Expression Profiling

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4/4/2011

Review

- Sequence analysis
- hmmbuild (not hmmfit)
- JackHMMer

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

Expression Profiling

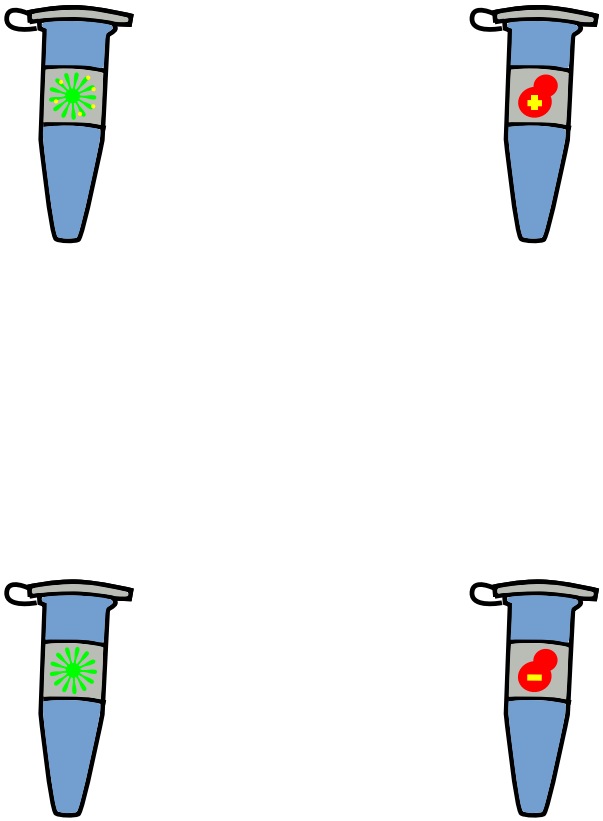
Why profile *transcription*?

Expression Profiling

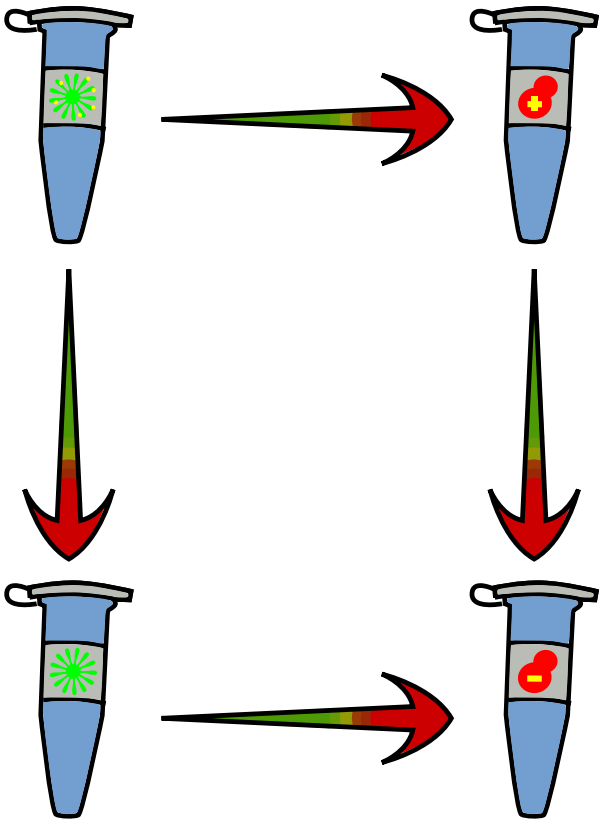
Why profile *transcription*?

- Major mode of replication
- Due to feedback, "shadows" other modes of regulation
- Thanks to Watson-Crick base pairing, we can assay arbitrary nucleic acids in a uniform way

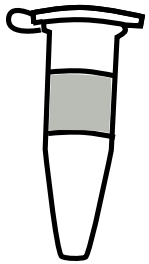
Sample Preparation



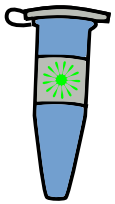
Circuit Design



Pooled Reference Design



Transforming Ratios



Transforming Ratios

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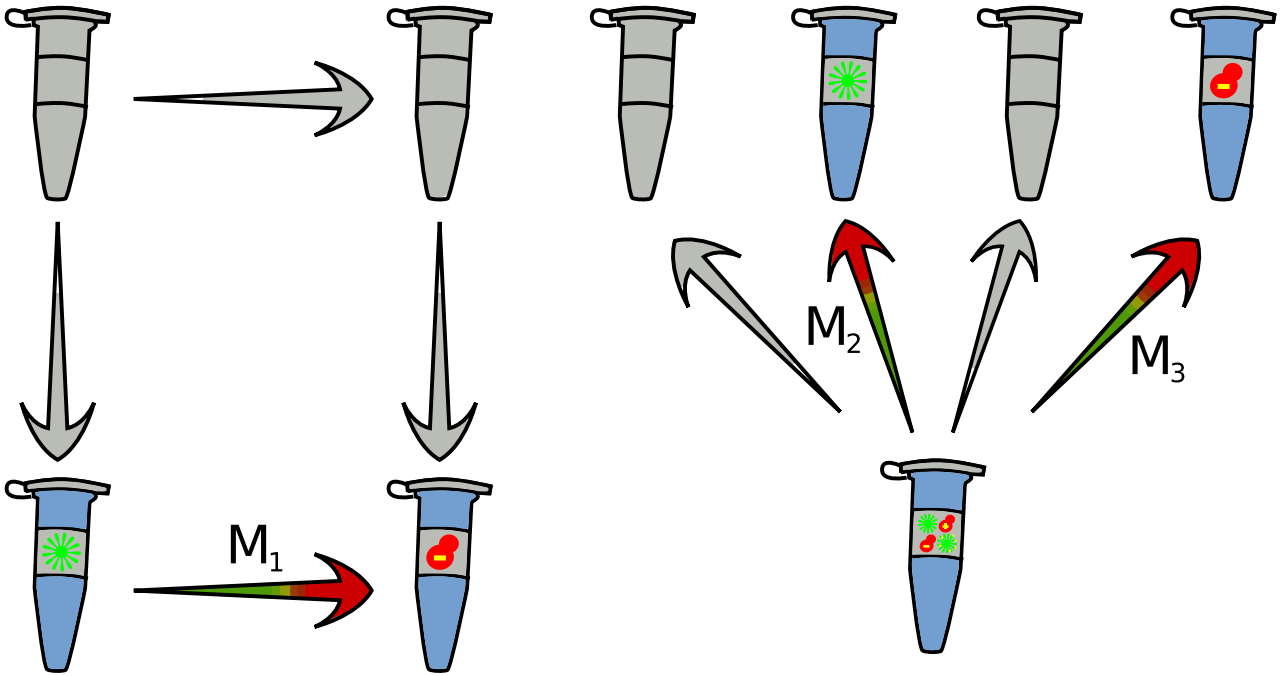
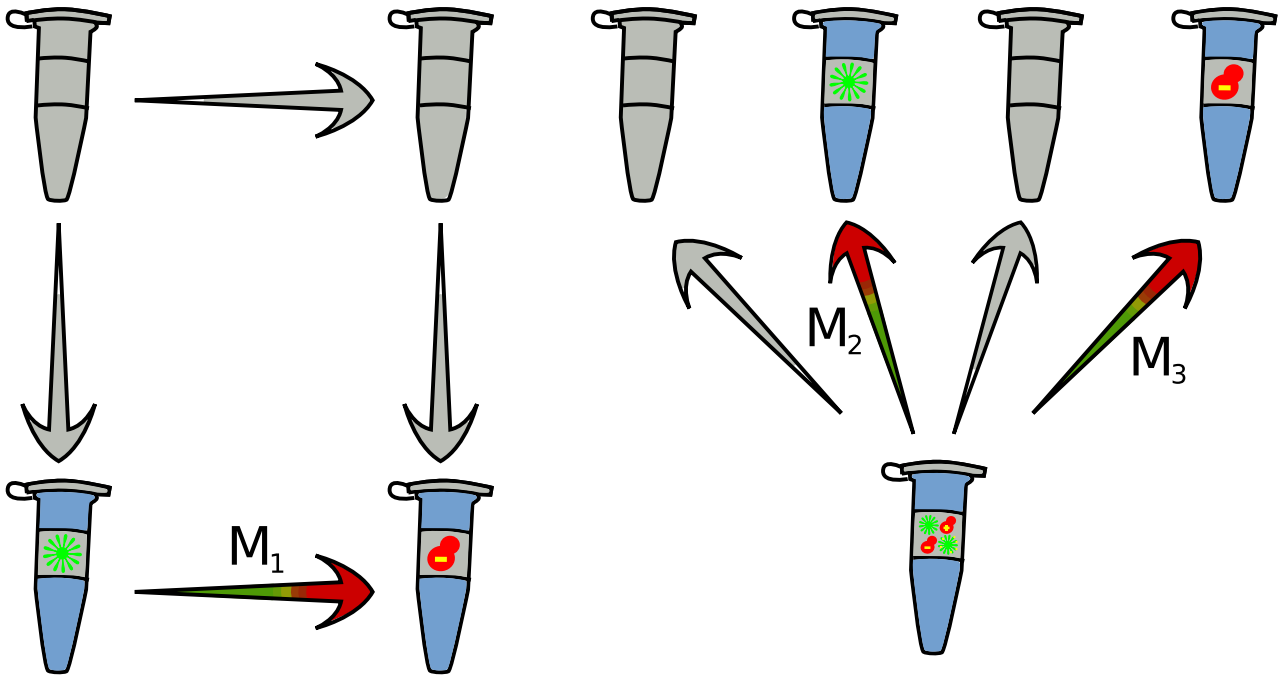


