Distance Metrics

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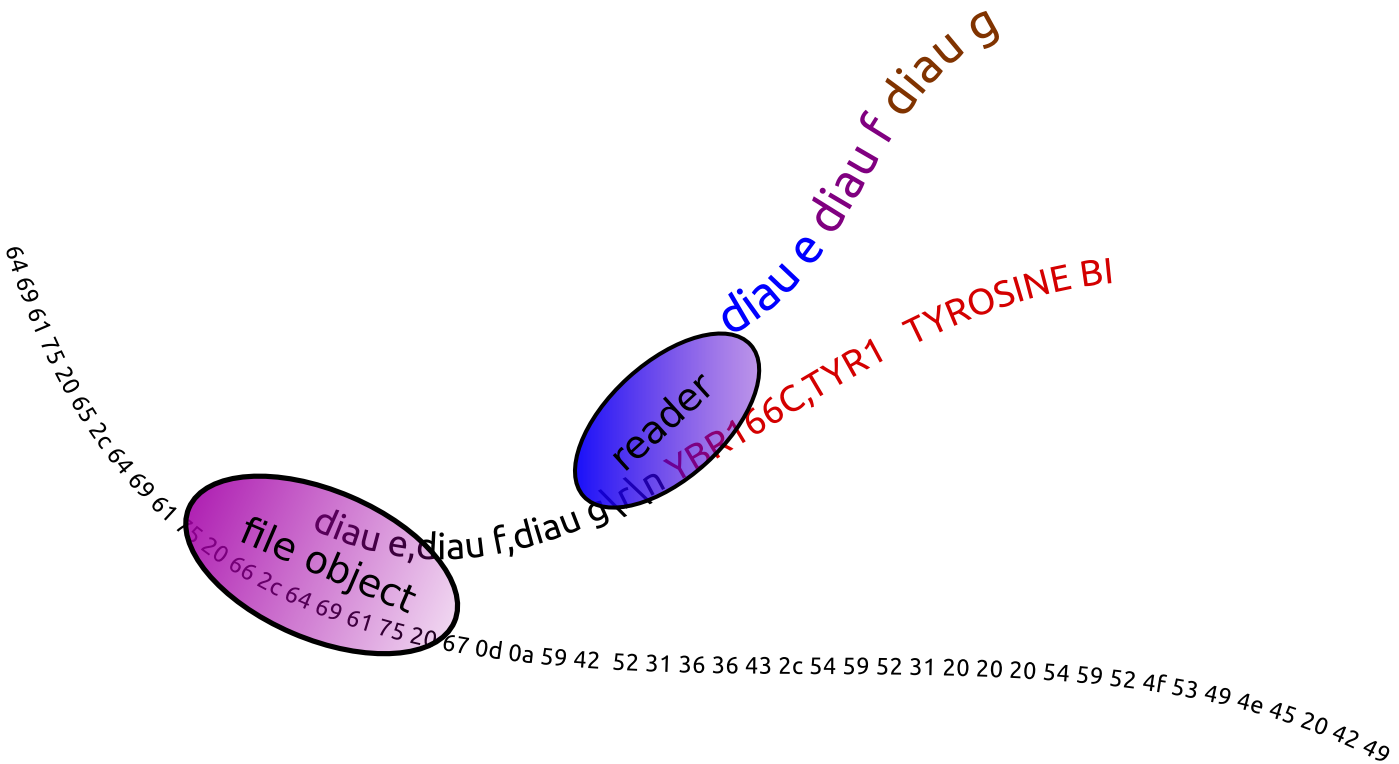
New verbs

```
def function(parameter1, parameter2):
    """Do this!"""
