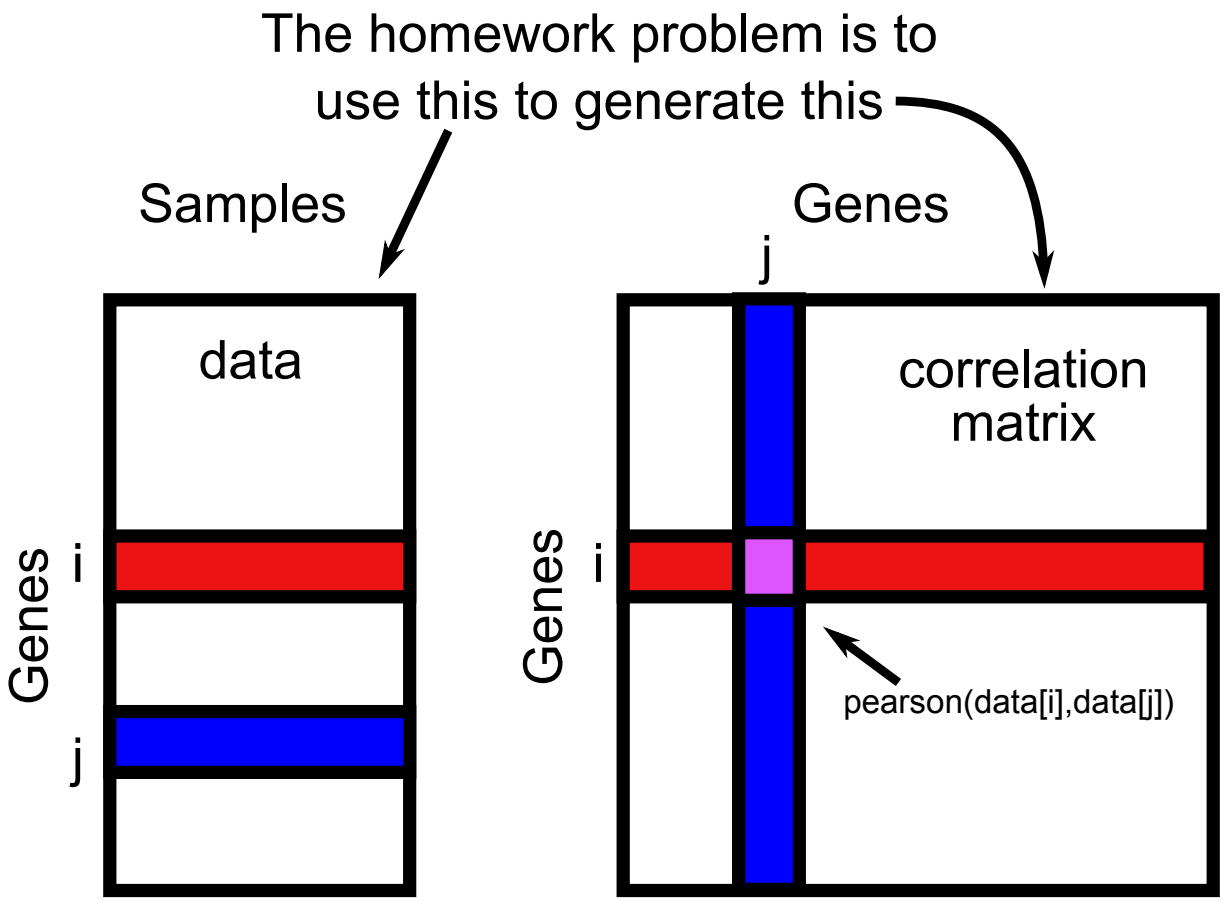
Practical Bioinformatics

Mark Voorhies

5/16/2019

What was Mark even asking for yesterday?



List tricks

Adding data to a list:

```
mylist = []
mylist.append(3)
mylist += [4,5,6]
```

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```

Lists of lists:

```
matrix = [[ 1, 2, 3, 4],
          [ 5, 6, 7, 8],
          [ 9,10,11,12]]
```

Pearson distances

Pearson similarity

$$s(x,y) = \frac{\sum_i^N (x_i - x_{offset})(y_i - y_{offset})}{\sqrt{\sum_i^N (x_i - x_{offset})^2}\sqrt{\sum_i^N (y_i - y_{offset})^2}}$$

Pearson distances

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Pearson distance

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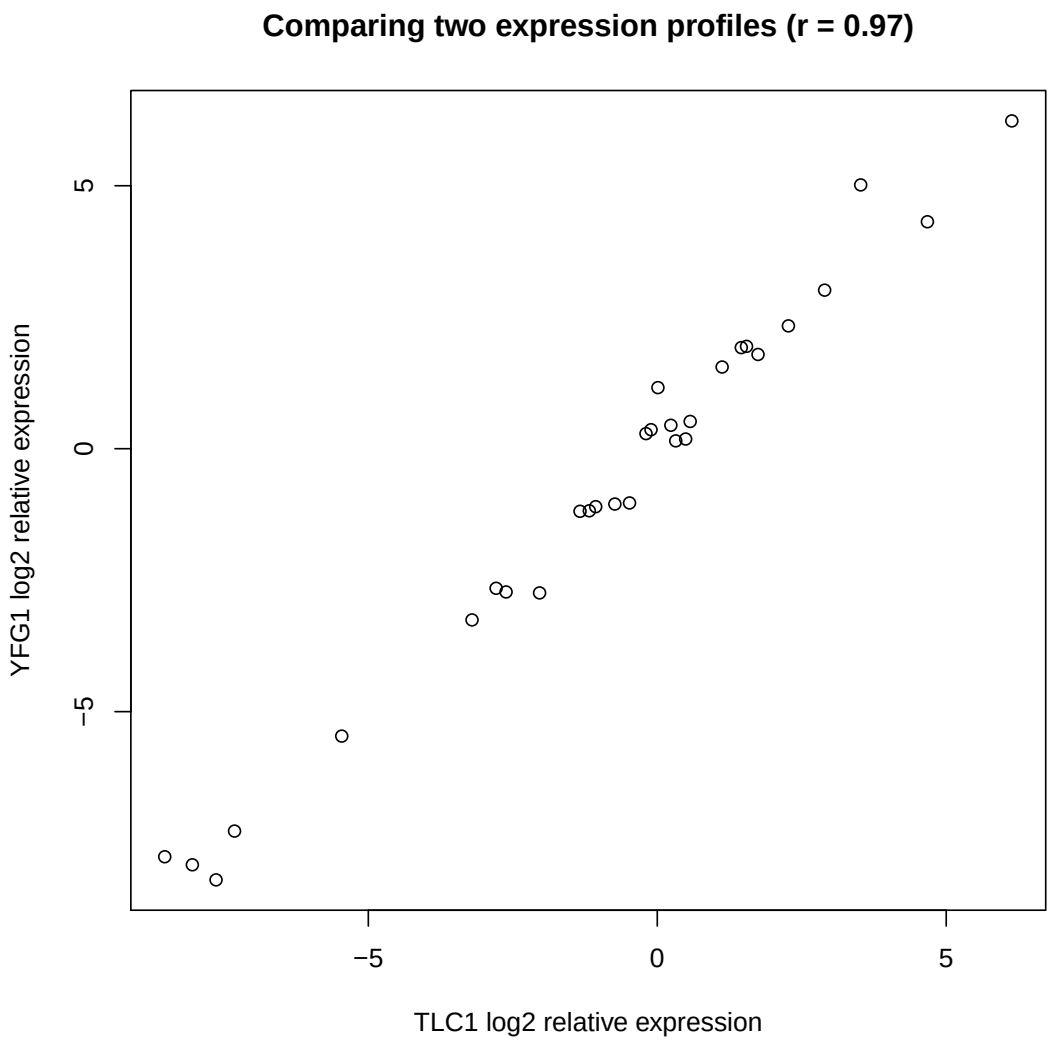
Pearson distance

