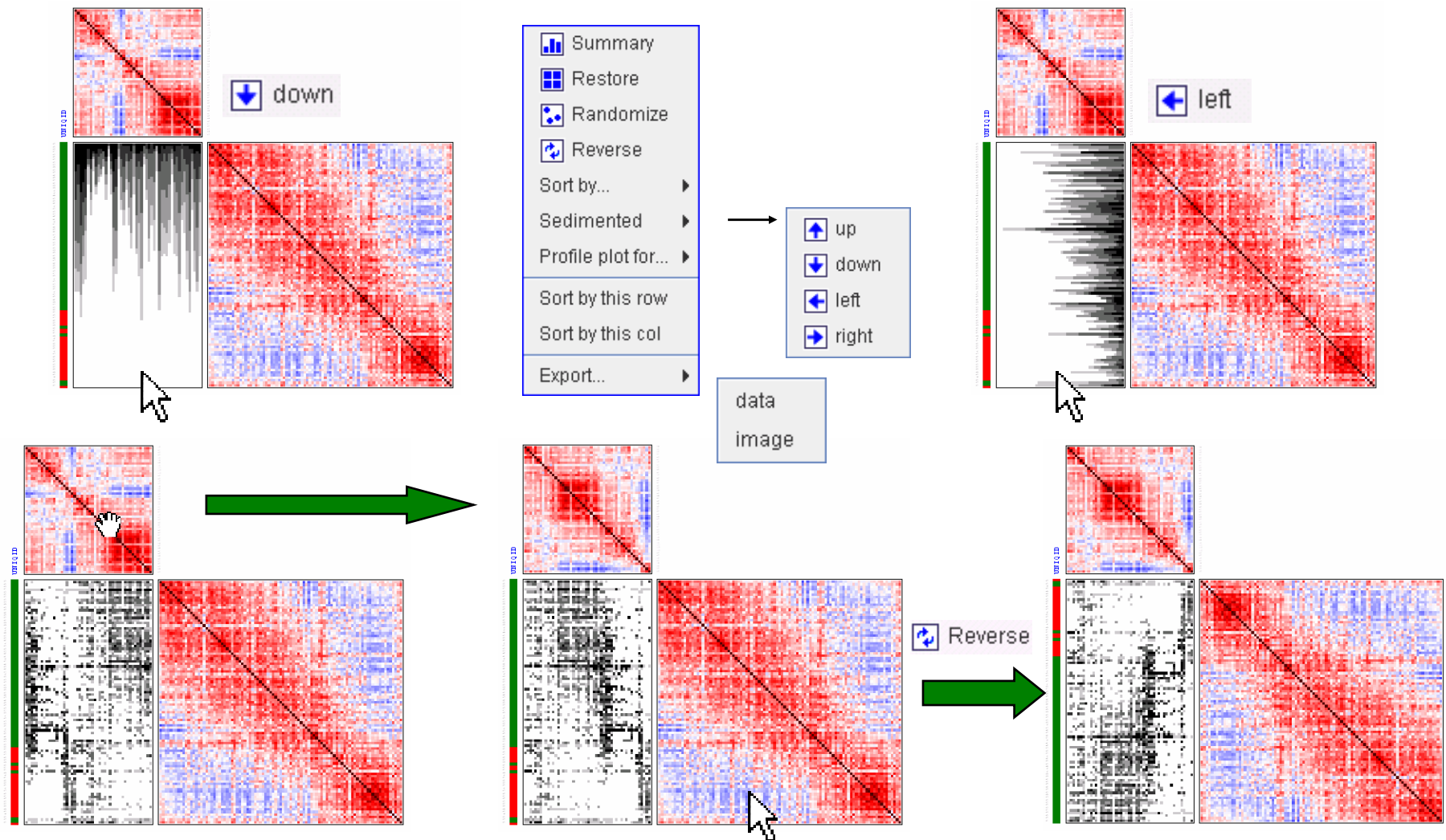
Reverse

Sort by...  
Means

# Pop-Up Menu: Sedimented plot

Generalized Association Plots 1: SAPSSANS9550 [95x50]: as continuous, [Pearson's Correlation, Pearson's Correlation]

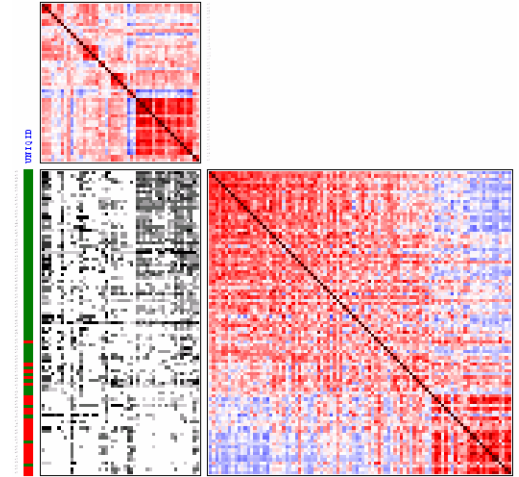
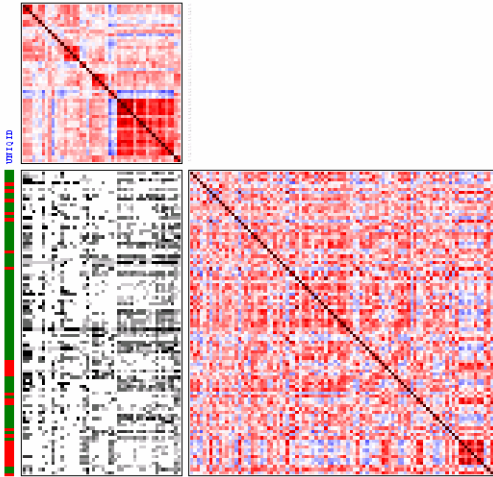
Row: Ellipse Sorting | Elliptical Guide | Col: Ellipse Sorting | Elliptical Guide | **Update** | Raw Data



# Mouse Tool: Find Similar Patterns

Generalized Association Plots 1: SAPSSANS9550 [95x50]: as continuous, [Pearson's Correlation, Pearson's Correlation]

Row: Original Order    Flip: None    Col: Original Order    Flip: None    **Update**



