CANB7640
Practical Workshop
Class 02

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9/10/2018
http://tanlab.ucdenver.edu/labHomePage/teaching/CANB7640/

Some thoughts - Assignment #1

- Applaud to those that have submitted on time

- Can a biologist do programming? – YES

- Is there a “right” or “wrong” program?

- Many ways to program - efficiency

@chomp

- New line can be a character (when you hit “Enter” in your keyboard, it generates a new line)
- You don’t see it, but it is there
- Cutting out new line

Reading in file

```
while (<>) # read in a file line by line
```

```
@array = (<>); # read in the file as any array, every line is an array element
```

Reading in file

`open (MYFILE, “file.txt”)` # open a file name `file.txt` and assign it to the variable `MYFILE`.

while (<MYFILE>) #read in the `file.txt` and read in line by line

`@array = (<MYFILE>);` # read in the `file.txt` as any array, every line is an array element

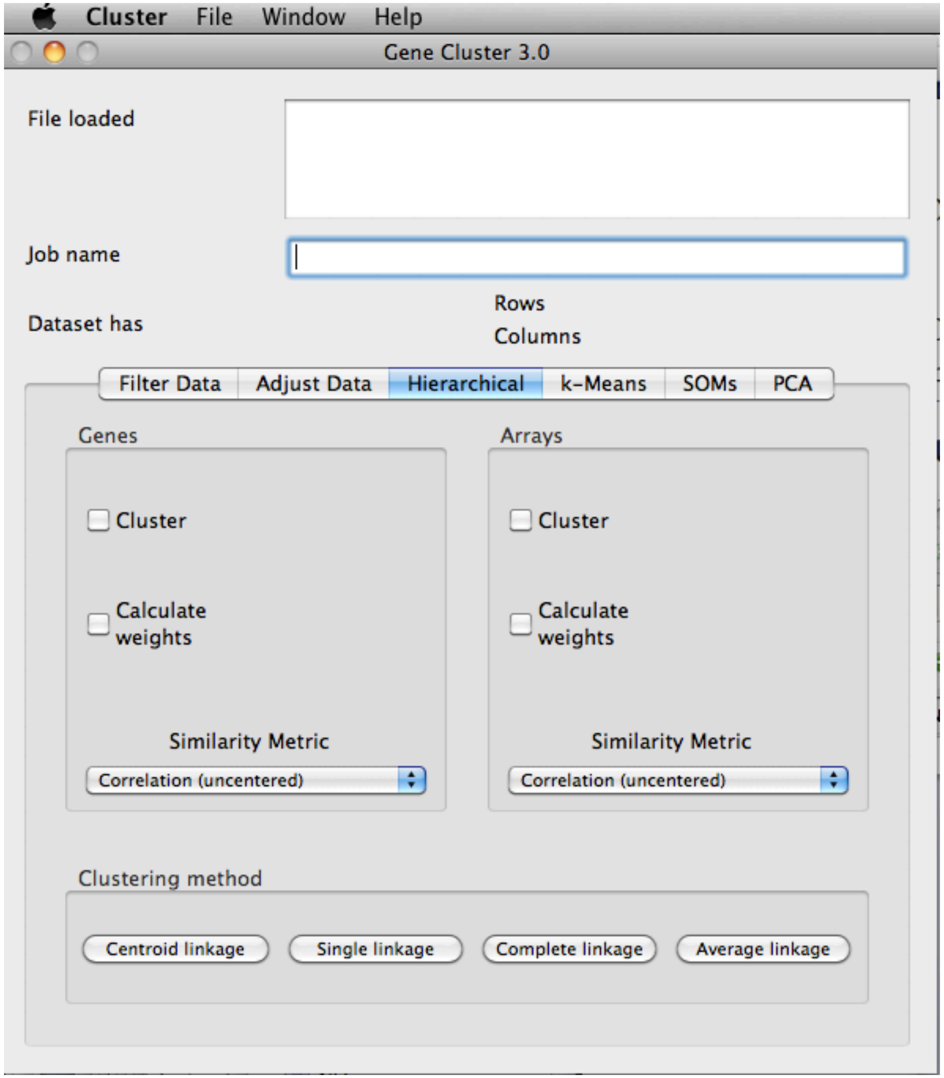
ReadFile_WHILE.pl

```
#! /usr/bin/perl -w

open (MYFILE, "file.txt");
open (OUTFILE, "> outfile_while.txt");
while (<MYFILE>)
{
        @tmp = split (/\t/);
        chomp @tmp;

        print OUTFILE "$tmp[0] || $tmp[1]\n";
}

close (MYFILE);
close (OUTFILE);
```

ReadFile_ARRAY.pl

```
#! /usr/bin/perl -w

open (MYFILE, "file.txt");
open (OUTFILE, "> outfile_array.txt");

@array = (<MYFILE>);
chomp @array;

for ($i = 0; $i <= $#array; $i++)
{
        print OUTFILE "$array[$i]\n";
}

close (MYFILE);
close (OUTFILE);
```