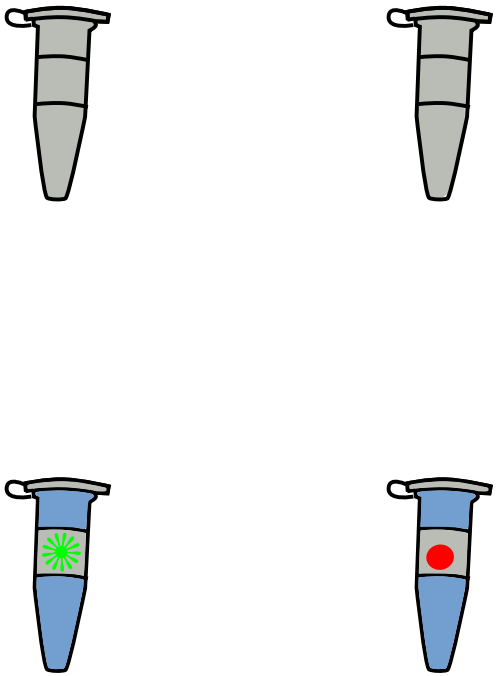
$$M_1 = M_3 / M_2$$

Transforming Ratios



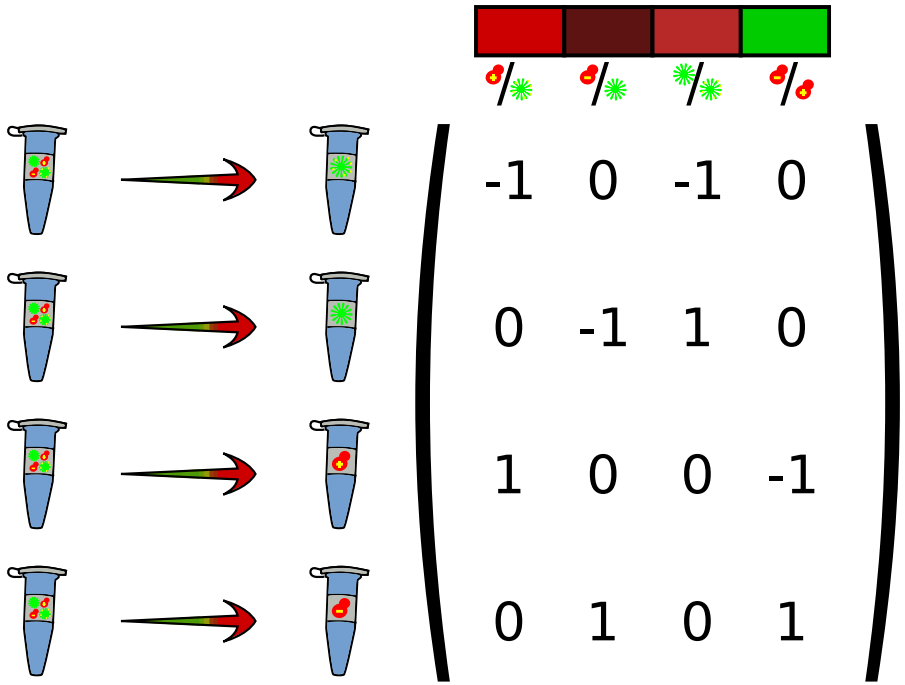
$$log_2 M_1 = log_2 M_3 - log_2 M_2$$

Linear Representation

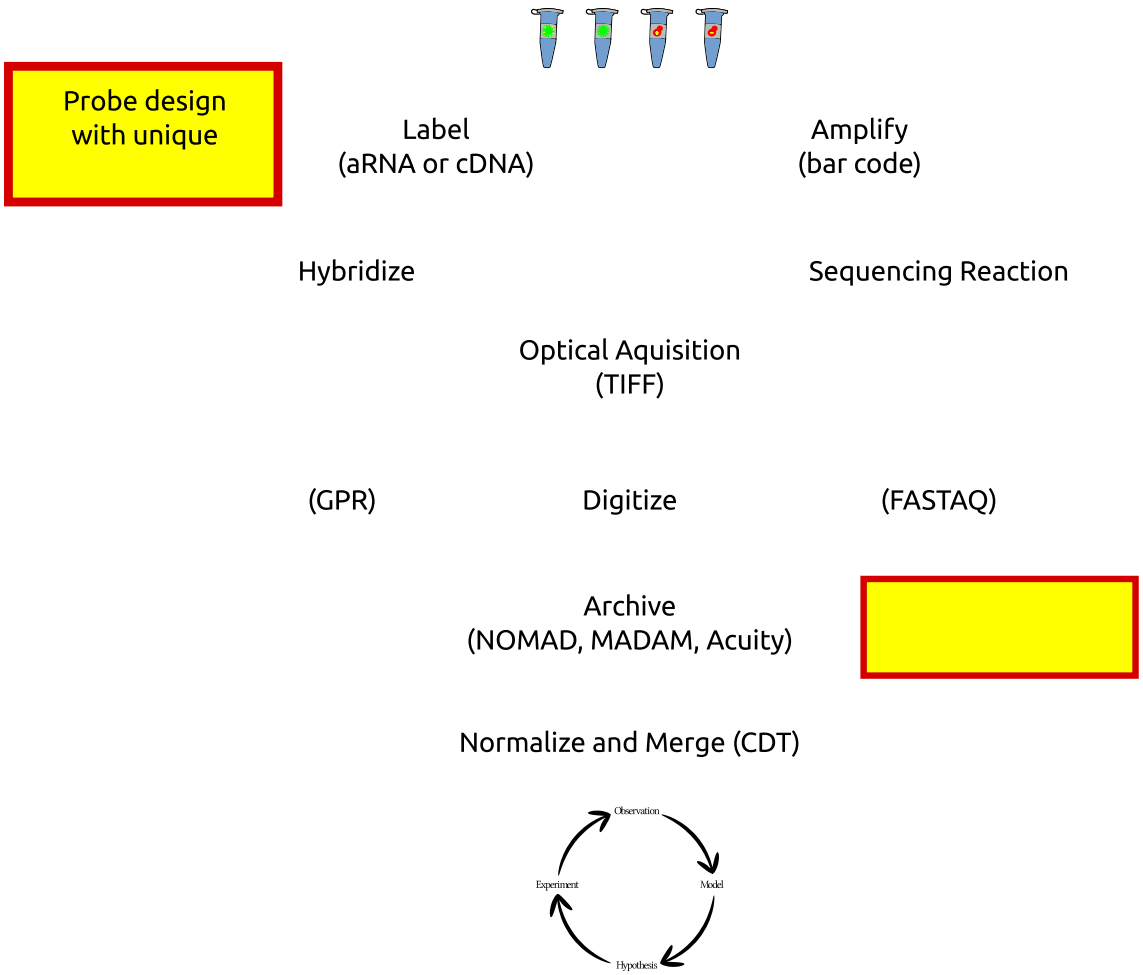


$$(1)log_2 M_1 = (-1)log_2 M_2 + (1)log_2 M_3$$

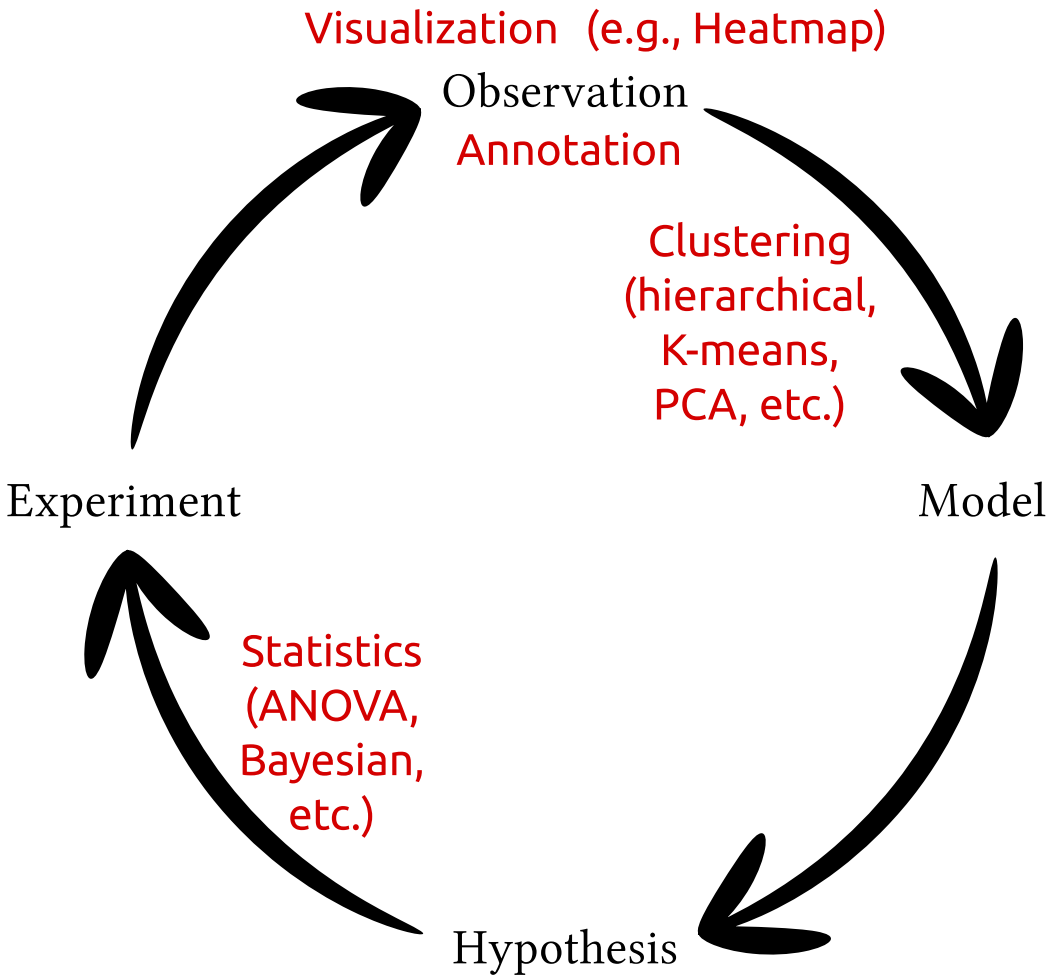
Linear Representation



Expression Profiling Workflow

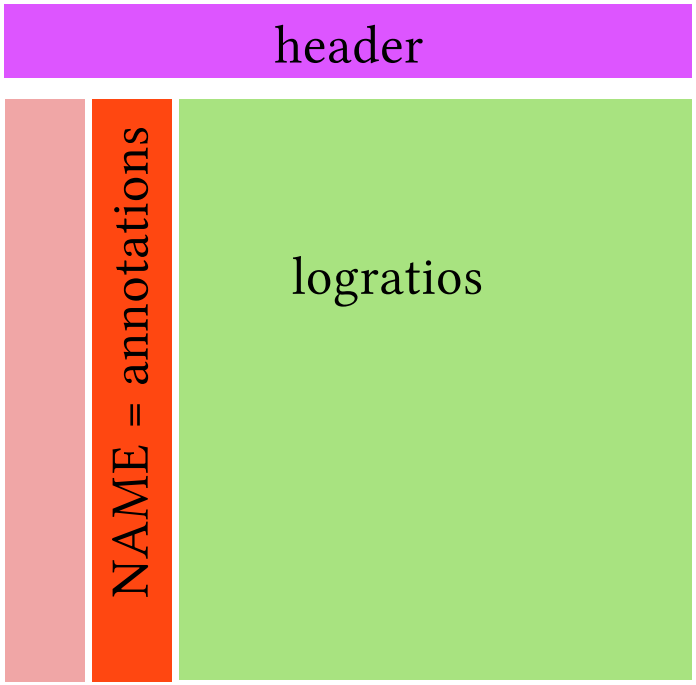


