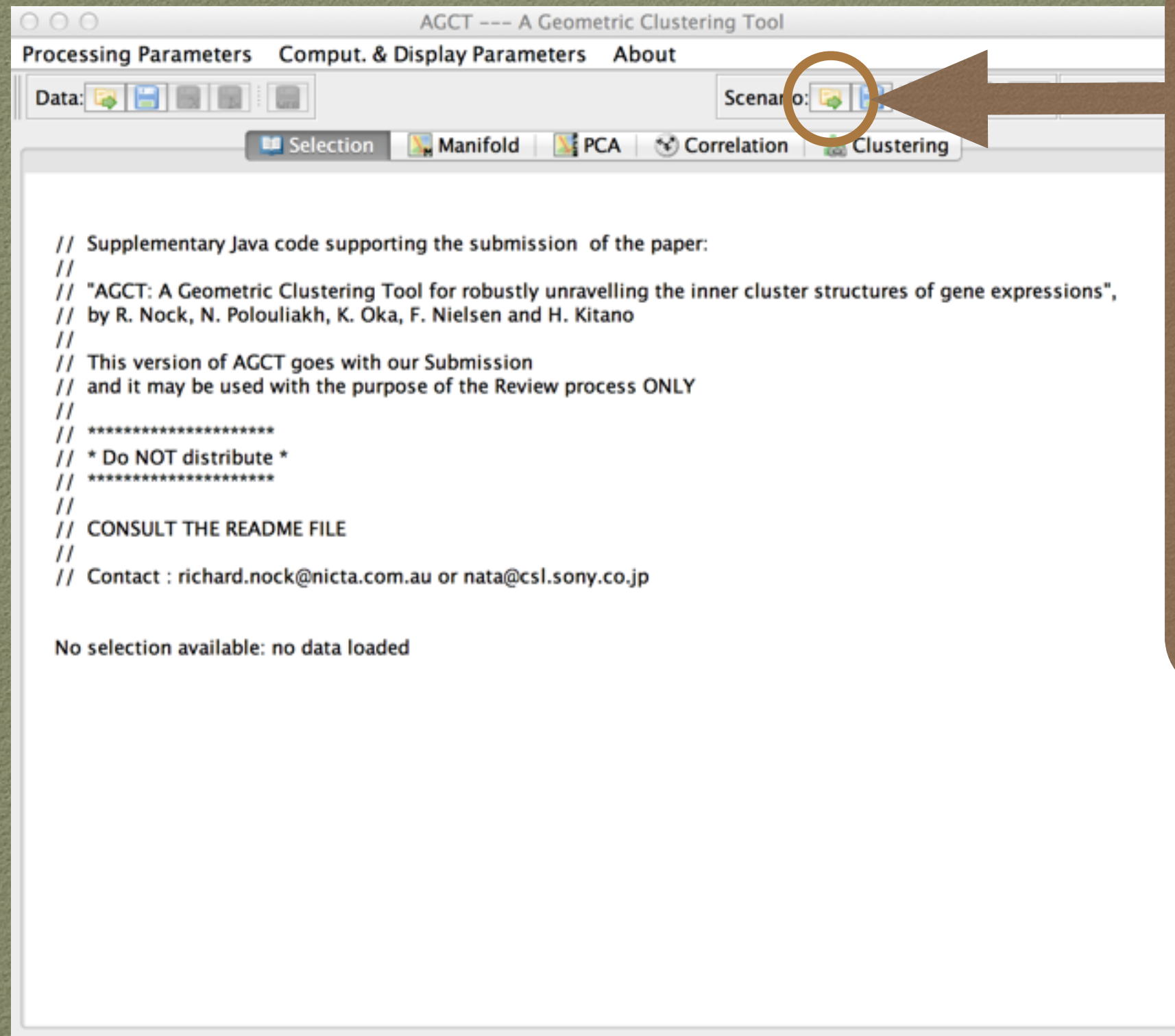


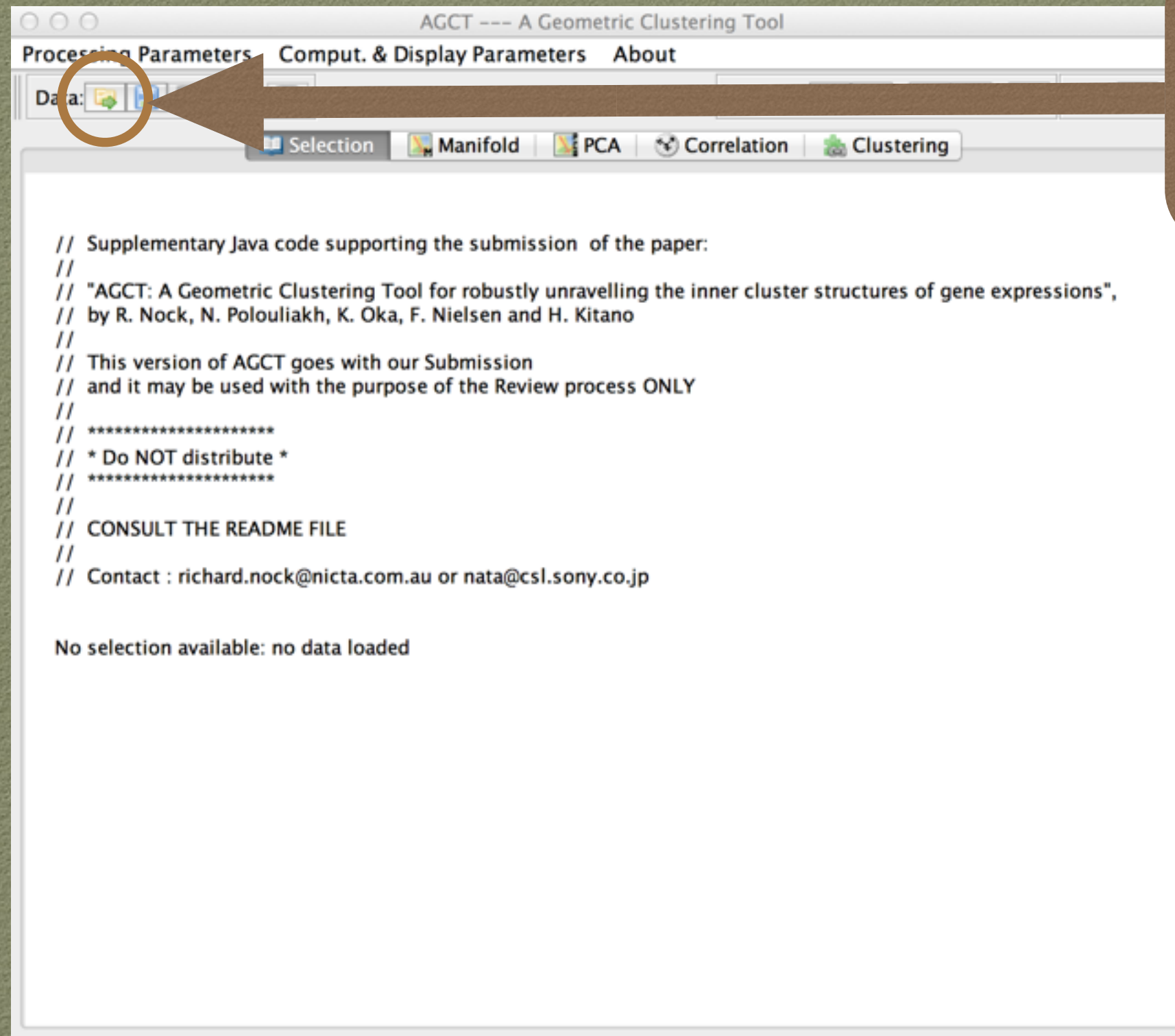
USING AGCT

RUN AGCT WITH SCENARIO

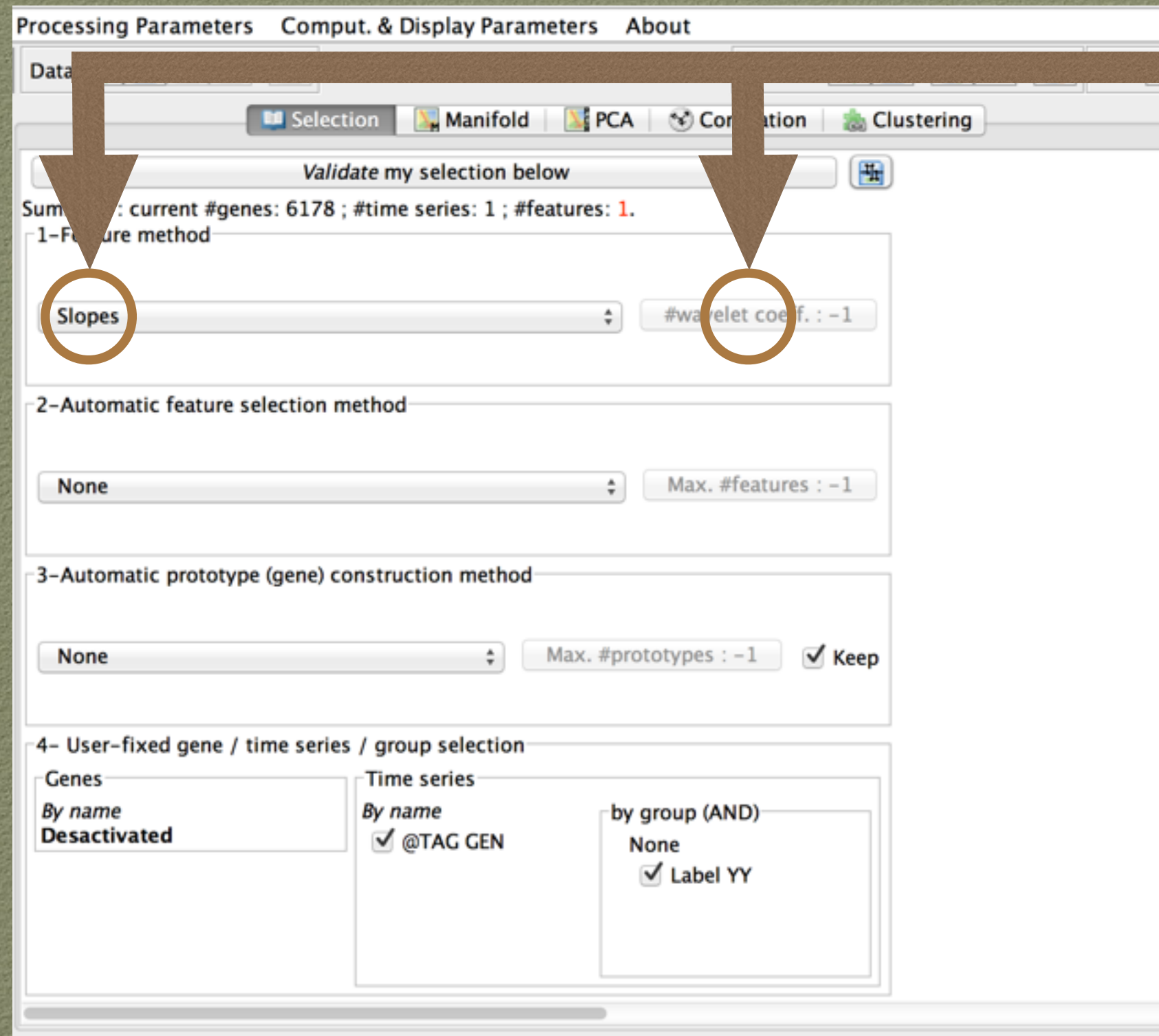


Click here
to load the
scenario
... then just
wait until it
finishes (Cf
Information
Frame)

**RUN AGCT WITH
DATASET**



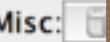


Click here
to load a
dataset



Click here
to select
Haar
wavelets and
then 64
coefficients
(all other
AGCT
parameters
are set by
default to
the paper's)

Processing Parameters Comput. & Display Parameters About

Data:  Scenario:  Misc: 

Selection Manifold PCA Correlation Clustering

Validate my selection

Summary : current #genes: 6178 ; #time series: 1 ; #features: 63.