    #  Code to do this
    return return_value
```

Generators are like polymerases: iterable but not indexable



List tricks

Adding data to a list:

```
mylist = []
mylist.append(3)
mylist += [4,5,6]
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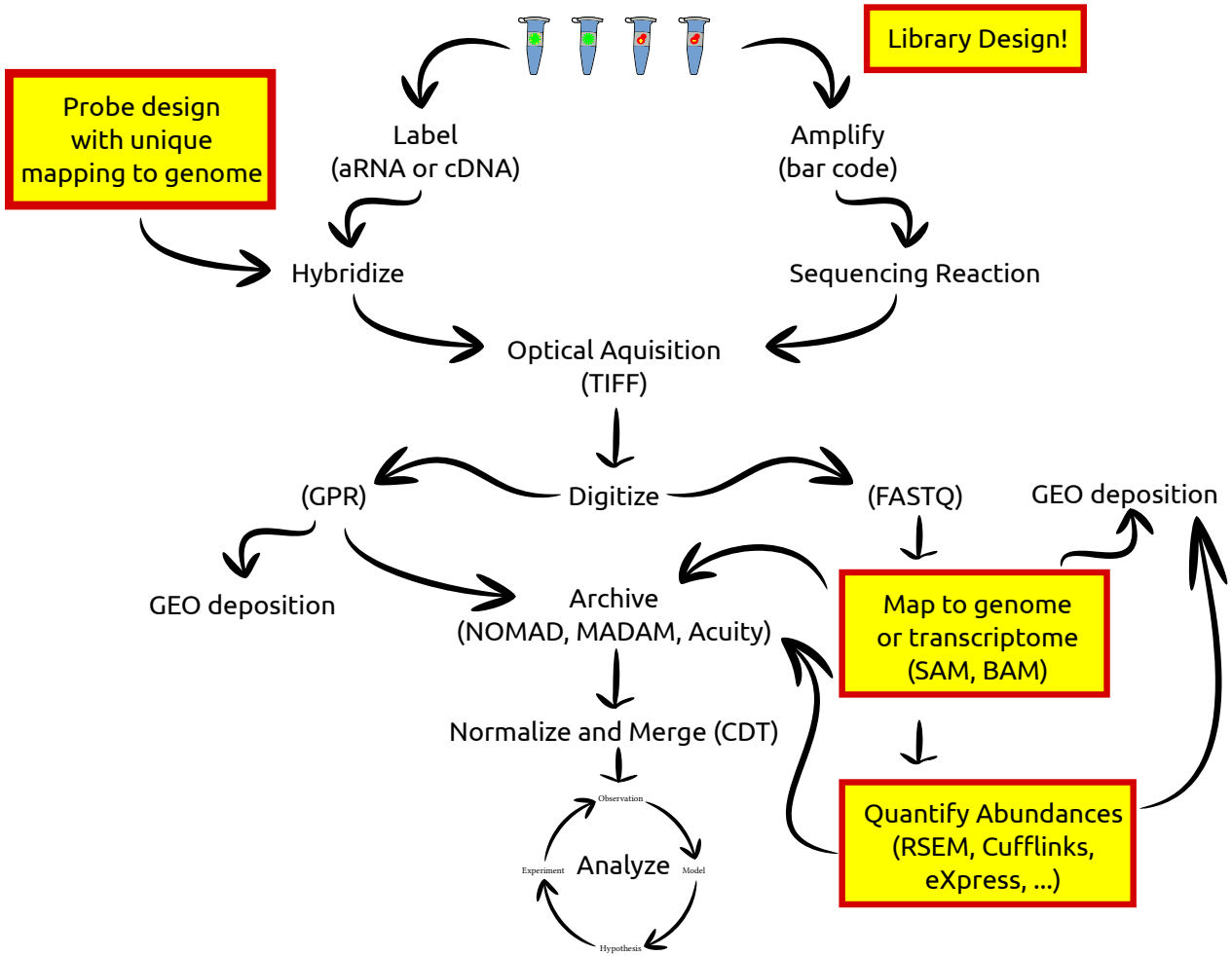
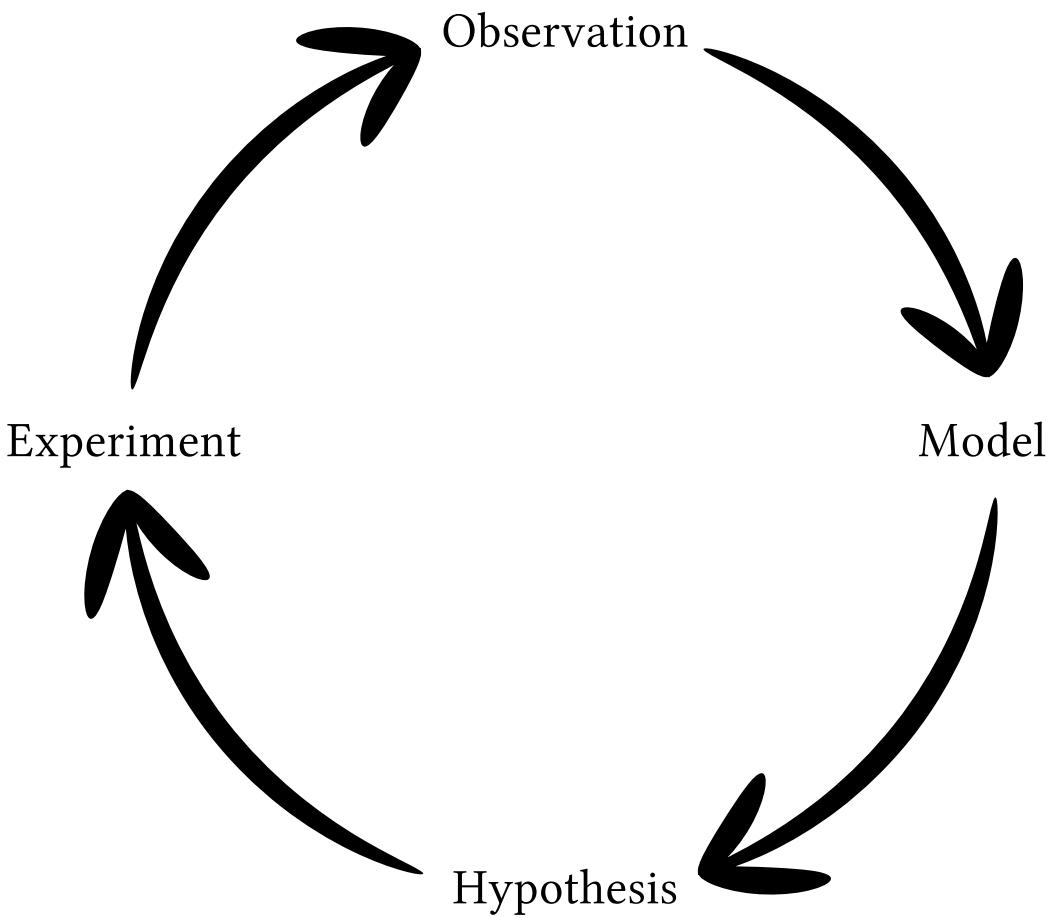
Lists of lists:

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

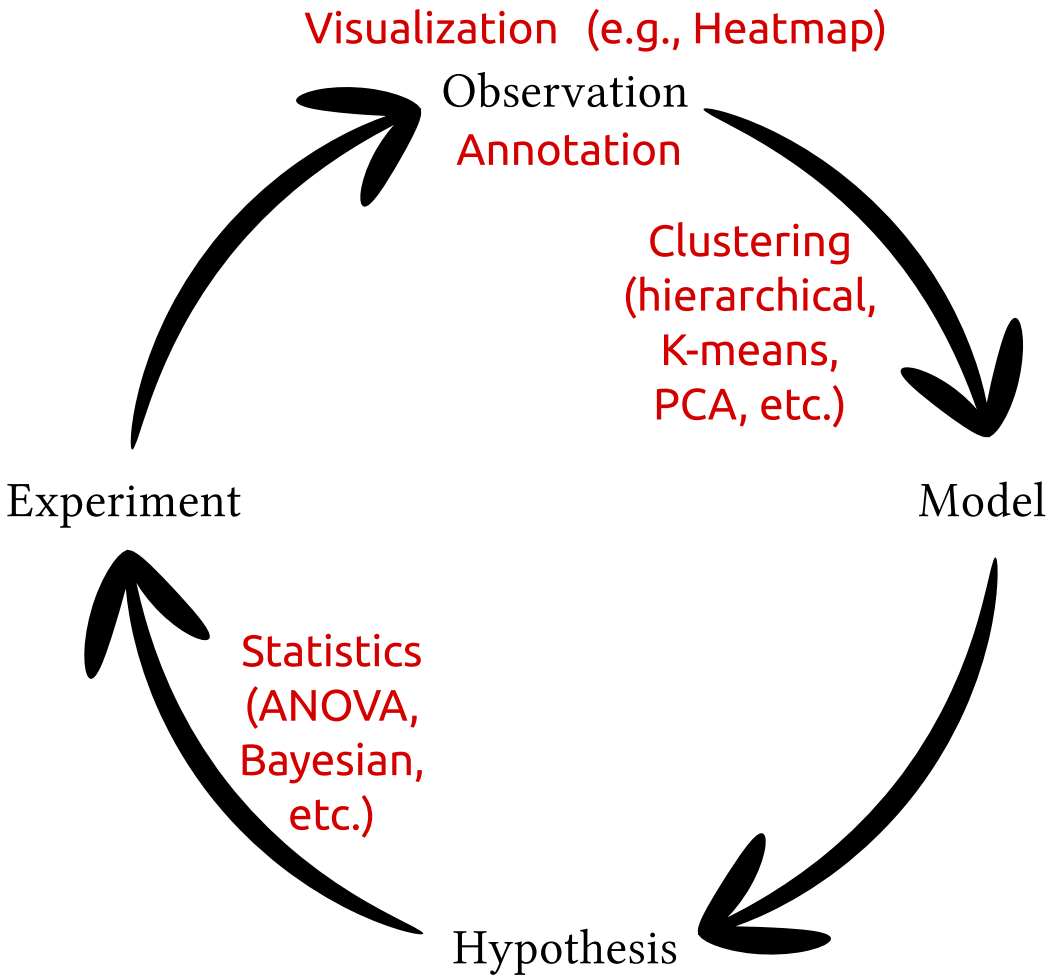
Expression profiling pipelines



Expression profiling pipelines