Expression Profiling Analysis

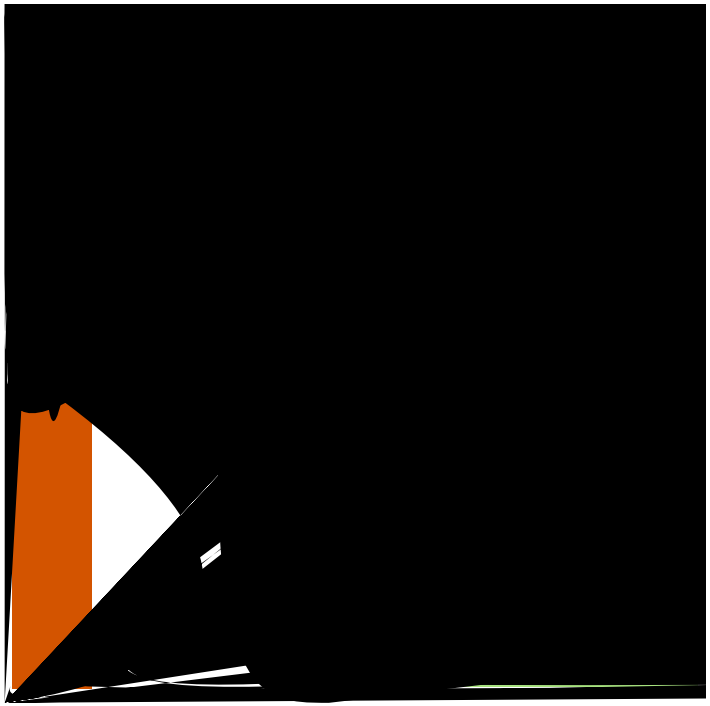


The CDT file format

Minimal CLUSTER input

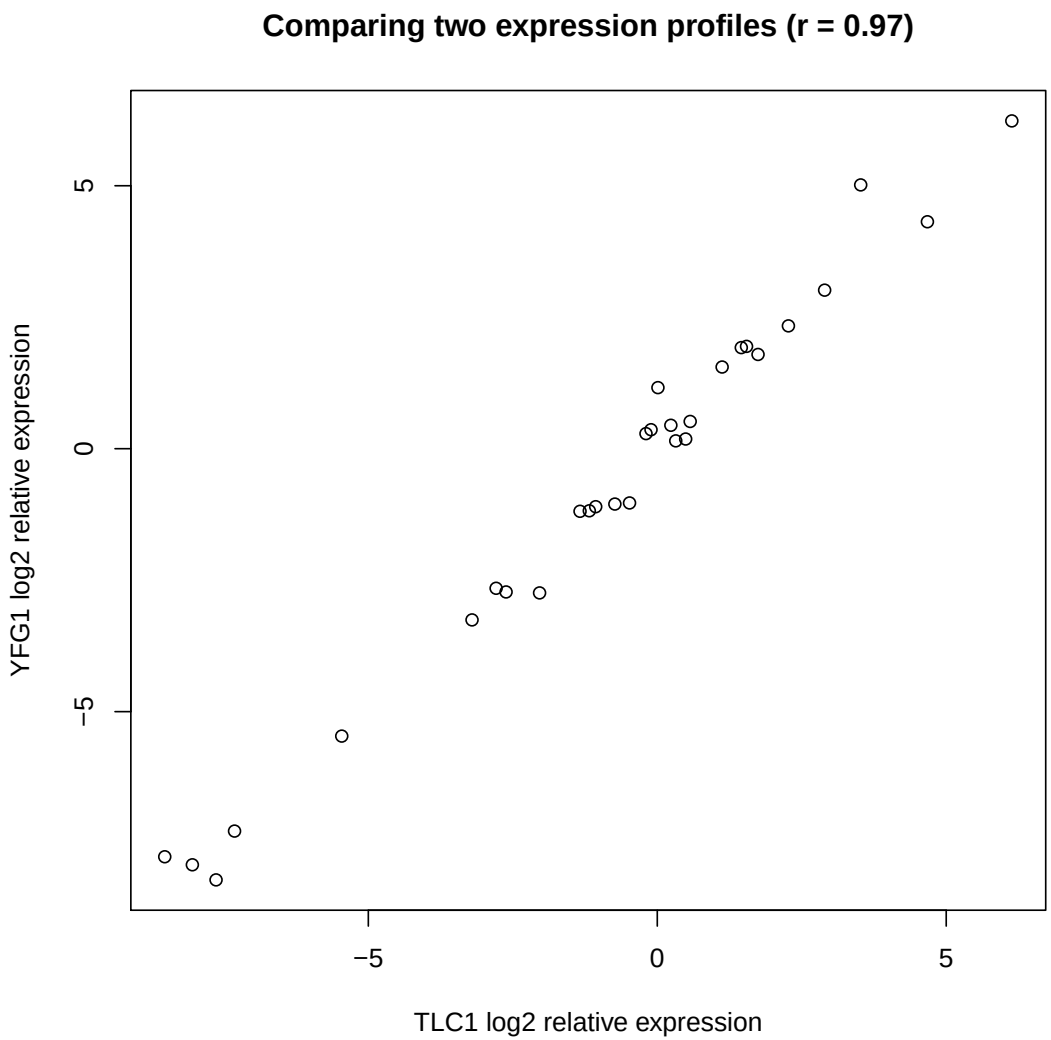


Cluster3 CDT output

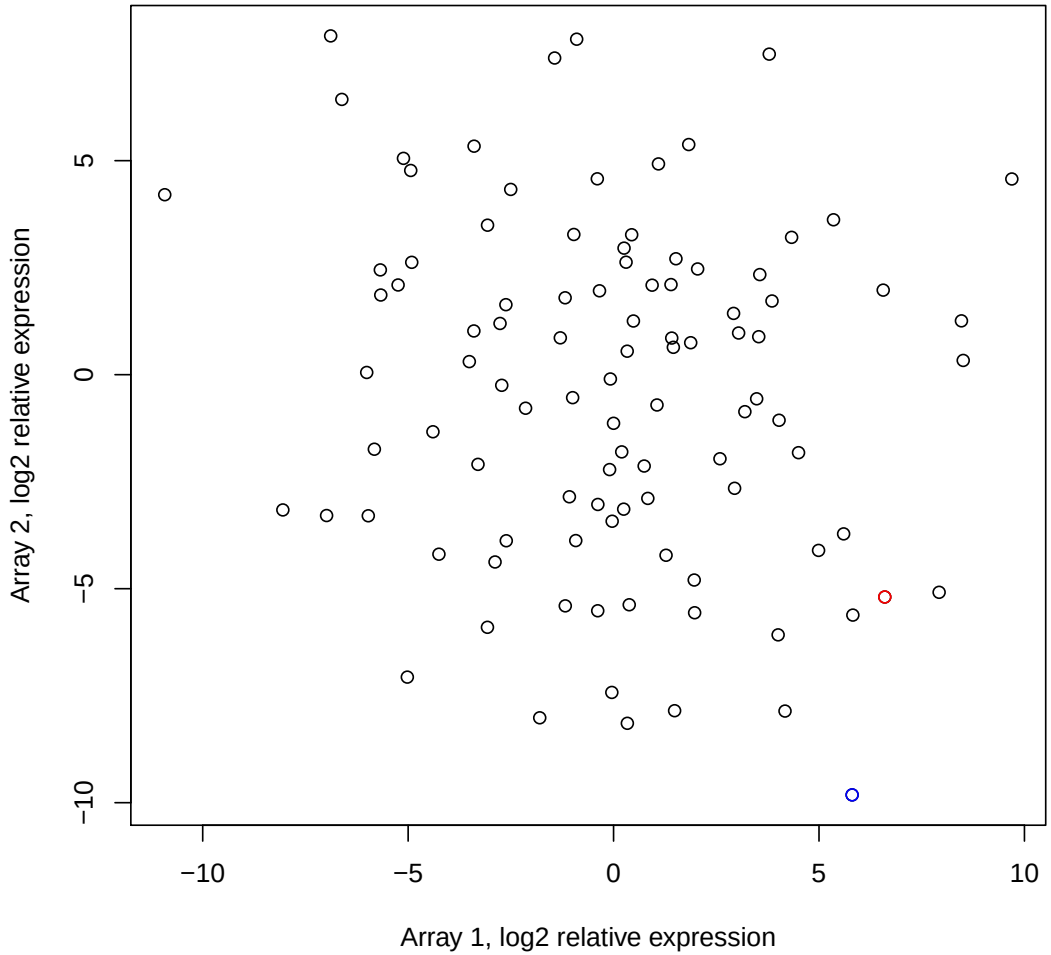


- Tab delimited (\t)
- UNIX newlines (\n)
- Missing values $\rightarrow$ empty cells

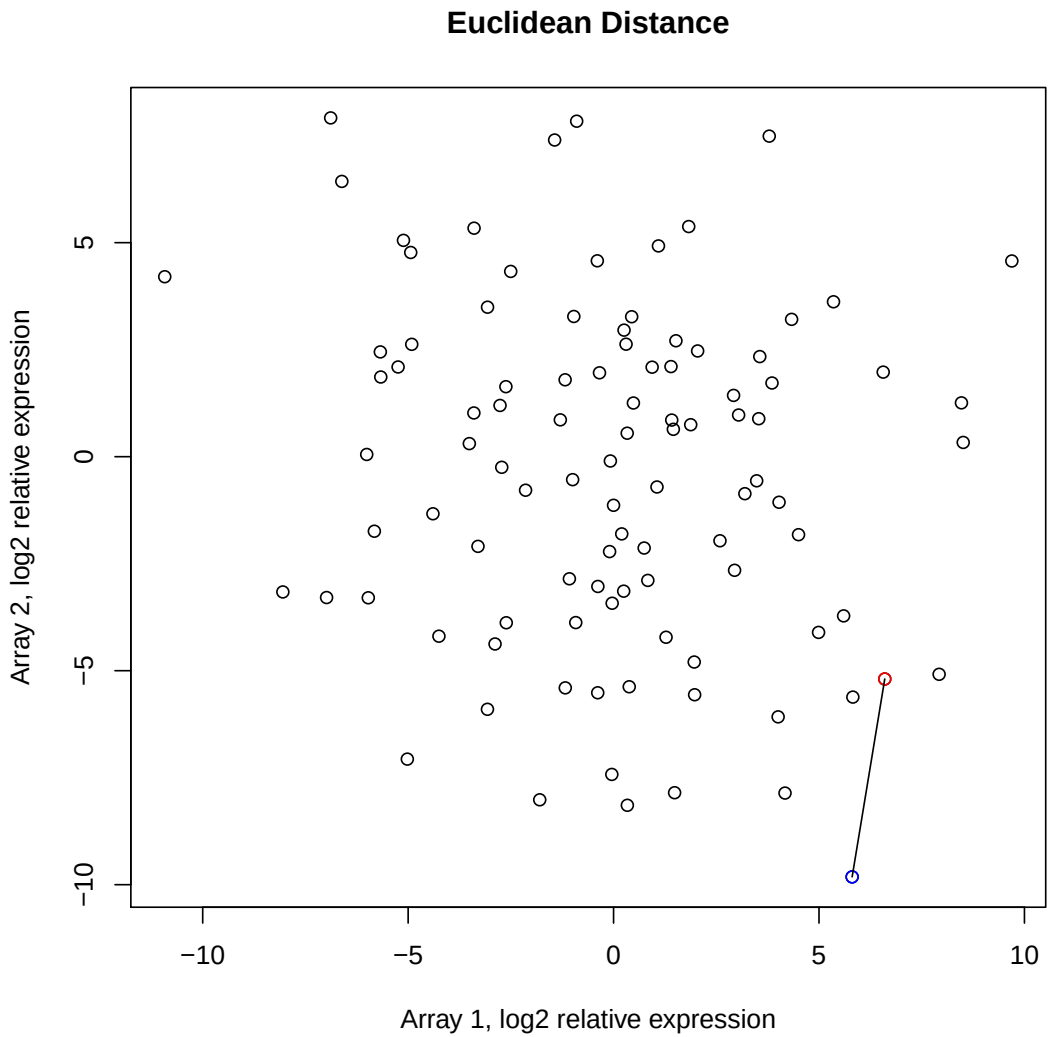
Comparing all measurements for two genes