Input pattern

**Finding Similar Patterns Dialog**

Option

Subject: Subject

Pattern: 4 4 4 1 4 3 5 5 4 1 3 3 3 0

Data Type: Continuous

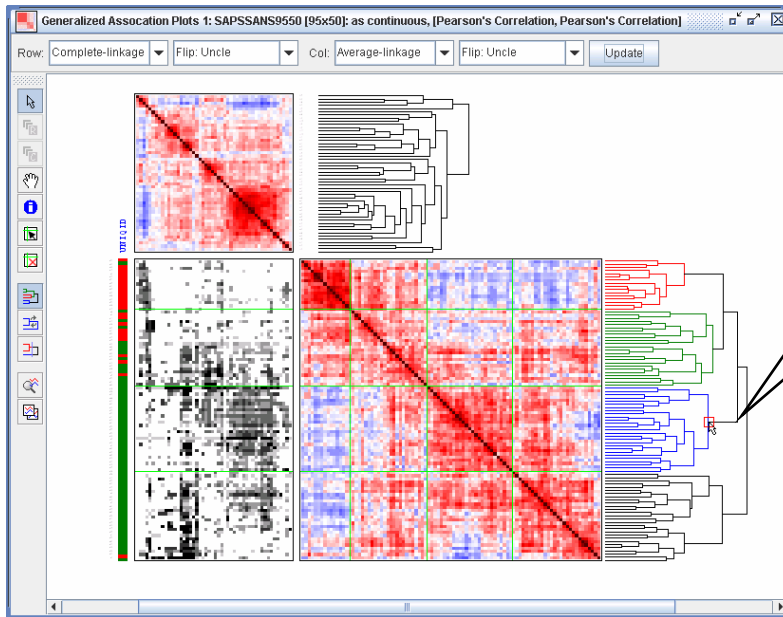
Similarity: Euclidean Distance

Preview

Compute    Close

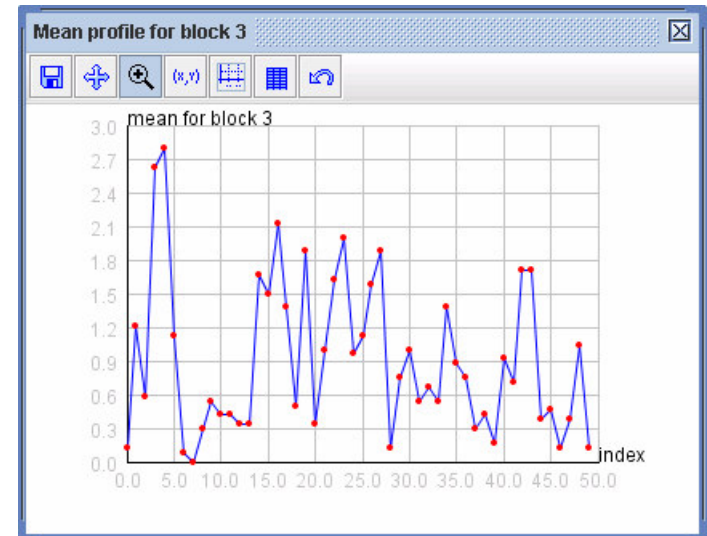
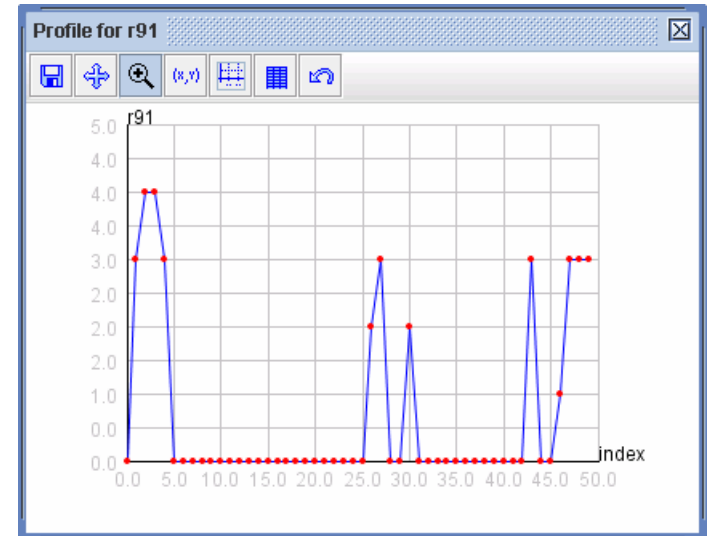


# Pop-Up Menu: Profile plot

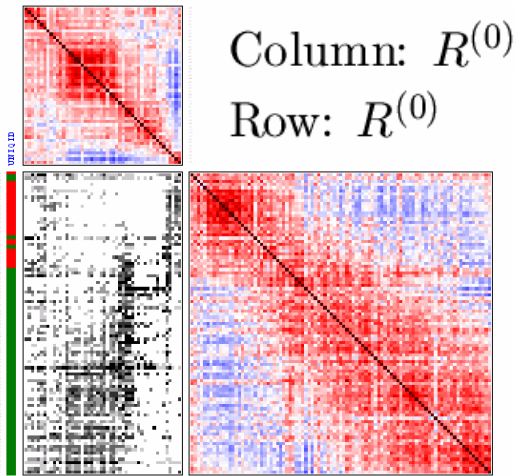


Select subtree

- Summary
- Restore
- Randomize
- Reverse
- Sort by...
- Sedimented
- Profile plot for...
  - this row
  - this block (mean)
  - this block (all)
  - all blocks (mean)
  - all blocks (all)
- Sort by this row
- Sort by this col
- Export...



# Converging Correlation Matrices



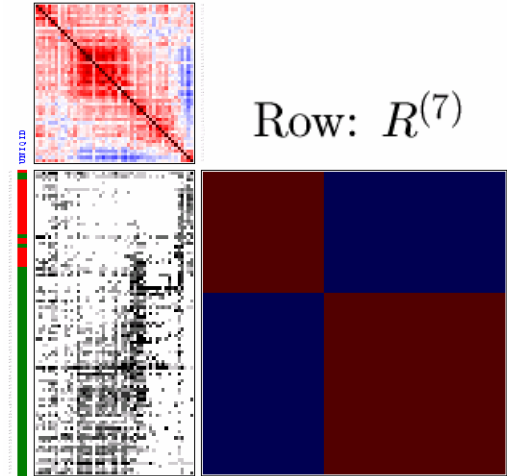
Converging Correlation Matrices

Row: 3  2D Plot  3D Plot

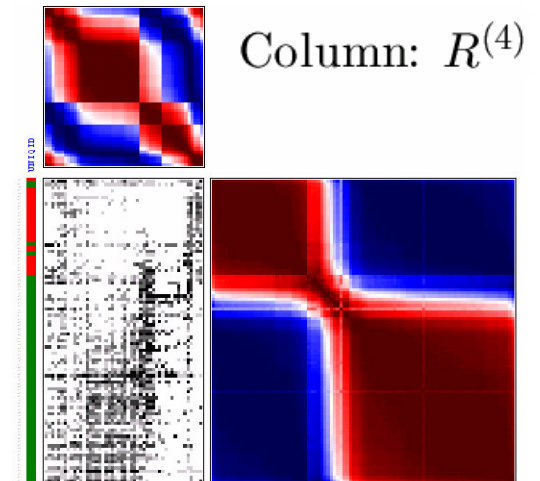
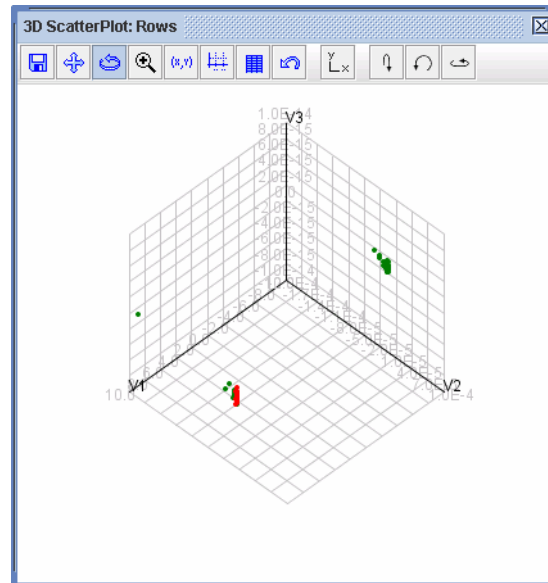
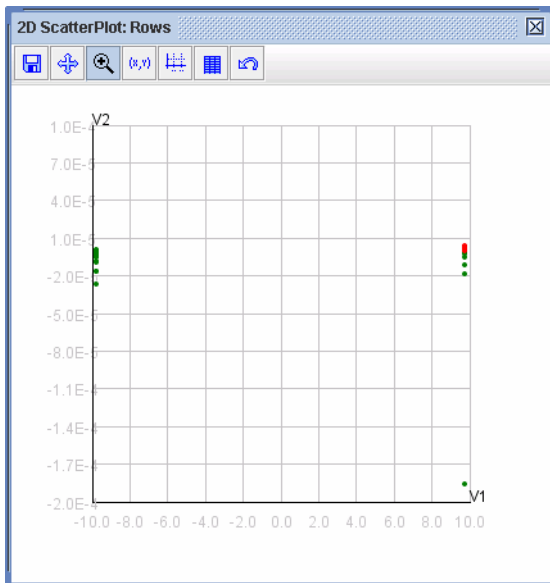
Column: 4  2D Plot  3D Plot

