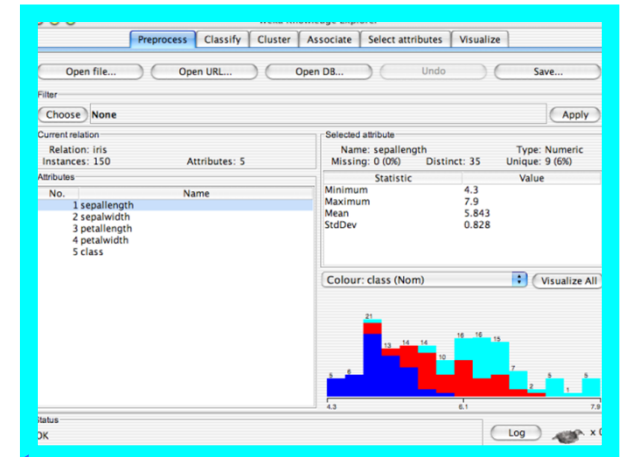


Clustering

Explorer: clustering data

- WEKA contains “clusterers” for finding groups of similar instances in a dataset
- Implemented schemes are:
 - *k*-Means, EM, Cobweb, *X*-means, FarthestFirst
- Clusters can be visualized and compared to “true” clusters (if given)



Open file...

Open URL...

Open DB...

Undo

Edit...

Save...

Filter

Choose

None

Apply

Current relation

Relation: None

Instances: None

Attributes: None

Selected attribute

Name: None

Missing: None

Distinct: None

Type: None

Unique: None

Attributes

All

None

Invert

Remove

Visualize All

Status

Welcome to the Weka Explorer

Log

x 0

Preprocess | Classify | Cluster | Associate | Select attributes | Visualize

Open file...

Open URL...

Open DB...

Undo

Edit...

Save...

Filter

Choose

None

Apply

Current relation

Relation: None

Instances: None

Attributes: None

Selected attribute

Name: None

Missing: None

Distinct: None

Type: None

Unique: None

Attributes

All

None

Invert

Remove

Visualize All

Status

Welcome to the Weka Explorer

Log

x 0

Open file...

Open URL...

Open DB...

Undo

Edit...

Save...

Filter

Choose

None

Apply

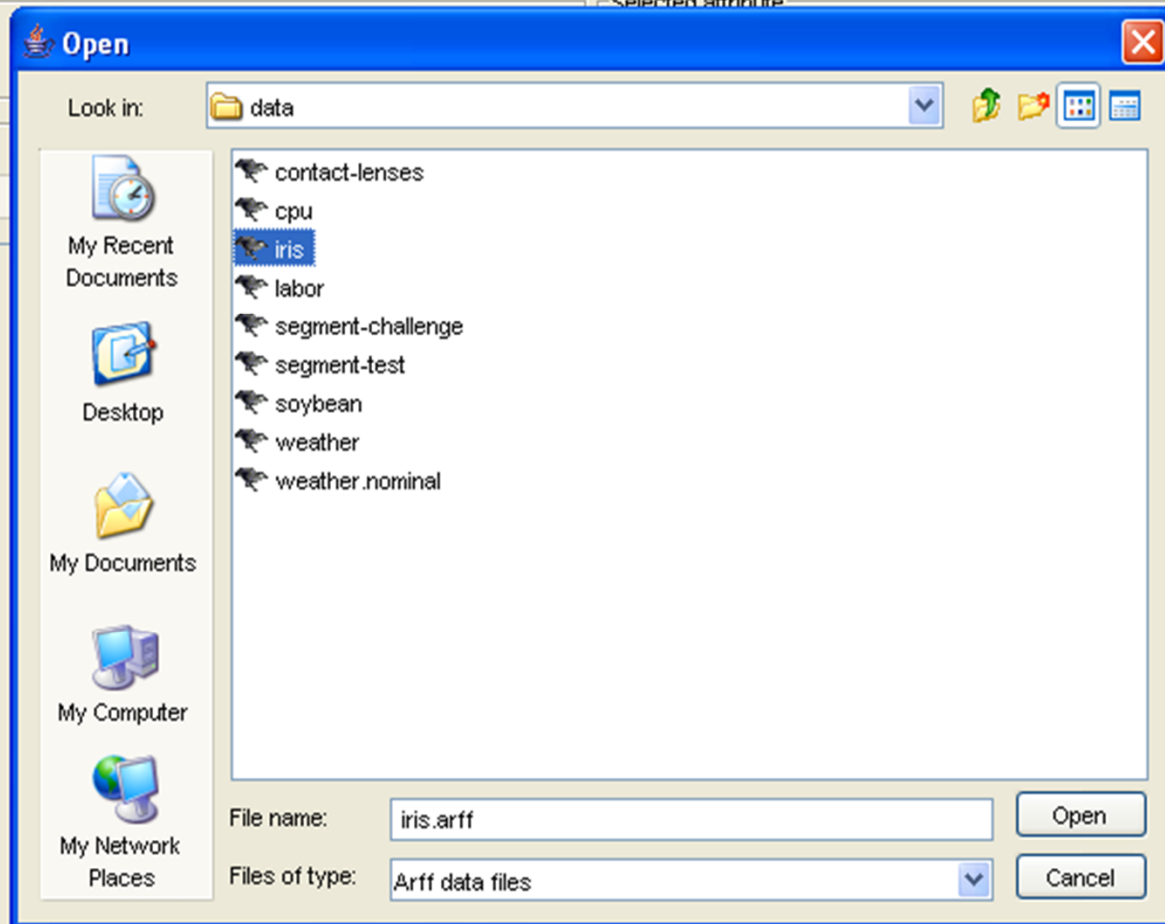
Current relation

Relation: None

Instances: None

Attributes

All



Type: None

Unique: None

Visualize All

Remove

Status

Welcome to the Weka Explorer

Log

x 0

Preprocess Classify Cluster Associate Select attributes Visualize

Open file...

Open URL...

Open DB...

Undo

Edit...

Save...

Filter

Choose **None**

Apply

Current relation

Relation: iris
Instances: 150

Attributes: 5

Attributes

All

None

Invert

No.	Name
1	<input checked="" type="checkbox"/> sepallength
2	<input type="checkbox"/> sepalwidth
3	<input type="checkbox"/> petallength
4	<input type="checkbox"/> petalwidth
5	<input type="checkbox"/> class

Remove

Selected attribute

Name: sepallength

Missing: 0 (0%)

Distinct: 35

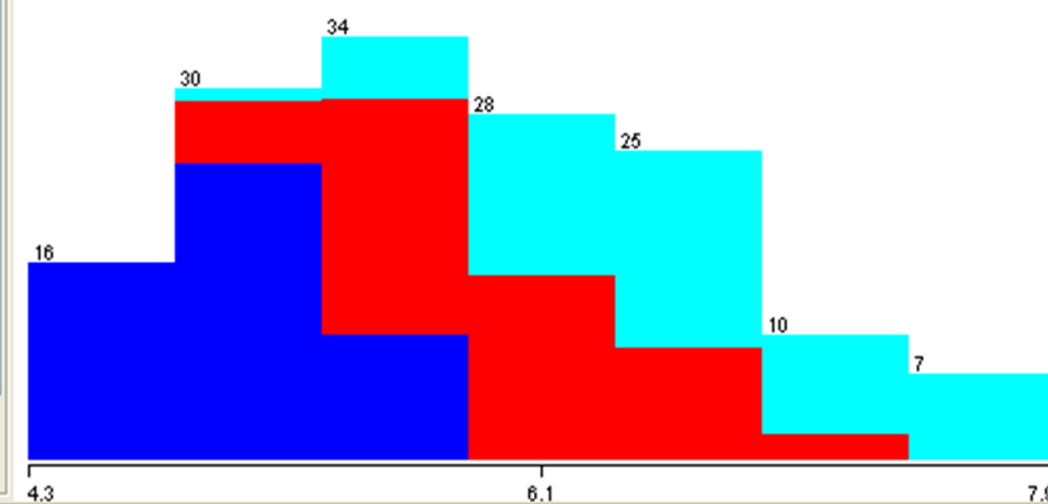
Type: Numeric

Unique: 9 (6%)

Statistic	Value
Minimum	4.3
Maximum	7.9
Mean	5.843
StdDev	0.828

Class: class (Nom)

Visualize All



Status

OK

Log

x 0

Preprocess **Classify** Cluster Associate Select attributes Visualize

Open file...

Open URL...

Open DB...

Undo

Edit...

Save...

Filter

Choose **None**

Apply

Current relation

Relation: iris
Instances: 150

Attributes: 5

Attributes

All

None

Invert

No.	Name
1	<input checked="" type="checkbox"/> sepallength
2	<input type="checkbox"/> sepalwidth
3	<input type="checkbox"/> petallength
4	<input type="checkbox"/> petalwidth
5	<input type="checkbox"/> class

Remove

Selected attribute

Name: sepallength

Missing: 0 (0%)

Distinct: 35

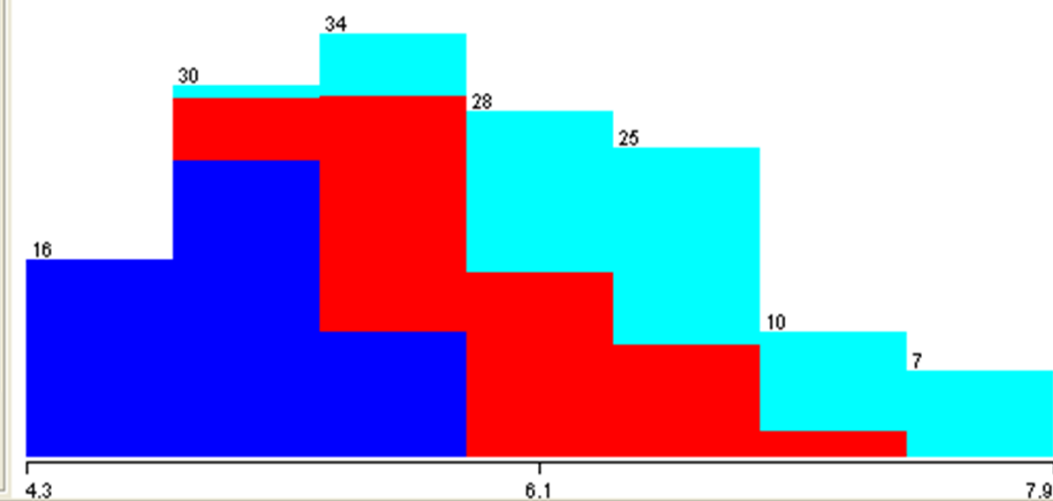
Type: Numeric

Unique: 9 (6%)

Statistic	Value
Minimum	4.3
Maximum	7.9
Mean	5.843
StdDev	0.828

Class: class (Nom)

Visualize All



Status

OK

Log

x 0

Preprocess Classify Cluster Associate Select attributes Visualize

Clusterer

Choose EM -I 100 -N -1 -S 100 -M 1.0E-6

Cluster mode

 Use training set Supplied test set

Set...

 Percentage split

%

66

 Classes to clusters evaluation (Nom) class Store clusters for visualization

Ignore attributes

Start

Stop

Result list (right-click for options)

Clusterer output

Status

OK

Log

 x 0

Clusterer

 EM -I 100 -N -1 -S 100 -M 1.0E-6

Cluster mode

 Use training set Supplied test set

Set...

 Percentage split

%

66

 Classes to clusters evaluation (Nom) class Store clusters for visualization

Result list (right-click for options)

Clusterer output

Status

OK

 x 0

Clusterer

- weka
 - clusterers
 - Cobweb
 - EM
 - FarthestFirst
 - MakeDensityBasedClusterer
 - SimpleKMeans

Clusterer output

Preprocess Classify Cluster Associate Select attributes Visualize

Clusterer

Choose SimpleKMeans -N 2 -S 10

Cluster mode

 Use training set Supplied test set Percentage split Classes to clusters evaluation (Nom) class Store clusters for visualization

right-click

Ignore attributes

Start

Stop

Result list (right-click for options)

Clusterer output

Status

OK

Log

x 0

Preprocess Classify Cluster Associate Select attributes Visualize

Clusterer

Choose SimpleKMeans -N 2 -S 10

Cluster mode

 Use training set Supplied test set

Set...

 Percentage split

%

66

 Classes (Nom) class Store cluster

Result list (right)

Clusterer output

weka.gui.GenericObjectEditor

weka.clusterers.SimpleKMeans

About

Cluster data using the k means algorithm

More

numClusters

2

seed

10

Open...

Save...