Comparing all genes for two measurements



Comparing all genes for two measurements



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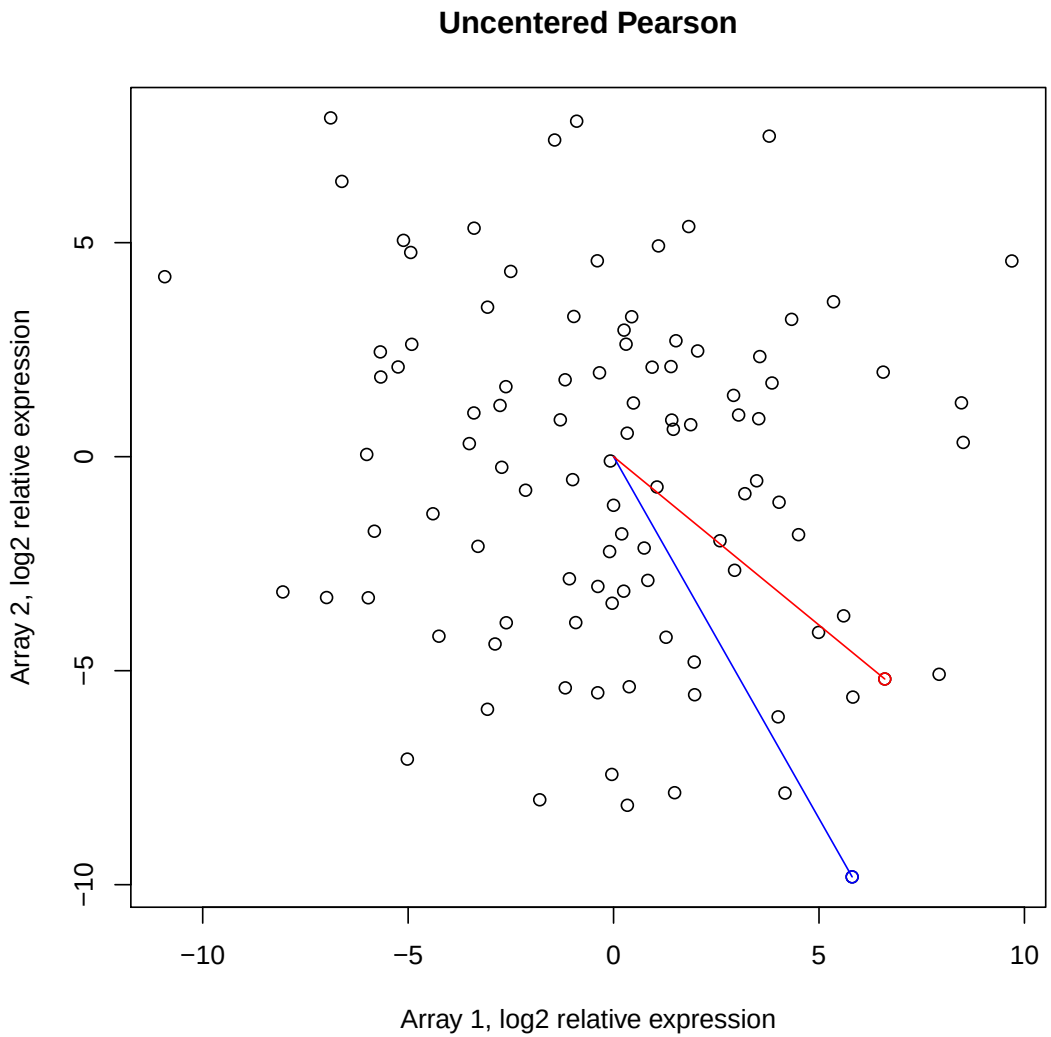
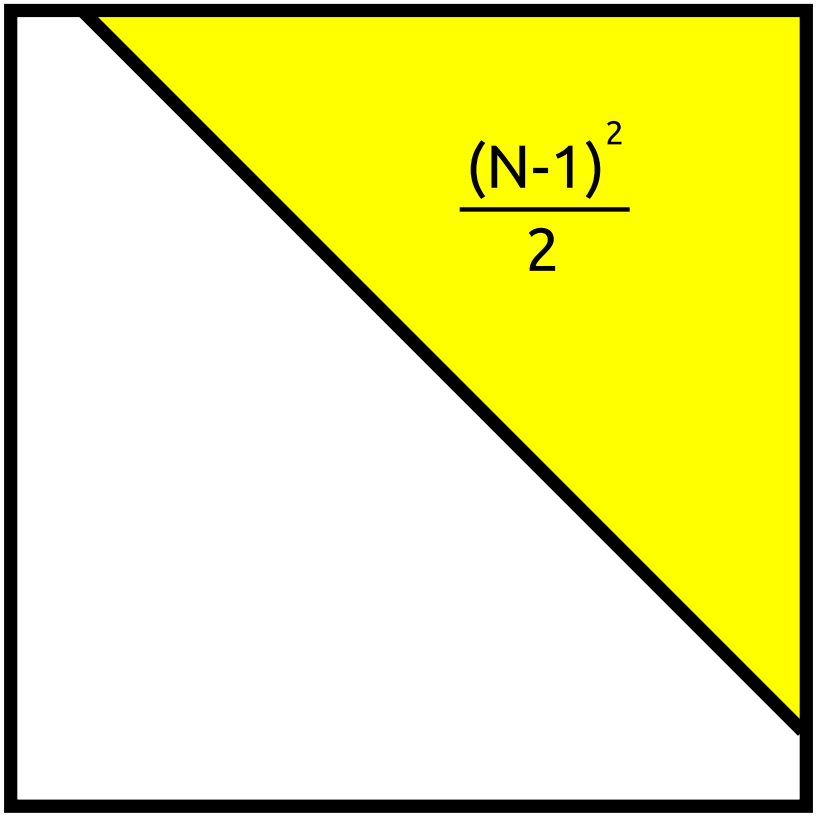
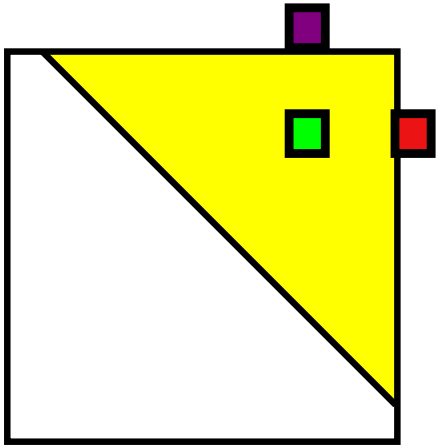
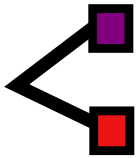


Measure all pairwise distances under distance metric



Hierarchical Clustering





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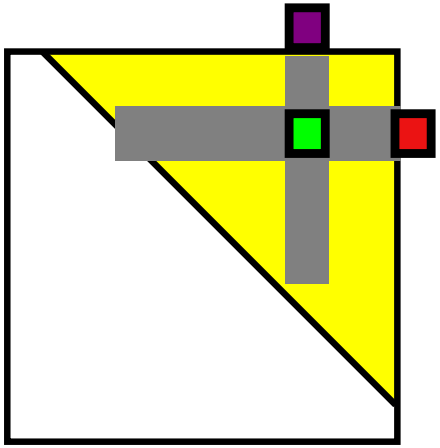

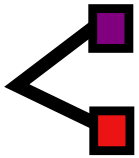

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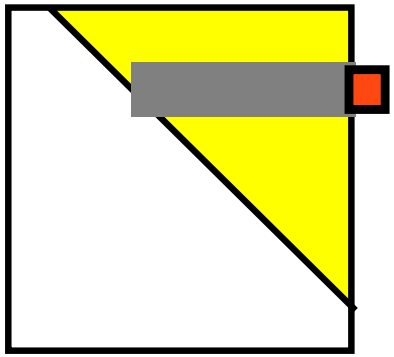

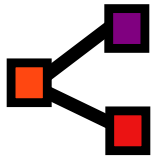

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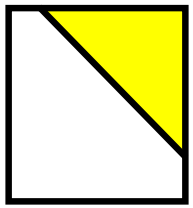