Navigation icons: Home, Previous, Play, Next

↑ ↑



Row:  $R^{(7)}$





# GAP Step 3: Partitions of Permuted Matrix Maps

**Finding Blocks:**

Row       Column

Simple      Simple

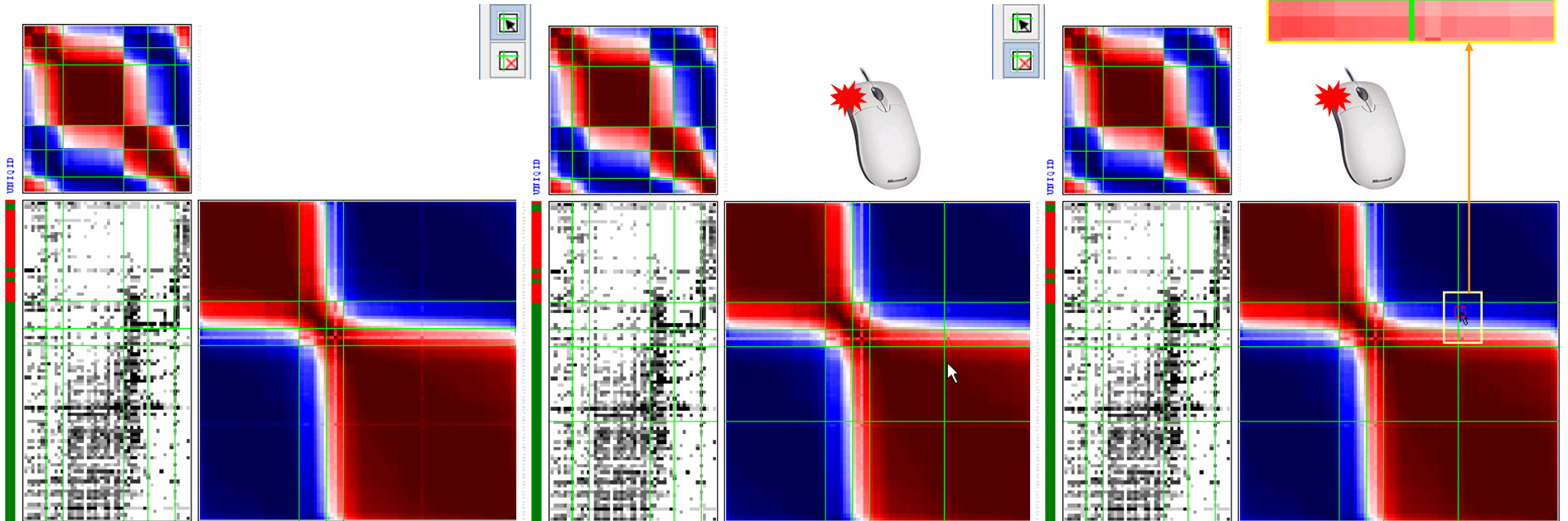
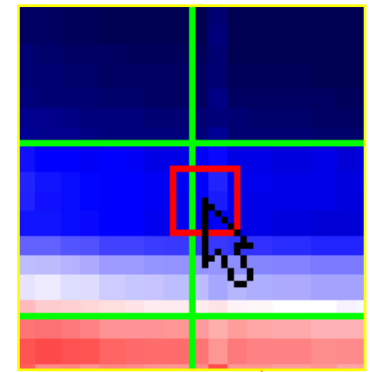
**Update**      **Clear**

- Simple
- Dendrogram
- max(BSS/WSS)

Generalized Association Plots 2: SAPSSANS9550 [95x50]: as continuous, [Pea

Row: Ellipse Sorting      Elliptical Guide      Col: Ellipse Sorting

UIQ ID







# GAP Step 4: Sufficient Graph

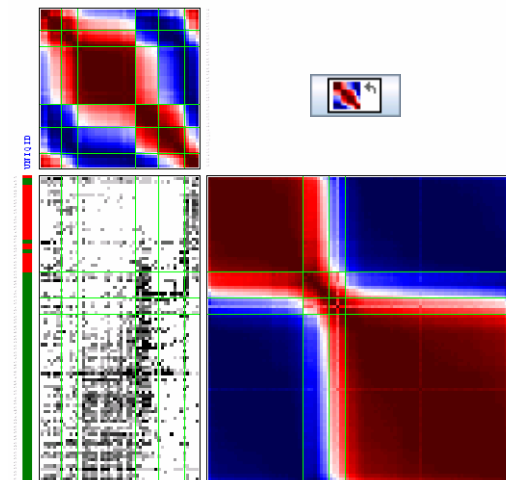
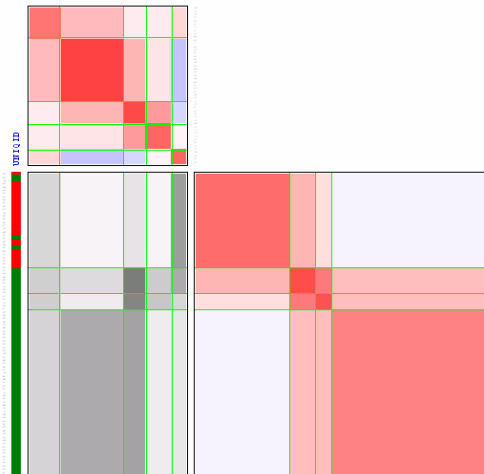
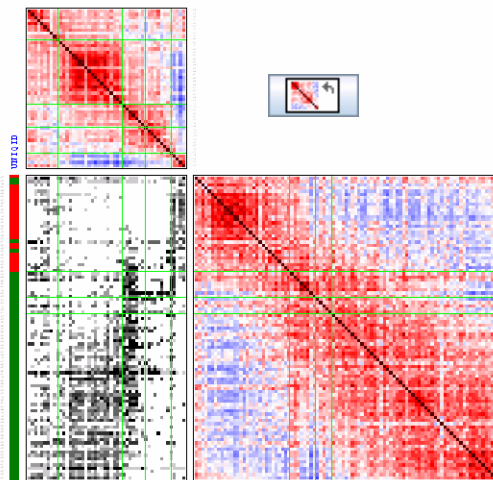
**Sufficient Graphs**

