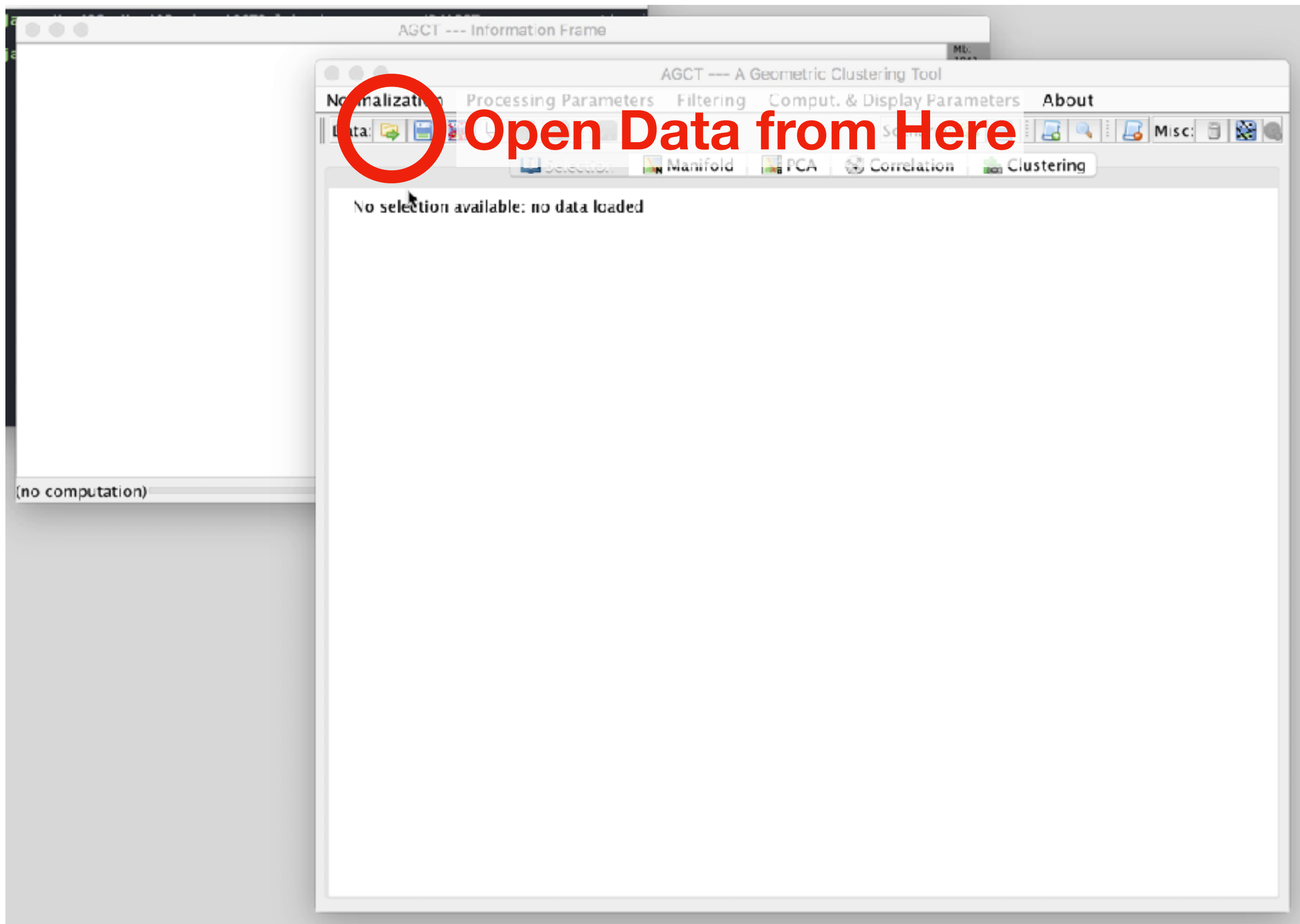


AGCT Tutorial

Step-by-step introduction



Press the button to start a calculation.

Validate my selection below

Summary : mean : 0.0 ; Geometric mean : 0.0 ; SD Threshold : 0.0
all #genes: 564 ; current #genes: 564 ; #time series: 36; #features: 255.