CLUSTER 3.0



File loaded

Job name

Dataset has
Rows
Columns

Genes

☐ Cluster

☐ Calculate weights

Similarity Metric: Correlation (uncentered)

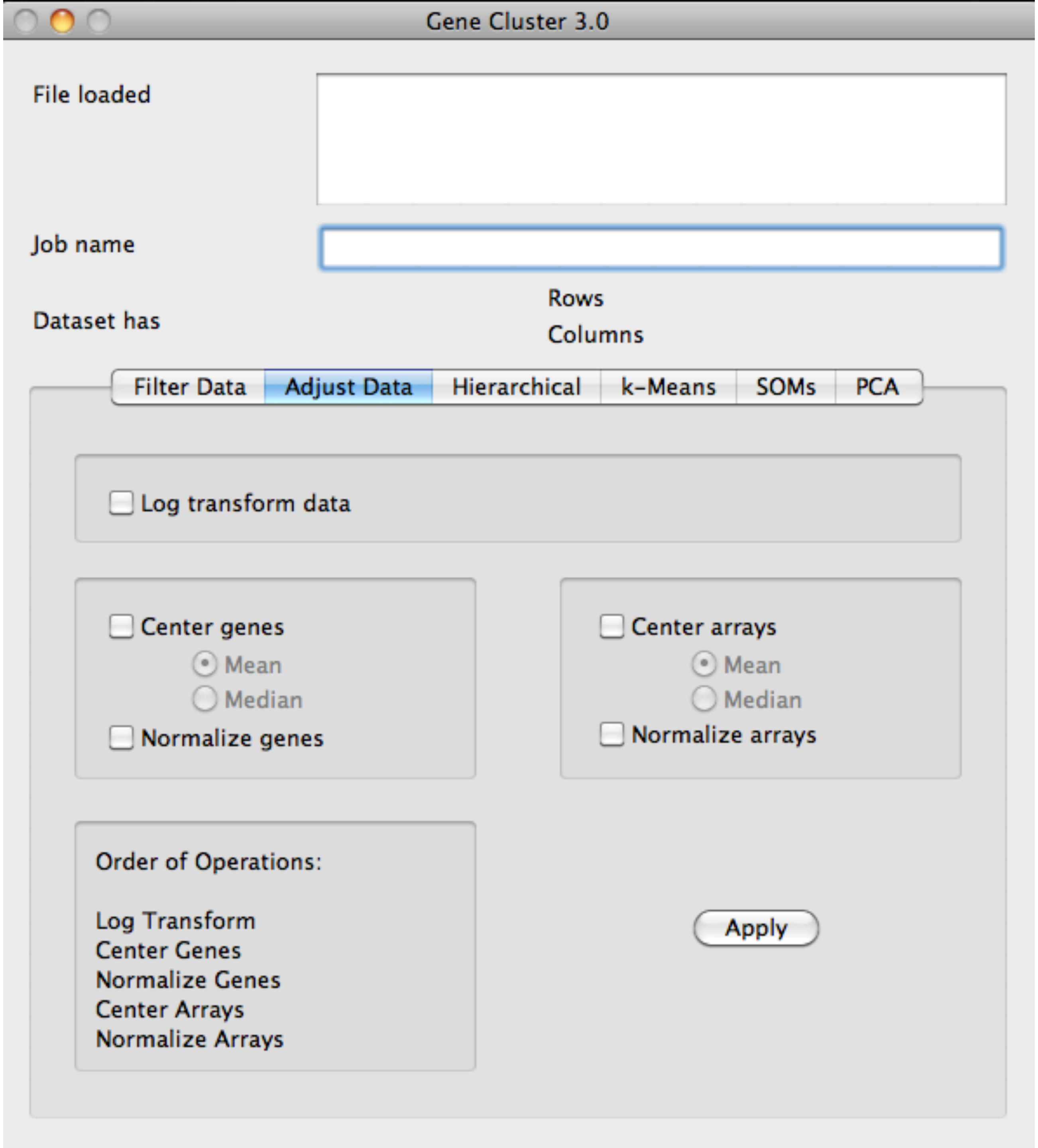
Arrays

☐ Cluster

☐ Calculate weights

Similarity Metric: Correlation (uncentered)