Matrix     Row     Column

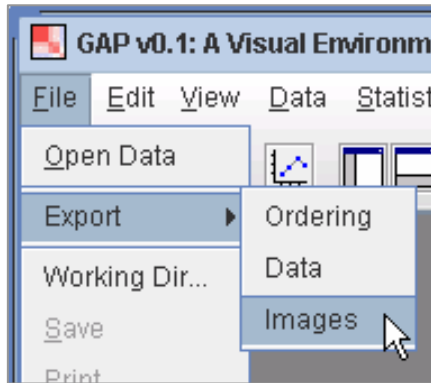
Mean    Mean    Mean

**Update**        

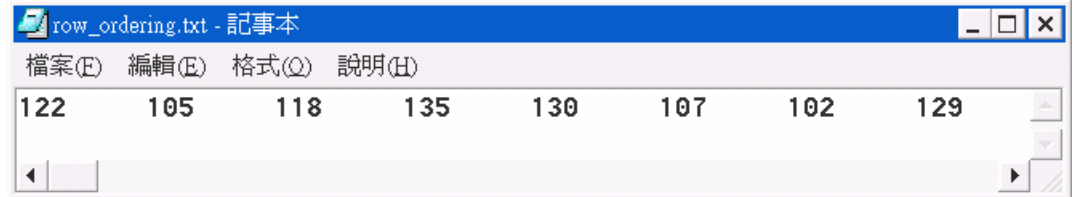
- Mean
- Median
- Std.
- CV



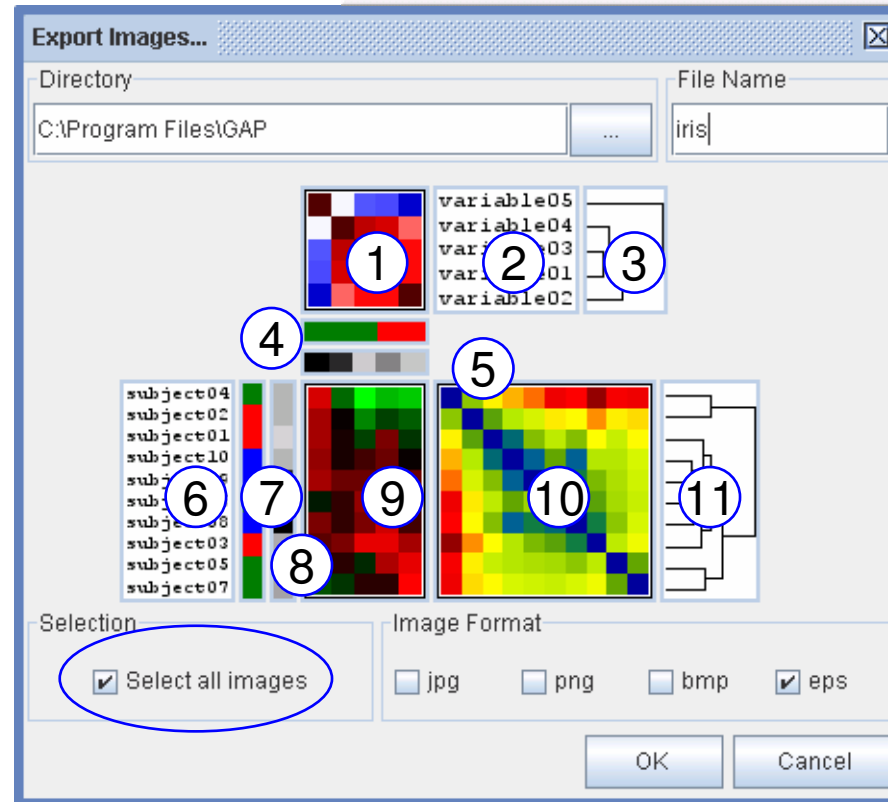
# Export Ordering, Data, Images



row\_ordering.txt  
col\_ordering.txt

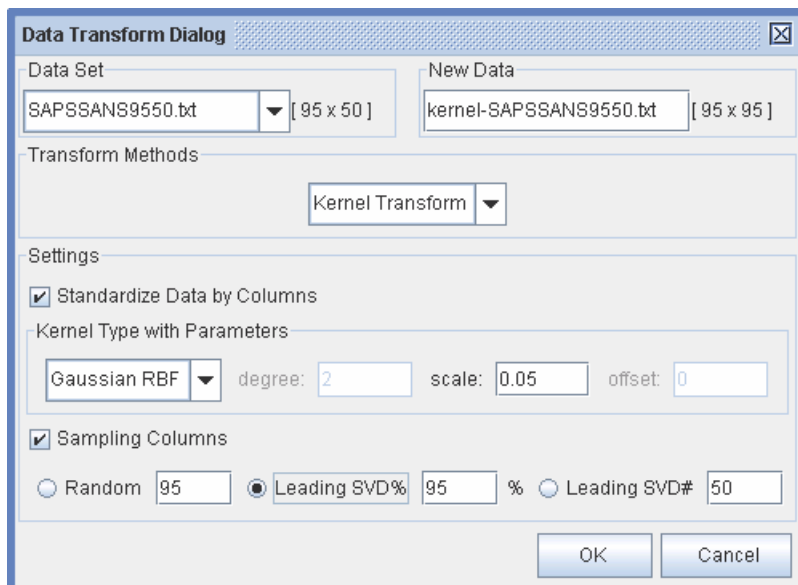
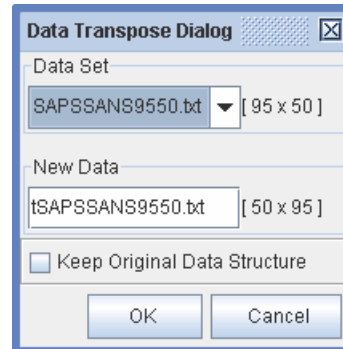
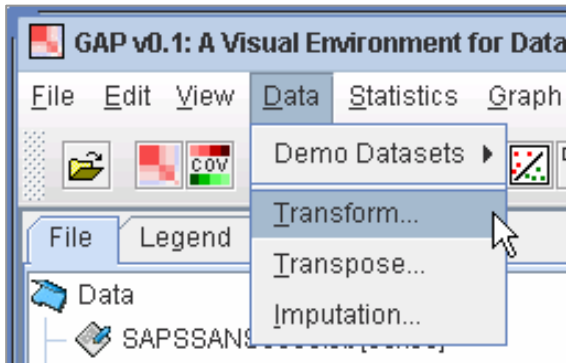


	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	LINGID	TH3	TH4	TH2	TH5	TH1	NE2	NE1	DL2	BE1	BE2	NA6	NC1	DL3	NC2	NE2	NE1
2	r62	1	1	5	1	5	5	5	0	2	3	1	1	4	4	2	
3	r27	2	2	1	2	1	1	2	0	0	2	0	1	0	2	2	
4	r52	0	0	2	0	2	0	3	0	0	0	0	0	0	2	0	
5	r4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
6	r89	0	0	1	2	2	2	1	0	0	0	0	0	0	0	0	
7	r84	0	0	1	0	2	1	1	0	0	2	1	1	1	1	1	
8	r88	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	
9	r60	2	0	3	1	3	3	3	2	0	0	0	0	0	3	0	
10	r90	0	0	3	0	2	0	2	0	0	0	0	0	0	0	0	
11	r87	0	0	0	0	0	1	1	0	2	3	2	2	0	1	0	
12	r91	0	0	0	0	0	2	3	3	3	3	0	2	0	3	0	
13	r86	0	0	0	0	0	0	3	0	2	3	0	0	0	0	0	
14	r15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
15	r6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
16	r72	0	0	0	0	0	1	3	0	1	0	1	0	1	0	2	
17	r90	0	0	0	0	2	1	1	0	2	2	1	0	0	0	0	
18	r86	0	0	0	0	0	1	3	0	1	0	2	0	0	2	1	
19	r71	0	0	0	0	3	4	0	0	3	0	0	0	0	0	0	
20	r9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
21	r94	0	0	0	2	0	0	3	0	0	0	0	0	0	3	0	
22	r51	5	5	5	0	5	0	2	0	0	2	2	0	3	0	2	
23	r91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
24	r82	0	2	3	0	3	2	3	0	0	0	0	0	0	0	0	
25	r24	0	0	0	0	3	2	0	0	2	0	1	0	0	0	0	
26	r25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	r80	0	0	0	0	2	0	3	0	1	0	0	0	2	0	0	
28	r13	0	0	0	0	0	3	3	0	0	0	0	0	1	0	0	
29	r89	3	3	0	4	2	3	0	0	2	2	0	0	2	0	4	
30	r83	0	3	4	4	0	0	1	0	0	2	0	0	0	0	0	
31	r89	0	0	3	0	0	2	0	0	3	3	2	1	0	2	0	
32	r29	4	4	3	1	4	1	1	0	0	1	1	0	0	1	1	
33	r19	0	0	0	0	2	2	2	0	0	1	0	0	3	0	2	
34	r64	3	4	4	2	5	5	4	0	2	4	2	0	4	0	0	
35	r42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
36	r75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
37	r33	0	0	0	0	0	2	0	0	0	0	0	0	0	2	0	
38	r3	0	3	0	0	0	0	0	0	0	1	0	0	0	0	0	
39	r73	2	3	0	0	3	2	2	0	0	2	2	0	0	4	0	
40	r86	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	
41	r10	0	0	0	0	0	2	0	0	0	0	0	0	0	3	0	
42	r20	3	4	3	0	4	5	4	0	2	4	0	3	0	3	0	
43	r1	0	0	0	0	0	2	0	0	0	2	0	0	0	3	0	
44	r56	0	2	1	2	2	1	2	0	0	0	0	0	0	3	1	
45	r11	0	0	0	0	0	1	1	1	3	0	3	0	2	0	0	
46	r7	0	3	0	0	0	1	0	0	0	0	0	0	0	3	0	
47	r57	0	3	0	0	0	1	1	0	0	2	0	0	0	0	3	
48	r70	0	0	0	0	0	2	2	0	0	0	2	0	3	0	0	
49	r40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