OK

Cancel

Information

NAME

weka.clusterers.SimpleKMeans

SYNOPSIS

Cluster data using the k means algorithm

OPTIONS

numClusters -- set number of clusters

seed -- random number seed

Status

OK

Log

x 0

Clusterer
Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

Use training set

Supplied test set

Percentage split

Classes to cluster

(Nom) class

Store clusters

Clusterer output

Result list (right)

weka.gui.GenericObjectEditor

weka.clusterers.SimpleKMeans

About

Cluster data using the k means algorithm

numClusters

seed

Clusterer

Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

- Use training set
- Supplied test set
- Percentage split %
- Classes to clusters evaluation
- Evaluate clusters with respect to a class
- Store clusters for visualization

Result list (right-click for options)

Clusterer output

Status

OK

x 0

Preprocess | Classify | Cluster | Associate | Select attributes | Visualize

Clusterer

Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

 Use training set Supplied test set

Set...

 Percentage split

%

66

 Classes to clusters evaluation

(Nom) class

 Store clusters for visualization

Ignore attributes

Start

Stop

Result list (right-click for options)

Clusterer output

Status

OK

Log

x 0

Clusterer

 Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

 Use training set

 Supplied test set

Set...

 Percentage split

%

66

 Classes to clusters evaluation

(Nom) class

 Store clusters for visualization

Ignore attributes

Start

Stop

Result list (right-click for options)

12:19:11 - SimpleKMeans

Clusterer output

=== Run information ===

Scheme: weka.clusterers.SimpleKMeans -N 3 -S 10

Relation: iris

Instances: 150

Attributes: 5

sepallength

sepalwidth

petallength

petalwidth

Ignored:

class

Test mode: Classes to clusters evaluation on training data

=== Model and evaluation on training set ===

kMeans

=====

Number of iterations: 6

Within cluster sum of squared errors: 6.9981140048267605

Cluster centroids:

Cluster 0

Mean/Mode: 5.8885 2.7377 4.3967 1.418

Std Devs: 0.4487 0.2934 0.5269 0.2723

Cluster 1

Mean/Mode: 5.006 3.418 1.464 0.244

Std Devs: 0.3525 0.381 0.1735 0.1072

Cluster 2

Mean/Mode: 6.8462 3.0821 5.7026 2.0795

Status

OK

Log

x 0

Clusterer

 Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

 Use training set

 Supplied test set

 Percentage split
 %

 Classes to clusters evaluation

 Store clusters for visualization

Result list (right-click for options)

12:19:11 - SimpleKMeans

Clusterer output

```
Cluster 0
  Mean/Mode:  5.8885 2.7377 4.3967 1.418
  Std Devs:   0.4487 0.2934 0.5269 0.2723
Cluster 1
  Mean/Mode:  5.006  3.418  1.464  0.244
  Std Devs:   0.3525 0.381  0.1735 0.1072
Cluster 2
  Mean/Mode:  6.8462 3.0821 5.7026 2.0795
  Std Devs:   0.5025 0.2799 0.5194 0.2811
```

Clustered Instances

```
0      61 ( 41%)
1      50 ( 33%)
2      39 ( 26%)
```

Class attribute: class

Classes to Clusters:

```
  0  1  2  <-- assigned to cluster
  0 50  0  | Iris-setosa
 47  0  3  | Iris-versicolor
 14  0 36  | Iris-virginica
```

Cluster 0 <-- Iris-versicolor

Cluster 1 <-- Iris-setosa

Cluster 2 <-- Iris-virginica

Incorrectly clustered instances : 17.0 11.3333 %

Status

OK

x 0

Clusterer

 Choose **SimpleKMeans -N 3 -S 10**

Cluster mode

- Use training set
 Supplied test set
 Percentage split %
 Classes to clusters evaluation

 Store clusters for visualization

right-click

Result list (right-click for options)

12:19:11 - SimpleKMeans

- View in main window
- View in separate window
- Save result buffer
- Load model
- Save model
- Re-evaluate model on current test set
- Visualize cluster assignments**
- Visualize tree

Clusterer output

```

Cluster 0
  Mean/Mode:  5.8885 2.7377 4.3967 1.418
  Std Devs:   0.4487 0.2934 0.5269 0.2723
Cluster 1
  Mean/Mode:  5.006  3.418  1.464  0.244
  Std Devs:   0.3525 0.381  0.1735 0.1072
Cluster 2
  Mean/Mode:  6.8462 3.0821 5.7026 2.0795
  Std Devs:   0.5025 0.2799 0.5194 0.2811
  
```

Clustered Instances

```

0      61 ( 41%)
1      50 ( 33%)
      39 ( 26%)
  
```

Class attribute: class

Classes to Clusters:

```

1 2 <-- assigned to cluster
50 0 | Iris-setosa
0 3 | Iris-versicolor
0 36 | Iris-virginica
  
```

Cluster 0 <-- Iris-versicolor

Cluster 1 <-- Iris-setosa

Cluster 2 <-- Iris-virginica

Incorrectly clustered instances : 17.0 11.3333 %

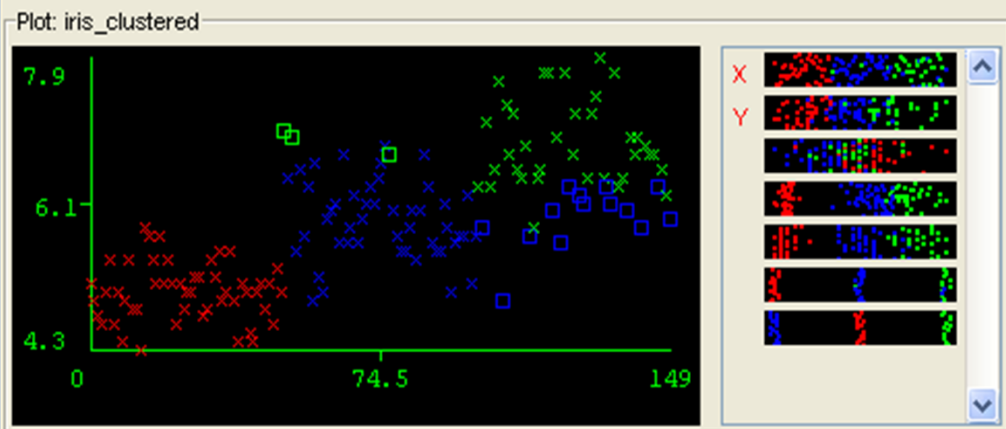
Status

OK

x 0

X: Instance_number (Num) Y: sepallength (Num)
 Colour: Cluster (Nom) Select Instance

Reset Clear Save Jitter



Class colour

cluster0 cluster1 cluster2

85	2.7377	4.3967	1.418
87	0.2934	0.5269	0.2723
5	3.418	1.464	0.244
25	0.381	0.1735	0.1072
52	3.0821	5.7026	2.0795
25	0.2799	0.5194	0.2811

```

Class attribute: class
Classes to Clusters:

 0  1  2  <-- assigned to cluster
 0 50  0  | Iris-setosa
47  0  3  | Iris-versicolor
14  0 36  | Iris-virginica

Cluster 0 <-- Iris-versicolor
Cluster 1 <-- Iris-setosa
Cluster 2 <-- Iris-virginica

Incorrectly clustered instances :      17.0      11.3333 %
    
```

X: Instance_number (Num)

Y: sepallength (Num)

Colour: Cluster (Nom)

Select Instance

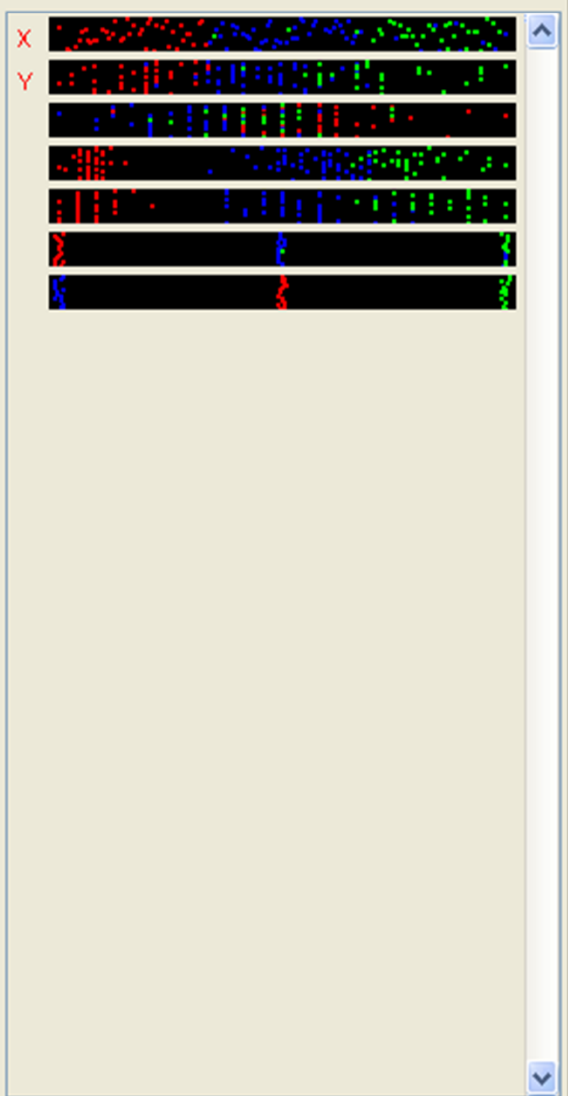
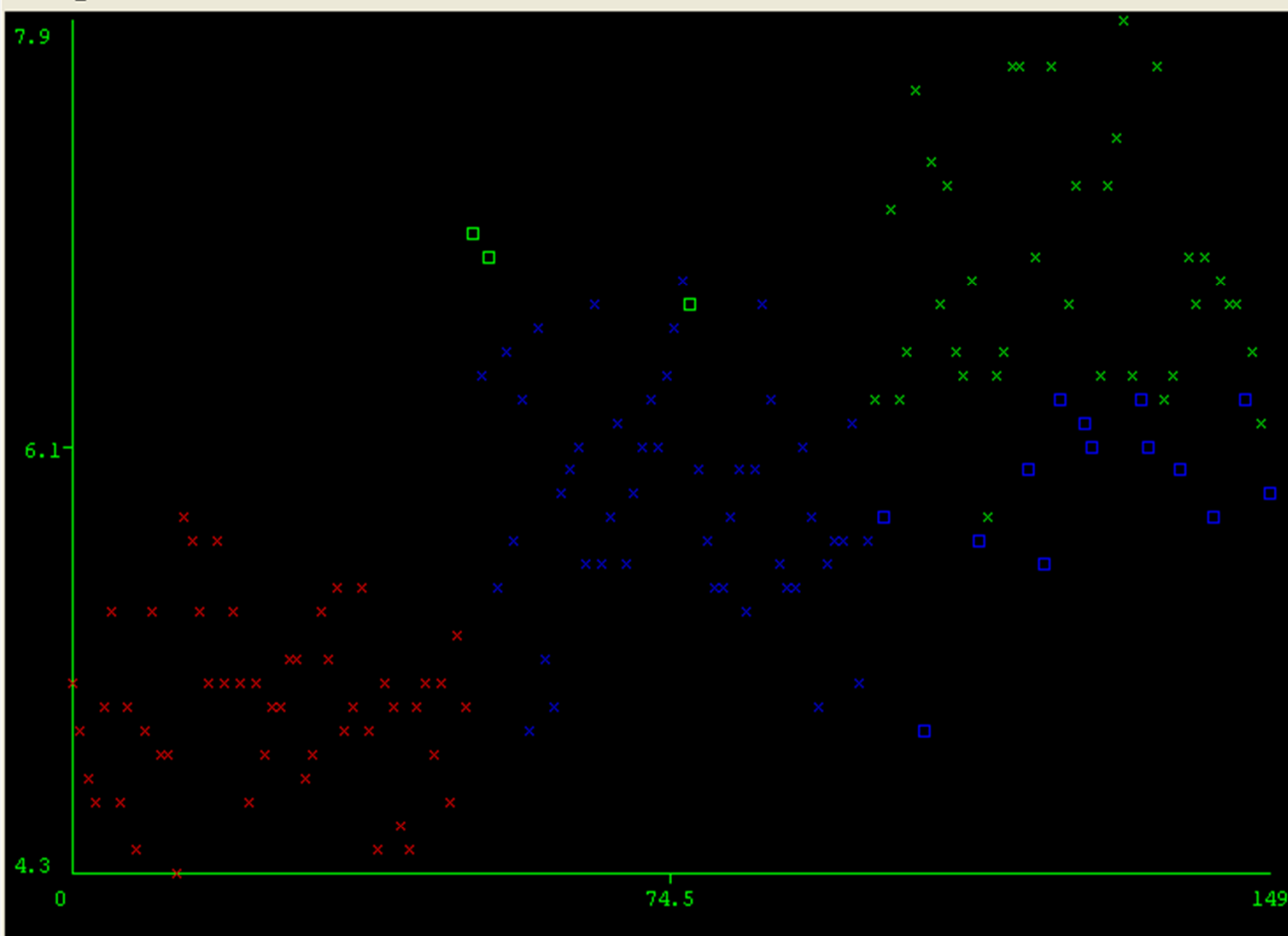
Reset