$$d(x,y) = 1 - s(x,y)$$

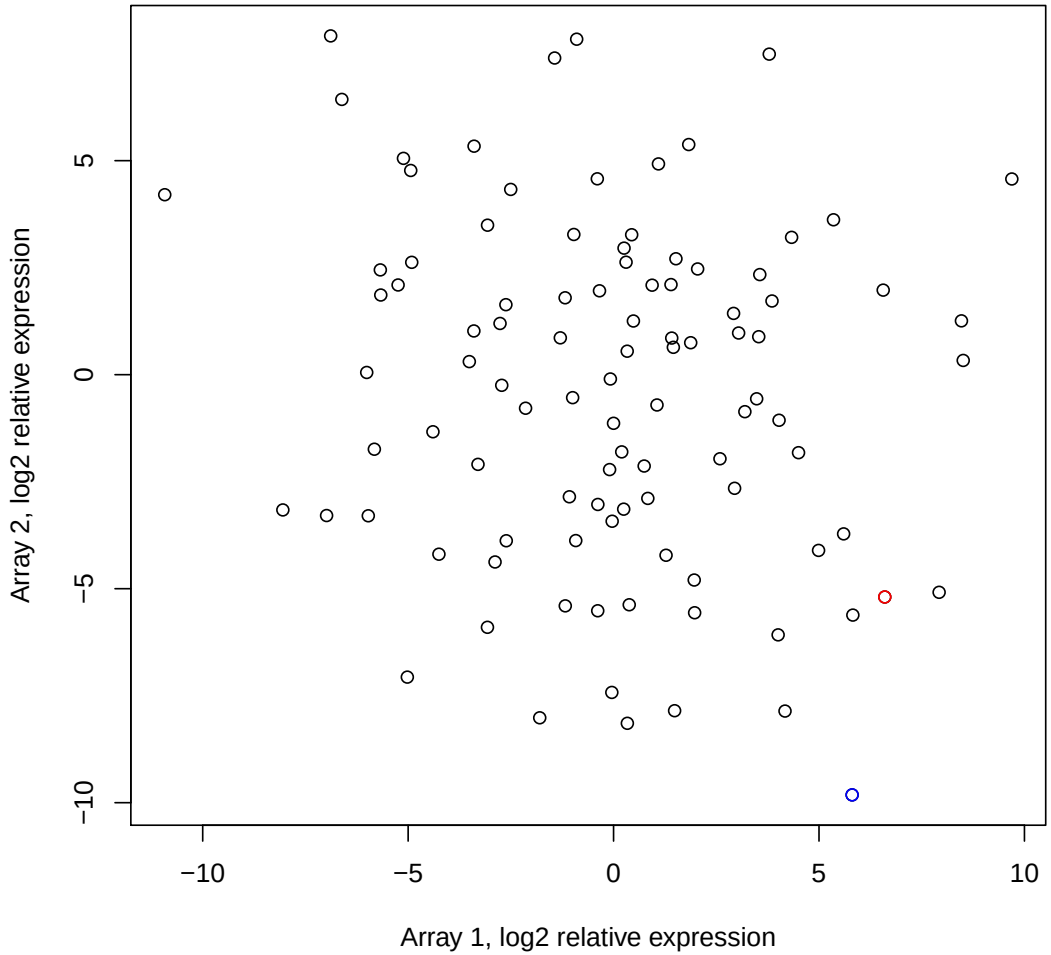
Euclidean distance

$$\frac{\sum_i^N (x_i - y_i)^2}{N}$$

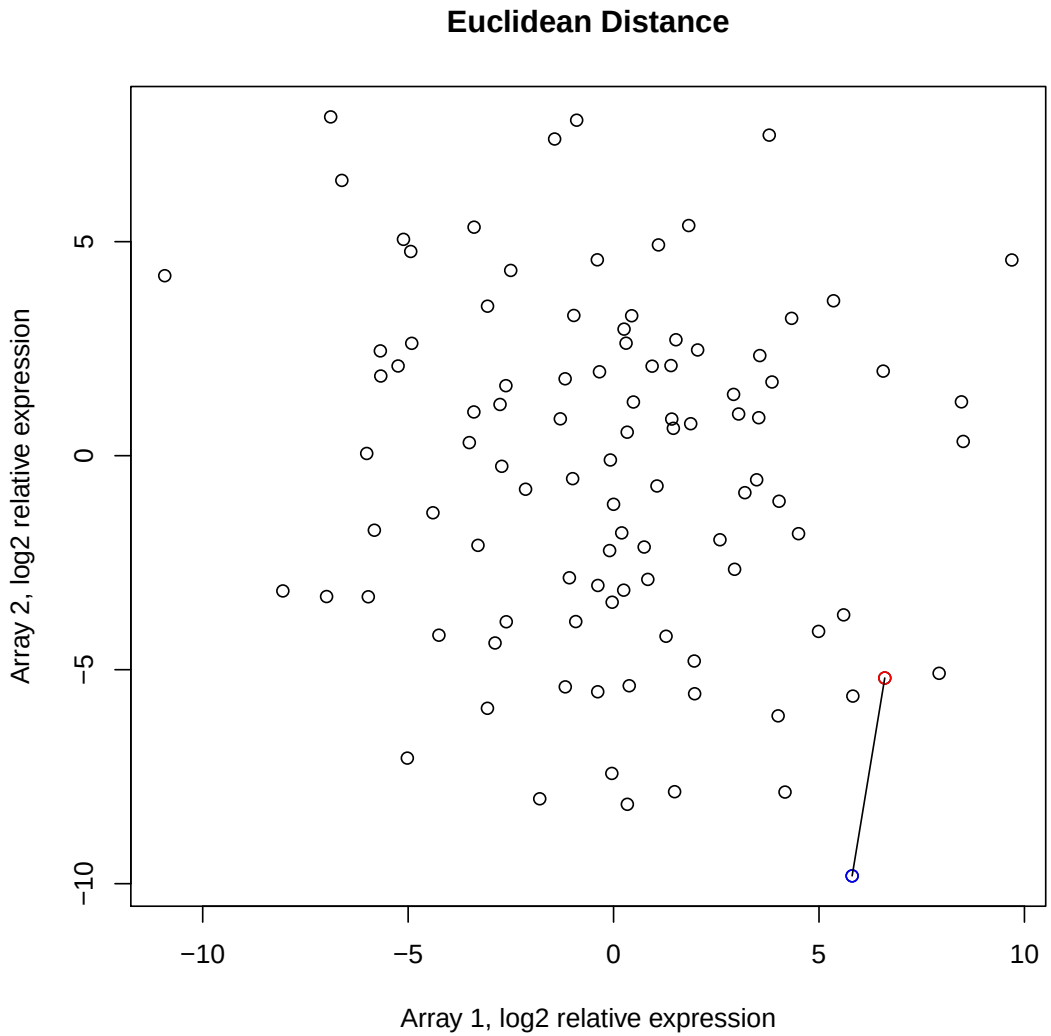
Comparing all measurements for two genes