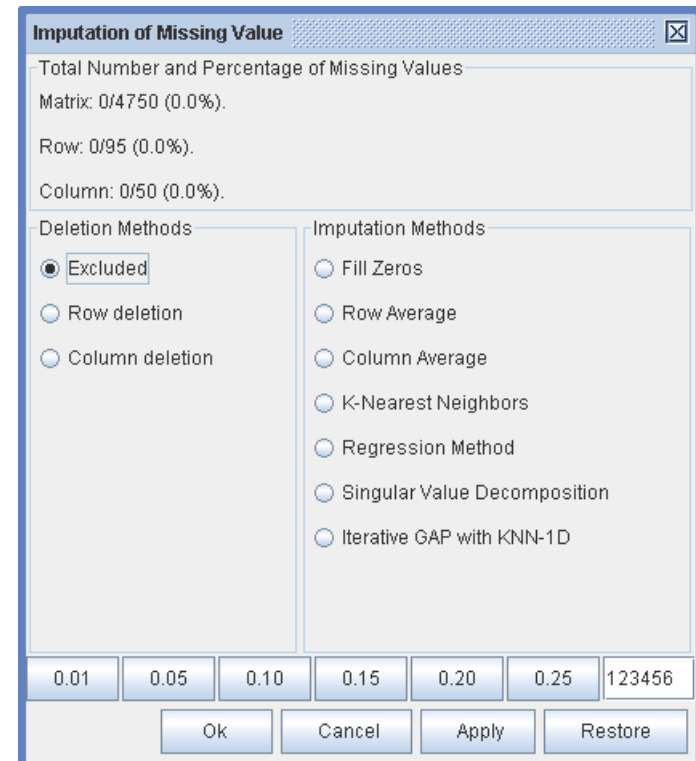


- 1 \_gapCol.eps
- 2 \_gapColName.eps
- 3 \_TreeCol.eps
- 4 \_gapXd.eps
- 5 \_gapXc.eps
- 6 \_gapRowName.eps
- 7 \_gapYd.eps
- 8 \_gapYc.eps
- 9 \_gapMatrix.eps
- 10 \_gapRow.eps
- 11 \_TreeRow.eps

# Data Processing



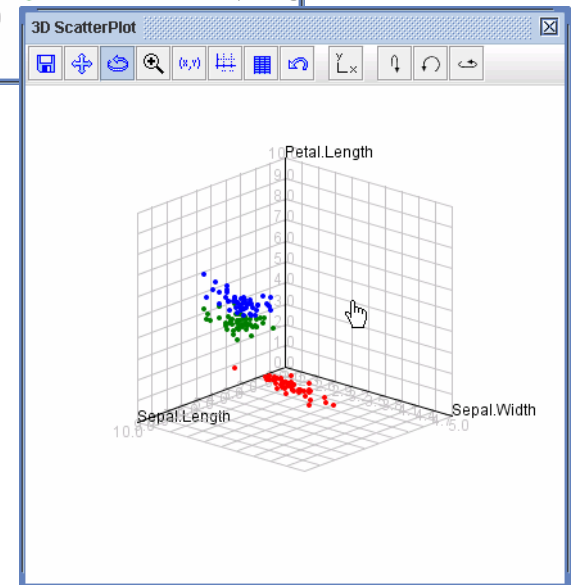
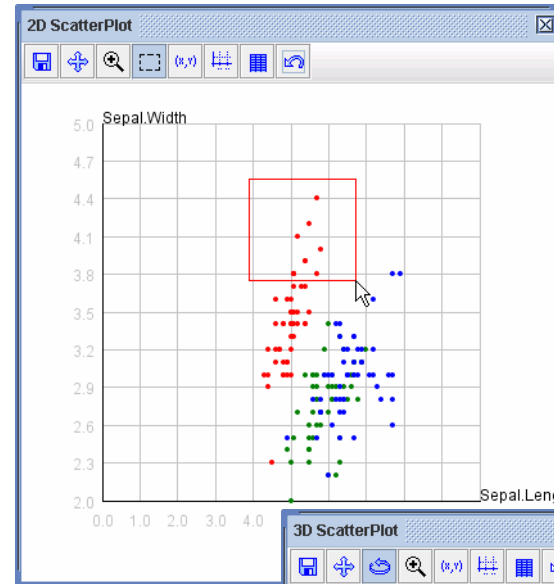
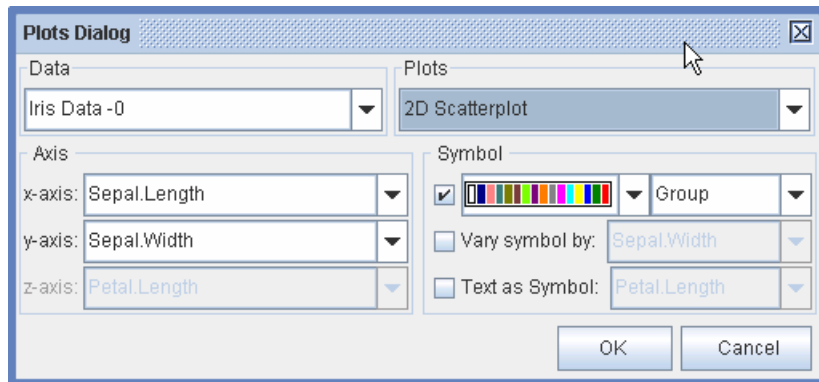
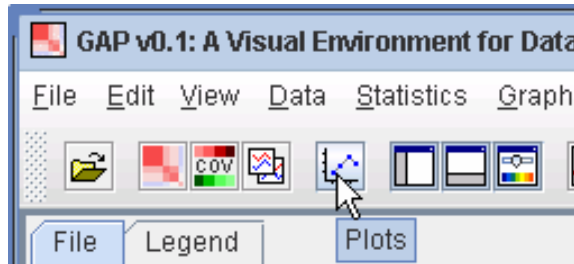
- Log
- Power
- (x) Transpose
- Center
- Scale
- Standardize
- Kernel Transform