1-Feature method

Haar_Wavelets

#wavelet coeff. : 256

2-Automatic feature selection method

None

Max. #features : -1

4-Automatic prototype (gene) construction method

None

Max. #prototypes : -1

☒ Keep

3- User-fixed gene / time series / group selection

Genes

By name

- ☒ gene 10001_at
- ☒ gene 10003_f_at
- ☒ gene 10005_at
- ☒ gene 10006_at
- ☒ gene 10010_at
- ☒ gene 10011_at
- ☒ gene 10012_at
- ☒ gene 10013_at
- ☒ gene 10015_at
- ☒ gene 10016_at
- ☒ gene 10018_at
- ☒ gene 10019_at
- ☒ gene 10021_at

Time series

By name

- ☒ Test_570.Cell1

by group (AND)

Group

- ☒ Test_570.1

Show the results in these tabs

10768_at_MST1

AGCT --- Information Frame

Normalization Processing Parameters Filtering Comput. & Display Parameters About

Data: [Icons]

Selection **Manifold** PCA Correlation Clustering

Up XYZ [Dropdown] X-axis: 0 Y-axis: 1 Z-axis: 2 Gene to find

(no computation):

- ☐ _5-phosphoribose_1-diphosphate_biosynthesis
- ☐ _ATP_biosynthetic_process_
- ☐ _ATP_metabolic_process_
- ☐ _ATP_synthesis_coupled_proton_transport_
- ☐ _ATP_transport_
- ☐ _Arp2/3_complex-mediated_actin_nucleation_
- ☐ _CTP_biosynthetic_process_
- ☐ _CVT_pathway_
- ☐ _D-xylose_catabolic_process_
- ☐ _D-xylose_metabolic_process_
- ☐ _DNA_damage_checkpoint_
- ☐ _DNA_metabolic_process_
- ☐ _DNA_recombination_

Visualization shows up here.

Manifold edges: ☐ All ☐ Pointed ☒ None

Gene names & annotations: ☐ ID ☐ Name ☒ -1 ☒ -2 ☐ F: ☐ P: ☐ C:

Clusterings, Clusters and Members: ☐ Show C#0 [Dropdown] [Buttons]

Execute Clustering in this tab

Selection Manifold PCA Correlation **Clustering**

Compute clusterings

Clustering type

Affinity Propagation

Command line

AP -Point Manifold3D -P -2 -B 2 -I 0

Search clusterings

-Help

Help

(Help on Clustering type)

Affinity Propagation

-Point :