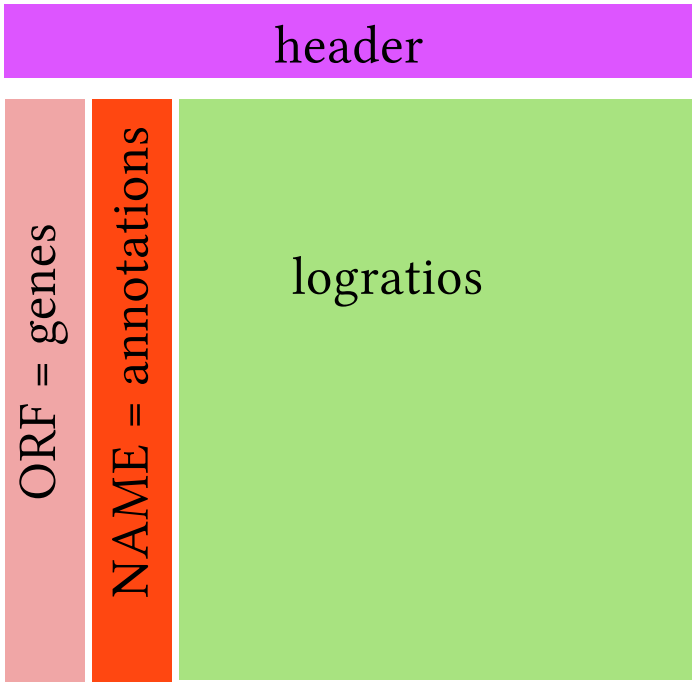


Expression profiling pipelines

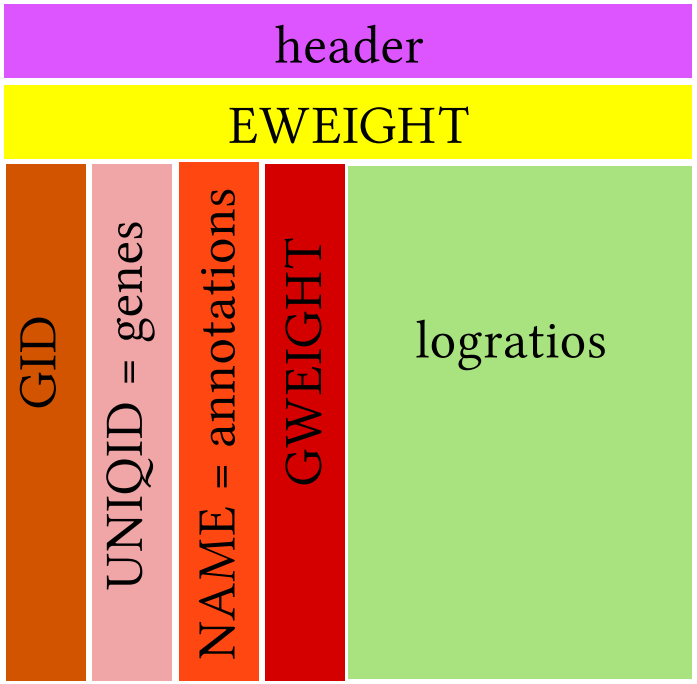


The CDT file format

Minimal CLUSTER input

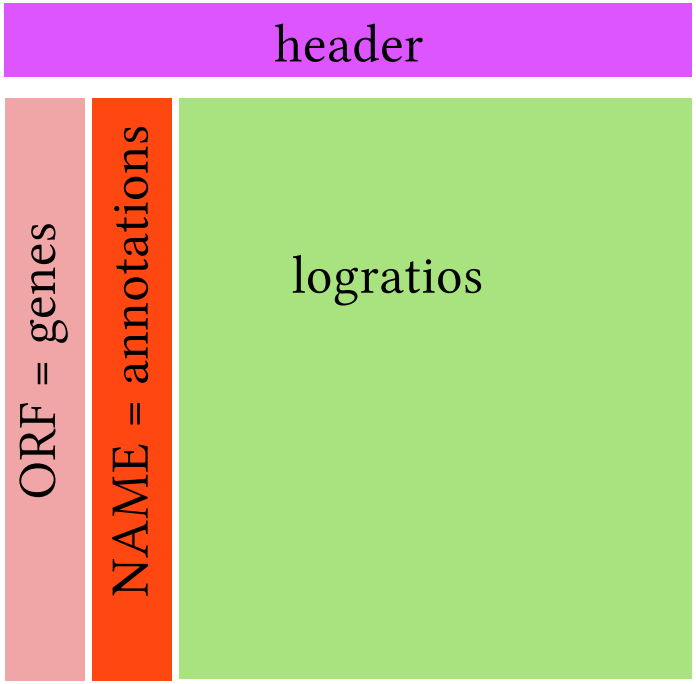


Cluster3 CDT output