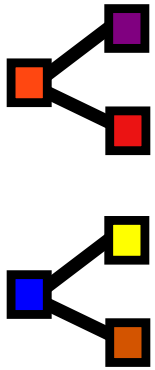

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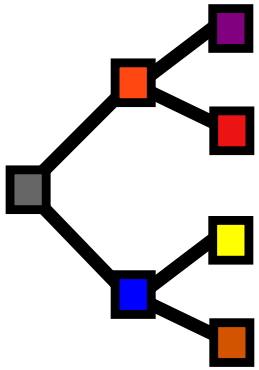
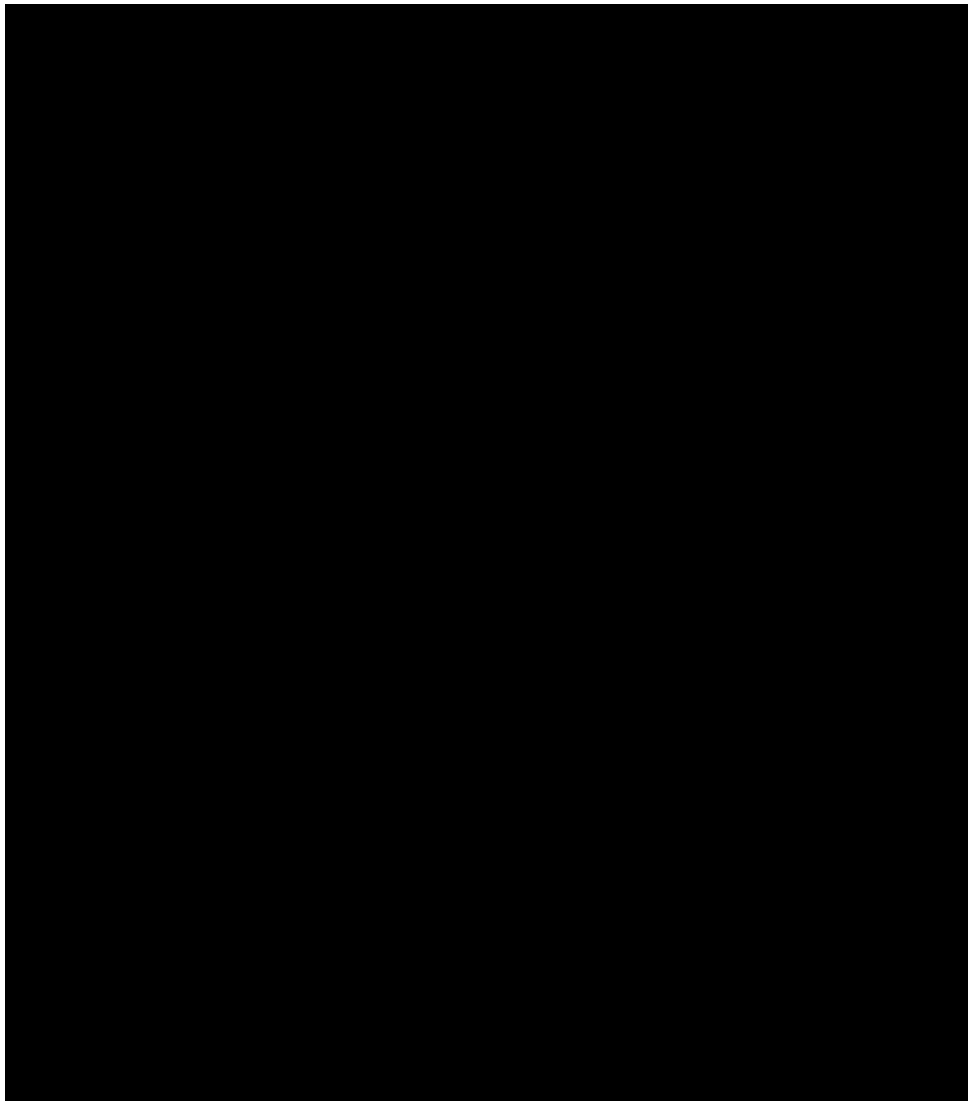
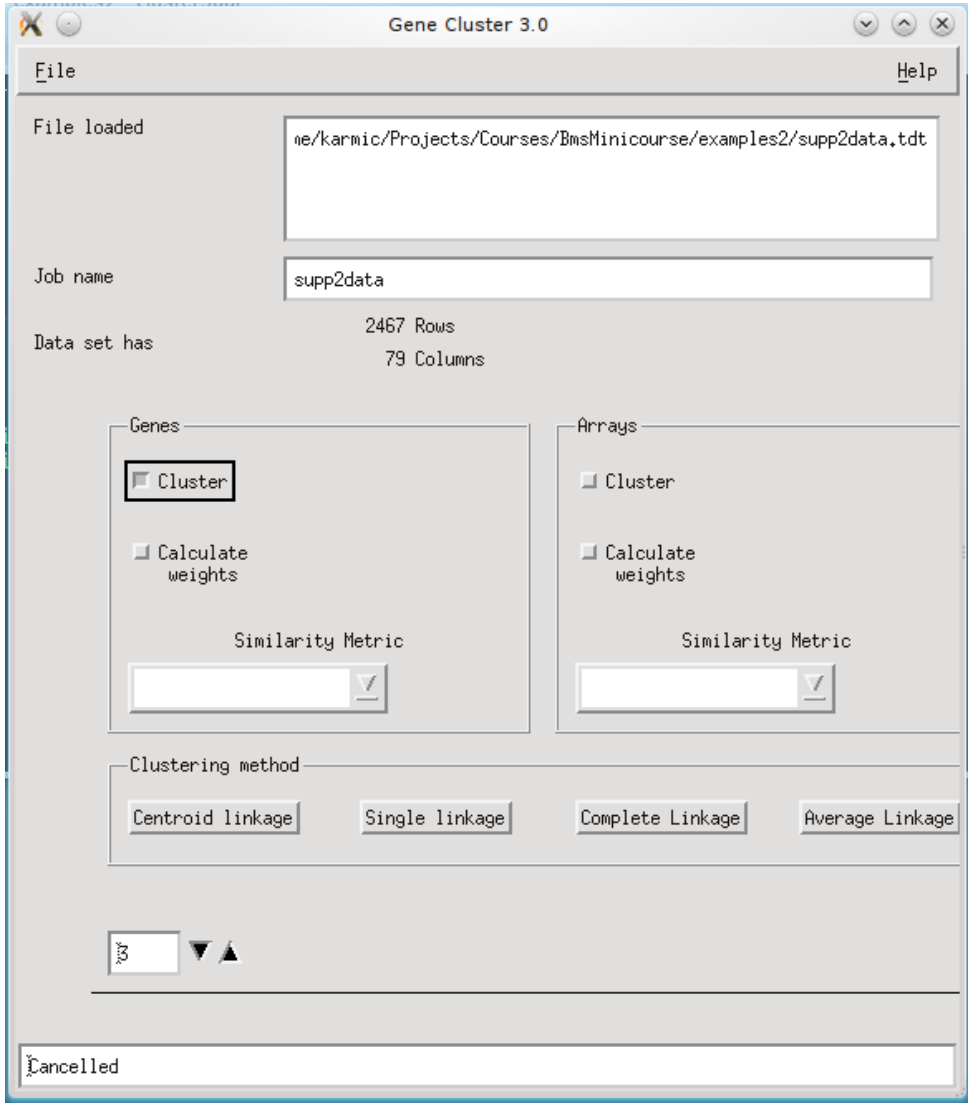