Manifold -> use manifold points

Manifold3D -> use the CURRENT 3D view of manifold points

PCA -> use the CURRENT 3D view of principal components

-P : preferences

-2 -> use the median of the similarities

Ordered list of clusterings

None

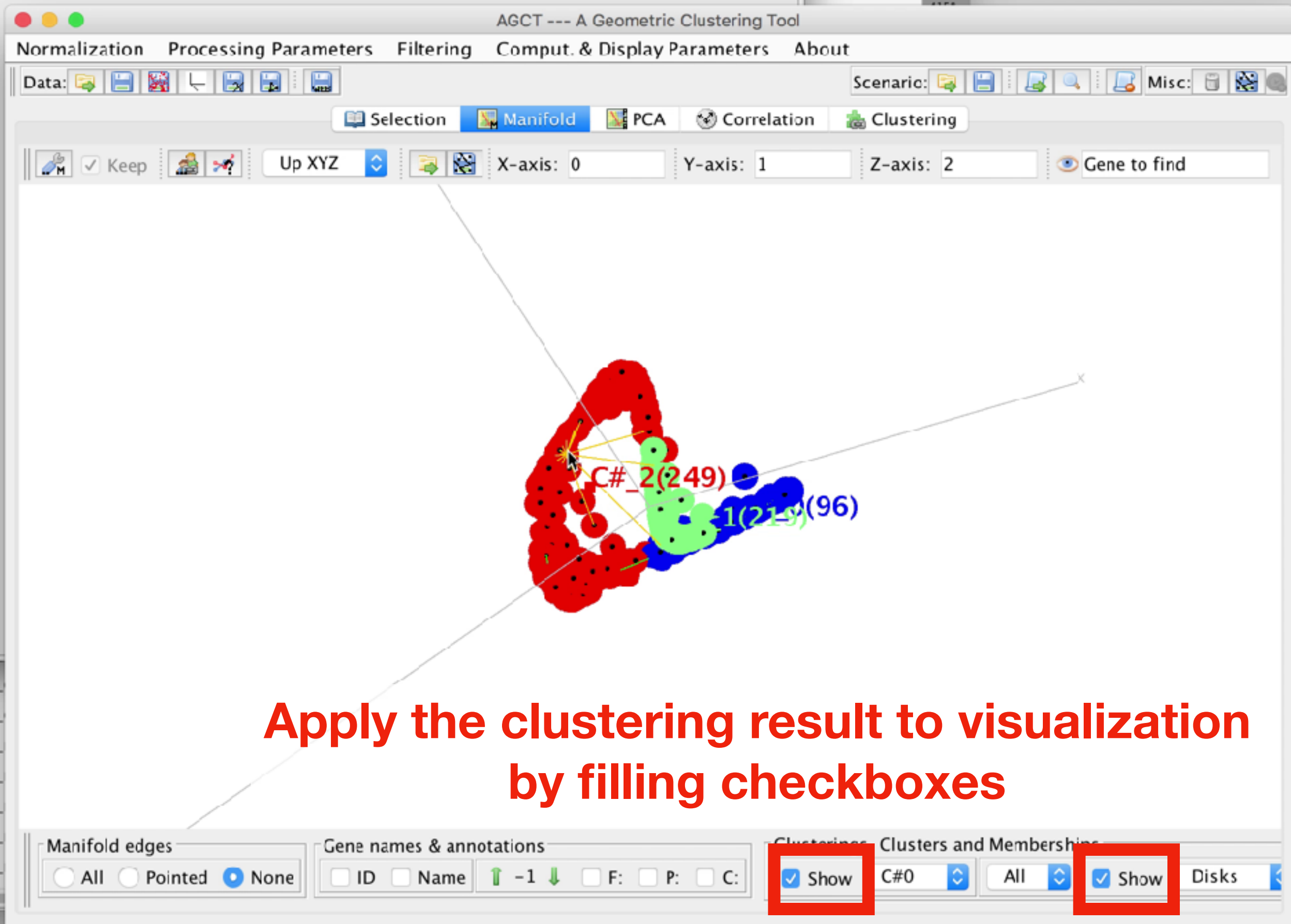
GO

**Select a method
and press the "GO" button.**

10061_at_HSP60

(no computation):

- ☐ _5-phosphoribose_1-diphosphate_bios
- ☐ _ATP_biosynthetic_process_
- ☐ _ATP_metabolic_process_
- ☐ _ATP_synthesis_coupled_proton_transp
- ☐ _ATP_transport_
- ☐ _Arp2/3_complex-mediated_actin_nucle
- ☐ _CTP_biosynthetic_process_
- ☐ _CVT_pathway_
- ☐ _D-xylose_catabolic_process_
- ☐ _D-xylose_metabolic_process_
- ☐ _DNA_damage_checkpoint_
- ☐ _DNA_metabolic_process_
- ☐ _DNA_recombination_