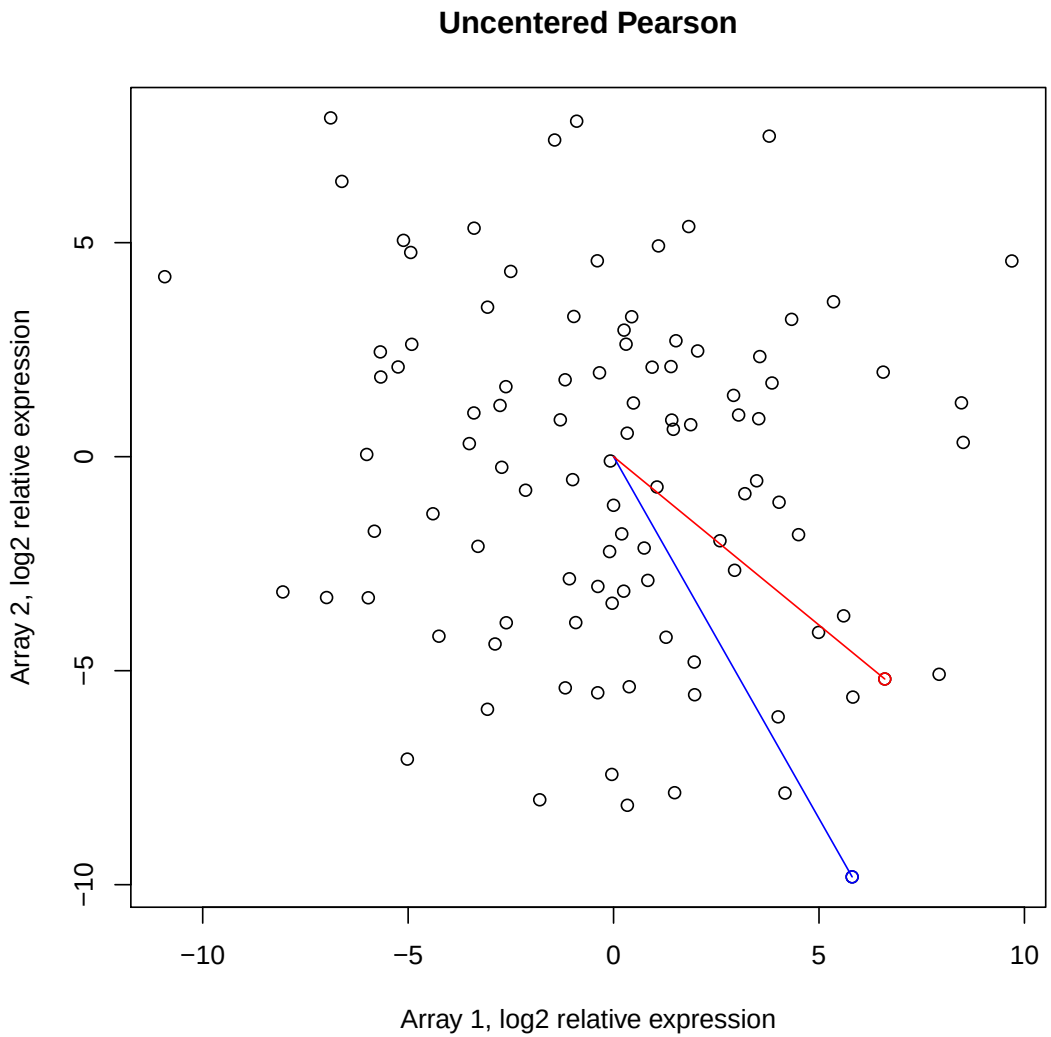
Comparing all genes for two measurements



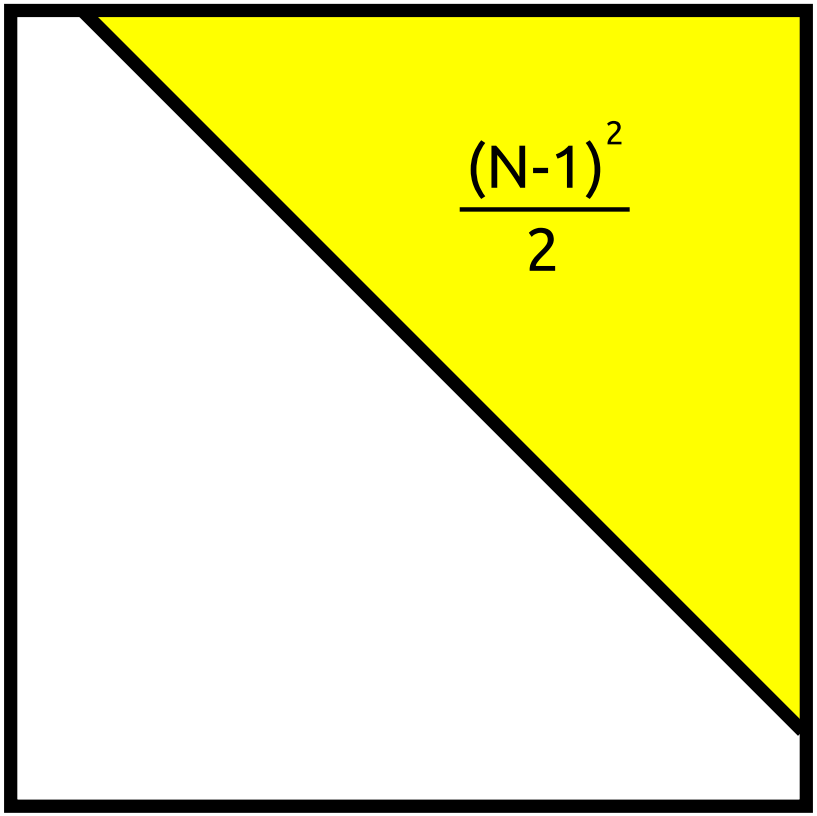
Comparing all genes for two measurements



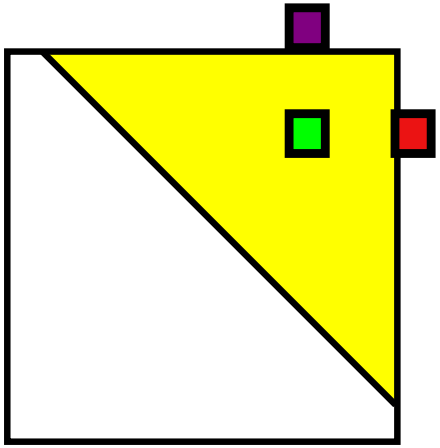
Comparing all genes for two measurements

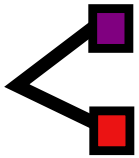


Measure all pairwise distances under distance metric

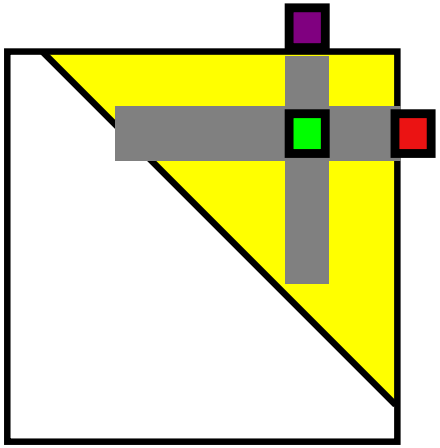


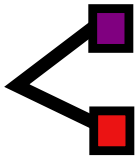
Hierarchical Clustering





Hierarchical Clustering





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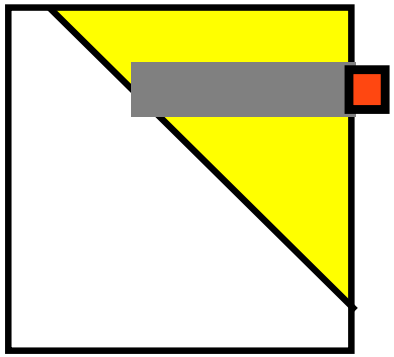

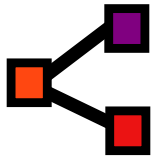

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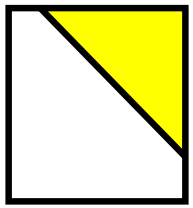