Clear

Save

Jitter

Plot: iris_clustered



Class colour

cluster0

cluster1

cluster2

Experiment other visualization options

Experiment different
clustering parameters and algorithms

gCLUTO - Graphical Clustering Toolkit | Karypis Lab - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Refresh Home Search Favorites

Google gcluto Go

Bookmarks 11692 blocked Check AutoLink AutoFill Send to gcluto Settings

Address http://glaros.dtc.umn.edu/gkhome/cluto/gcluto/overview Go

Home | Contact | METIS | CLUTO | Forums

Karypis Lab

Search

Navigation

- Home
- Research
 - Projects
 - Software
 - METIS
 - CLUTO
 - CLUTO
 - gCLUTO
 - wCLUTO
 - PAFI
 - YASSPP
 - AFGen
 - SUGGEST
 - MGridGen
 - PSPASES
 - Publications
- Education
- Lab Information

Home » Research » Software » CLUTO

gCLUTO - Graphical Clustering Toolkit

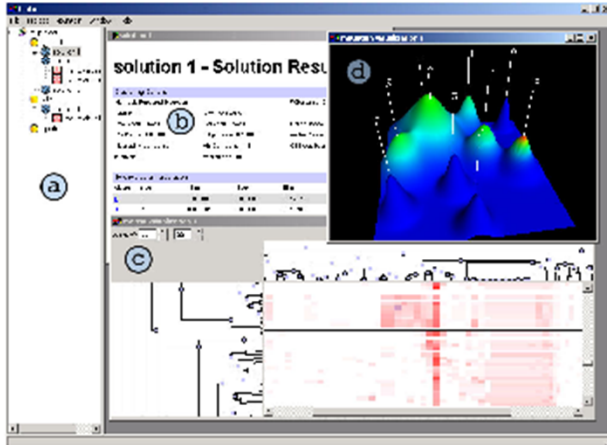
Overview Download Changes Publications

Current version: 1.0, 11/27/03

gCLUTO is a cross-platform graphical application for clustering low- and high-dimensional datasets and for analyzing the characteristics of the various clusters. gCLUTO is build on-top of the CLUTO clustering library.

gCLUTO provides tools for visualizing the resulting clustering solutions using tree, matrix, and an OpenGL-based mountain visualization.

Here are some screenshots of gCLUTO's various screens and visualizations.



Support

Forum

If you encounter any problems or have any "how to use" questions take a look at the community discussion [forums](#).

Bugs or Suggestions?

If you have any suggestions or you have found a bug please use the [online bug & issue](#) tracking system.

Open positions

The lab has open postdoctoral positions on research projects related to [chemical informatics](#) and [data mining](#).

Active forum topics

- Mesh2Dual -> AdaptiveRapart
- 64bit CLUTO

<http://glaros.dtc.umn.edu/gkhome/cluto/gcluto/overview>

gCLUTO - Graphical Clustering Toolkit | Karypis Lab - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Home Search Favorites Refresh Print Mail W Go

Google G gcluto Go 11692 blocked Check AutoLink AutoFill Send to gcluto Settings Go

Address http://glaros.dtc.umn.edu/gkhome/cluto/gcluto/overview

Home | Contact | METIS | CLUTO | Forums

Karypis Lab

Search

Navigation

- Home
- Research
 - Projects
 - Software
 - METIS
 - CLUTO
 - CLUTO
 - gCLUTO**
 - wCLUTO
 - PAFI
 - YASSPP
 - AFGen
 - SUGGEST
 - MGridGen
 - PSPASES
 - Publications
- Education
- Lab Information

Home » Research » Software » CLUTO

gCLUTO - Graphical Clustering Toolkit

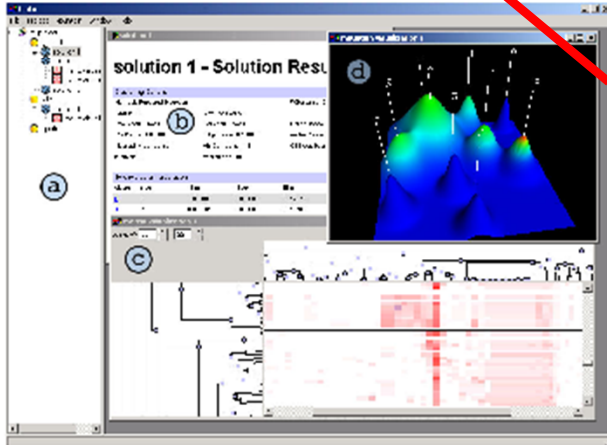
Overview **Download** Changes Publications

Current version: 1.0, 11/27/03

gCLUTO is a cross-platform graphical application for clustering low- and high-dimensional datasets and for analyzing the characteristics of the various clusters. gCLUTO is build on-top of the CLUTO clustering library.

gCLUTO provides tools for visualizing the resulting clustering solutions using tree, matrix, and an OpenGL-based mountain visualization.

Here are some screenshots of gCLUTO's various screens and visualizations.



Support

Forum

If you encounter any problems or have any "how to use" questions take a look at the community discussion [forums](#).

Bugs or Suggestions?

If you have any suggestions or you have found a bug please use the [online bug & issue](#) tracking system.

Open positions

The lab has open postdoctoral positions on research projects related to [chemical informatics](#) and [data mining](#).

Active forum topics

- Mesh2Dual -> AdaptiveRapart
- 64bit CLUTO

<http://glaros.dtc.umn.edu/gkhome/cluto/gcluto/overview>

Obtaining gCLUTO | Karypis Lab - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Home Search Favorites

Google G gcluto Go 11692 blocked Check AutoLink AutoFill Send to gcluto Settings

Address http://glaros.dtc.umn.edu/gkhome/cluto/gcluto/download

Home | Contact | METIS | CLUTO | Forums

Karypis Lab

Search

Navigation

- Home
- Research
 - Projects
 - Software
 - METIS
 - CLUTO
 - CLUTO
 - gCLUTO
 - wCLUTO
 - PAFI
 - YASSPP
 - AFGen
 - SUGGEST
 - MGridGen
 - PSPASES
 - Publications
- Education
- Lab Information

Home » Research » Software » CLUTO

gCLUTO - Graphical Clustering Toolkit

Overview Download Changes Publications

The gCLUTO data clustering package is currently distributed as a single file that contains binary distributions for Linux, and MS Windows platforms.

Getting the files

The first step in setting up gCLUTO is to download the binary distribution file. gCLUTO's distribution is available as either a Unix gzipped tar file or as a Windows zip file.

Available files for download

[gzipped tar file](#) [zip file](#)

Older versions of gCLUTO can be found [here](#).

Installing

On Unix systems, after downloading gCLUTO you need to uncompress and untar it. This is achieved by executing the following command:

```
gunzip gcluto-1.0.tar.gz
tar -xvf gcluto-1.0.tar
```

On Windows systems, you need to have a zip/unzip program (e.g., [winzip](#)) in order to unzip the files. In

Support

Forum

If you encounter any problems or have any "how to use" questions take a look at the community discussion [forums](#).

Bugs or Suggestions?

If you have any suggestions or you have found a bug please use the [online bug & issue](#) tracking system.

Open positions

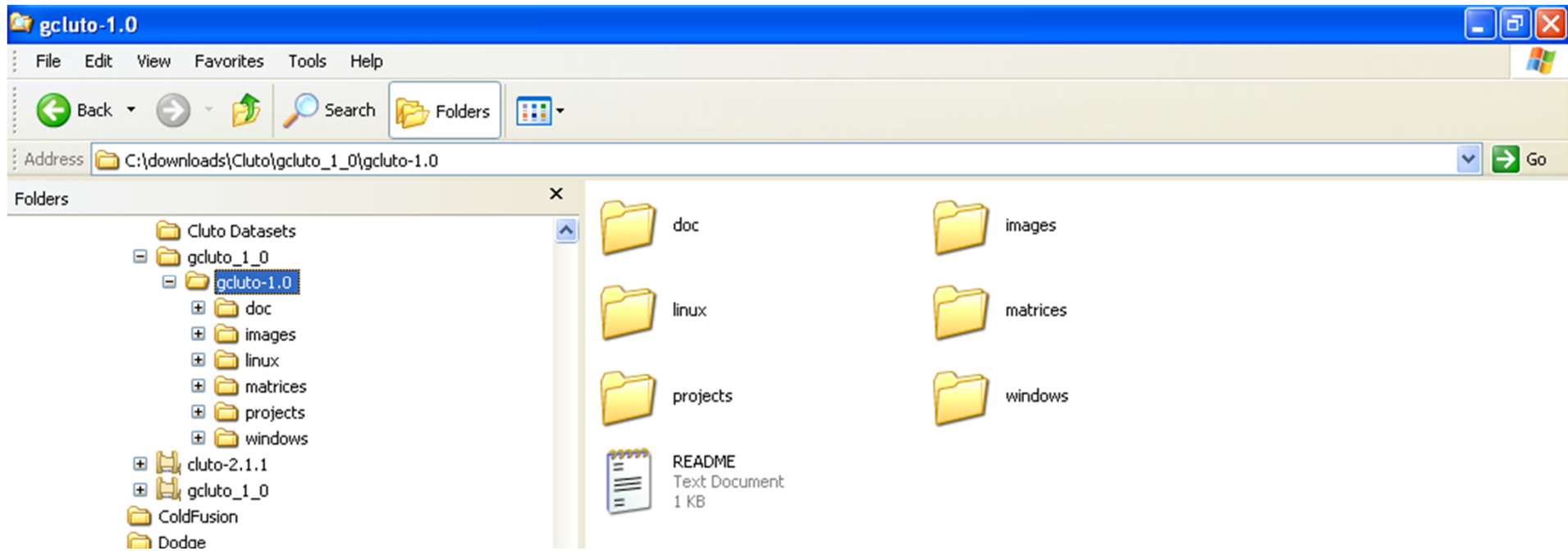
The lab has open postdoctoral positions on research projects related to [chemical informatics](#) and [data mining](#).

Active forum topics

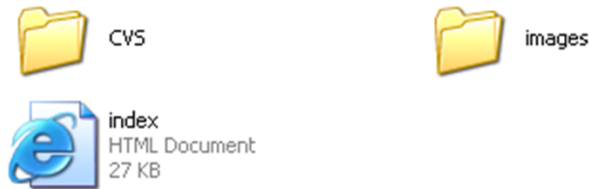
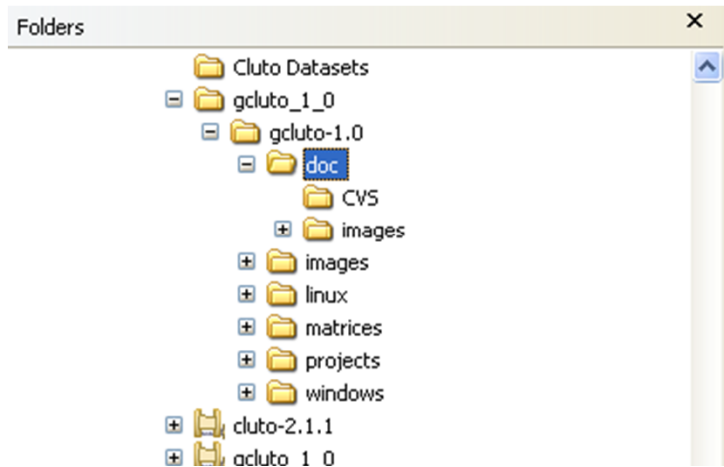
- Mesh2Dual -> AdaptiveRapart
- 64bit CLUTO

Download and Unzip "gcluto_1_0.zip"

gCLUTO Folders and Files (extracted)

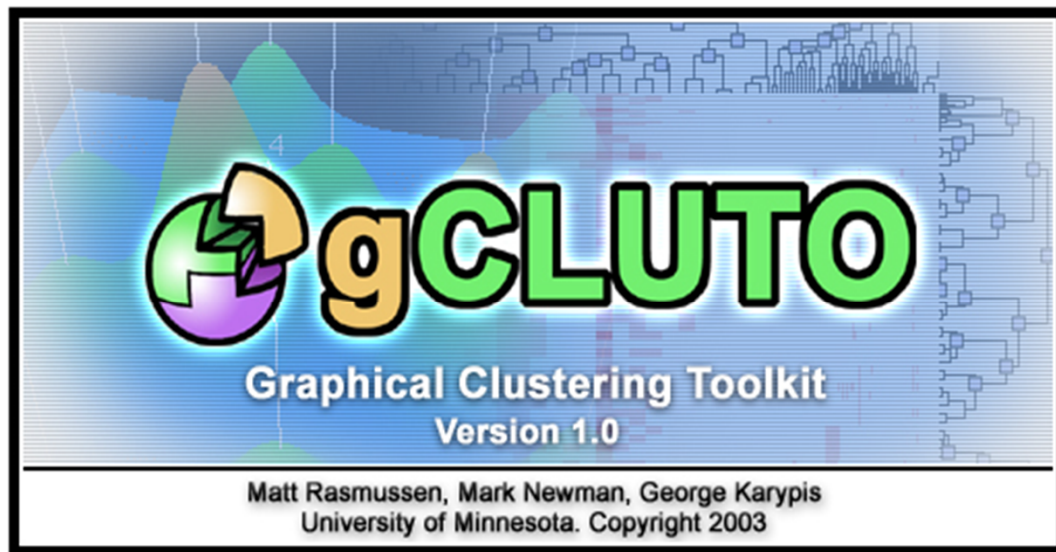


gCLUTO "doc" Subfolder and Files



gCLUTO Documentation





gCLUTO Documentation

Version 1.0

Matt Rasmussen, Mark Newman, George Karypis
University of Minnesota. Copyright 2003