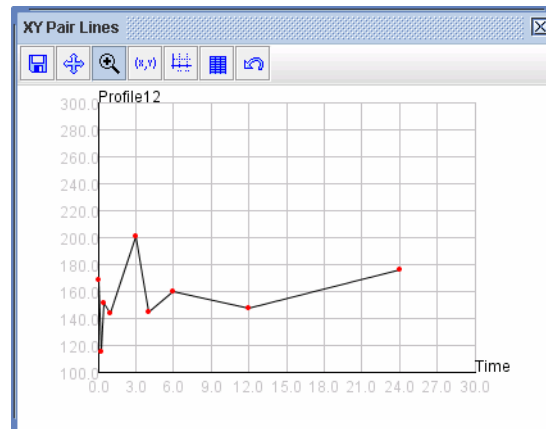




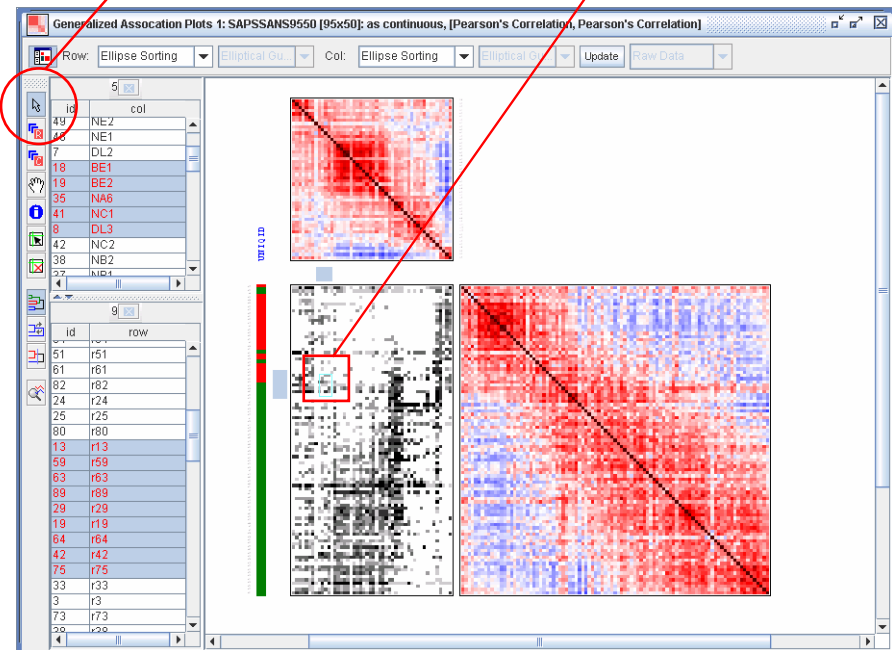
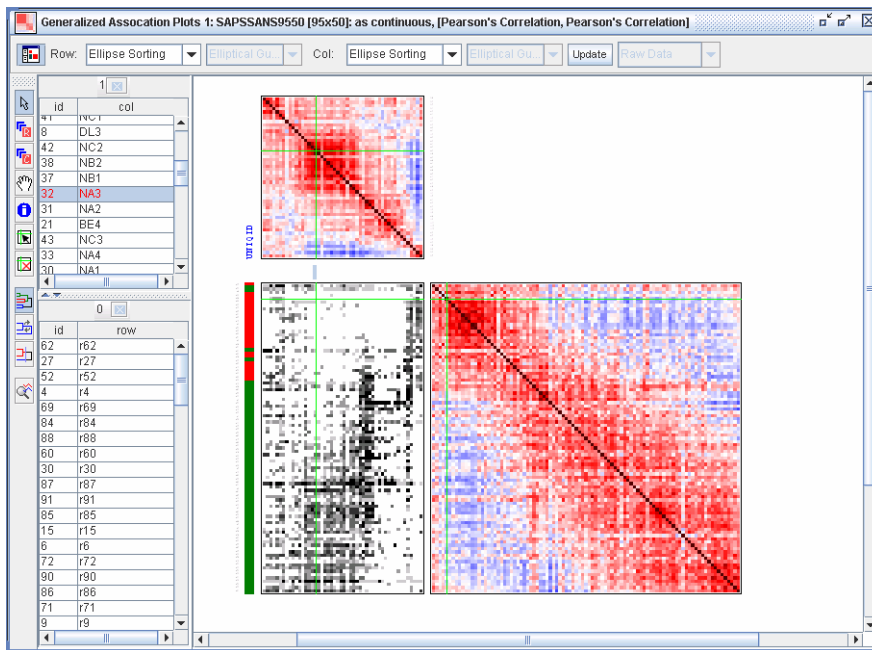
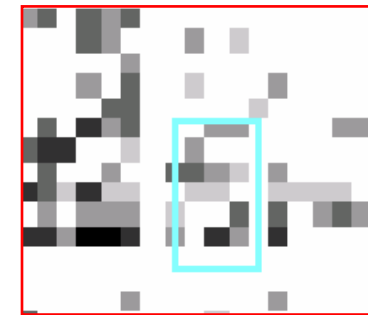
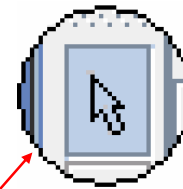
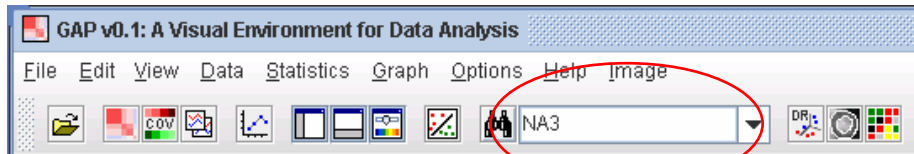
# Plots



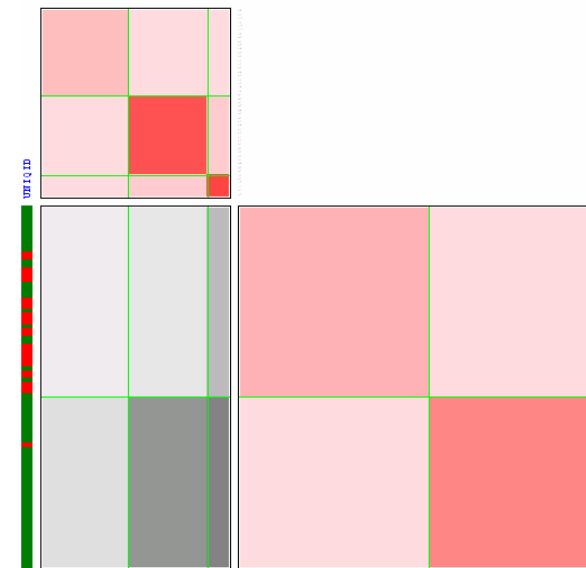
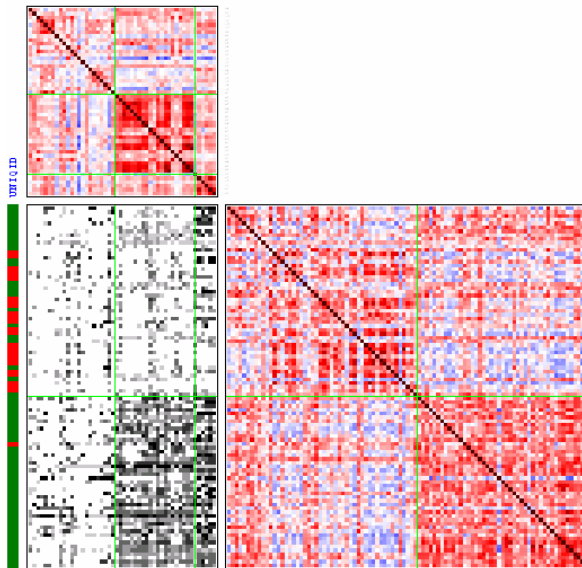
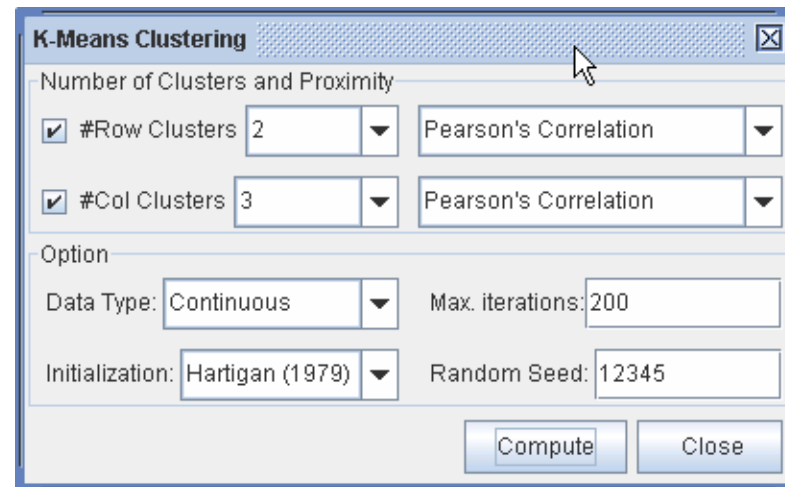
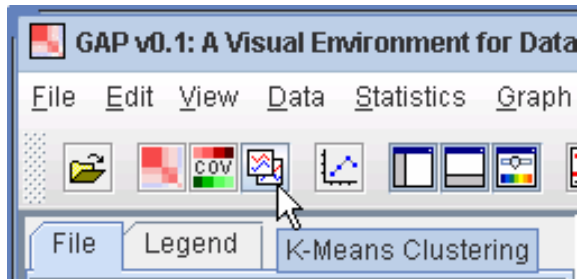
- 2D Scatterplot
- 3D Scatterplot
- XY PairLines Plot
- 2D Boxplot (X)
- 3D Boxplot (X)
- Histogram (X)