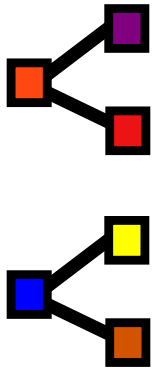

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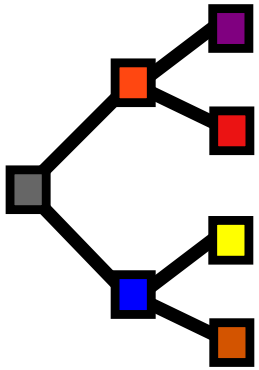
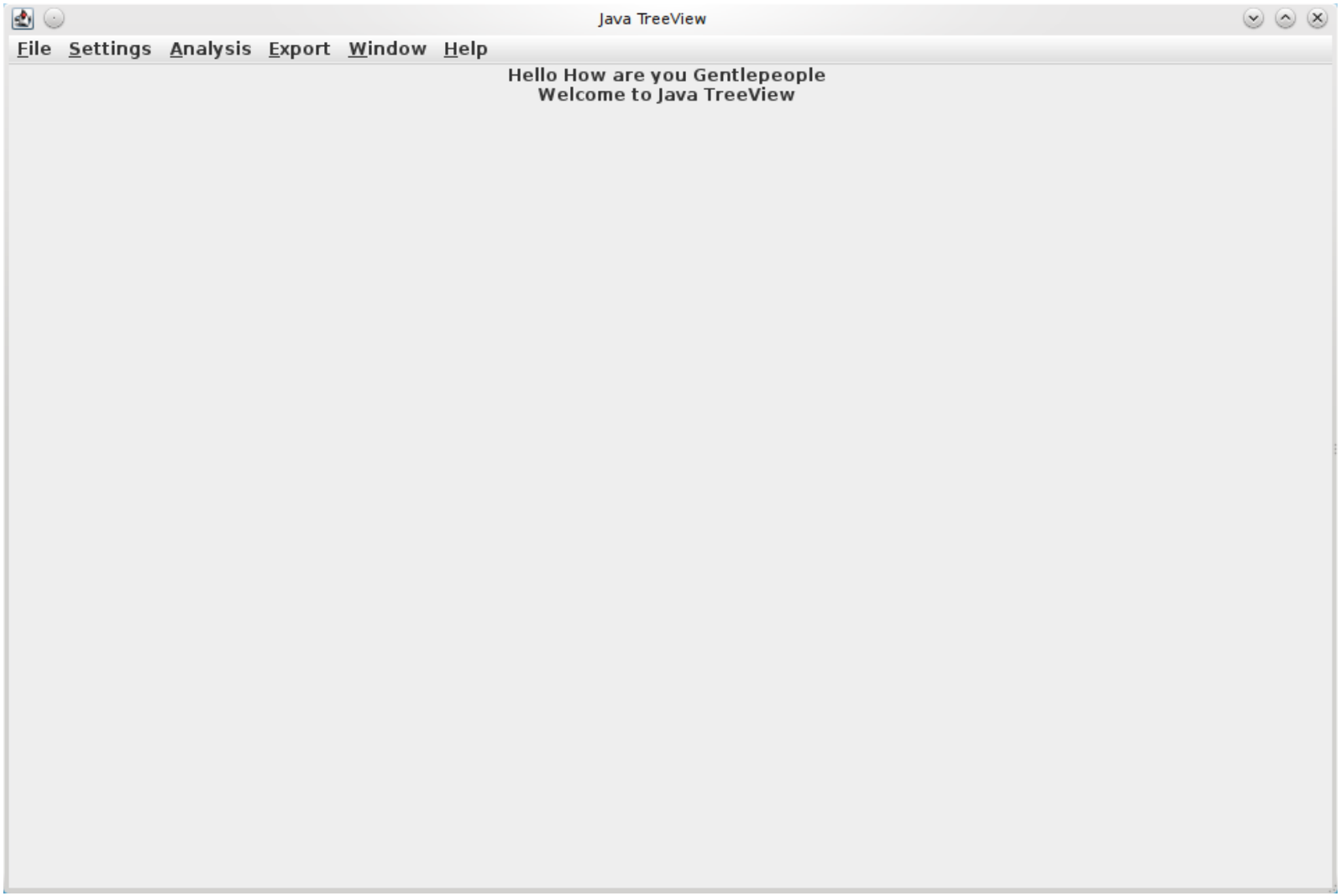


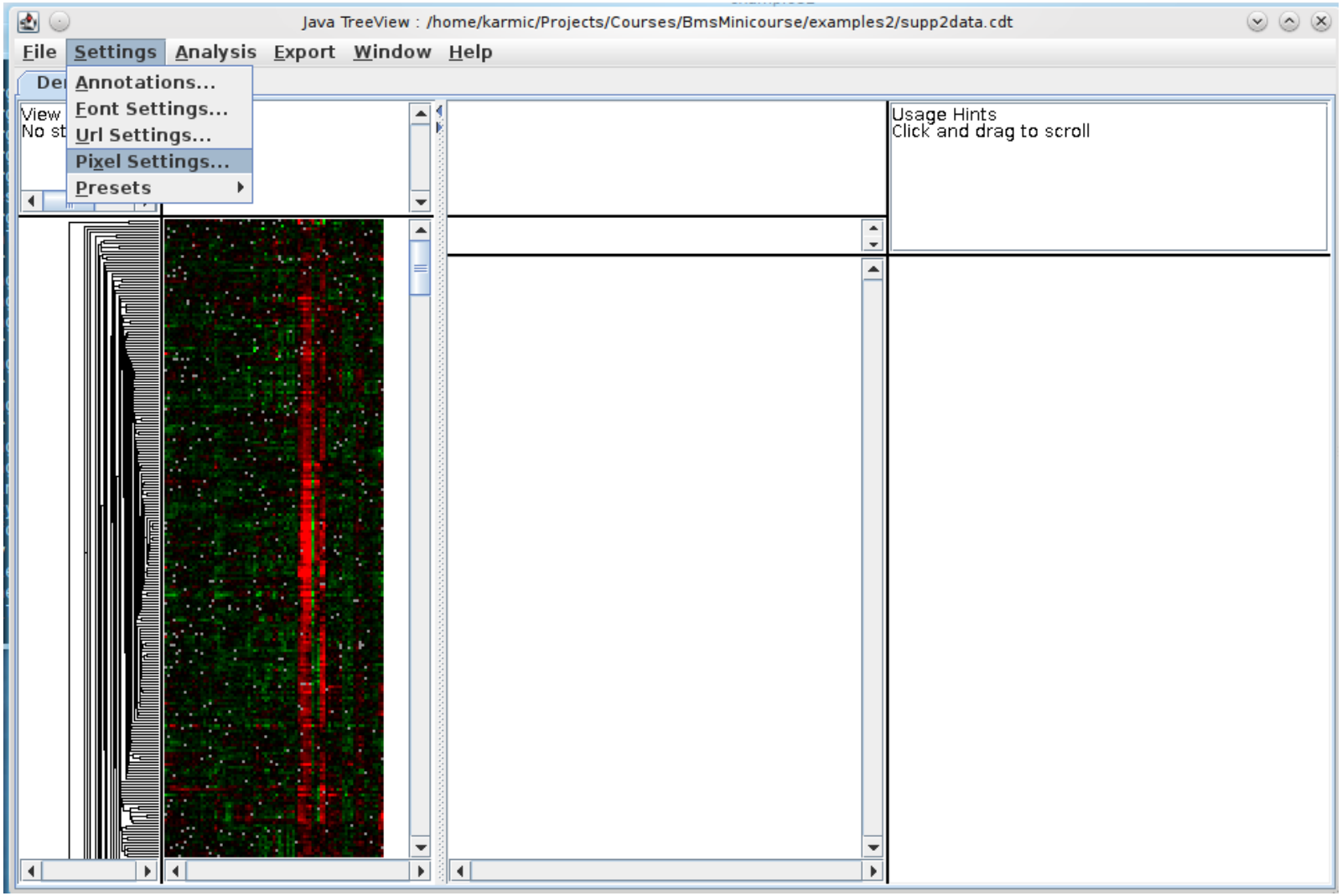
It's hard work at times, but you have to be realistic. If you have a large database with many variables and your goal is to get a good understanding of the interrelationships, then, unless you get lucky, this complex structure is bound to require some hard work to understand.