Last Modified: Wed Nov 19 15:16:53 CST 2003

<http://www.cs.umn.edu/~mrasmus/gcluto>

Table of Contents

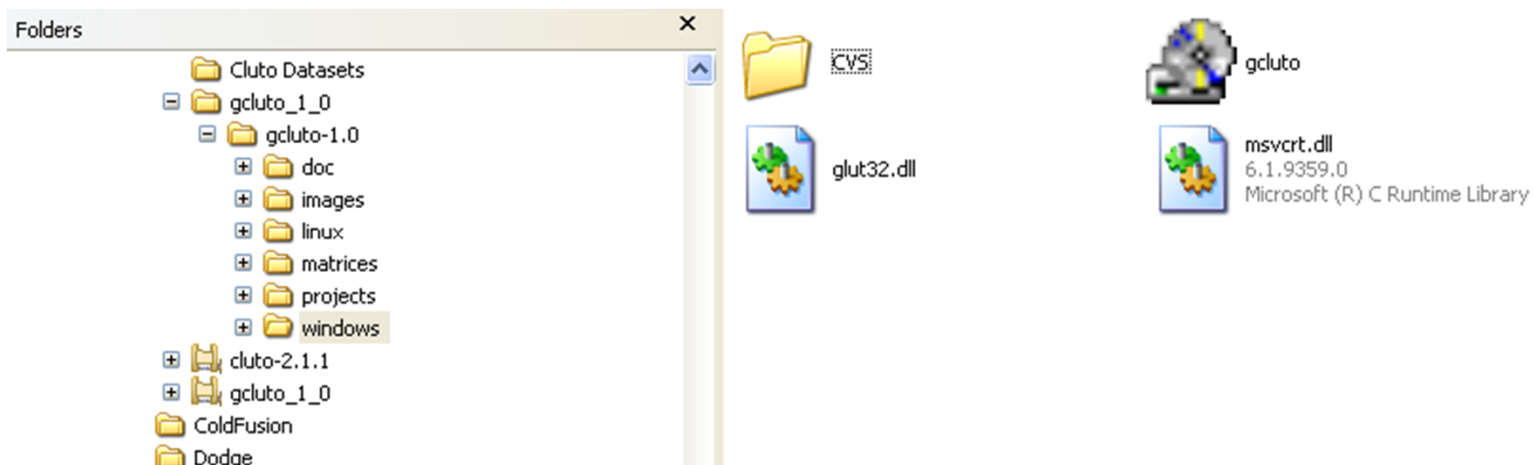
- [1 Introduction](#)
 - [1.1 What is gCLUTO](#)
 - [1.2 Features](#)

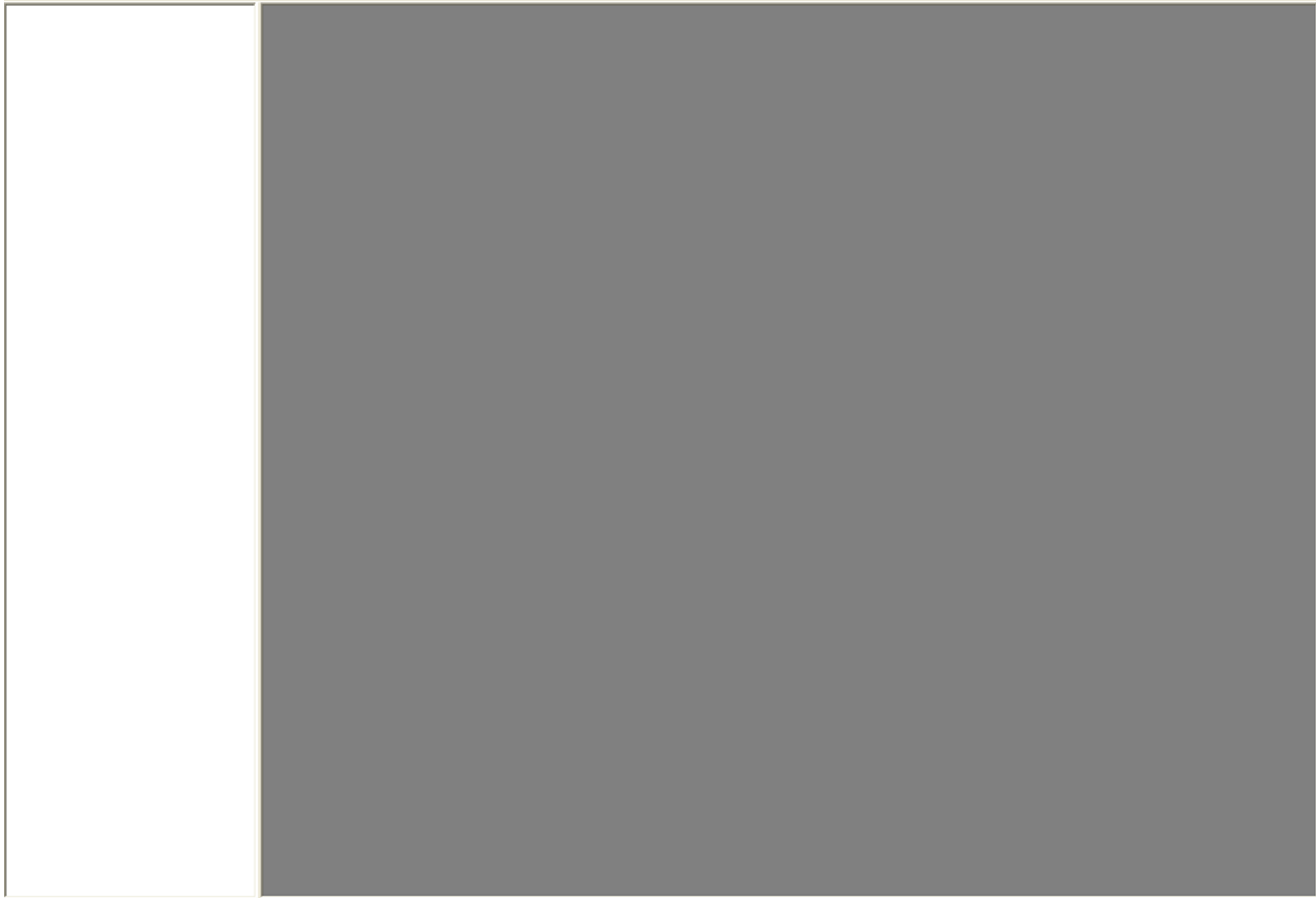
For more information on CLUTO (original non-graphical version), download and Unzip "cluto-2.1.1.zip" at:

<http://glaros.dtc.umn.edu/gkhome/cluto/cluto/download>

gCLUTO "windows" Subfolder and Files

**Executable file;
Double-click to run the program**





- New Project Ctrl-N
- Open Project Ctrl-O
- Save Project Ctrl-S
- Close Project

- Print Ctrl-P
- Print Setup
- Page Setup
- Print Preview

- Show Error Log Ctrl-E
- Quit Ctrl-Q



New Project

Save in: gcluto-1.0

- My Recent Documents
- Desktop
- My Documents
- My Computer
- My Network Places

- doc
- images
- linux
- matrices
- projects
- windows
- README

Create a new "projects" subfolder

File name:

Save as type: All files (*.*)

Save Cancel

New Project

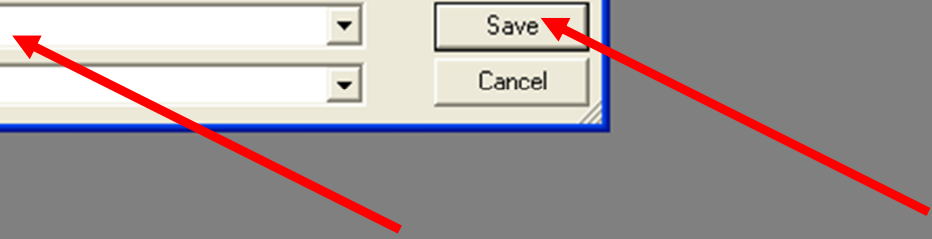
Save in: projects

- My Recent Documents
- Desktop
- My Documents
- My Computer
- My Network Places

File name: genes1-test

Save as type: All files (*.*)

Save Cancel



genes1-test



- Import Data Ctrl-I
- Export Ctrl-E



genes1-test

Import Data

Label
[]

Matrix File Graph File Delimited File

[] Browse

Row File
[] Browse

Column File
[] Browse

Row Class File
[] Browse


Delimited File Options

Use 1st column as Row Labels
 Use 1st row as Column Labels

Delimiters

Tab Semicolon Comma Space Other []

OK Cancel



Matrix File

Look in: gcluto-1.0

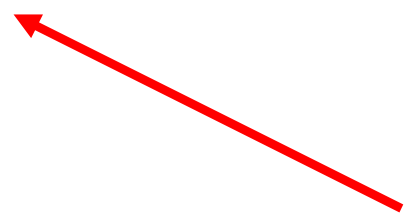
- doc
- images
- linux
- matrices
- projects
- windows

File name:

Files of type: Cluto Matrix (*.mat)

Open as read-only

Open Cancel



There are a couple of examples at the "matrices" subfolder

Delimited File

Browse

Browse

Browse

Browse

Browse

Delimited File Options

Use 1st column as Row Labels

Use 1st row as Column Labels

Delimiters

Tab Semicolon Comma Space Other

OK Cancel

Matrix File

Look in:

- My Recent Documents
- Desktop
- My Documents
- My Computer
- My Network Places

Files in 'matrices':

- CVS
- genes1
- genes2

File name:

Files of type:

Open as read-only

Open Cancel

Delimited File

Browse

Browse

Browse

Browse

Browse

Delimited File Options

Use 1st column as Row Labels

Use 1st row as Column Labels

Delimiters

Tab Semicolon Comma Space Other

OK Cancel

genes1-test

Import Data

Label
[]

Matrix File Graph File Delimited File

C:\downloads\Cluto\gcluto_1_0\gcluto-1.0\matrices\genes1. [Browse]

Row File
C:\downloads\Cluto\gcluto_1_0\gcluto-1.0\matrices\genes1. [Browse]

Column File
[] [Browse]

Row Class File
[] [Browse]

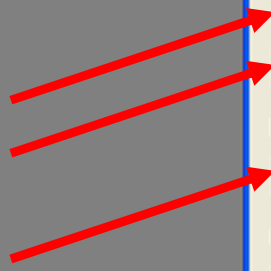
Delimited File Options

Use 1st column as Row Labels
 Use 1st row as Column Labels

Delimiters

Tab Semicolon Comma Space Other []