Clustering method



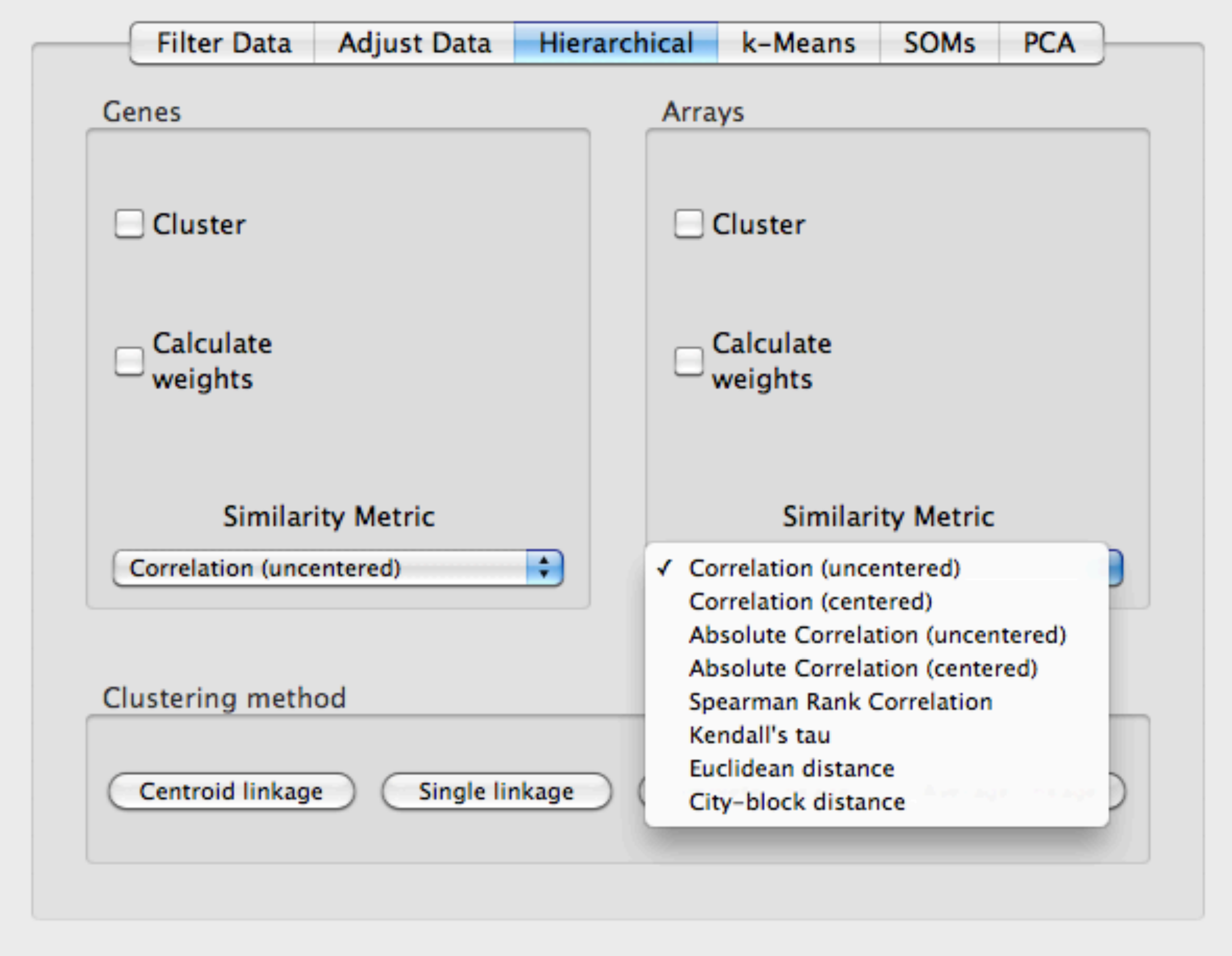
☐ Log transform data

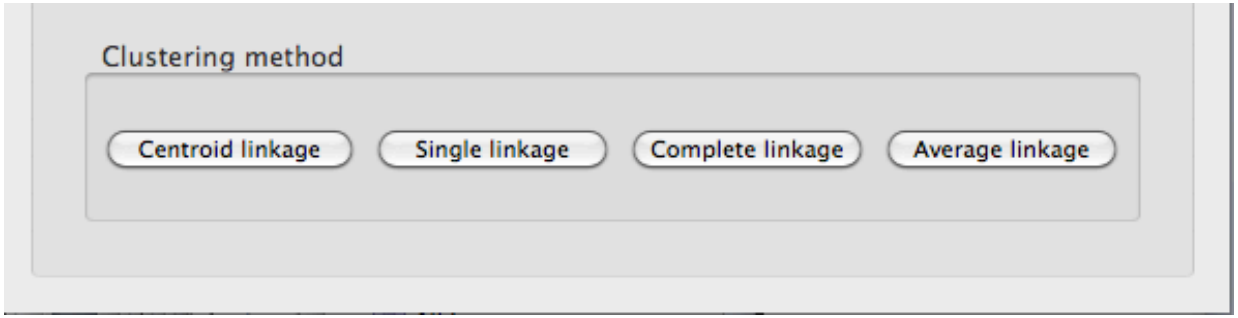
☐ Center genes
● Mean
○ Median
☐ Normalize genes

☐ Center arrays
● Mean
○ Median
☐ Normalize arrays

Order of Operations:

Log Transform
Center Genes
Normalize Genes
Center Arrays
Normalize Arrays

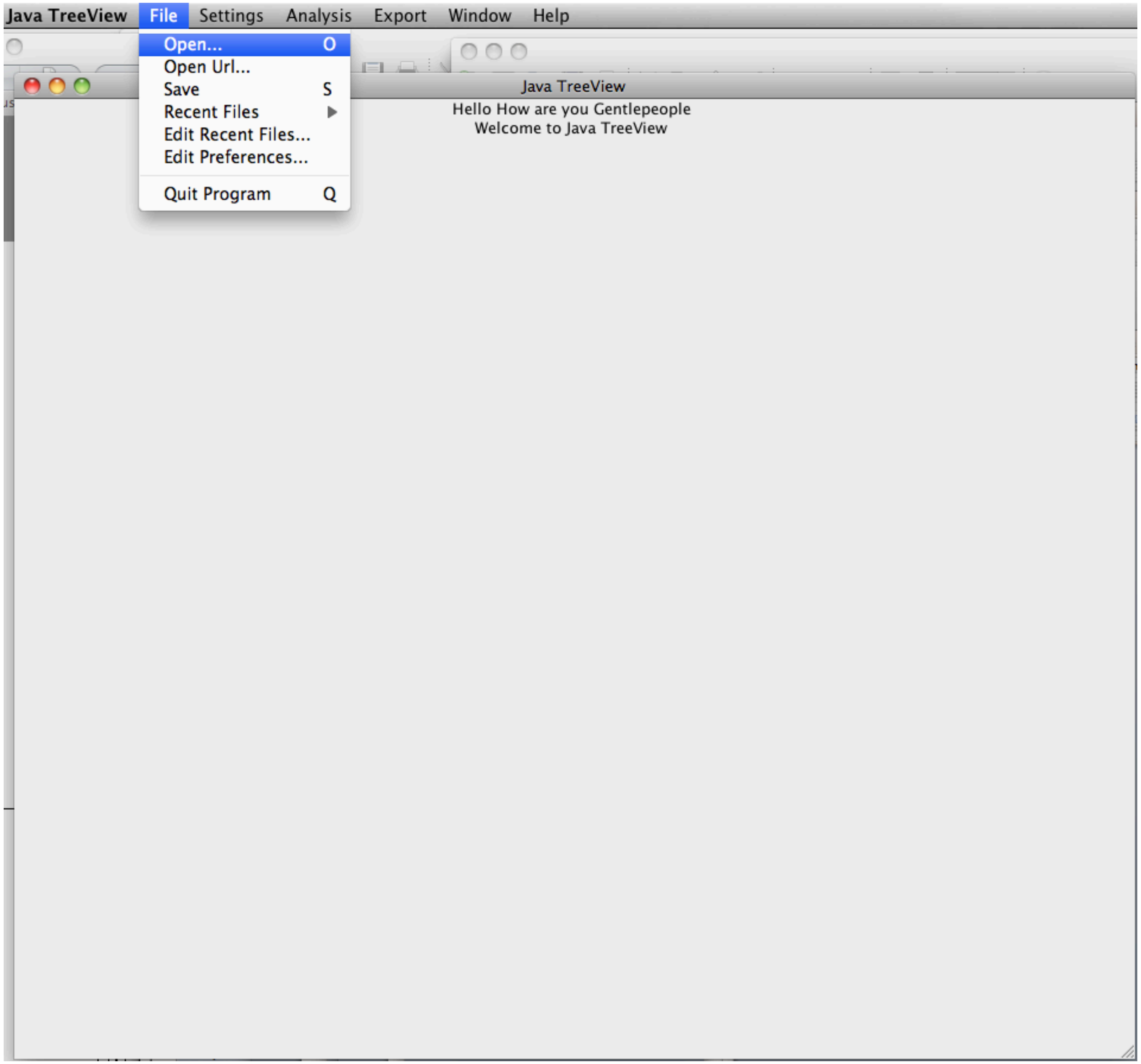

Filter Data
Adjust Data
Hierarchical
k-Means
SOMs
PCA
Genes
☐ Cluster
☐ Calculate weights
Similarity Metric
Correlation (uncentered)
Arrays
☐ Cluster
☐ Calculate weights
Similarity Metric
✓ Correlation (uncentered)
Correlation (centered)
Absolute Correlation (uncentered)
Absolute Correlation (centered)
Spearman Rank Correlation
Kendall's tau
Euclidean distance
City-block distance
Clustering method
Centroid linkage
Single linkage


Clustering method
Centroid linkage
Single linkage
Complete linkage
Average linkage

Clustering Results

- *.cdt – clustered data table
- *.atr – array tree (samples)
- *.gtr – gene tree (genes)