Bill Cleveland and Rick Becker
http://stat.bell-labs.com/project/trellis/interview.html

Using JavaTreeView



Adjust pixel settings for global view



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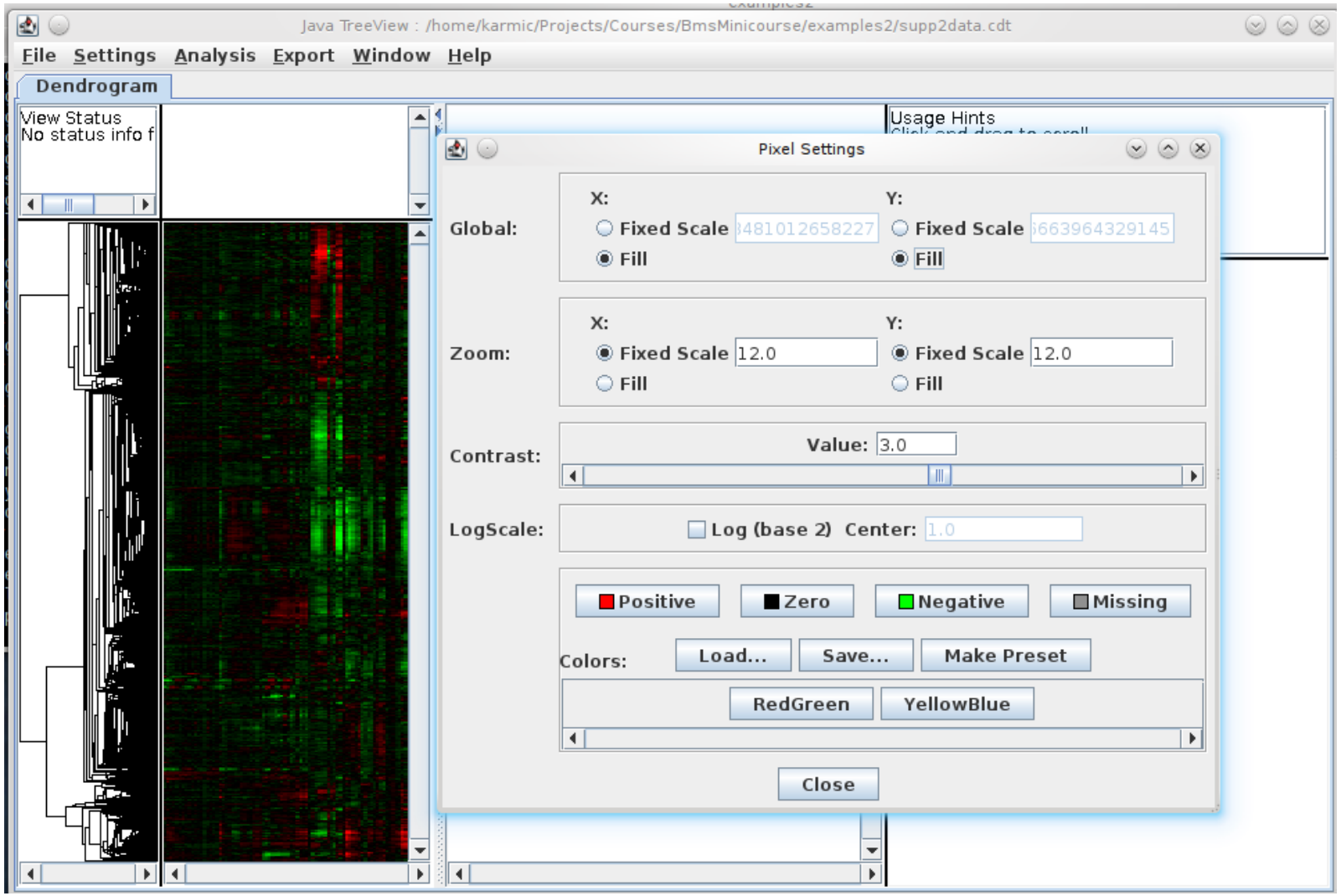
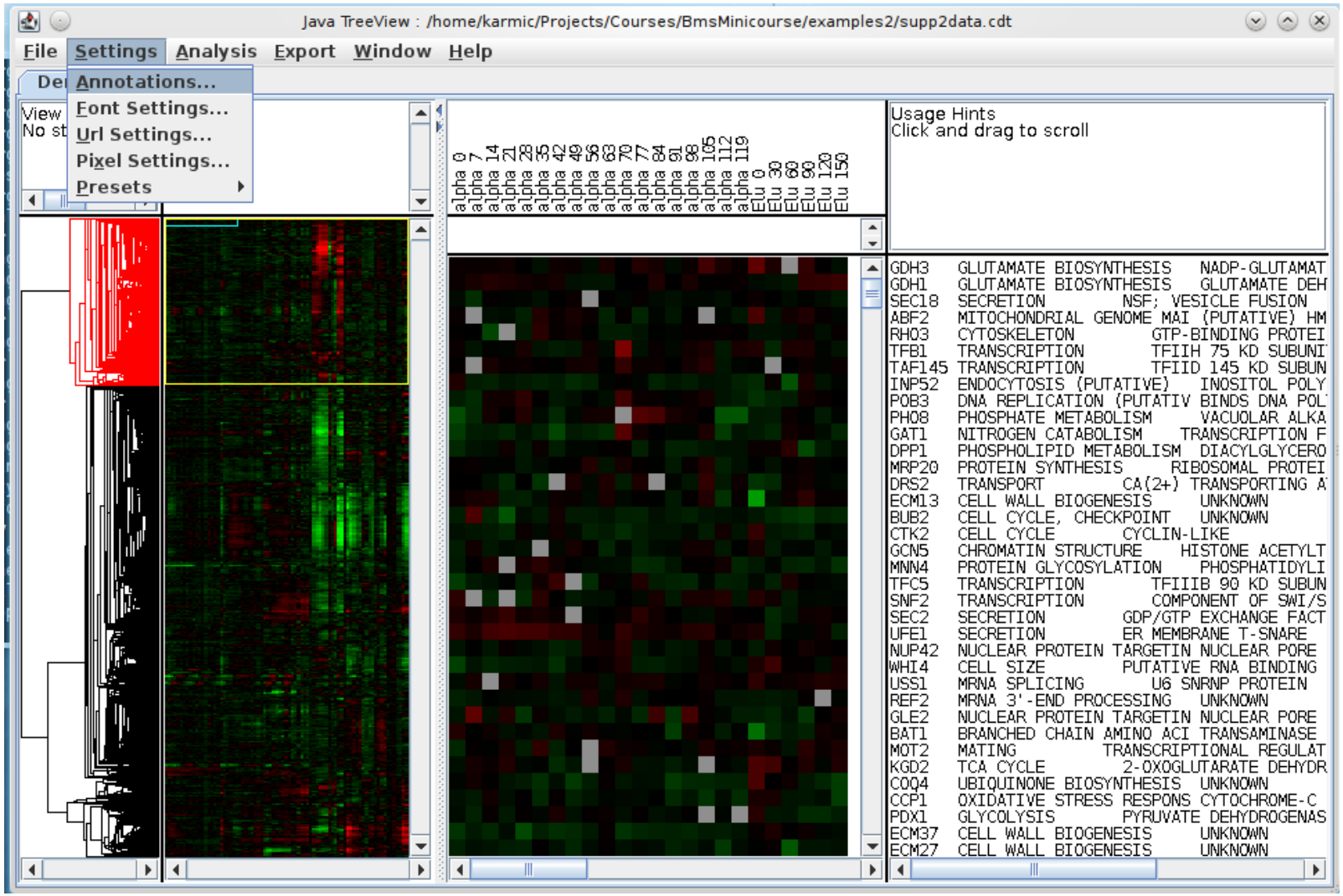