[OK] [Cancel]



genes1-test
genes1

Dense Matrix

	1	2	3	4	5	6	7	8	9
5HT1b	0.340000	0.490000	0.880000	1.000000	0.790000	0.980000	0.750000	0.660000	0.720000
5HT2	0.350000	0.610000	0.890000	0.810000	1.000000	0.970000	0.390000	0.550000	0.660000
5HT3	0.510000	0.360000	0.660000	1.000000	0.660000	0.560000	0.360000	0.180000	0.170000
ACHE	0.570000	0.530000	0.750000	0.760000	0.890000	0.960000	1.000000	0.840000	0.540000
actin	0.720000	0.900000	1.000000	0.930000	0.760000	0.850000	0.880000	0.650000	0.580000
aFGF	0.160000	0.210000	0.530000	0.770000	0.320000	0.650000	1.000000	0.250000	0.230000
BDNF	0.020000	0.040000	0.290000	0.260000	0.280000	0.430000	0.330000	0.260000	1.000000
bFGF	0.630000	0.530000	0.850000	0.900000	1.000000	0.930000	0.950000	0.940000	0.970000
Brm	0.870000	1.000000	0.520000	0.360000	0.360000	0.230000	0.130000	0.060000	0.070000
CC01	0.870000	0.920000	0.980000	0.950000	0.610000	1.000000	0.930000	0.870000	0.840000
CC02	1.000000	0.890000	0.740000	0.700000	0.810000	0.830000	0.960000	0.740000	0.860000
cellubrevin	0.780000	1.000000	0.990000	0.920000	0.750000	0.830000	0.760000	0.240000	0.380000
cjun	0.710000	0.680000	0.670000	0.680000	0.660000	0.800000	0.700000	0.760000	1.000000
CNTF	1.000000	0.930000	0.660000	0.890000	0.910000	0.790000	0.810000	0.750000	0.820000
CNTFR	1.000000	0.900000	0.780000	0.830000	0.970000	0.830000	0.990000	0.990000	0.810000
CX43	0.880000	0.750000	0.990000	1.000000	0.900000	0.970000	0.980000	0.880000	1.000000
cyclinA	1.000000	0.890000	0.830000	0.720000	0.750000	0.710000	0.640000	0.640000	0.550000
cyclinB	1.000000	0.980000	0.770000	0.590000	0.610000	0.480000	0.280000	0.090000	
EGF	0.860000	0.870000	1.000000	0.720000	0.790000	0.680000	0.790000	0.710000	0.580000
FABP	0.730000	0.750000	0.830000	0.900000	0.890000	1.000000	0.850000	0.690000	0.680000
G67I8086	0.900000	1.000000	0.680000	0.680000	0.560000	0.410000	0.250000	0.160000	0.150000
G67I86	0.970000	1.000000	0.720000	0.770000	0.440000	0.420000	0.260000	0.110000	0.070000
GAD65	0.910000	0.830000	0.860000	0.970000	0.870000	1.000000	0.790000	0.720000	0.510000
GAD67	0.350000	0.460000	0.950000	0.830000	0.810000	1.000000	0.810000	0.660000	0.720000
GAP43	0.580000	0.650000	1.000000	0.630000	0.630000	0.640000	0.650000	0.630000	0.540000
GFAP			0.520000	0.380000	0.810000	1.000000	0.940000	0.560000	0.910000
GMFb	1.000000	0.970000	0.890000	0.940000	0.920000	0.510000	0.880000	0.750000	0.430000
GRa1	0.050000	0.230000	0.800000	0.620000	0.850000	0.850000	0.850000	1.000000	1.000000
GRa2	0.660000	0.690000	1.000000	0.980000	0.980000	0.990000	0.940000	0.840000	0.890000
GRa3	0.440000	0.690000	0.720000	1.000000	0.860000	0.900000	0.810000	0.570000	0.260000

genes1-test

- genes1

Open
Close
Save
Delete
Cluster



Dense Matrix

	1	2	3	4	5	6	7	8	9
5HT1b	0.340000	0.490000	0.880000	1.000000	0.790000	0.980000	0.750000	0.660000	0.720000
5HT2	0.350000	0.610000	0.890000	0.810000	1.000000	0.970000	0.390000	0.550000	0.660000
5HT3	0.510000	0.360000	0.660000	1.000000	0.660000	0.560000	0.360000	0.180000	0.170000
ACHE	0.570000	0.530000	0.750000	0.760000	0.890000	0.960000	1.000000	0.840000	0.540000
actin	0.720000	0.900000	1.000000	0.930000	0.760000	0.850000	0.880000	0.650000	0.580000
aFGF	0.160000	0.210000	0.530000	0.770000	0.320000	0.650000	1.000000	0.250000	0.230000
BDNF	0.020000	0.040000	0.290000	0.260000	0.280000	0.430000	0.330000	0.260000	1.000000
bFGF	0.630000	0.530000	0.850000	0.900000	1.000000	0.930000	0.950000	0.940000	0.970000
Brm	0.870000	1.000000	0.520000	0.360000	0.360000	0.230000	0.130000	0.060000	0.070000
CCO1	0.870000	0.920000	0.980000	0.950000	0.610000	1.000000	0.930000	0.870000	0.840000
CCO2	1.000000	0.890000	0.740000	0.700000	0.810000	0.830000	0.960000	0.740000	0.860000
cellubrevin	0.780000	1.000000	0.990000	0.920000	0.750000	0.830000	0.760000	0.240000	0.380000
cjun	0.710000	0.680000	0.670000	0.680000	0.660000	0.800000	0.700000	0.760000	1.000000
CNTF	1.000000	0.930000	0.660000	0.890000	0.910000	0.790000	0.810000	0.750000	0.820000
CNTFR	1.000000	0.900000	0.780000	0.830000	0.970000	0.830000	0.990000	0.990000	0.810000
CX43	0.880000	0.750000	0.990000	1.000000	0.900000	0.970000	0.980000	0.880000	1.000000
cyclinA	1.000000	0.890000	0.830000	0.720000	0.750000	0.710000	0.640000	0.640000	0.550000
cyclinB	1.000000	0.980000	0.770000	0.590000	0.610000	0.480000	0.280000	0.090000	
EGF	0.860000	0.870000	1.000000	0.720000	0.790000	0.680000	0.790000	0.710000	0.580000
FABP	0.730000	0.750000	0.830000	0.900000	0.890000	1.000000	0.850000	0.690000	0.680000
G67I8086	0.900000	1.000000	0.680000	0.680000	0.560000	0.410000	0.250000	0.160000	0.150000
G67I86	0.970000	1.000000	0.720000	0.770000	0.440000	0.420000	0.260000	0.110000	0.070000
GAD65	0.910000	0.830000	0.860000	0.970000	0.870000	1.000000	0.790000	0.720000	0.510000
GAD67	0.350000	0.460000	0.950000	0.830000	0.810000	1.000000	0.810000	0.660000	0.720000
GAP43	0.580000	0.650000	1.000000	0.630000	0.630000	0.640000	0.650000	0.630000	0.540000
GFAP			0.520000	0.380000	0.810000	1.000000	0.940000	0.560000	0.910000
GMFb	1.000000	0.970000	0.890000	0.940000	0.920000	0.510000	0.880000	0.750000	0.430000
GRa1	0.050000	0.230000	0.800000	0.620000	0.850000	0.850000	0.850000	1.000000	1.000000
GRa2	0.660000	0.690000	1.000000	0.980000	0.980000	0.990000	0.940000	0.840000	0.890000
GRa3	0.440000	0.690000	0.720000	1.000000	0.860000	0.900000	0.810000	0.570000	0.260000

genes1-test
 genes1

Dense Matrix

	1	2	3	4	5	6	7	8	9
5HT1b	0.340000	0.490000	0.880000	1.000000	0.790000	0.980000	0.750000	0.660000	0.720000
5HT2	0.350000	0.610000	0.890000	0.810000	1.000000	0.970000	0.390000	0.550000	0.660000
5HT3	0.510000	0.360000	0.660000	1.000000	0.660000	0.560000	0.360000	0.180000	0.170000

Edit Clustering Options

Cluster Method

Repeated Bisection
 Direct
 Agglomerative
 Graph

Number of Clusters:

Similarity Function:

Row Model:

Column Model:

Graph Model:

Number of Trials:

Cluster Selection:

K-Way Refine

Criterion Function:

Number of Iterations:

Minimum Component:

Nearest Neighbors:

Edge Prune:

Vertex Prune:

Column Prune:

GMFb	1.000000	0.970000	0.890000	0.940000	0.920000	0.510000	0.880000	0.750000	0.430000
GRa1	0.050000	0.230000	0.800000	0.620000	0.850000	0.850000	0.850000	1.000000	1.000000
GRa2	0.660000	0.690000	1.000000	0.980000	0.980000	0.990000	0.940000	0.840000	0.890000
GRa3	0.440000	0.690000	0.720000	1.000000	0.860000	0.900000	0.810000	0.570000	0.260000



solution 1 - Solution Results

Clustering Options

Method: Repeated Bisection	#Clusters: 10	
CRfun: l2	Simfun: Cosine	
RowModel: None	ColModel: None	Graph Model: Asymmetric-Direct
ColPrune: 1.000	EdgePrune: 0.000	VertexPrune: 0.000
Nearest Neighbors: 4	MinComponent: 1	CSType: Best
#Trials: 10	#Iterations: 10	

10-way clustering: [70 of 70]

Cluster	Size	ISim	ISdev	ESim	ESdev
0	2	0.985	0.000	0.752	0.034
1	2	0.949	0.000	0.770	0.036
2	2	0.897	0.000	0.723	0.053
3	2	0.954	0.000	0.817	0.051
4	3	0.940	0.013	0.814	0.034
5	29	0.968	0.009	0.875	0.014
6	7	0.919	0.013	0.836	0.050
7	3	0.965	0.005	0.884	0.007
8	6	0.930	0.016	0.851	0.033
9	14	0.953	0.022	0.885	0.029

[Go to Top](#)

Descriptive & Discriminating Features

Cluster	Size	ISim	ESim						
Cluster 0	Size: 2	ISim: 0.985	ESim: 0.752						
Descriptive:	1		19.7%	11	19.7%	0	17.1%	3	10.3%
Discriminating:	1		14.7%	0	13.2%	11	10.5%	16	8.7%
Cluster 1	Size: 2	ISim: 0.949	ESim: 0.770						
Descriptive:	8		12.3%	13	10.5%	11	9.8%	15	9.1%
Discriminating:	3		15.8%	1	13.8%	2	13.2%	0	12.1%
Cluster 2	Size: 2	ISim: 0.897	ESim: 0.723						
Descriptive:	0		18.5%	1	15.2%	2	13.6%	4	11.5%
Discriminating:	0		15.5%	11	10.5%	13	9.7%	1	9.0%
Cluster 3	Size: 2	ISim: 0.954	ESim: 0.817						
Descriptive:	11		17.1%	3	14.8%	12	13.3%	13	11.5%

genes1-test

genes1

solution 1

Open

Close

Save

Delete

Recluster

Create Matrix Visualization

Create Mountain Visualization

solution 1 - Solution Results

Options

Repeated Bisection

None

0.000

Neighbors: 4

#Trials: 10

Simfun: Cosine

ColModel: None

EdgePrune: 0.000

MinComponent: 1

#Iterations: 10

#Clusters: 10

Graph Model: Asymmetric-Direct

VertexPrune: 0.000

CSType: Best

10-way clustering: [70 of 70]

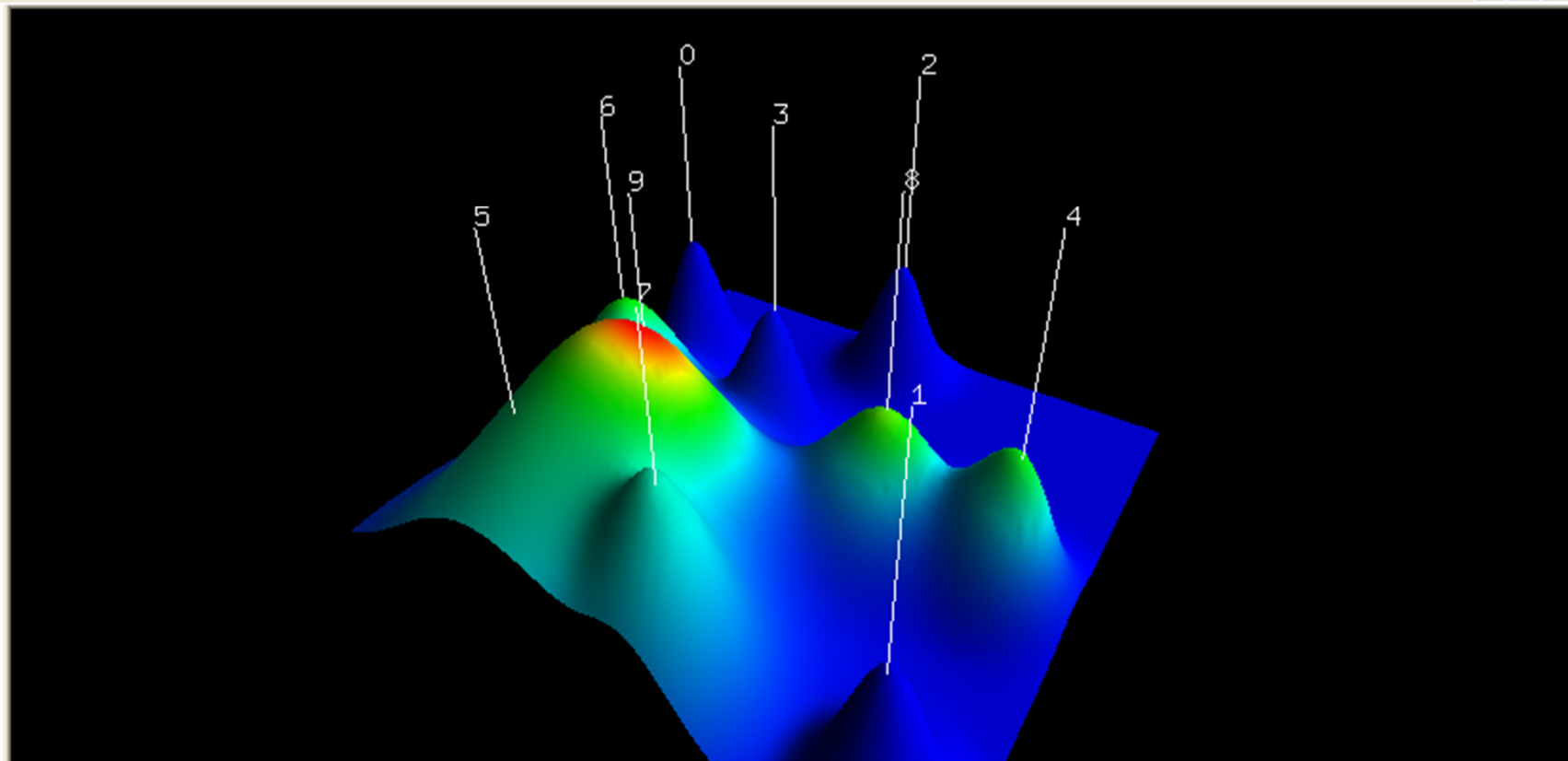
Cluster	Size	ISim	ISdev	ESim	ESdev
0	2	0.985	0.000	0.752	0.034
1	2	0.949	0.000	0.770	0.036
2	2	0.897	0.000	0.723	0.053
3	2	0.954	0.000	0.817	0.051
4	3	0.940	0.013	0.814	0.034
5	29	0.968	0.009	0.875	0.014
6	7	0.919	0.013	0.836	0.050
7	3	0.965	0.005	0.884	0.007
8	6	0.930	0.016	0.851	0.033
9	14	0.953	0.022	0.885	0.029