10018_at_MET17

AGCT --- Information Frame

AGCT --- [Clustering|Gene] Profile Visualization Frame

C#0 (KM) (default: average) SD B

C#0 (KM) Time-ExpressionLevel Plot

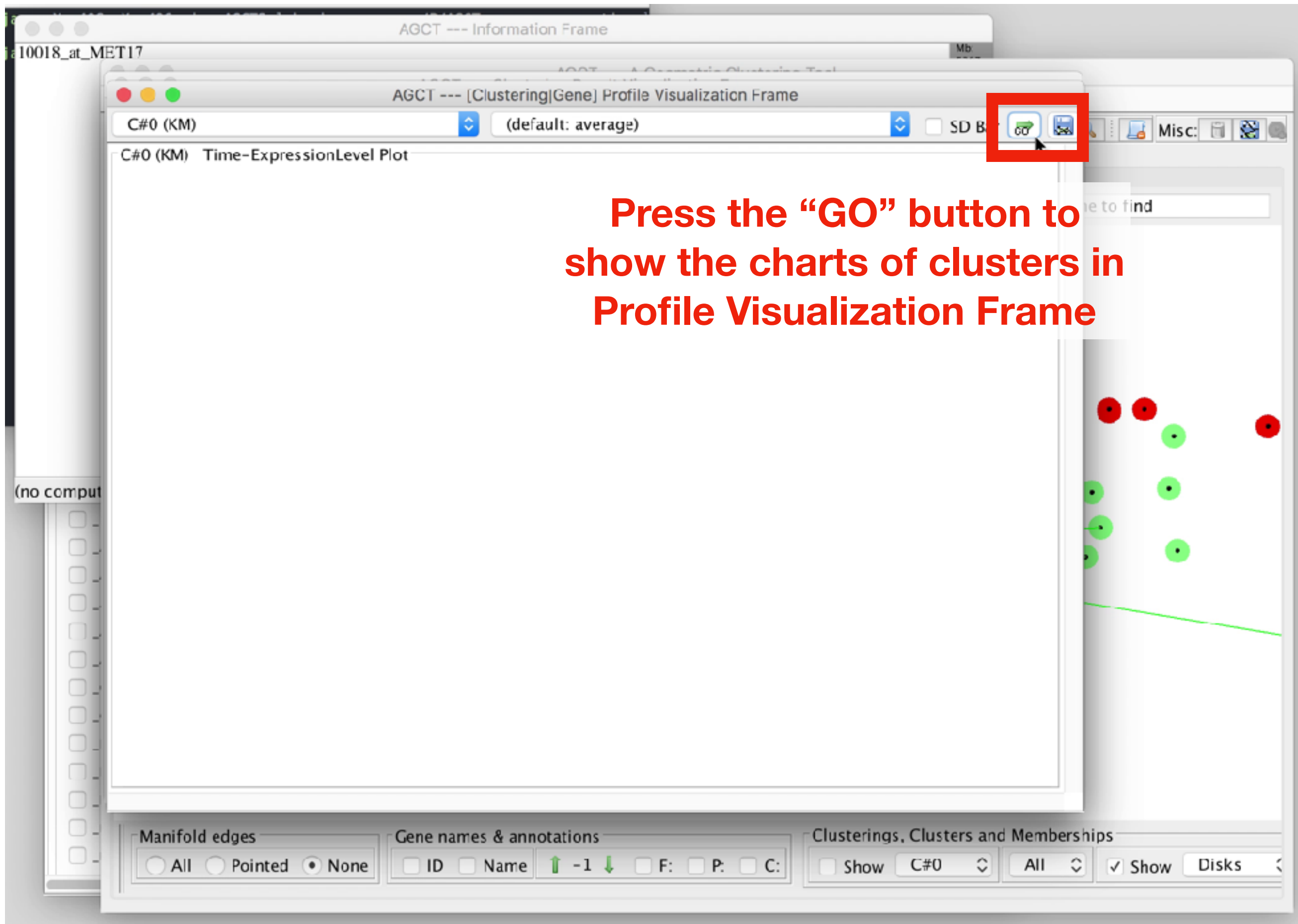
Press the “GO” button to show the charts of clusters in Profile Visualization Frame

(no comput

Manifold edges: ☐ All ☐ Pointed ☒ None

Gene names & annotations: ☐ ID ☐ Name ☒ -1 ☒ -2 ☐ F: ☐ P: ☐ C:

Clusterings, Clusters and Memberships: ☐ Show C#0 ☐ All ☒ Show Disks



C#0 (KM)

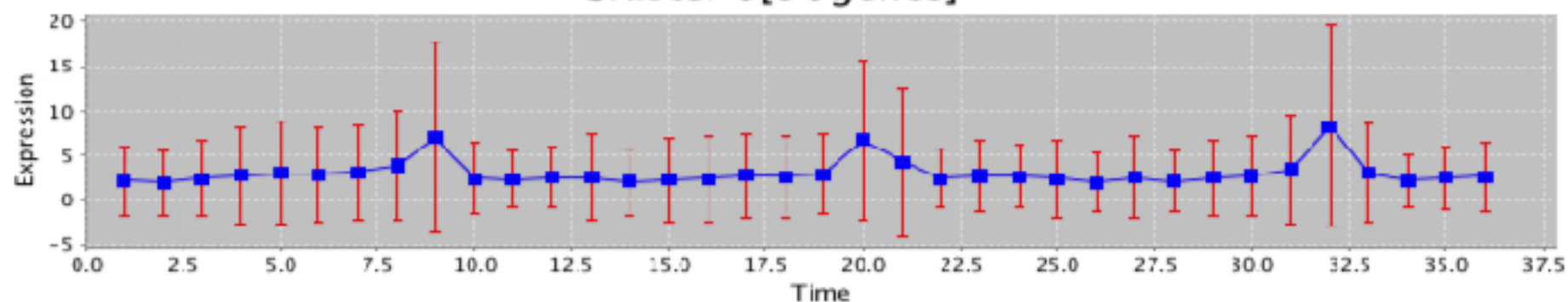
(default: average)