Select annotation columns



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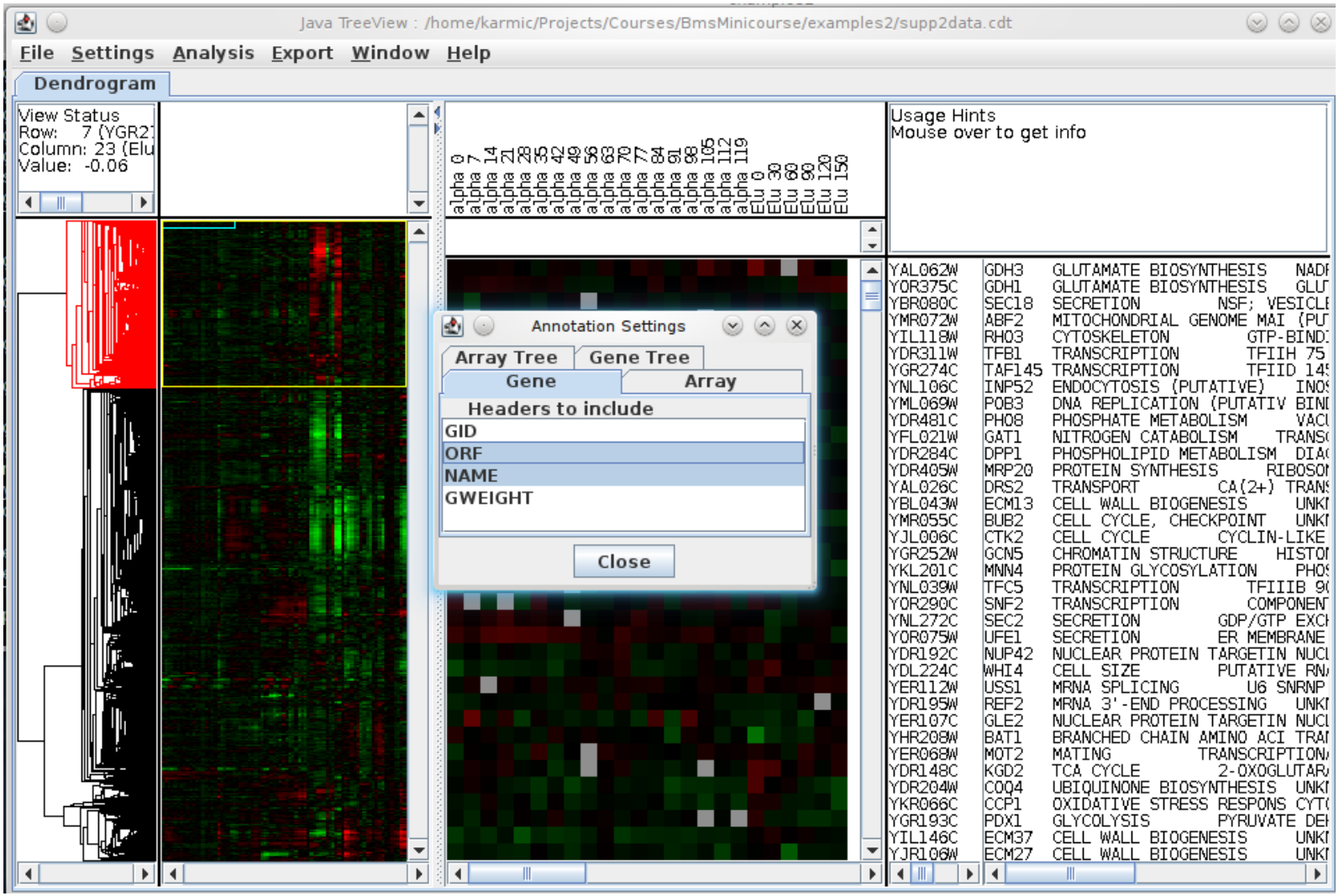
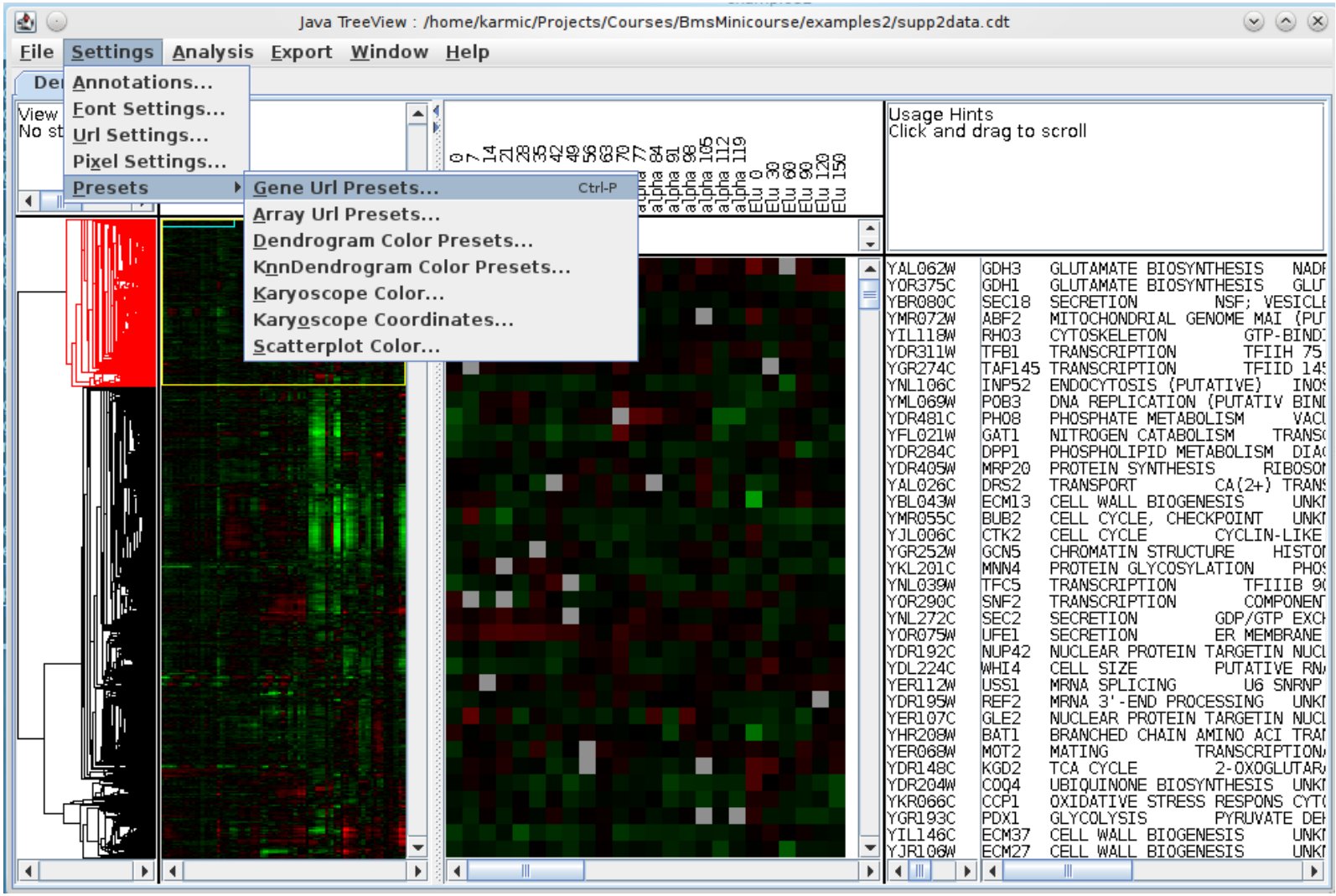