1-Feature method

Haar_Wavelets #wavelet coeff. : 64

2-Automatic feature selection method

None Max. #features : -1

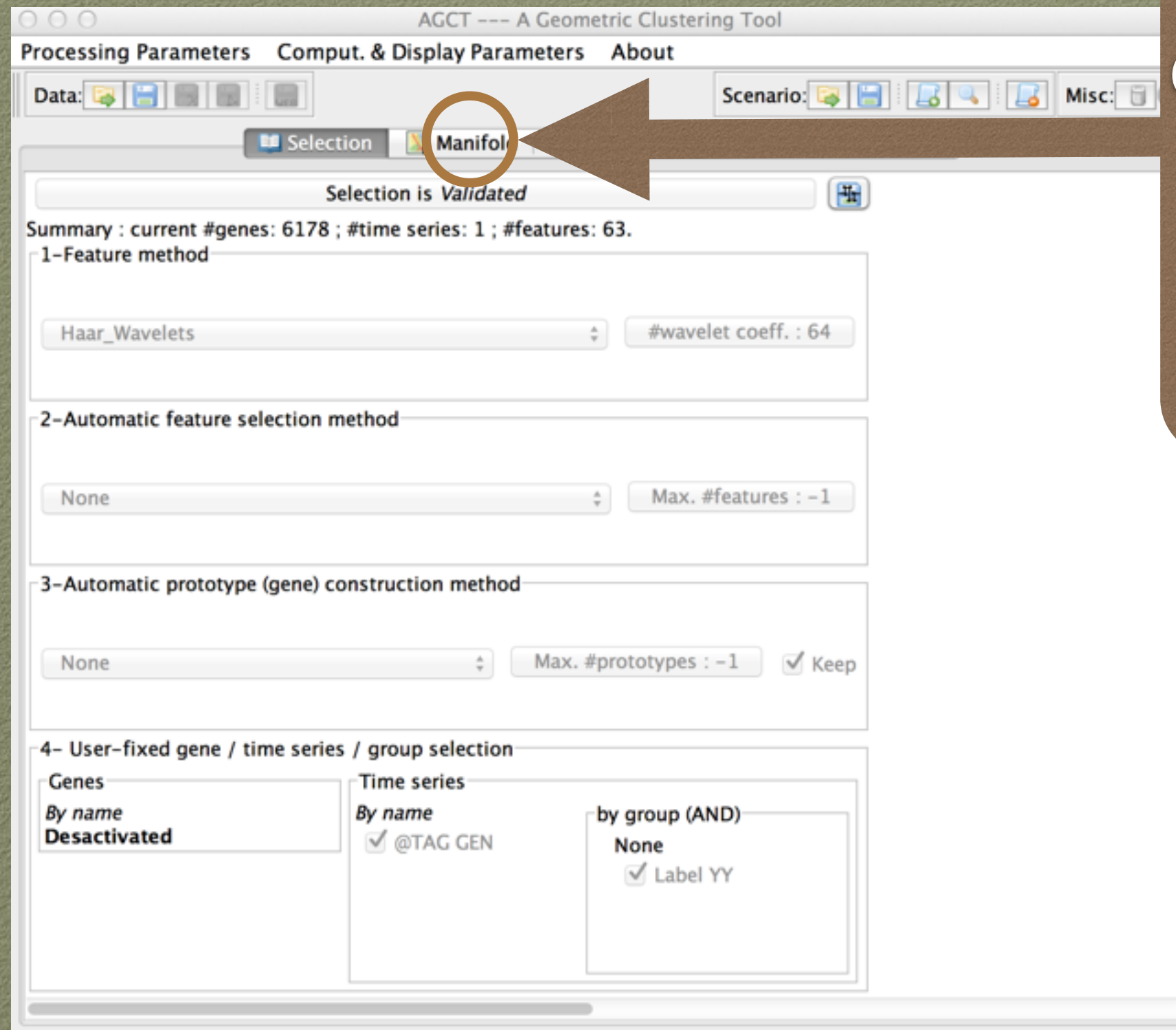
3-Automatic prototype (gene) construction method