Java Tree



Hello How are you Gentlepeople
Welcome to Java TreeView

View Status
No status info for ArrayName

Usage Hints
Click and drag to scroll

MB-1 gene (U05259_rna1_at)
HKR-T1 (S50223_at)
Inducible protein mRNA (L47738_at)
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Interleukin 8 (IL8) gene (M28130_rna1_s_at)
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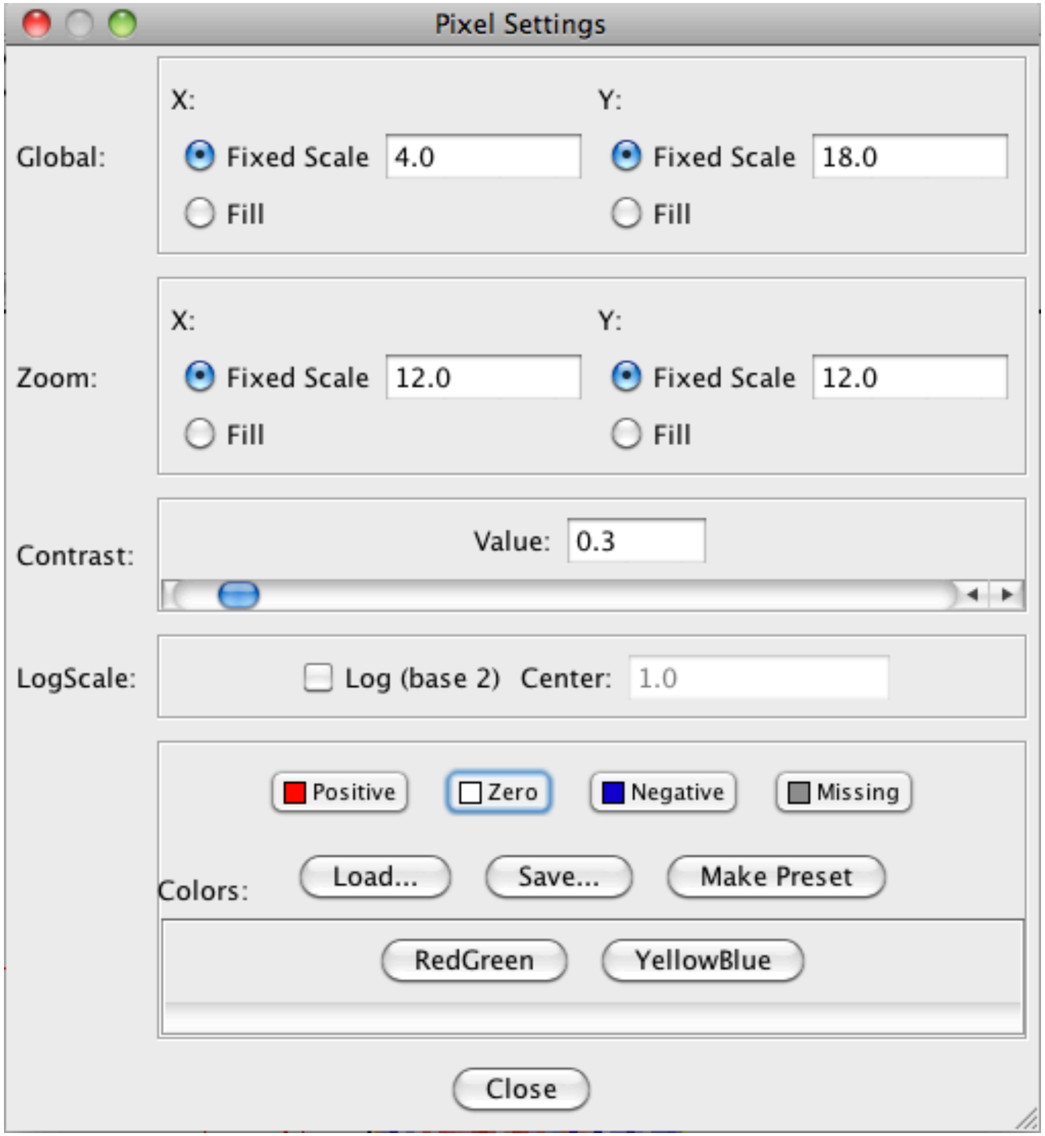