SD Bar

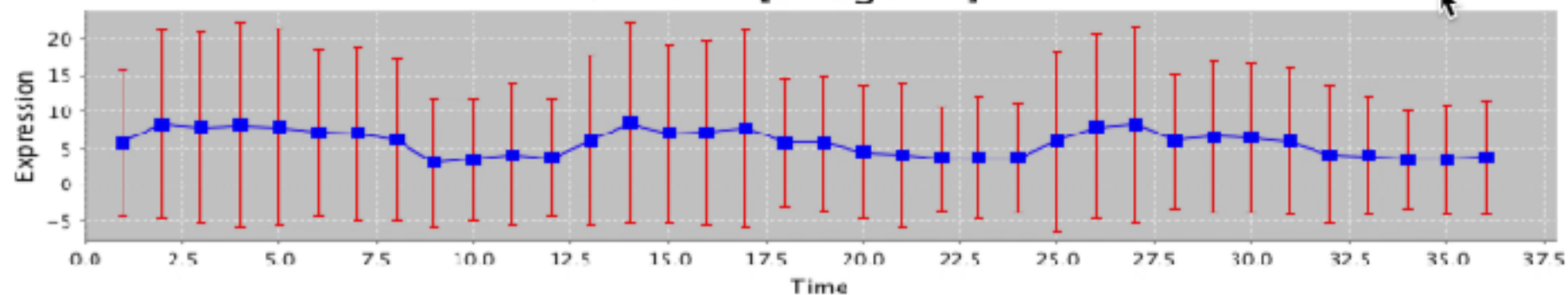
GO

C#0 (KM) Time-ExpressionLevel Plot

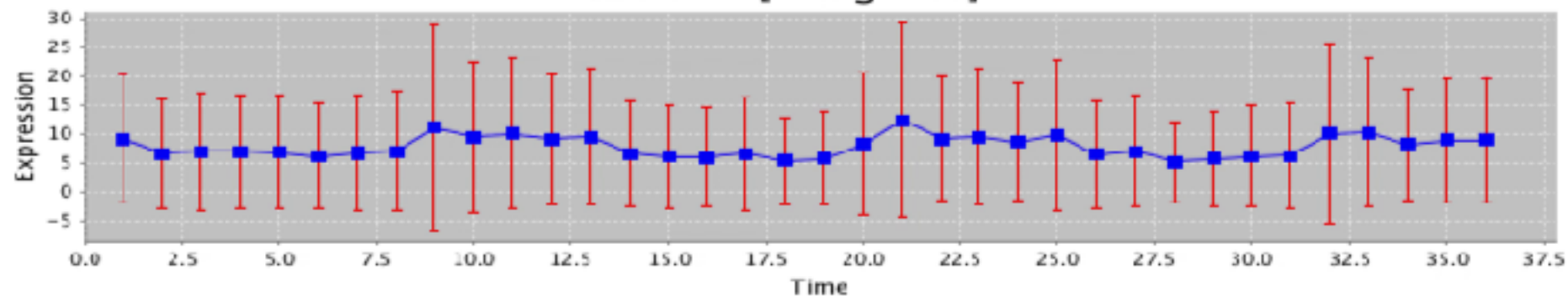
Cluster 0[96genes]



Cluster 1[219genes]



Cluster 2[249genes]