None Max. #prototypes : -1 ☒ Keep

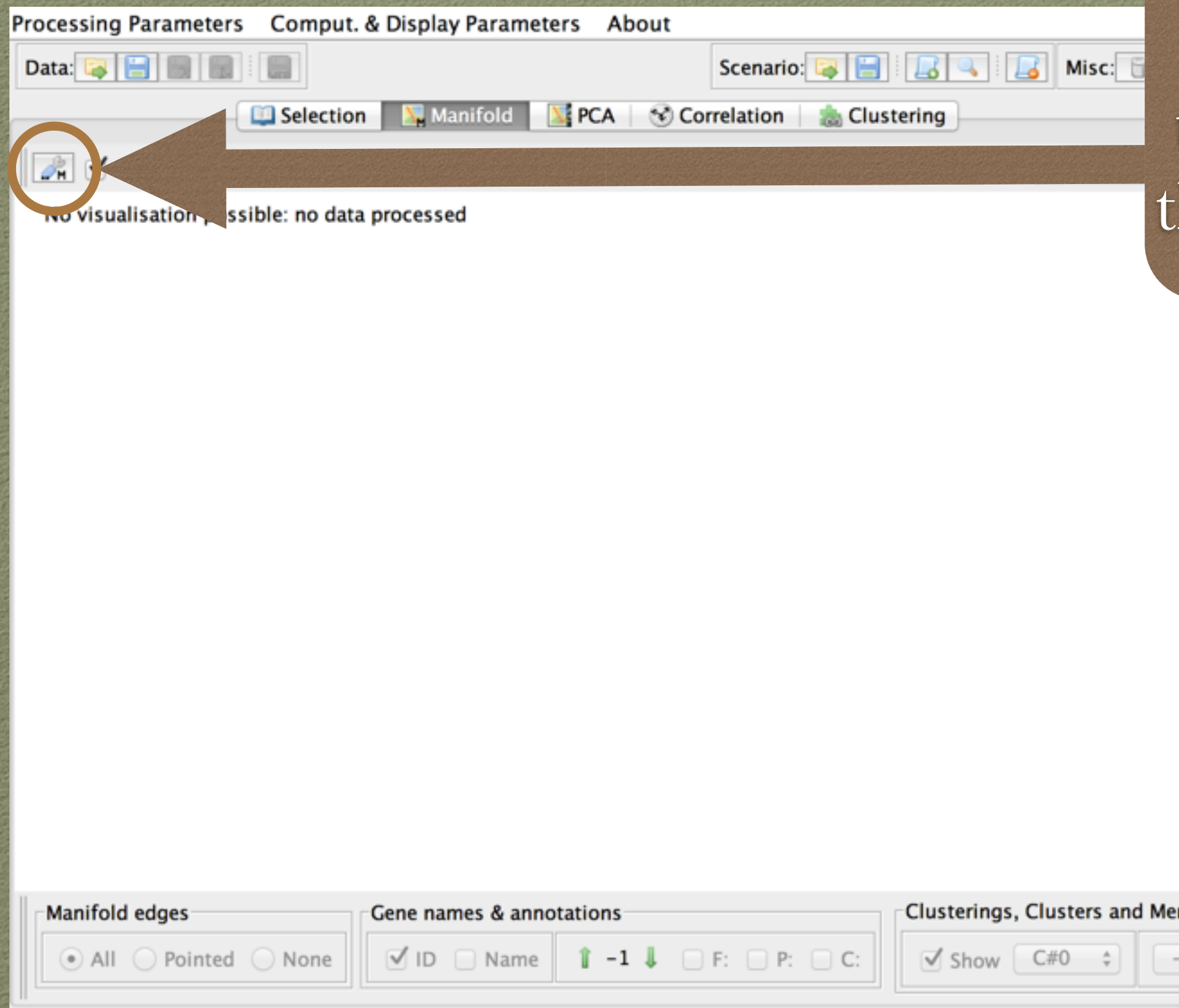
4- User-fixed gene / time series / group selection