# Find... and Select

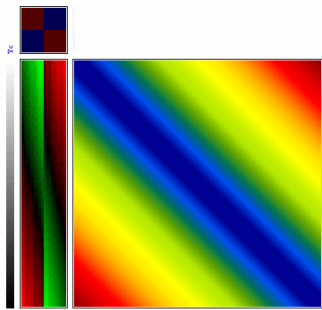


# K-means Clustering



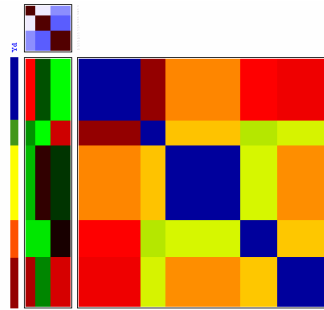


# GAP with Covariate Adjustment



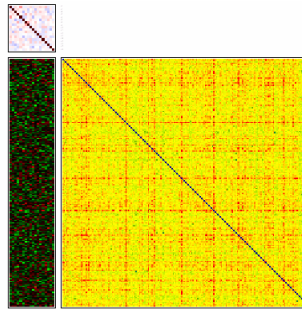
**Data (model):  
continuous pattern**

+



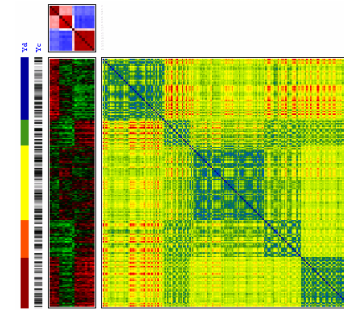
**Data (model):  
discrete pattern**

+



**Gaussian noise**

=



**Noisy data:  
mixed pattern**

**Generalized Association Plots**

Data Sets: noise.data.txt

as Continuous  as Binary  as Nominal  as Ordinal

Options:  Row Processing  Column Processing

Proximity Measure: Euclidean Distance | Pearson's Correlation

Seriation Method: Original Order | Original Order

Extensions:  Covariate Adjustment  Nonlinear Association

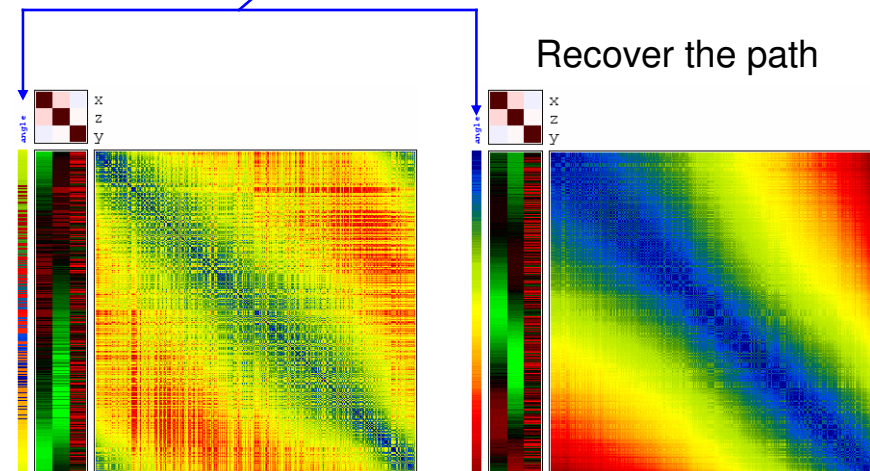
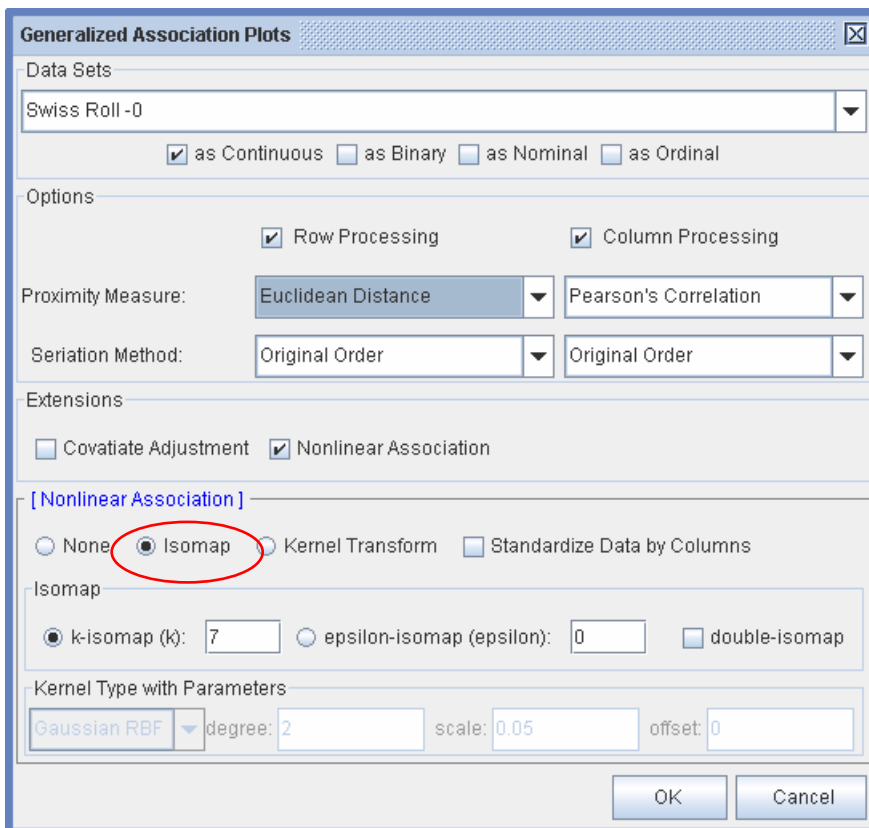
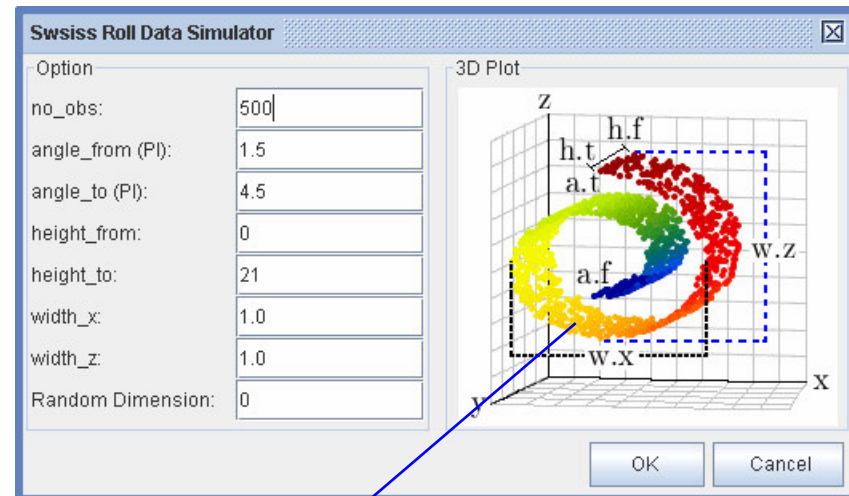
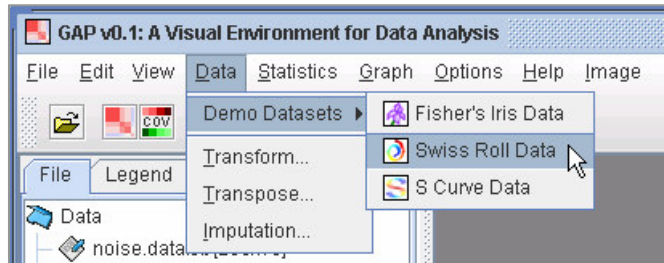
[ Covariate Adjustment ]