Using the Cluster3 GUI

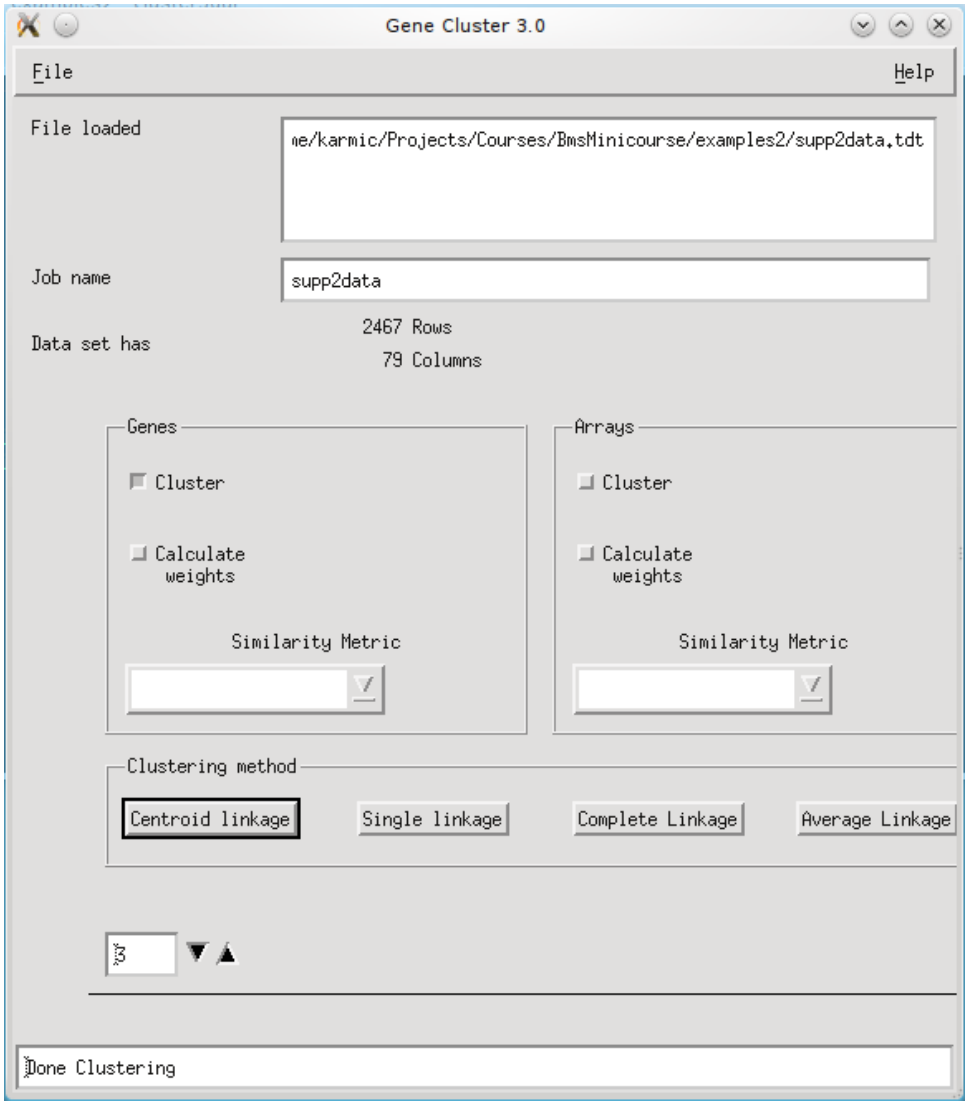
Load your data



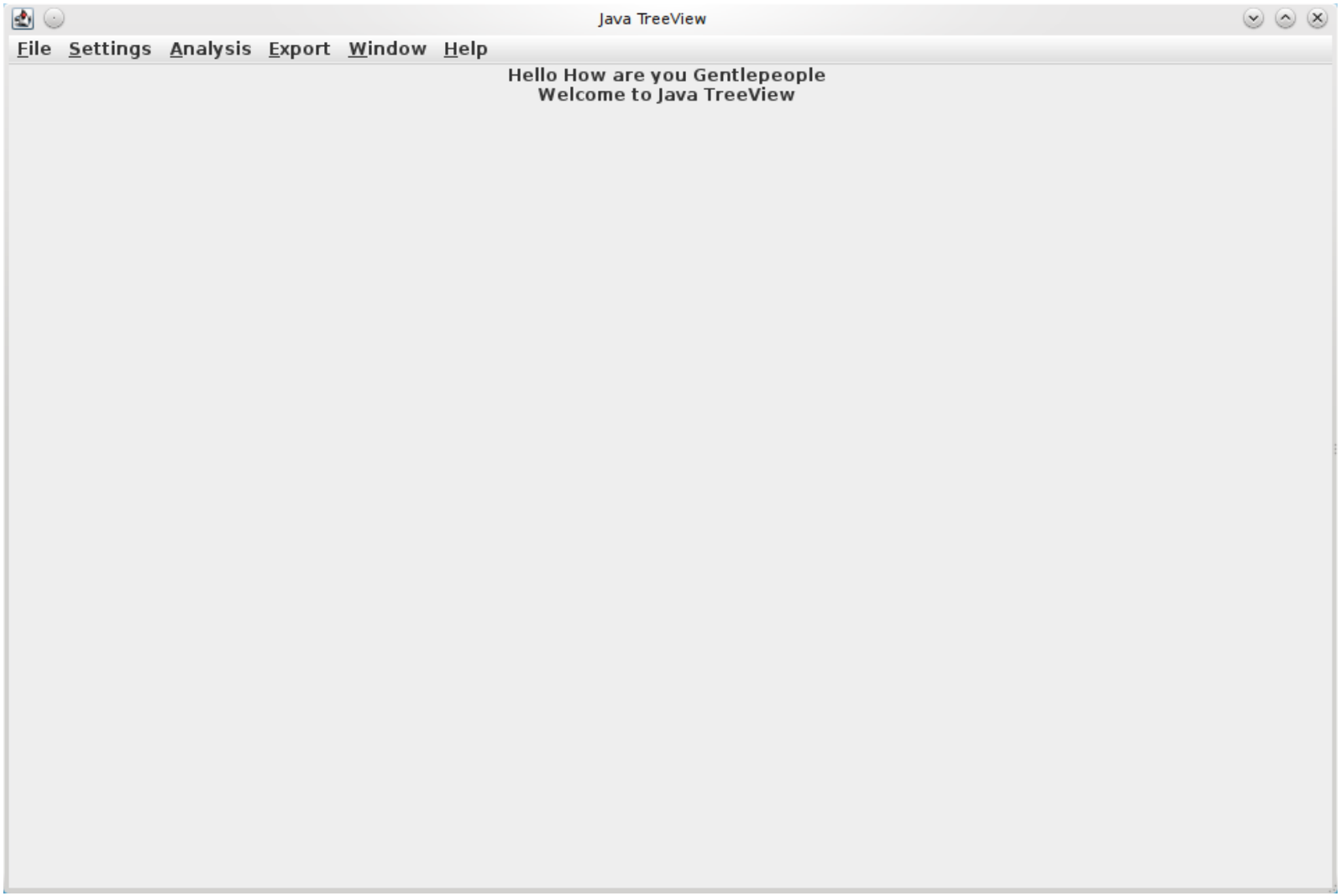
Choose distance function



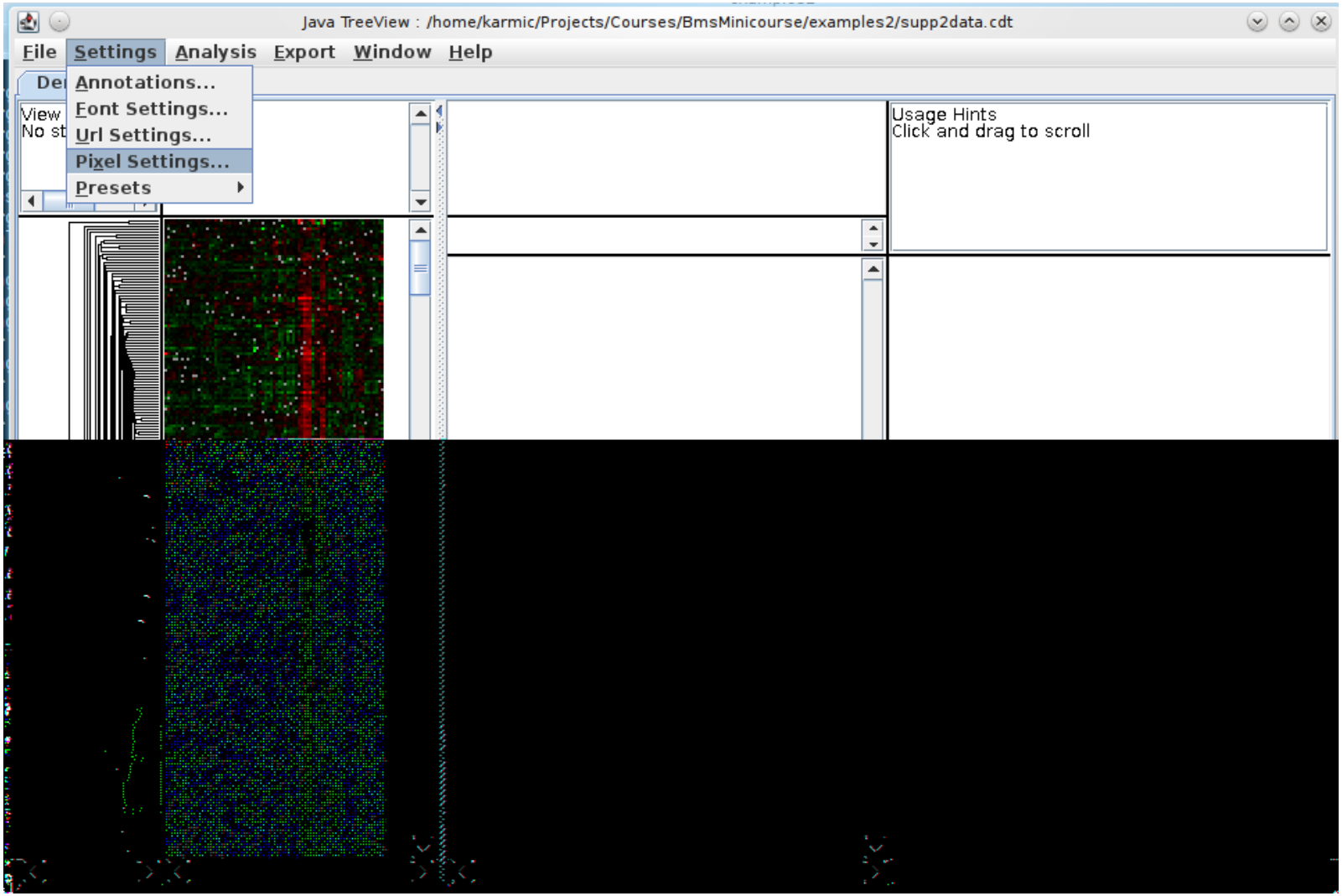
Choose linking method



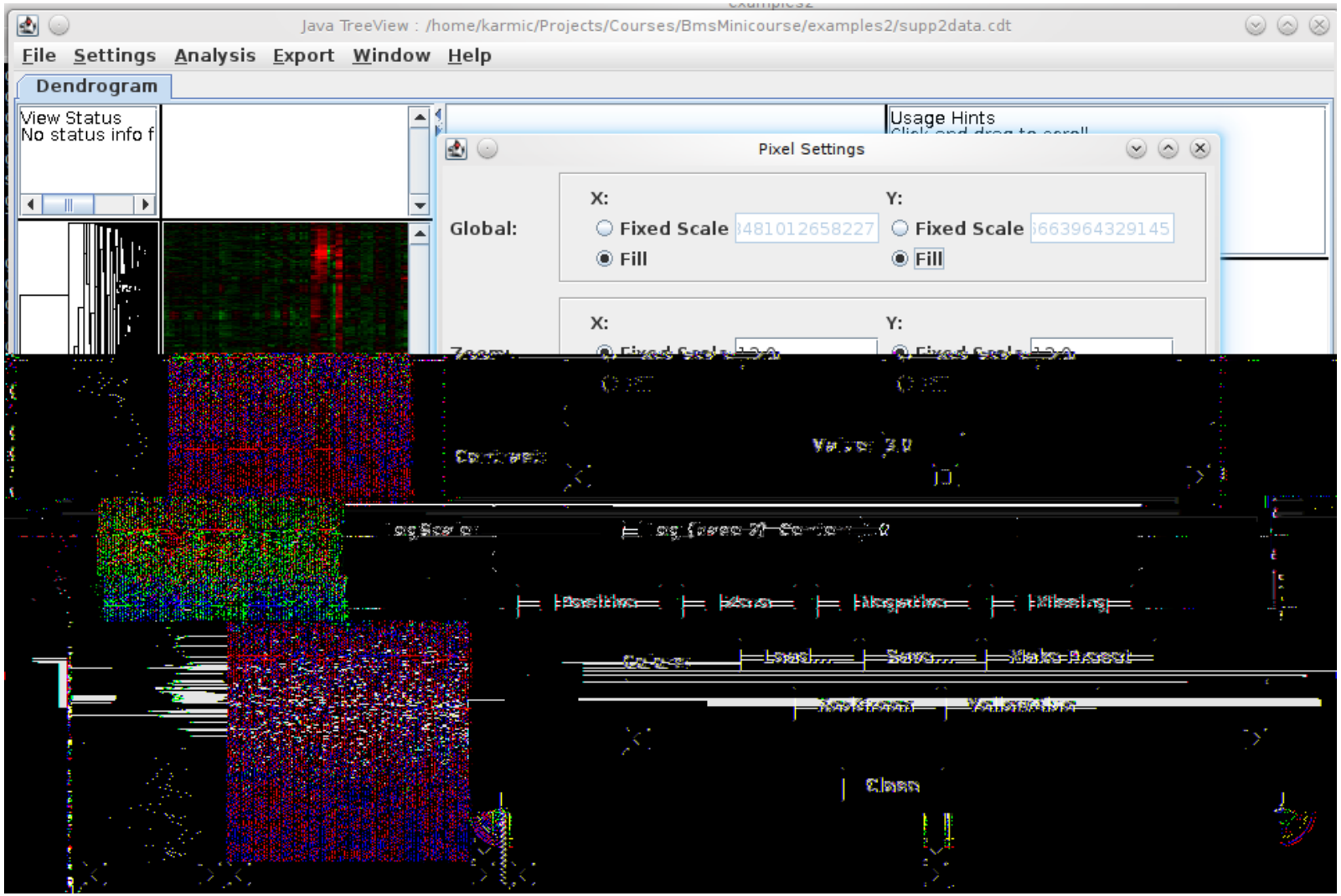
Using JavaTreeView



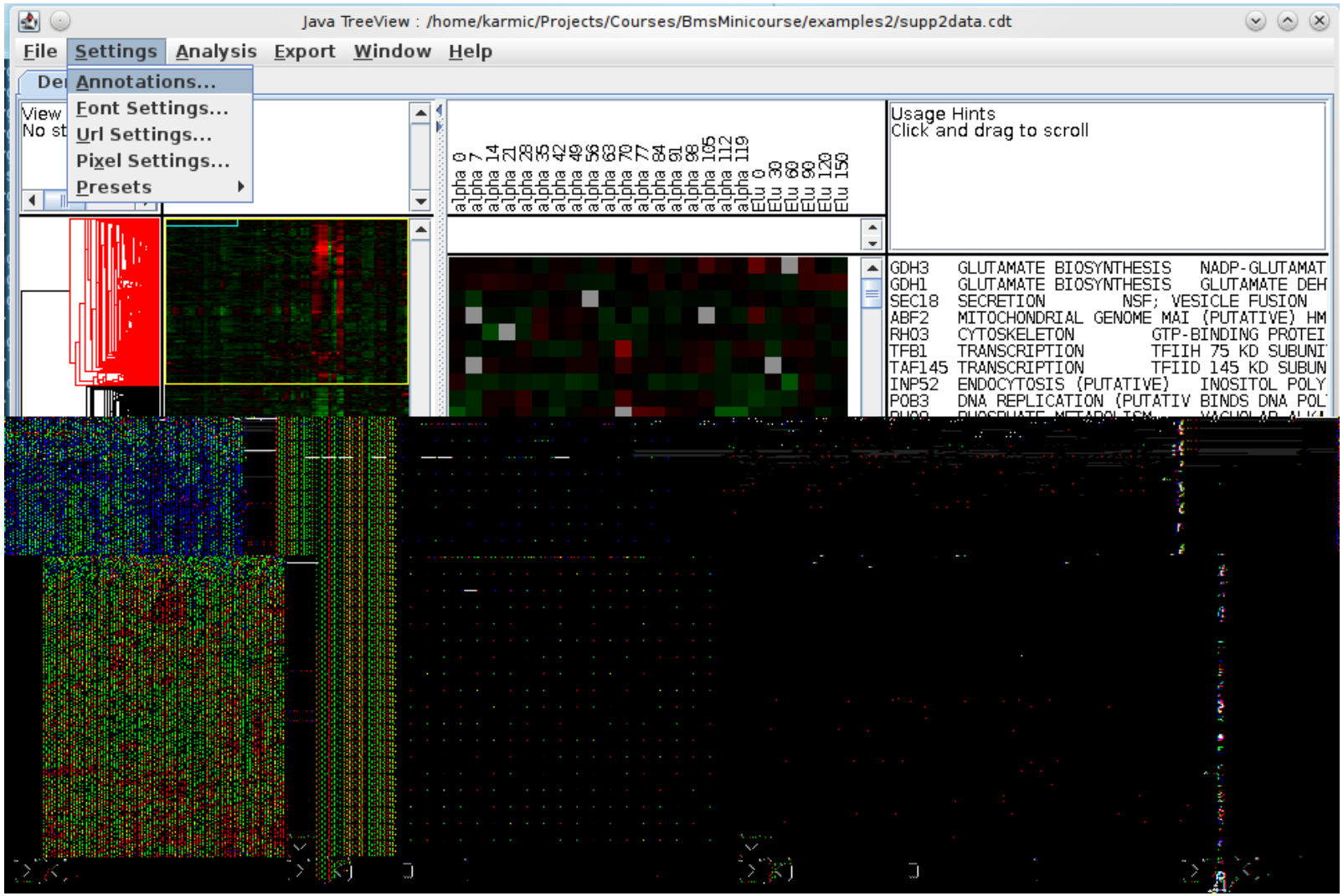