Select URL for gene annotations



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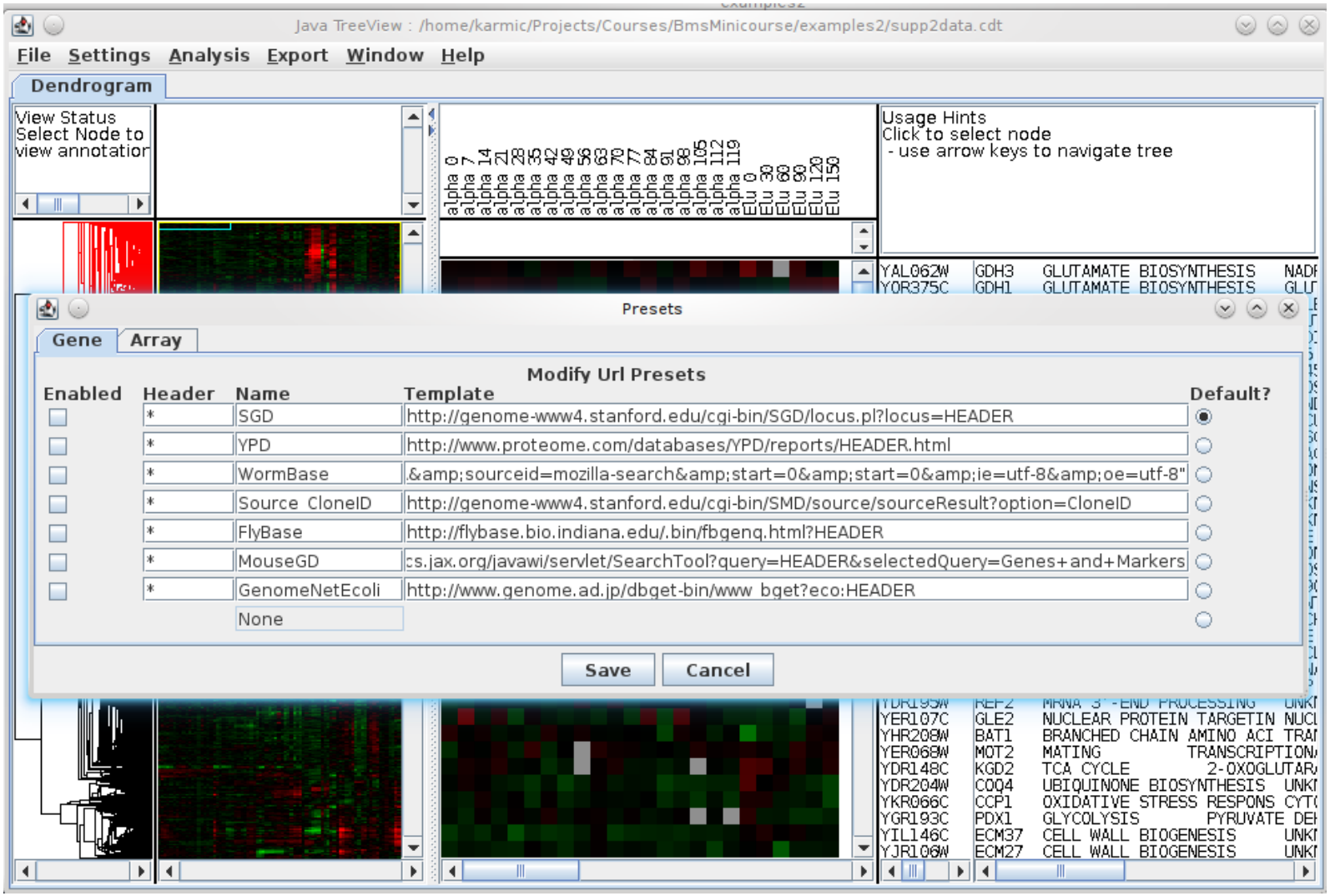
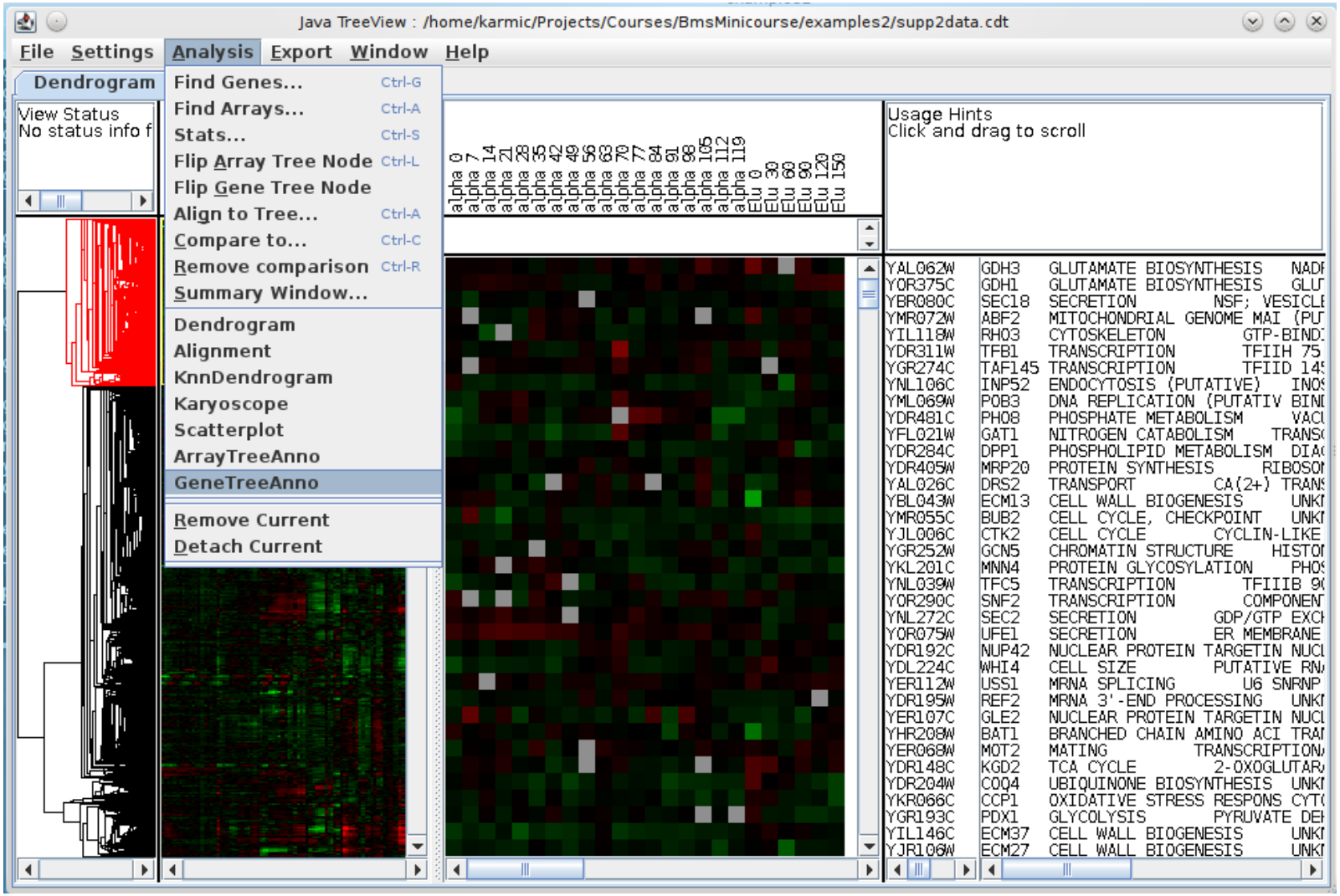