Pixel Settings

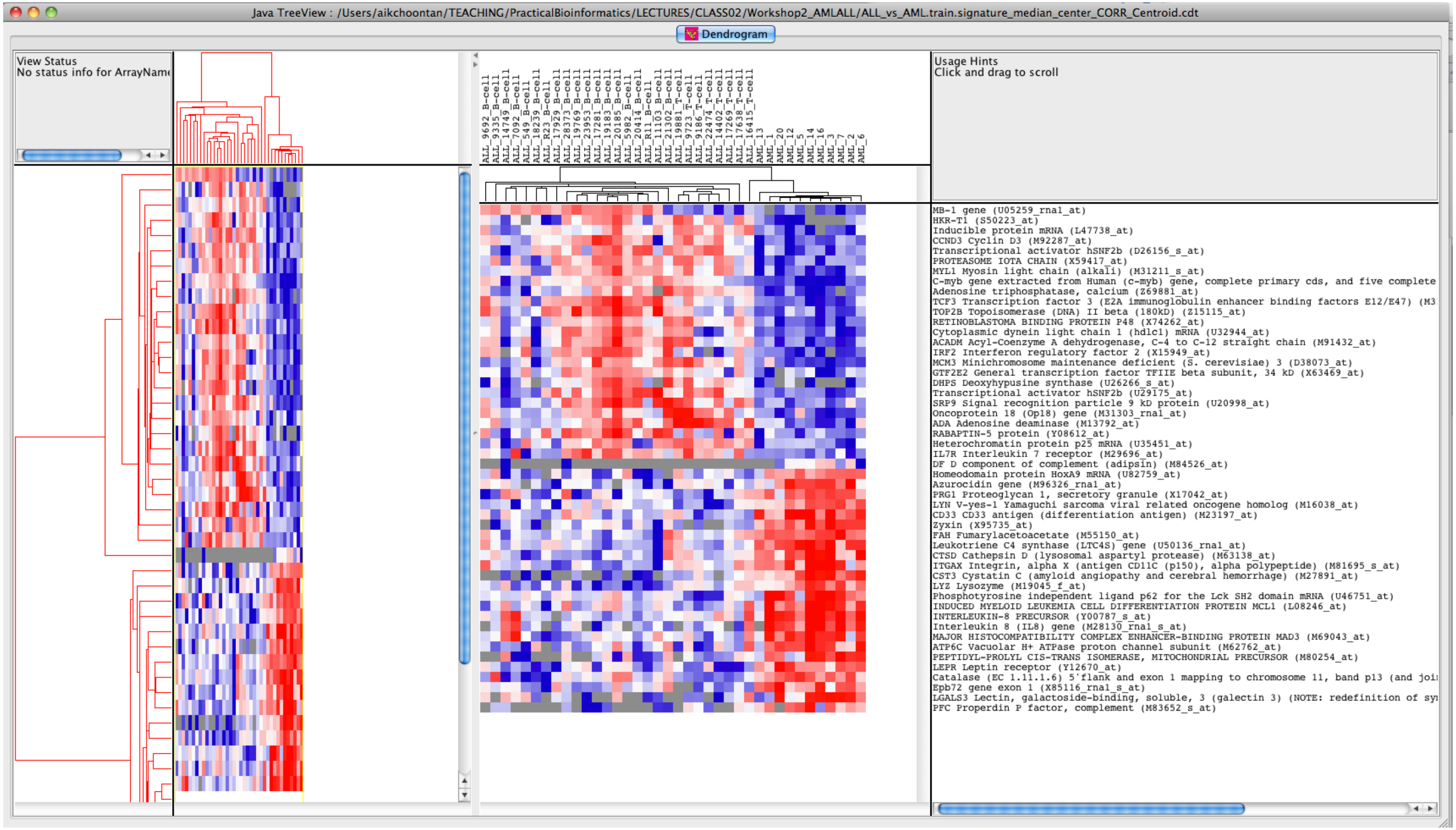
Global:
X: ● Fixed Scale 4.0 ○ Fill
Y: ● Fixed Scale 18.0 ○ Fill

Zoom:
X: ● Fixed Scale 12.0 ○ Fill
Y: ● Fixed Scale 12.0 ○ Fill

Contrast: Value: 0.3

LogScale: ☐ Log (base 2) Center: 1.0

Colors:



Java TreeView : /Users/aikchoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS02/Workshop2_AMLALL/ALL_vs_AML.train.signature_median_center_CORR_Centroid.cdt

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No status info for ArrayName