Adjust pixel settings for global view



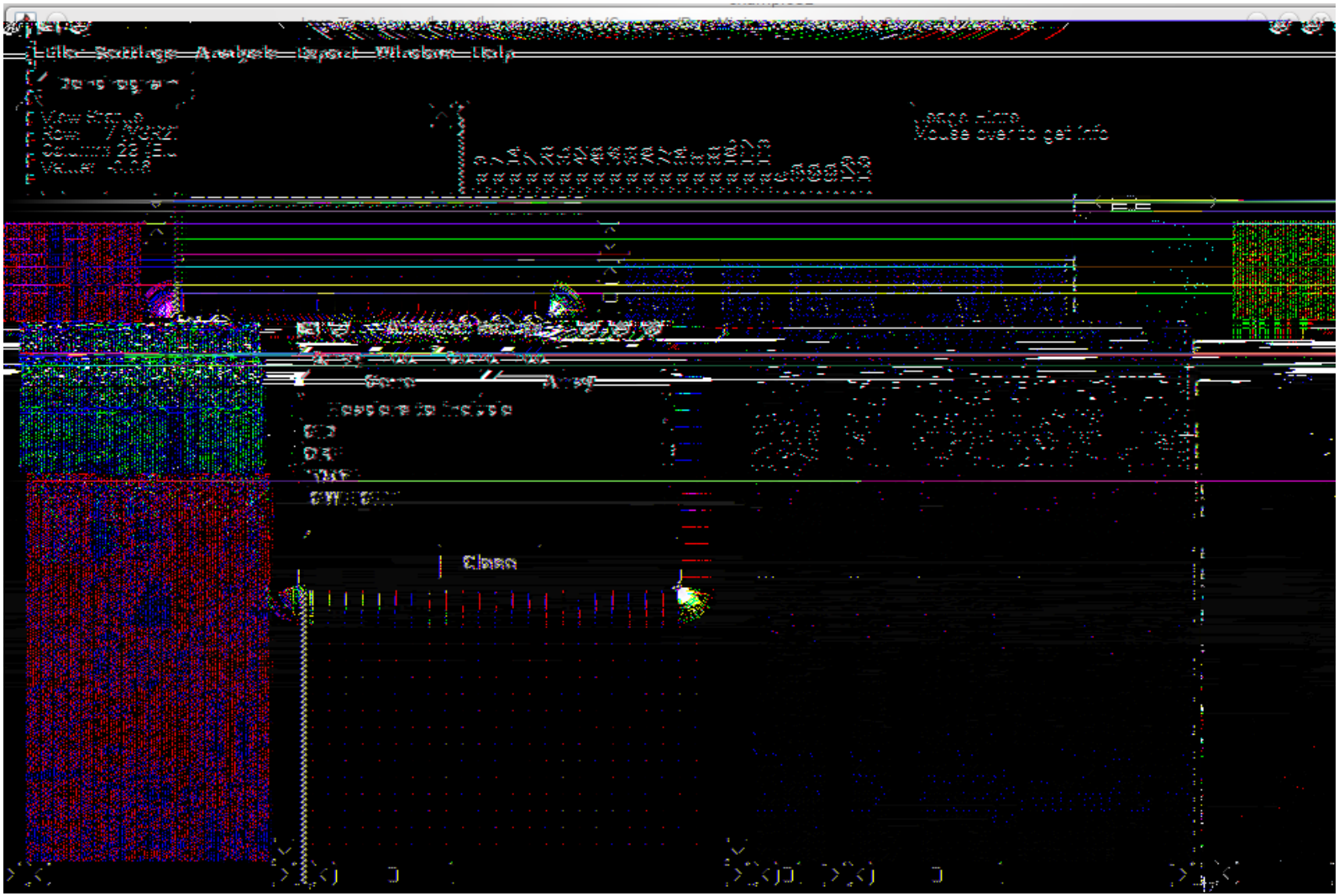
Adjust pixel settings for global view



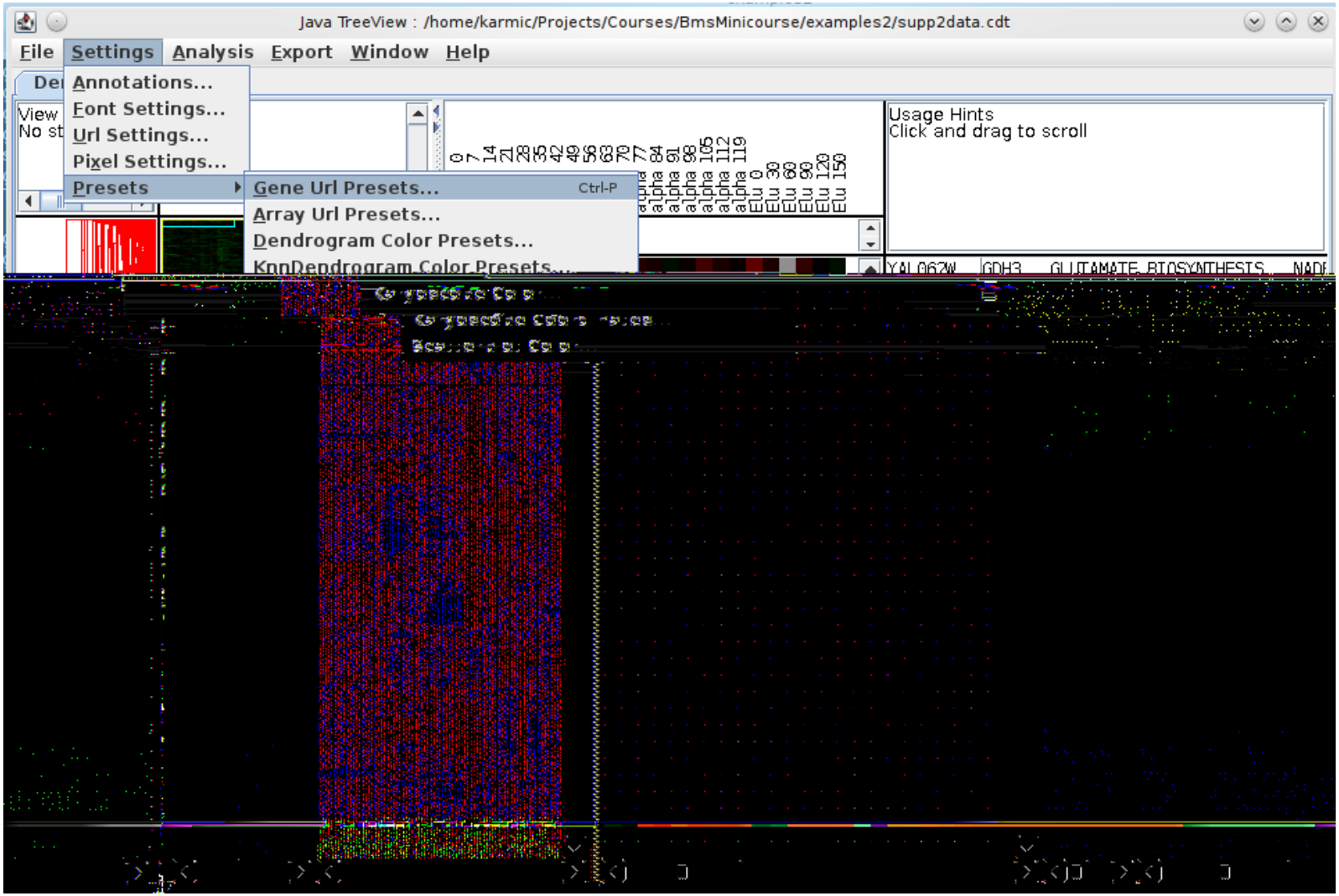
Select annotation columns



Select annotation columns



Select URL for gene annotations