Genes	Time series	by group (AND)
By name	By name	None
<input checked="" type="checkbox"/> Desactivated	<input checked="" type="checkbox"/> @TAG GEN	<input checked="" type="checkbox"/> Label YY

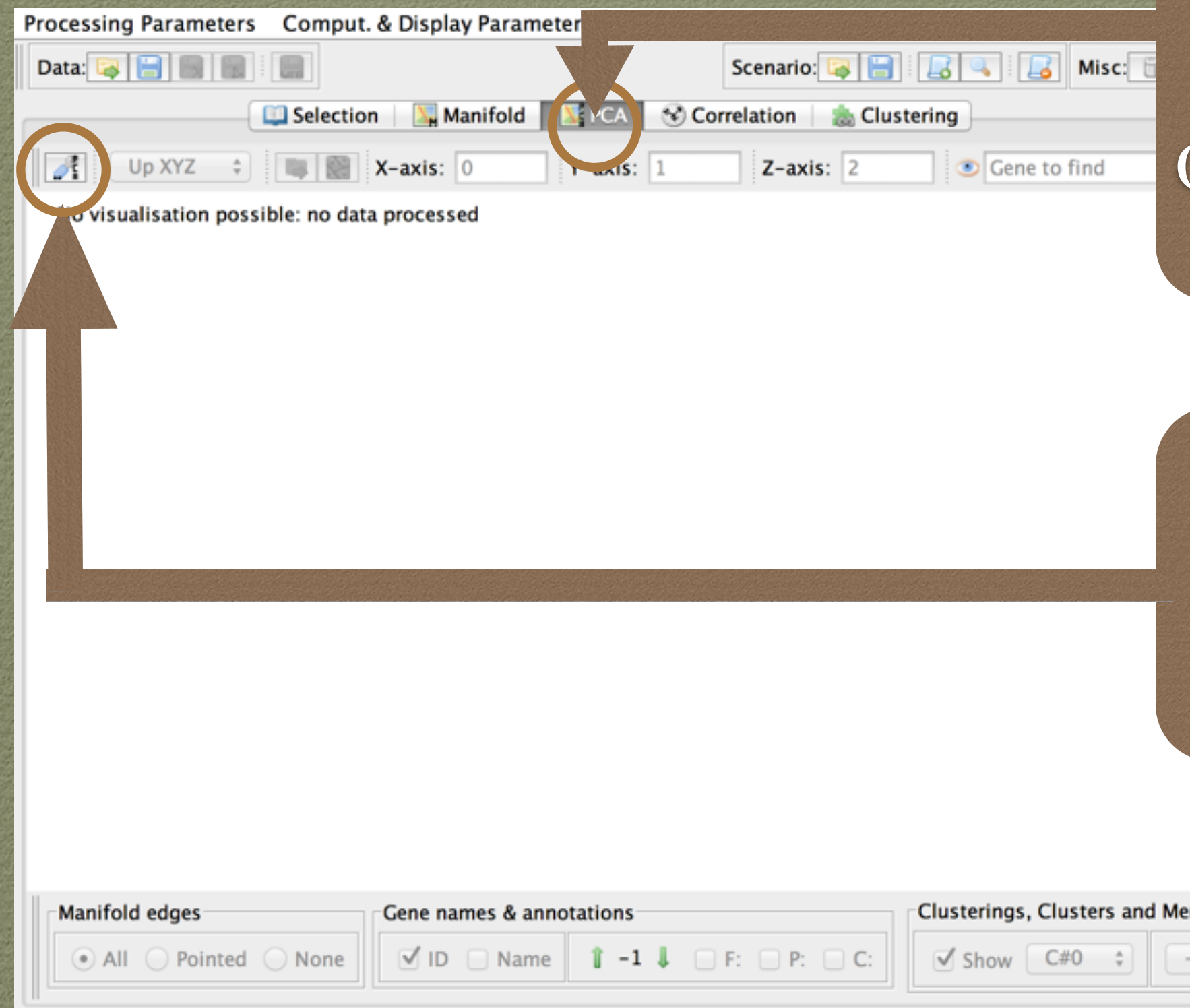
Click here
to validate