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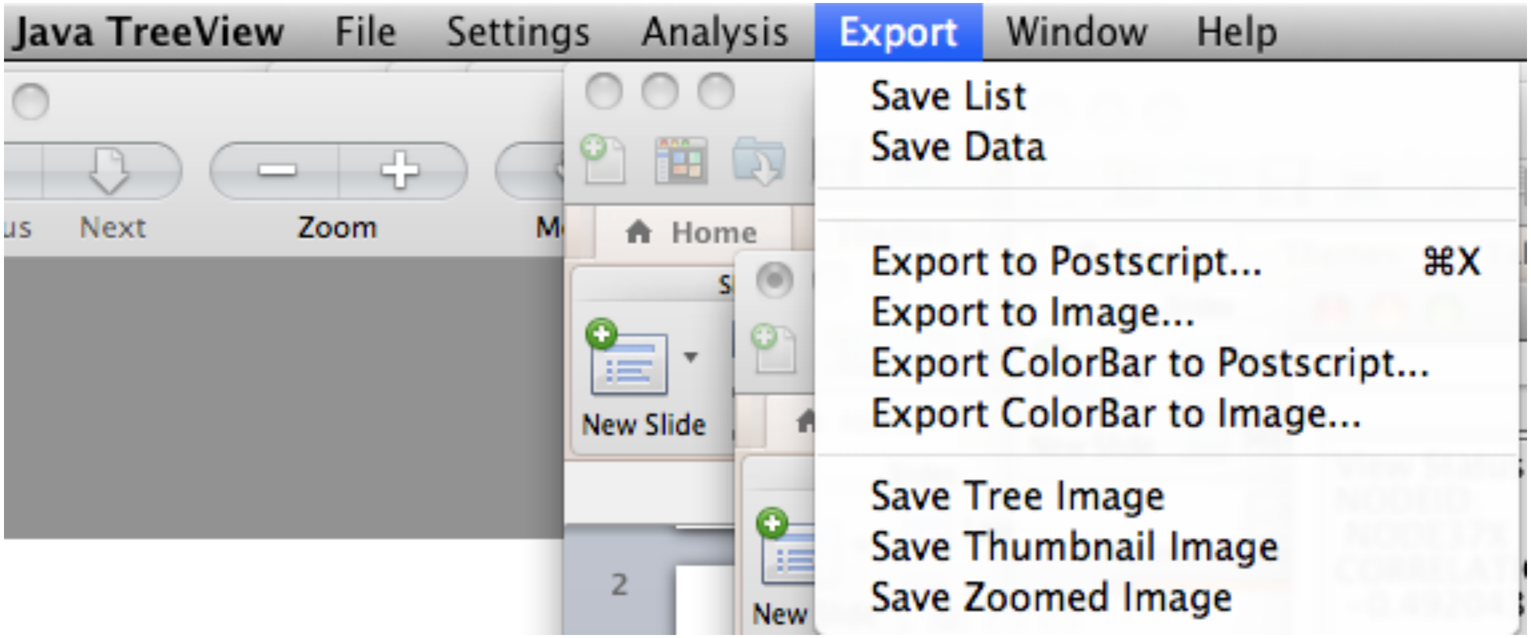
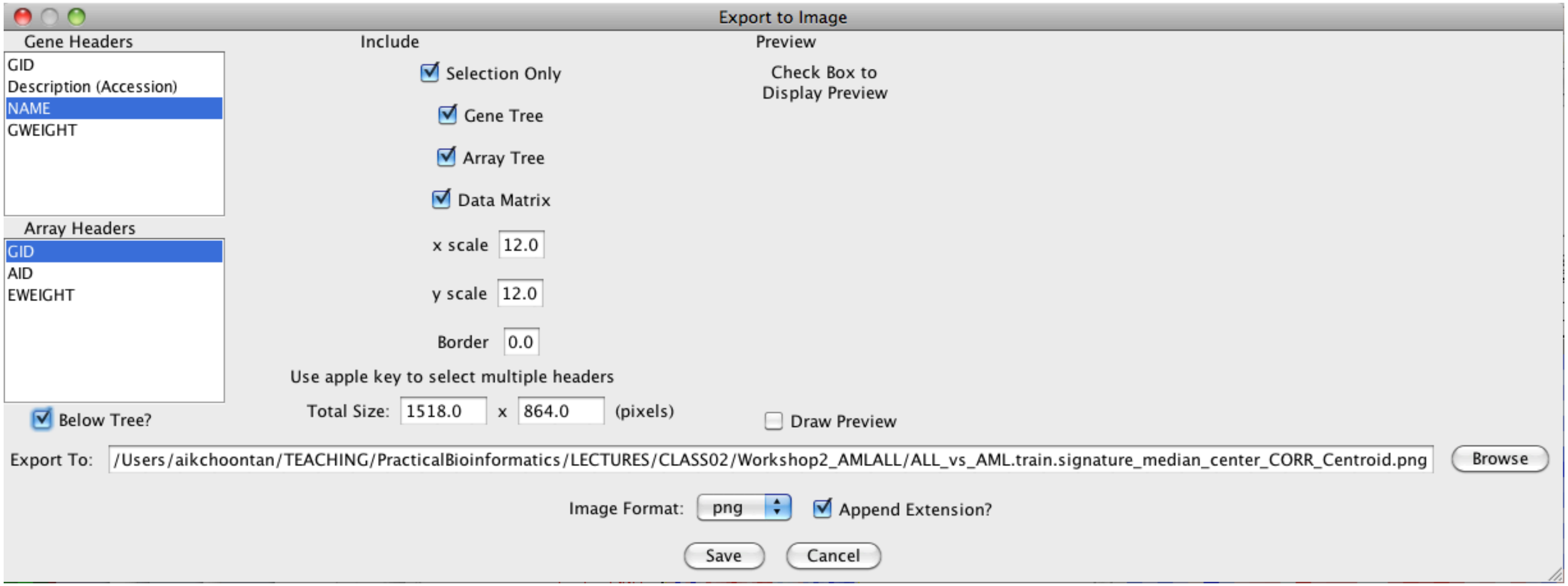

Java TreeView
File
Settings
Analysis
Export
Window
Help
Save List
Save Data
Export to Postscript... ⌘X
Export to Image...
Export ColorBar to Postscript...
Export ColorBar to Image...
Save Tree Image
Save Thumbnail Image
Save Zoomed Image
Next
Zoom
Home
New Slide
2
New



Export to Image

Gene Headers

GID
Description (Accession)
NAME
GWEIGHT

Array Headers

GID
AID
EWEIGHT

☑ Below Tree?