Manifold edges

☐ All ☐ Pointed ☒ None

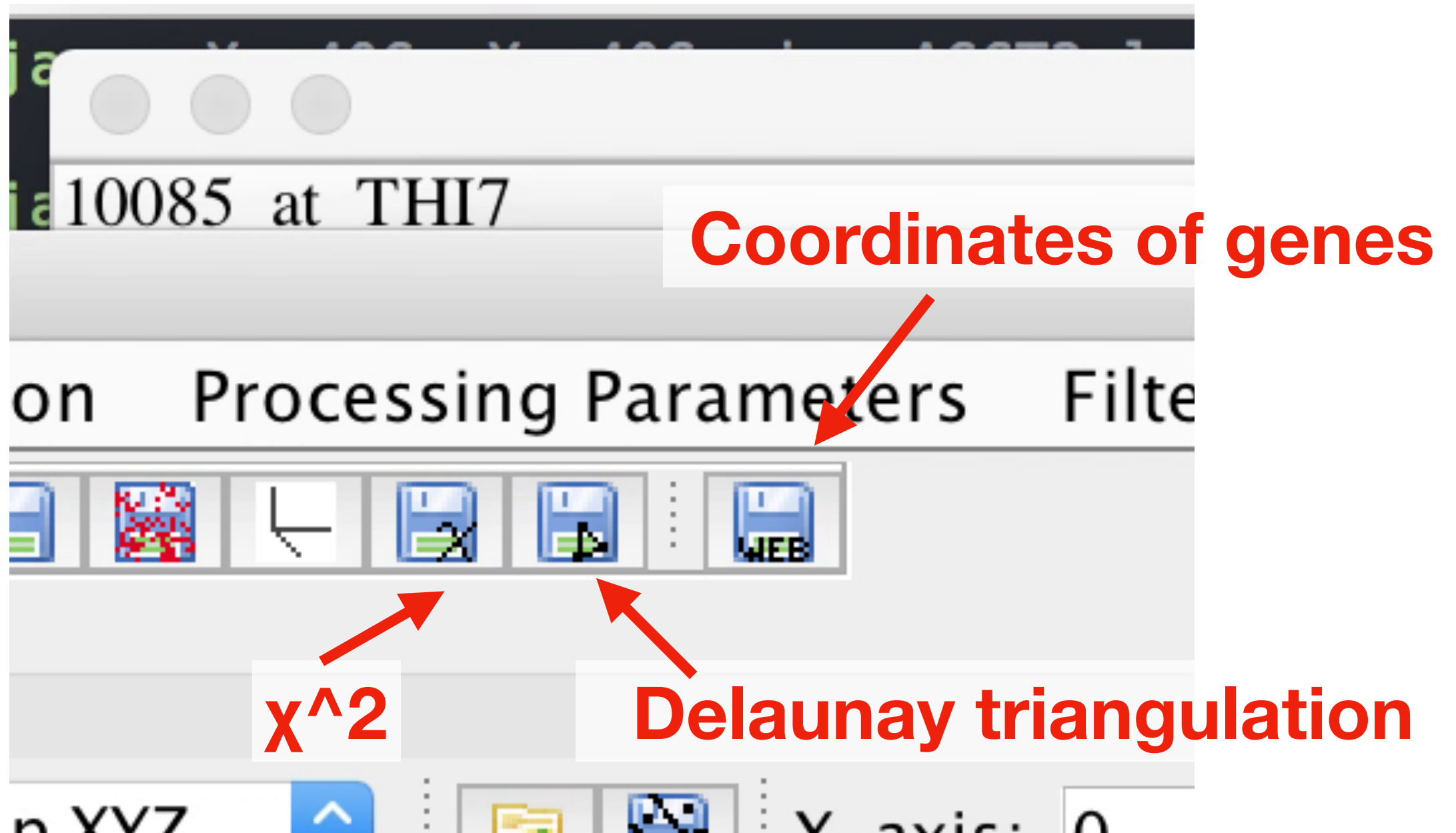
Gene names & annotations

☐ ID ☐ Name ☒ -1 ☒ -1 ☐ F: ☐ P: ☐ C:

Clusterings, Clusters and Memberships

☐ Show C#0 ☐ All ☒ Show Disks

Save the results of clustering.



Save the results of clustering.

The screenshot displays a software interface with three main components:

- File Explorer (Left):** A sidebar showing a file tree. Under the 'Today' section, four files are listed: `Test_570_cluster_1.txt`, `Test_570_cluster_2.txt`, `Test_570_cluster_3.txt`, and `Test_570...erProfile.txt`. These files are highlighted with a red rectangular box.
- Metadata Table (Middle):** A table with columns for various biological data points. The first row is: `ID`, `GB_ACC`, `SPOT_ID`. Other rows include `Species Scientific Name`, `Annotation Date Sequence`, `Type Sequence Source`, `Target Description`, `Representative Public ID`, `Gene Title`, `Gene Symbol`, `ENTREZ_GENE_ID RefSeq`, `Transcript ID Gene`, `Ontology Biological`, `Process Gene Ontology`, and `Cellular Component`. Below the table, the file `Test_570_cluster_1.txt` is selected, showing its details: `Plain Text - 101 KB`, `Created Today 10:29`, `Modified Today 10:29`, and `Last opened Today 10:29`. A link `Add Tags...` is also visible.
- Clustering Visualization (Right):** A window titled 'Clustering' showing a scatter plot of data points. The points are colored red and green, representing different clusters. A red rectangular box highlights a button in the top right corner of the 'Clustering' window, which appears to be a 'Save' or 'Export' icon.

Overlaid on the right side of the image is the text: **Save the all the results of clusters**.