the selection



Click here to
proceed to
manifold
pane

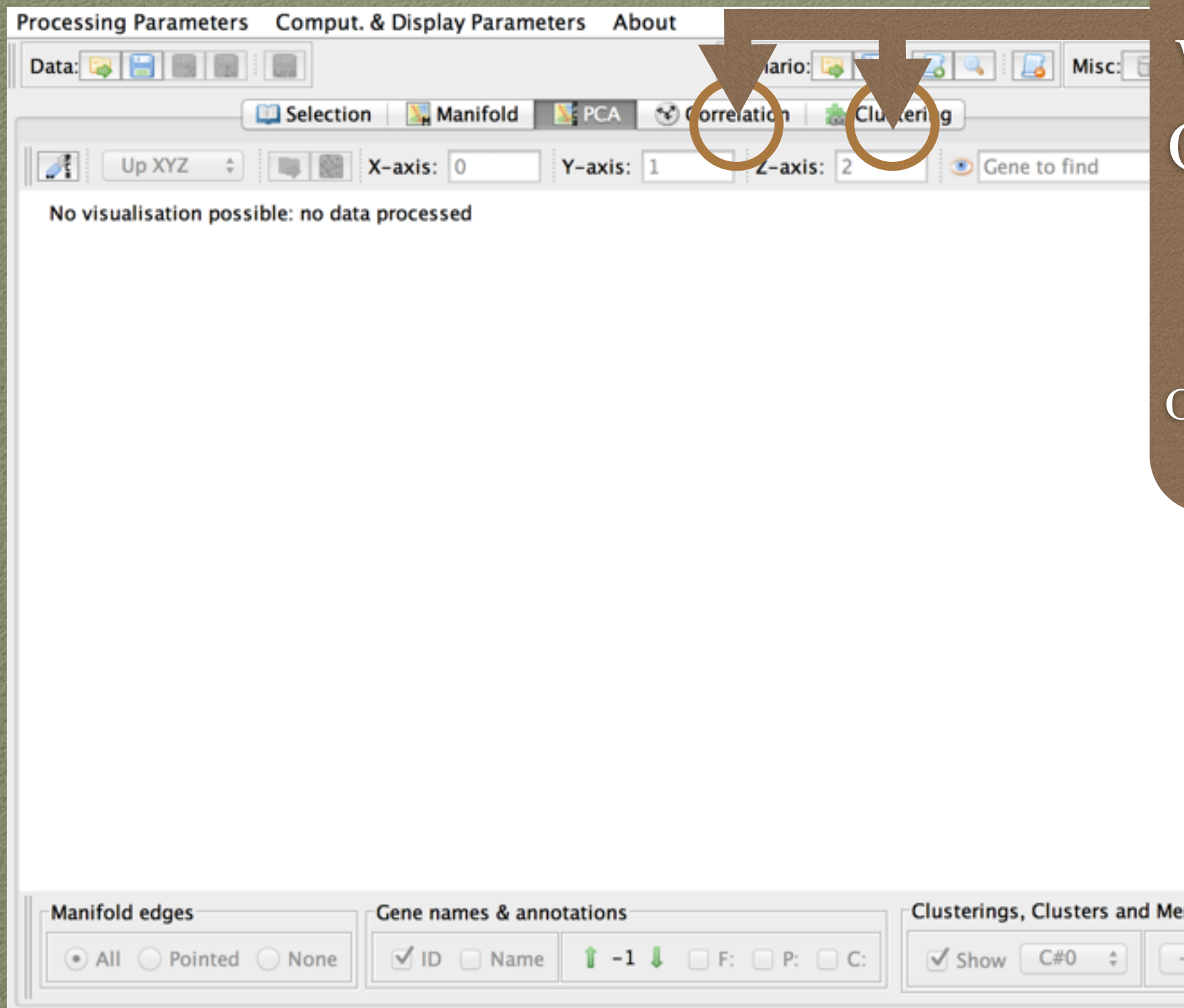


Click here
to compute
the manifold



When manifold
Ok, click on
PCA pane

Then click
here to
compute
PCA



When PCA
Ok, you can
go to
correlation
or clustering