Include

☑ Selection Only
☑ Gene Tree
☑ Array Tree
☑ Data Matrix

x scale 12.0
y scale 12.0
Border 0.0

Use apple key to select multiple headers

Total Size: 1518.0 x 864.0 (pixels)

Preview

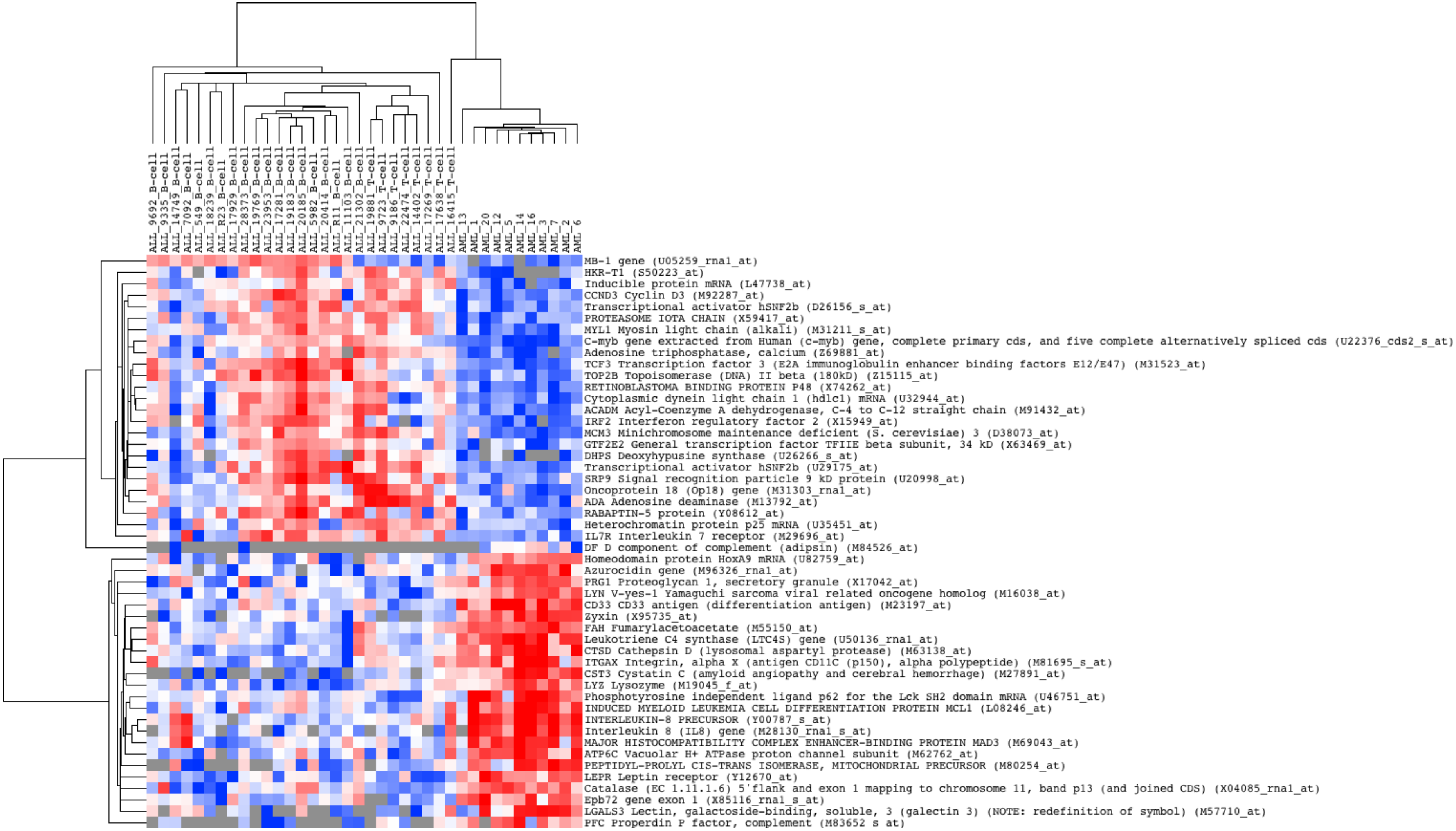
Check Box to Display Preview

☐ Draw Preview

Export To: /Users/aikchoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS02/Workshop2_AMLALL/ALL_vs_AML.train.signature_median_center_CORR_Centroid.png

Image Format: png

☑ Append Extension?


ALL_9692_B-cell
ALL_9335_B-cell
ALL_14749_B-cell
ALL_7092_B-cell
ALL_549_B-cell
ALL_18239_B-cell
ALL_R23_B-cell
ALL_17929_B-cell
ALL_28373_B-cell
ALL_19769_B-cell
ALL_23953_B-cell
ALL_17281_B-cell
ALL_19183_B-cell
ALL_20185_B-cell
ALL_5982_B-cell
ALL_20414_B-cell
ALL_R11_B-cell
ALL_11103_B-cell
ALL_21302_B-cell
ALL_19881_T-cell
ALL_9723_T-cell
ALL_9186_T-cell
ALL_22474_T-cell
ALL_14402_T-cell
ALL_17269_T-cell
ALL_17638_T-cell
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