[Go to Top](#)

Descriptive & Discriminating Features

Cluster	Size	ISim	ESim						
Cluster 0	Size: 2	ISim: 0.985	ESim: 0.752						
Descriptive:	1		19.7%	11	19.7%	0	17.1%	3	10.3%
Discriminating:	1		14.7%	0	13.2%	11	10.5%	16	8.7%
Cluster 1	Size: 2	ISim: 0.949	ESim: 0.770						
Descriptive:	8		12.3%	13	10.5%	11	9.8%	15	9.1%
Discriminating:	3		15.8%	1	13.8%	2	13.2%	0	12.1%
Cluster 2	Size: 2	ISim: 0.897	ESim: 0.723						
Descriptive:	0		18.5%	1	15.2%	2	13.6%	4	11.5%
Discriminating:	0		15.5%	11	10.5%	13	9.7%	1	9.0%
Cluster 3	Size: 2	ISim: 0.954	ESim: 0.817						
Descriptive:	11		17.1%	3	14.8%	12	13.3%	13	11.5%

genes1-test
genes1
solution 1
mountain visualization 1



genes1-test

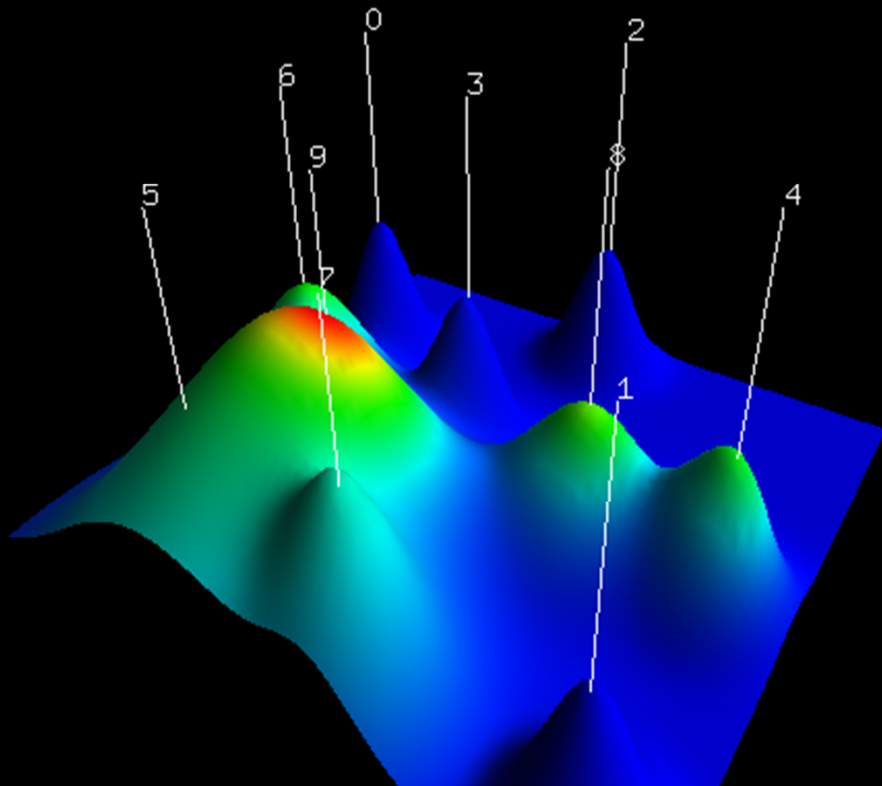
genes1

- Open
- Close
- Save
- Delete

Recluster

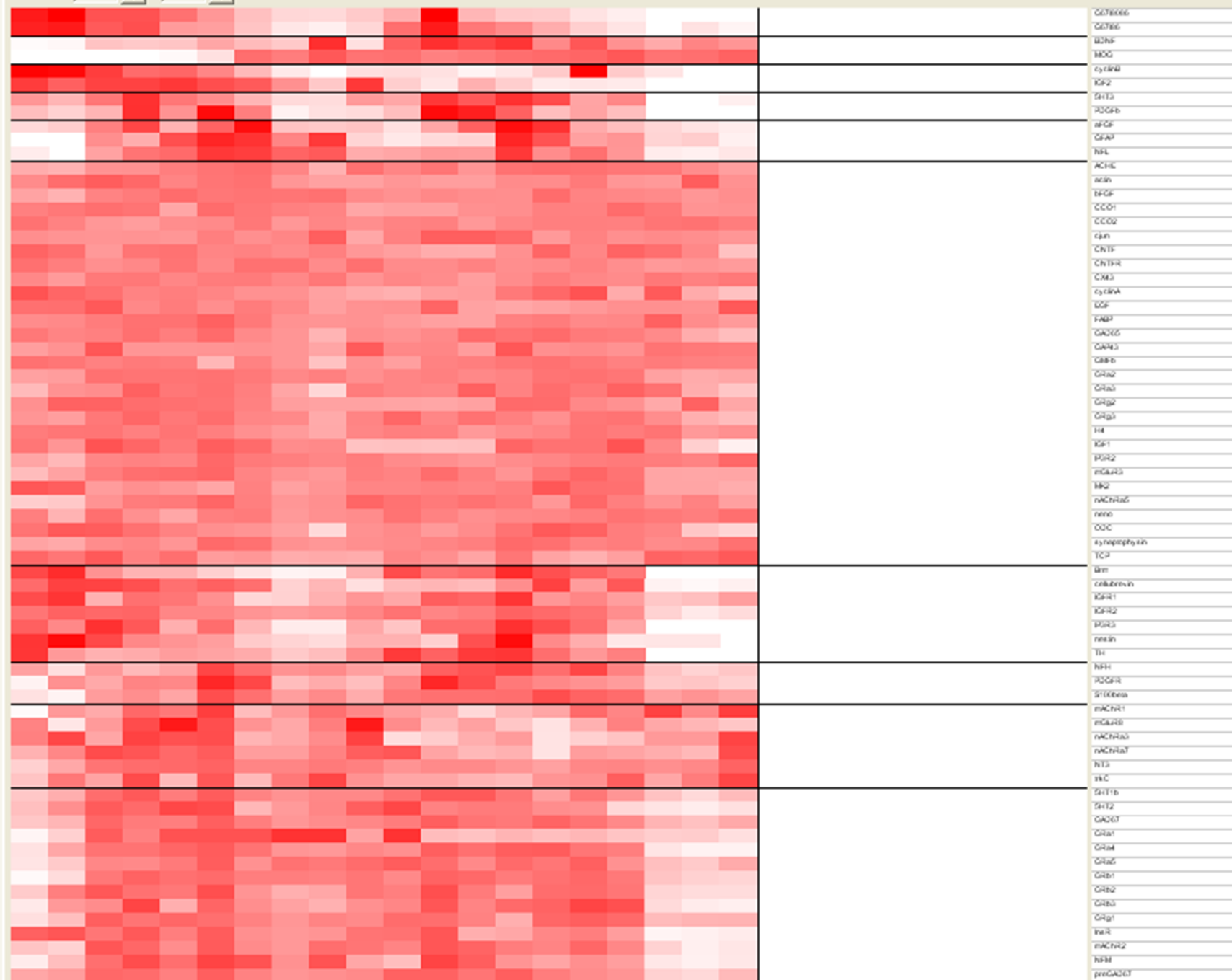
Create Matrix Visualization

Create Mountain Visualization





scale: W 100 H 36



Using other data sets

Preparing the data

Opening "housing.dat" in Excel

The screenshot shows the Microsoft Excel interface with the Text Import Wizard dialog box open. The dialog box is titled "Text Import Wizard - Step 1 of 3" and contains the following information:

The Text Wizard has determined that your data is Fixed Width.
If this is correct, choose Next, or choose the data type that best describes your data.

Original data type
Choose the file type that best describes your data:

- Delimited - Characters such as commas or tabs separate each field.
- Fixed width - Fields are aligned in columns with spaces between each field.

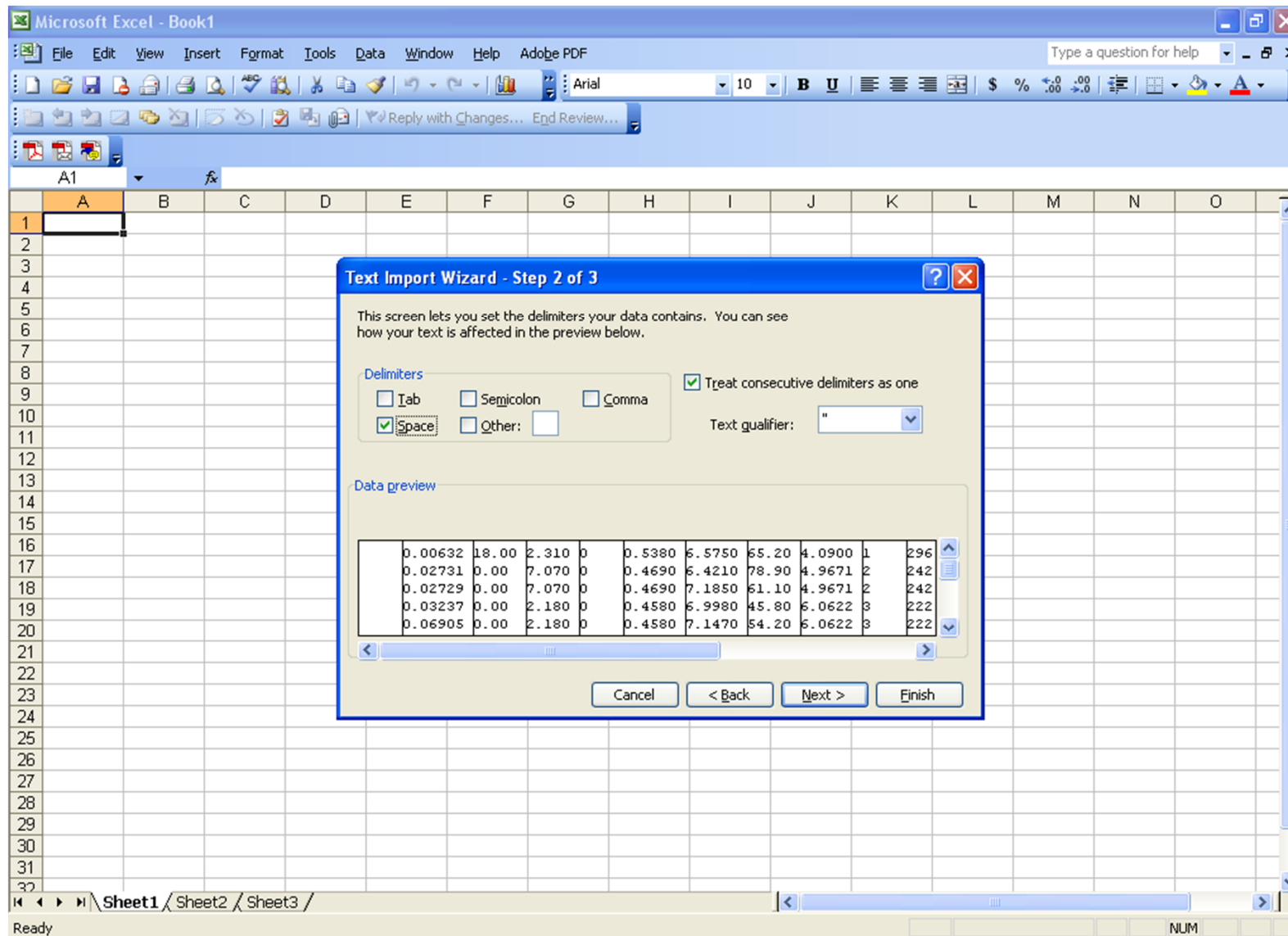
Start import at row: 1 File origin: 437 : OEM United States

Preview of file C:\Caldas\Teaching\CE 395R5 - Fall 2005\Datasets\UCI\housing.data.