None  Continuous Covariate  Discrete Covariate

Variables: Yd | #Groups: 5

OK Cancel

# GAP with Nonlinear Association

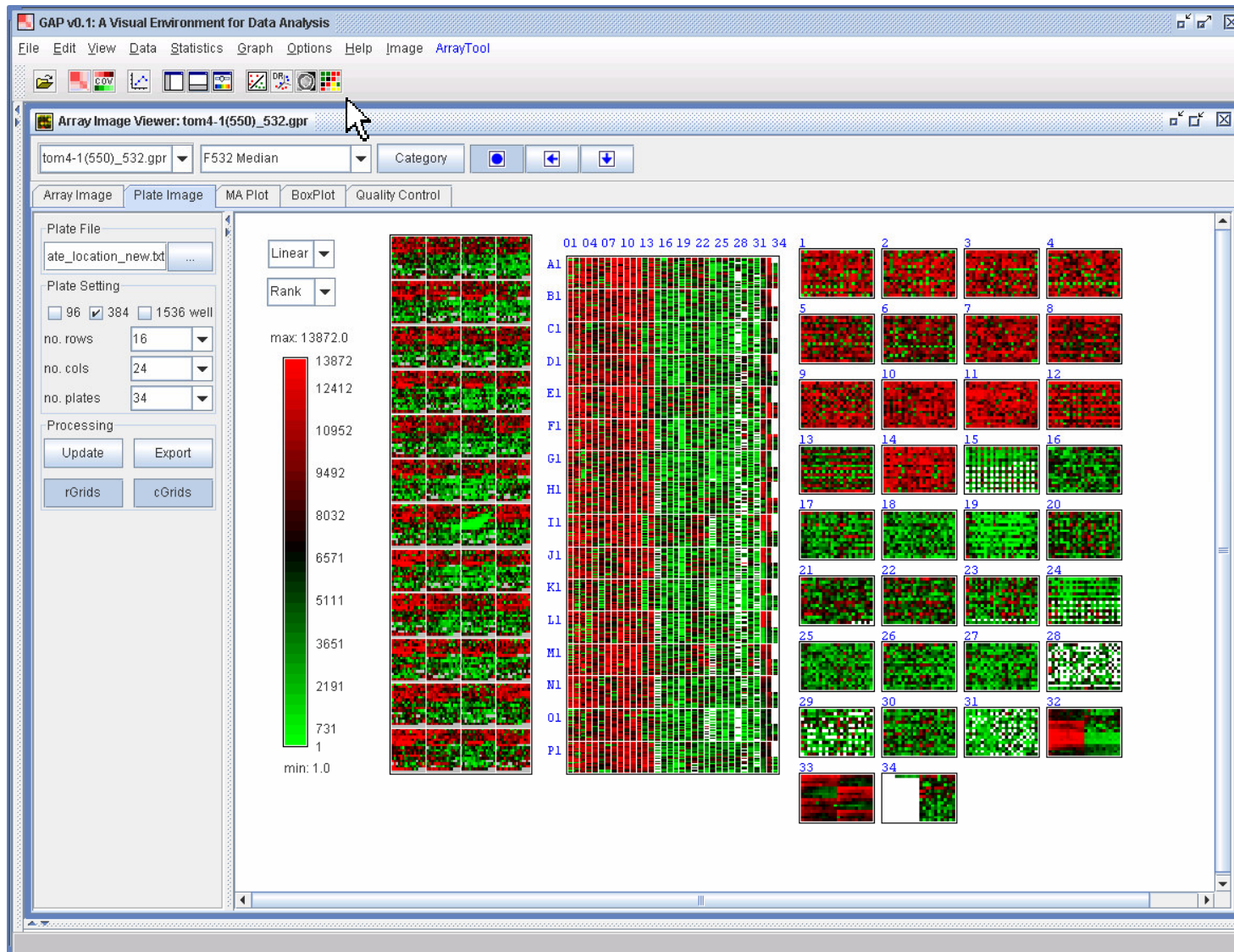


**GAP**

**isoGAP**



# GAP Module: Microarray Tool





# Web Site

## Lab for Information Visualization

Dimension Free Data Visualization  
Lab for Information Visualization  
資訊視覺化研究室  
中央研究院 統計科學研究所  
Institute of Statistical Science, Academia Sinica

Home | Research | Members | Database | Software

**Chun-houh Chen**  
陳君厚  
Associate Research Fellow  
Institute of Statistical Science  
Academia Sinica

- Information Visualization**
  - Generalized Association Plots (GAP)
  - Sliced Inverse Regression (SIR)
  - Multidimensional Scaling (MDS)
- Psychiatry Research**
  - Psychiatry
- Bioinformatics**
  - Microarray Data Analysis
  - SNPs
- Talks/Seminar**
  - Lecture Notes
  - Posters
- News/Conference** [more]
  - 2006: BIBE | CAMDA | CSB | GIW | IMS/ENAR | ISMB/ECCB | InfoVis | JSM | PSB

**H**andbook of Computational Statistics (Volume III): Data Visualization  
Chun-houh Chen, Wolfgang Härdle, and Antony Unwin (eds)  
Springer-Verlag, Heidelberg

<http://gap.stat.sinica.edu.tw>

<http://gap.stat.sinica.edu.tw/Software/GAP>

## GAP Software

GAP: Generalized Association Plots - Microsoft Internet Explorer

網址: <http://gap.stat.sinica.edu.tw/Software/GAP/index.htm>

GAP is a Java-designed software for generalized association plots (Chen, 2002) and exploratory data analysis. It is programmed for the Java runtime environment 1.5 (JRE version 1.5.0\_04), which is available for most operating systems.

**Authors:**  
[Han-Wine Wu](#) and [Chun-houh Chen](#) at  
[Lab for Information Visualization](#)  
Institute of Statistical Science,  
Academia Sinica  
Taipei, Taiwan, R. O. C.

**Official Website of GAP Software:**  
<http://gap.stat.sinica.edu.tw/Software/GAP>

**Current Version:**  
v0.1.014, Build 2006-02-07

**Contact:**  
[hmwu@stat.sinica.edu.tw](mailto:hmwu@stat.sinica.edu.tw)

**Features:**

- Clustering Analysis
- Various Display Conditions
- GAP with a Covariate Adjusted
- Nonlinear Association Analysis
- Missing Value Imputation
- Histogram, 2D Scatterplot, 3D Scatterplot (Rotatable)

More...

**Latest Features** The latest features of GAP.

**FAQ** Frequently asked questions.

**Bug Reports/Fixed** Bug reports and fixed.

## GAP Forum

Generalized Association Plots (GAP) Forum - Microsoft Internet Explorer

網址: <http://140.109.74.128/GAPforums/index.php>

**Generalized Association Plots (GAP) Forum**  
GAP: a graphical environment for matrix visualization and information mining

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**Announcement**

GAP is a Java-designed software for general purposes matrix visualization (MV) and exploratory data analysis (EDA). It provides powerful visual aids for rapid and dynamic exploration of a data matrix and the corresponding proximity matrices for variables and subjects interactively. Various clustering methods with internal/external permutation algorithms are developed. GAP also offers other unique functionalities with friendly graphical user interface. Please visit us at [Lab for Information Visualization](#)

GAP Forum	Topics	Posts	Last post
<b>News &amp; updates</b> Announcements, news and updates about GAP. (Moderated by <a href="#">hmwu</a> )	1	1	2006-02-05 17:02:23 by <a href="#">hmwu</a>
<b>General</b> Questions about using GAP (Moderated by <a href="#">hmwu</a> )	0	0	
<b>Suggestions &amp; Feedback</b> Give us your thoughts and comments to improve GAP. (Moderated by <a href="#">hmwu</a> )	0	0	
<b>Bug Report</b> Please report bugs here! (Moderated by <a href="#">hmwu</a> )	0	0	

Newest registered user: [hoh1](#)  
Registered users online: 0  
Guests online: 1

Total number of registered users: 2  
Total number of topics: 1  
Total number of posts: 1

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