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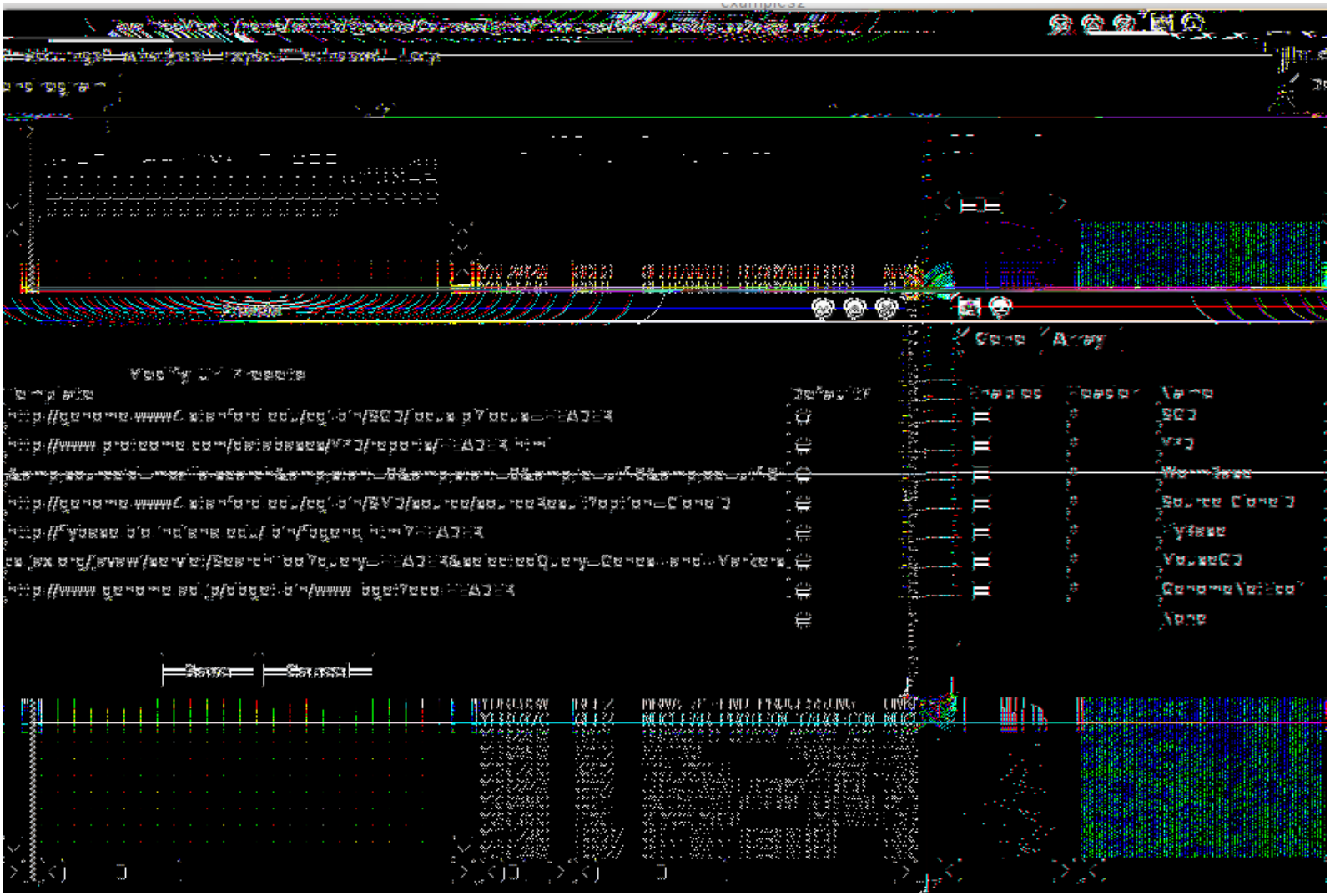
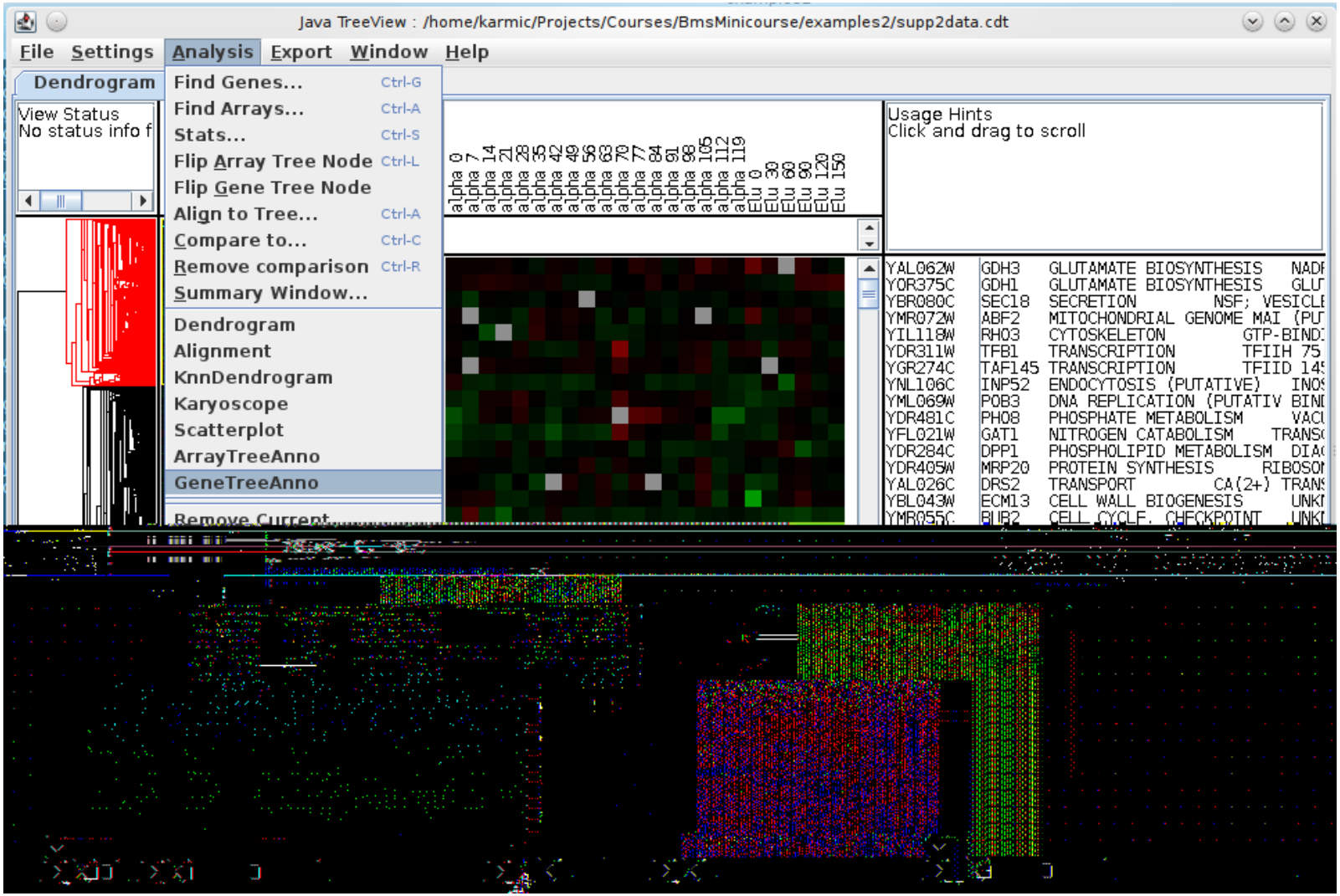


Activate and detach annotation window



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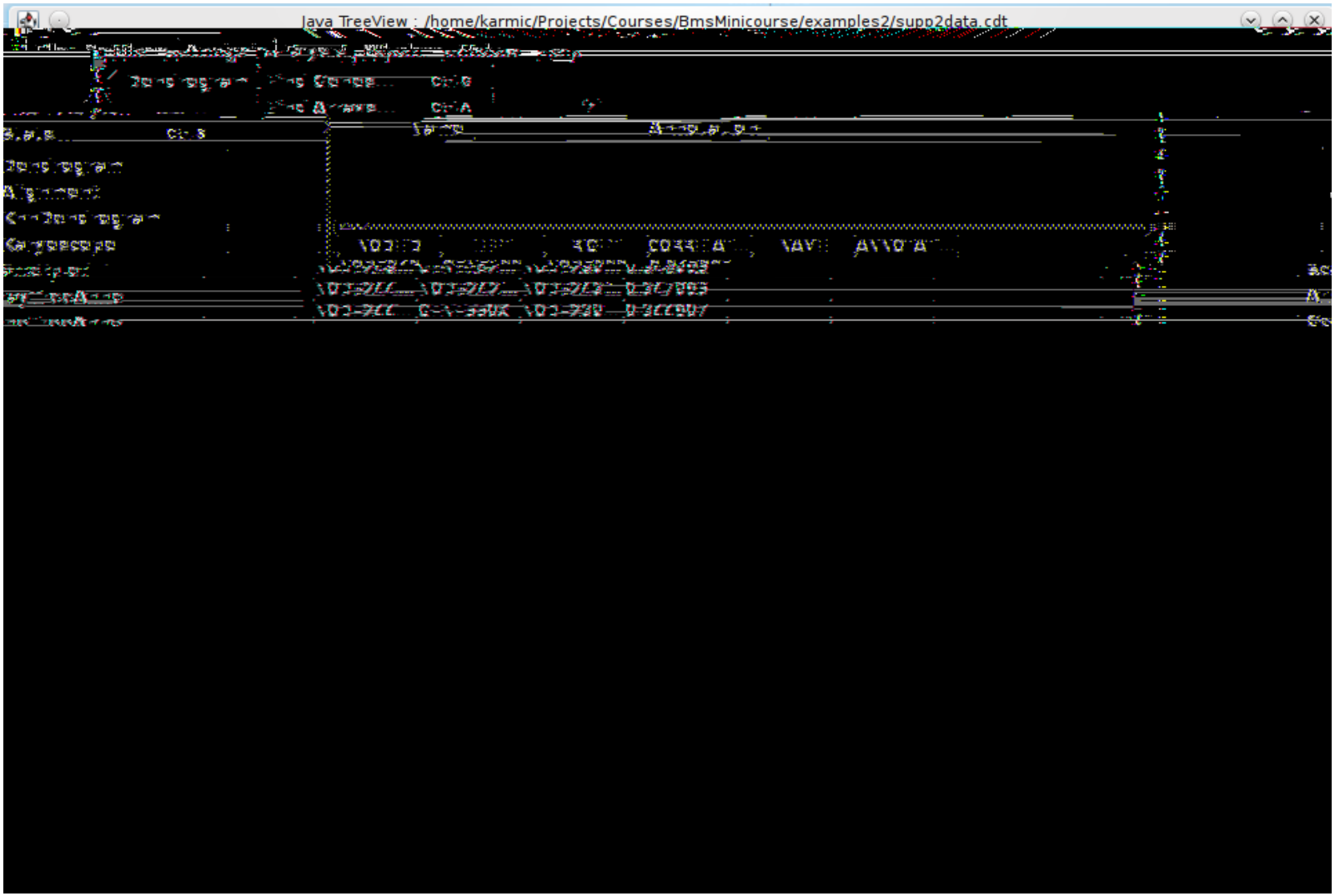

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