1	0.00632	18.00	2.310	0	0.5380	6.5750	65.20	4.0900	1
2	0.02731	0.00	7.070	0	0.4690	6.4210	78.90	4.9671	2
3	0.02729	0.00	7.070	0	0.4690	7.1850	61.10	4.9671	2
4	0.03237	0.00	2.180	0	0.4580	6.9980	45.80	6.0622	3
5	0.06905	0.00	2.180	0	0.4580	7.1470	54.20	6.0622	3

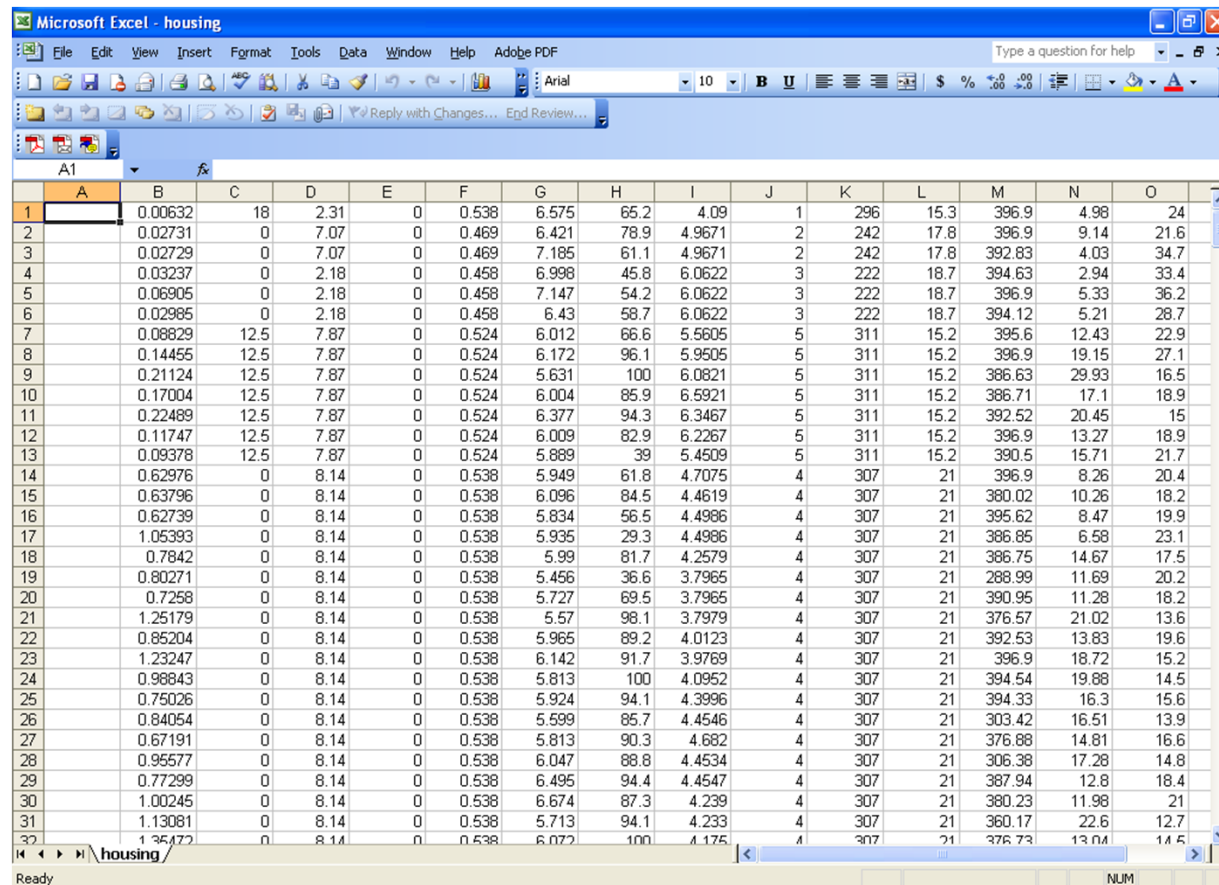
Buttons: Cancel, < Back, Next >, Finish

In this data set "space" is the delimiter
That's not always the case



Check the data

- make sure that all columns are complete
- preprocess the data, if needed
- eliminate unnecessary columns



The screenshot shows a Microsoft Excel spreadsheet titled "Microsoft Excel - housing". The spreadsheet contains a dataset with 32 rows and 15 columns (A through O). The data is as follows:

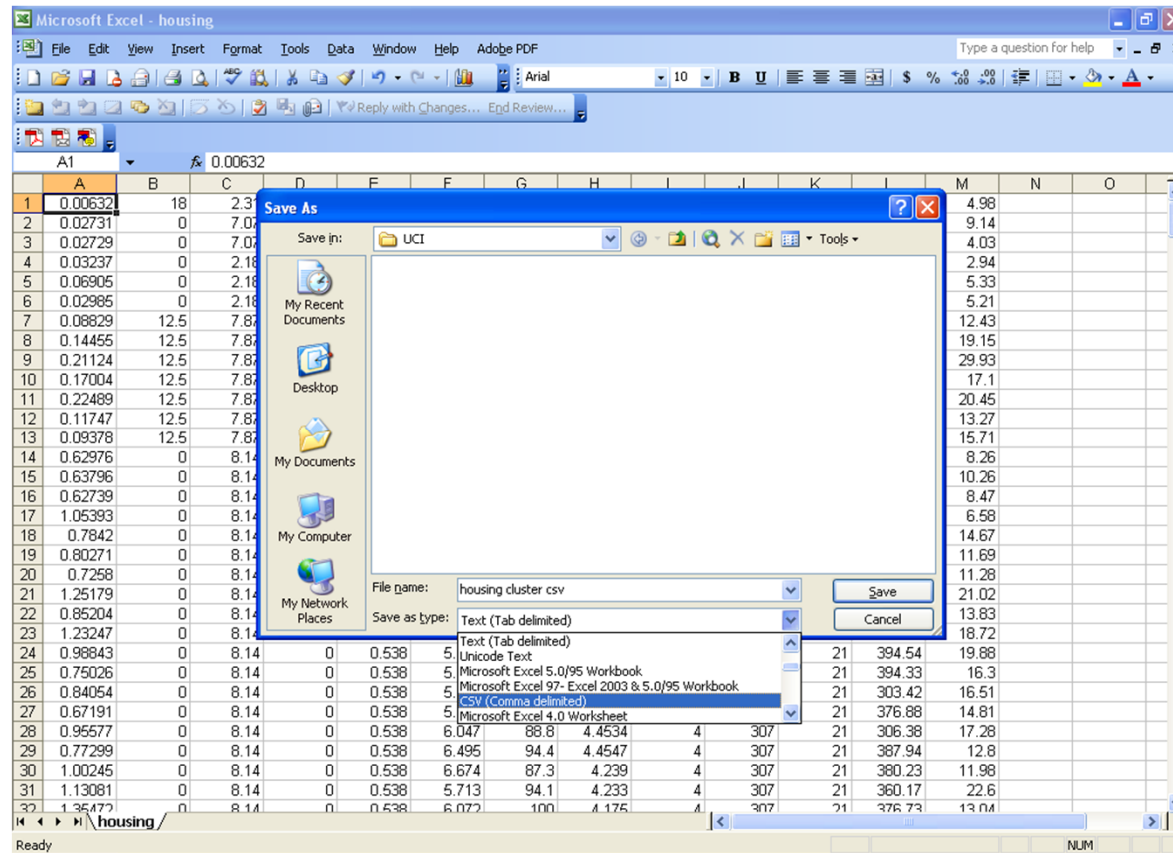
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1		0.00632	18	2.31	0	0.538	6.575	65.2	4.09	1	296	15.3	396.9	4.98	24
2		0.02731	0	7.07	0	0.469	6.421	78.9	4.9671	2	242	17.8	396.9	9.14	21.6
3		0.02729	0	7.07	0	0.469	7.185	61.1	4.9671	2	242	17.8	392.83	4.03	34.7
4		0.03237	0	2.18	0	0.458	6.998	45.8	6.0622	3	222	18.7	394.63	2.94	33.4
5		0.06905	0	2.18	0	0.458	7.147	54.2	6.0622	3	222	18.7	396.9	5.33	36.2
6		0.02985	0	2.18	0	0.458	6.43	58.7	6.0622	3	222	18.7	394.12	5.21	28.7
7		0.08829	12.5	7.87	0	0.524	6.012	66.6	5.5605	5	311	15.2	395.6	12.43	22.9
8		0.14455	12.5	7.87	0	0.524	6.172	96.1	5.9505	5	311	15.2	396.9	19.15	27.1
9		0.21124	12.5	7.87	0	0.524	5.631	100	6.0821	5	311	15.2	386.63	29.93	16.5
10		0.17004	12.5	7.87	0	0.524	6.004	85.9	6.5921	5	311	15.2	386.71	17.1	18.9
11		0.22489	12.5	7.87	0	0.524	6.377	94.3	6.3467	5	311	15.2	392.52	20.45	15
12		0.11747	12.5	7.87	0	0.524	6.009	82.9	6.2267	5	311	15.2	396.9	13.27	18.9
13		0.09378	12.5	7.87	0	0.524	5.889	39	5.4509	5	311	15.2	390.5	15.71	21.7
14		0.62976	0	8.14	0	0.538	5.949	61.8	4.7075	4	307	21	396.9	8.26	20.4
15		0.63796	0	8.14	0	0.538	6.096	84.5	4.4619	4	307	21	380.02	10.26	18.2
16		0.62739	0	8.14	0	0.538	5.834	56.5	4.4986	4	307	21	395.62	8.47	19.9
17		1.05393	0	8.14	0	0.538	5.935	29.3	4.4986	4	307	21	386.85	6.58	23.1
18		0.7842	0	8.14	0	0.538	5.99	81.7	4.2579	4	307	21	386.75	14.67	17.5
19		0.80271	0	8.14	0	0.538	5.456	36.6	3.7965	4	307	21	288.99	11.69	20.2
20		0.7258	0	8.14	0	0.538	5.727	69.5	3.7965	4	307	21	390.95	11.28	18.2
21		1.25179	0	8.14	0	0.538	5.57	98.1	3.7979	4	307	21	376.57	21.02	13.6
22		0.85204	0	8.14	0	0.538	5.965	89.2	4.0123	4	307	21	392.53	13.83	19.6
23		1.23247	0	8.14	0	0.538	6.142	91.7	3.9769	4	307	21	396.9	18.72	15.2
24		0.98843	0	8.14	0	0.538	5.813	100	4.0952	4	307	21	394.54	19.88	14.5
25		0.75026	0	8.14	0	0.538	5.924	94.1	4.3996	4	307	21	394.33	16.3	15.6
26		0.84054	0	8.14	0	0.538	5.599	85.7	4.4546	4	307	21	303.42	16.51	13.9
27		0.67191	0	8.14	0	0.538	5.813	90.3	4.682	4	307	21	376.88	14.81	16.6
28		0.95577	0	8.14	0	0.538	6.047	88.8	4.4534	4	307	21	306.38	17.28	14.8
29		0.77299	0	8.14	0	0.538	6.495	94.4	4.4547	4	307	21	387.94	12.8	18.4
30		1.00245	0	8.14	0	0.538	6.674	87.3	4.239	4	307	21	380.23	11.98	21
31		1.13081	0	8.14	0	0.538	5.713	94.1	4.233	4	307	21	360.17	22.6	12.7
32		1.35472	0	8.14	0	0.538	6.072	100	4.175	4	307	21	376.73	13.04	14.5

In this example, I will eliminate:

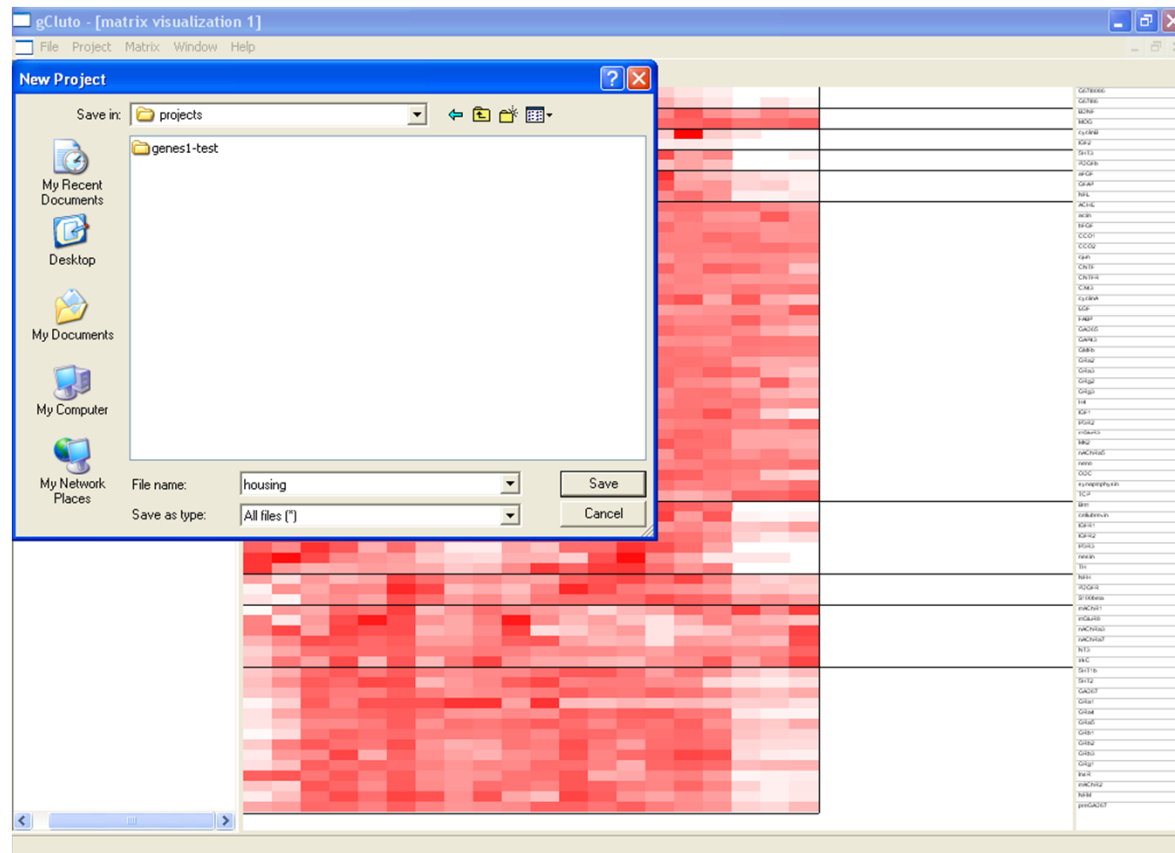
- First column: empty
- Last column: predicted value (don't need it for clustering)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	0.00632	18	2.31	0	0.538	6.575	65.2	4.09	1	296	15.3	396.9	4.98		
2	0.02731	0	7.07	0	0.469	6.421	78.9	4.9671	2	242	17.8	396.9	9.14		
3	0.02729	0	7.07	0	0.469	7.185	61.1	4.9671	2	242	17.8	392.83	4.03		
4	0.03237	0	2.18	0	0.458	6.998	45.8	6.0622	3	222	18.7	394.63	2.94		
5	0.06905	0	2.18	0	0.458	7.147	54.2	6.0622	3	222	18.7	396.9	5.33		
6	0.02985	0	2.18	0	0.458	6.43	58.7	6.0622	3	222	18.7	394.12	5.21		
7	0.08829	12.5	7.87	0	0.524	6.012	66.6	5.9605	5	311	15.2	395.6	12.43		
8	0.14455	12.5	7.87	0	0.524	6.172	96.1	5.9505	5	311	15.2	396.9	19.15		
9	0.21124	12.5	7.87	0	0.524	5.631	100	6.0821	5	311	15.2	386.63	29.93		
10	0.17004	12.5	7.87	0	0.524	6.004	85.9	6.5921	5	311	15.2	386.71	17.1		
11	0.22489	12.5	7.87	0	0.524	6.377	94.3	6.3467	5	311	15.2	392.52	20.45		
12	0.11747	12.5	7.87	0	0.524	6.009	82.9	6.2267	5	311	15.2	396.9	13.27		
13	0.09378	12.5	7.87	0	0.524	5.889	39	5.4509	5	311	15.2	390.5	15.71		
14	0.62976	0	8.14	0	0.538	5.949	61.8	4.7075	4	307	21	396.9	8.26		
15	0.63796	0	8.14	0	0.538	6.096	84.5	4.4619	4	307	21	380.02	10.26		
16	0.62739	0	8.14	0	0.538	5.834	56.5	4.4986	4	307	21	395.62	8.47		
17	1.05393	0	8.14	0	0.538	5.935	29.3	4.4986	4	307	21	386.85	6.58		
18	0.7842	0	8.14	0	0.538	5.99	81.7	4.2579	4	307	21	386.75	14.67		
19	0.80271	0	8.14	0	0.538	5.456	36.6	3.7965	4	307	21	288.99	11.69		
20	0.7258	0	8.14	0	0.538	5.727	69.5	3.7965	4	307	21	390.95	11.28		
21	1.25179	0	8.14	0	0.538	5.57	98.1	3.7979	4	307	21	376.57	21.02		
22	0.85204	0	8.14	0	0.538	5.965	89.2	4.0123	4	307	21	392.53	13.83		
23	1.23247	0	8.14	0	0.538	6.142	91.7	3.9769	4	307	21	396.9	18.72		
24	0.98843	0	8.14	0	0.538	5.813	100	4.0952	4	307	21	394.54	19.88		
25	0.75026	0	8.14	0	0.538	5.924	94.1	4.3996	4	307	21	394.33	16.3		
26	0.84054	0	8.14	0	0.538	5.599	85.7	4.4546	4	307	21	303.42	16.51		
27	0.67191	0	8.14	0	0.538	5.813	90.3	4.682	4	307	21	376.88	14.81		
28	0.95577	0	8.14	0	0.538	6.047	88.8	4.4534	4	307	21	306.38	17.28		
29	0.77299	0	8.14	0	0.538	6.495	94.4	4.4547	4	307	21	387.94	12.8		
30	1.00245	0	8.14	0	0.538	6.674	87.3	4.239	4	307	21	380.23	11.98		
31	1.13081	0	8.14	0	0.538	5.713	94.1	4.233	4	307	21	360.17	22.6		
32	1.35472	0	8.14	0	0.538	6.072	100	4.175	4	307	21	376.73	13.04		

Save the file as CSV



Create a new project in gCLUTO



housing



- Import Data Ctrl-I
- Export Ctrl-E

housing

Import Data

Label

Matrix File Graph File Delimited File

Row File

Column File

Row Class File

Delimited File Options

Use 1st column as Row Labels

Use 1st row as Column Labels

Delimiters

Tab Semicolon Comma Space Other

housing
housing cluster csv

Dense Matrix

	1	2	3	4	5	6	7	8	9
1	0.006320	18.000000	2.310000		0.538000	6.575000	65.199997	4.090000	1.000000
2	0.027310		7.070000		0.469000	6.421000	78.900002	4.967100	2.000000
3	0.027290		7.070000		0.469000	7.185000	61.099998	4.967100	2.000000
4	0.032370		2.180000		0.458000	6.998000	45.799999	6.062200	3.000000
5	0.069050		2.180000		0.458000	7.147000	54.200001	6.062200	3.000000
6	0.029850		2.180000		0.458000	6.430000	58.700001	6.062200	3.000000
7	0.088290	12.500000	7.870000		0.524000	6.012000	66.599998	5.560500	5.000000
8	0.144550	12.500000	7.870000		0.524000	6.172000	96.099998	5.950500	5.000000
9	0.211240	12.500000	7.870000		0.524000	5.631000	100.000000	6.082100	5.000000
10	0.170040	12.500000	7.870000		0.524000	6.004000	85.900002	6.592100	5.000000
11	0.224890	12.500000	7.870000		0.524000	6.377000	94.300003	6.346700	5.000000
12	0.117470	12.500000	7.870000		0.524000	6.009000	82.900002	6.226700	5.000000
13	0.093780	12.500000	7.870000		0.524000	5.889000	39.000000	5.450900	5.000000
14	0.629760		8.140000		0.538000	5.949000	61.799999	4.707500	4.000000
15	0.637960		8.140000		0.538000	6.096000	84.500000	4.461900	4.000000
16	0.627390		8.140000		0.538000	5.834000	56.500000	4.498600	4.000000
17	1.053930		8.140000		0.538000	5.935000	29.299999	4.498600	4.000000
18	0.784200		8.140000		0.538000	5.990000	81.699997	4.257900	4.000000
19	0.802710		8.140000		0.538000	5.456000	36.599998	3.796500	4.000000
20	0.725800		8.140000		0.538000	5.727000	69.500000	3.796500	4.000000
21	1.251790		8.140000		0.538000	5.570000	98.099998	3.797900	4.000000
22	0.852040		8.140000		0.538000	5.965000	89.199997	4.012300	4.000000
23	1.232470		8.140000		0.538000	6.142000	91.699997	3.976900	4.000000
24	0.988430		8.140000		0.538000	5.813000	100.000000	4.095200	4.000000
25	0.750260		8.140000		0.538000	5.924000	94.099998	4.399600	4.000000
26	0.840540		8.140000		0.538000	5.599000	85.699997	4.454600	4.000000
27	0.671910		8.140000		0.538000	5.813000	90.300003	4.682000	4.000000
28	0.955770		8.140000		0.538000	6.047000	88.800003	4.453400	4.000000
29	0.772990		8.140000		0.538000	6.495000	94.400002	4.454700	4.000000
30	1.002450		8.140000		0.538000	6.674000	87.300003	4.239000	4.000000

housing
 housing cluster csv

Dense Matrix

	1	2	3	4	5	6	7	8	9
1	0.006320	18.000000	2.310000		0.538000	6.575000	65.199997	4.090000	1.000000
2	0.027310		7.070000		0.469000	6.421000	78.900002	4.967100	2.000000

Edit Clustering Options

Cluster Method

Repeated Bisection
 Direct
 Agglomerative
 Graph

Number of Clusters:

Similarity Function:

Row Model:

Column Model:

Graph Model:

Number of Trials:

Cluster Selection:

K-Way Refine

Criterion Function:

Number of Iterations:

Minimum Component:

Nearest Neighbors:

Edge Prune:

Vertex Prune:

Column Prune:

Cluster Cancel

26	0.840540		8.140000		0.538000	5.599000	85.699997	4.454600	4.000000
27	0.671910		8.140000		0.538000	5.813000	90.300003	4.682000	4.000000
28	0.955770		8.140000		0.538000	6.047000	88.800003	4.453400	4.000000
29	0.772990		8.140000		0.538000	6.495000	94.400002	4.454700	4.000000
30	1.002450		8.140000		0.538000	6.674000	87.300003	4.239000	4.000000

housing
 housing cluster csv

Dense Matrix

	1	2	3	4	5	6	7	€	solution 1
1	0.006320	18.000000	2.310000		0.538000	6.575000	65.199997	4.090000	10
2	0.027310		7.070000		0.469000	6.421000	78.900002	4.967100	8
3	0.027290		7.070000		0.469000	7.185000	61.099998	4.967100	8
4	0.032370		2.180000		0.458000	6.998000	45.799999	6.062200	8
5	0.069050		2.180000		0.458000	7.147000	54.200001	6.062200	8
6	0.029850		2.180000		0.458000	6.430000	58.700001	6.062200	8
7	0.088290	12.500000	7.870000		0.524000	6.012000	66.599998	5.560500	12
8	0.144550	12.500000	7.870000		0.524000	6.172000	96.099998	5.950500	12
9	0.211240	12.500000	7.870000		0.524000	5.631000	100.000000	6.082100	12
10	0.170040	12.500000	7.870000		0.524000	6.004000	85.900002	6.592100	12
11	0.224890	12.500000	7.870000		0.524000	6.377000	94.300003	6.346700	12
12	0.117470	12.500000	7.870000		0.524000	6.009000	82.900002	6.226700	12
13	0.093780	12.500000	7.870000		0.524000	5.889000	39.000000	5.450900	6
14	0.629760		8.140000		0.538000	5.949000	61.799999	4.707500	12
15	0.637960		8.140000		0.538000	6.096000	84.500000	4.461900	12
16	0.627390		8.140000		0.538000	5.834000	56.500000	4.498600	12
17	1.053930		8.140000		0.538000	5.935000	29.299999	4.498600	6
18	0.784200		8.140000		0.538000	5.990000	81.699997	4.257900	12
19	0.802710		8.140000		0.538000	5.456000	36.599998	3.796500	7
20	0.725800		8.140000		0.538000	5.727000	69.500000	3.796500	12
21	1.251790		8.140000		0.538000	5.570000	98.099998	3.797900	12
22	0.852040		8.140000		0.538000	5.965000	89.199997	4.012300	12
23	1.232470		8.140000		0.538000	6.142000	91.699997	3.976900	12
24	0.988430		8.140000		0.538000	5.813000	100.000000	4.095200	12
25	0.750260		8.140000		0.538000	5.924000	94.099998	4.399600	12
26	0.840540		8.140000		0.538000	5.599000	85.699997	4.454600	7
27	0.671910		8.140000		0.538000	5.813000	90.300003	4.682000	12
28	0.955770		8.140000		0.538000	6.047000	88.800003	4.453400	7
29	0.772990		8.140000		0.538000	6.495000	94.400002	4.454700	12
30	1.002450		8.140000		0.538000	6.674000	87.300003	4.239000	12