Activate and detach annotation window



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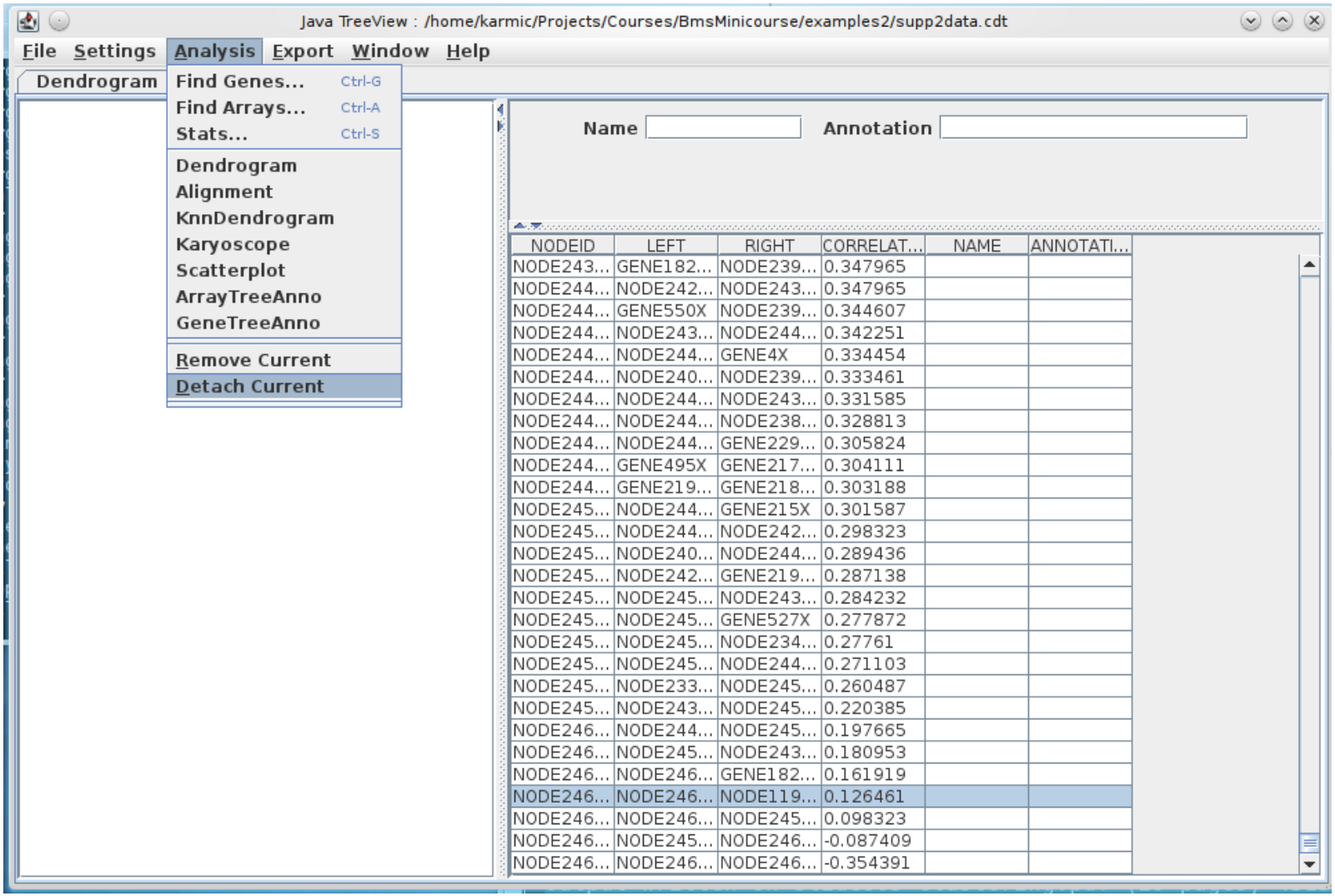

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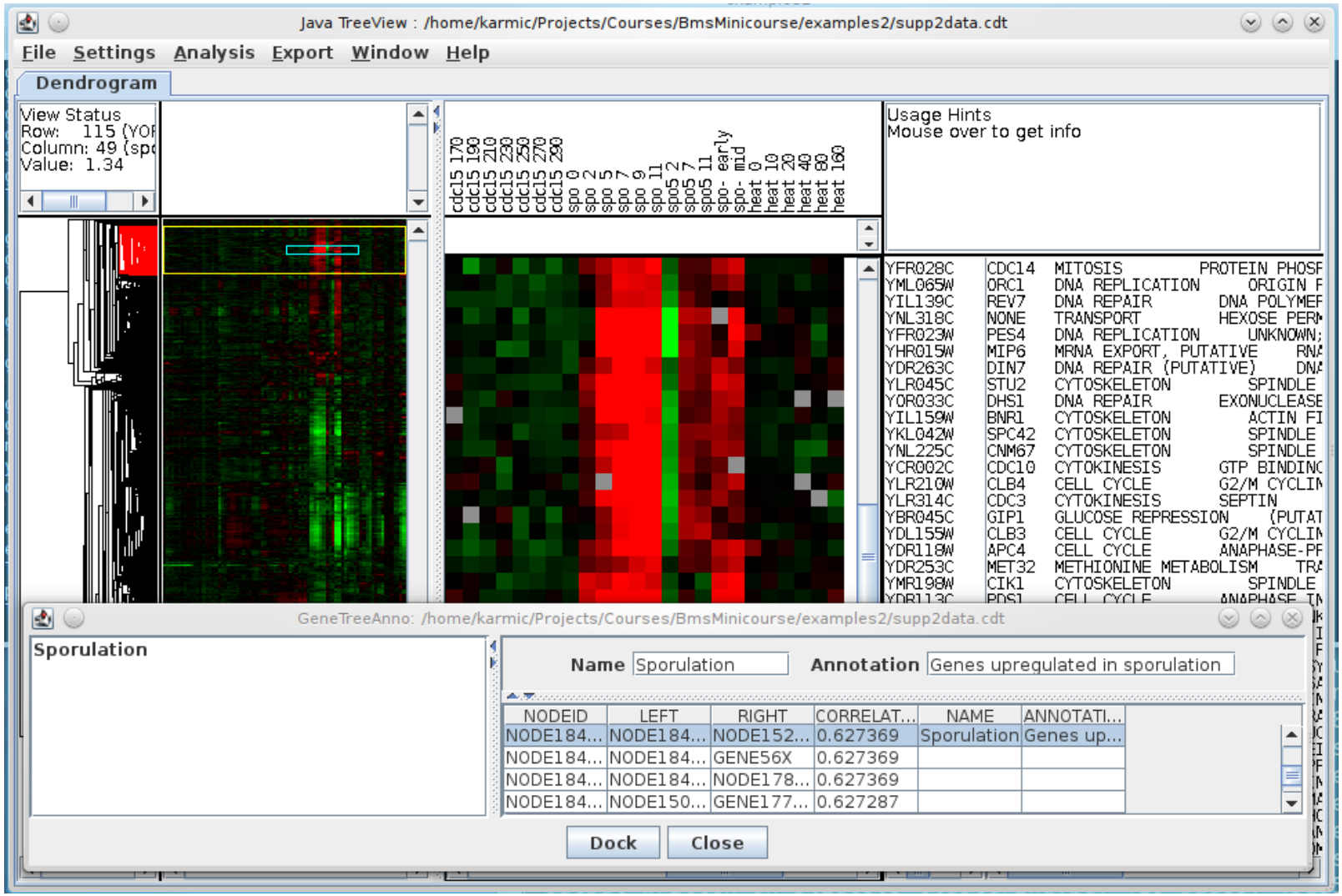

Homework

1. Write functions to reproduce the shuffling controls in figure 3 of the Eisen paper (removing correlations among genes and/or samples).