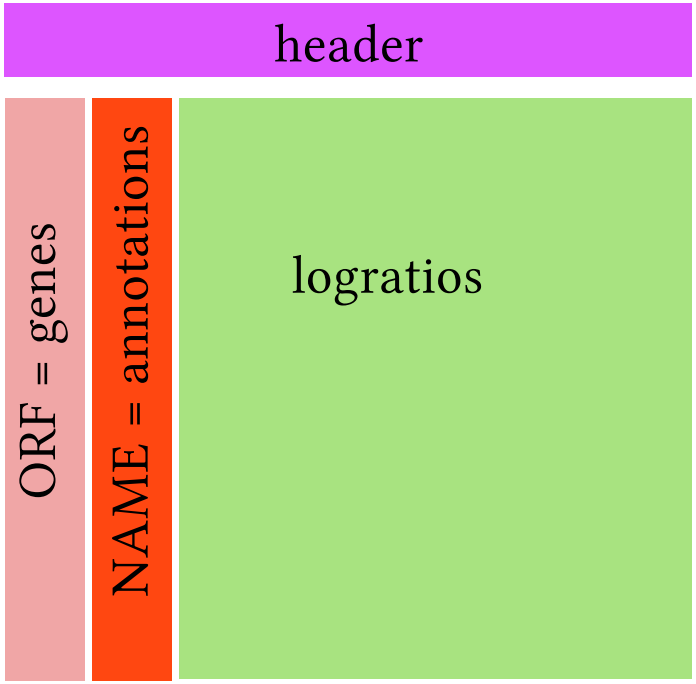


- Tab delimited (\t)
- UNIX newlines (\n)
- Missing values $\rightarrow$ empty cells

supp2data.cdt



supp2data.cdt




```
[["YBR166C", "YOR357C", "YLR292C", ...],

 ["TYR1 ...", "GRD19 ...", "SEC72 ...", ...],

 [[ 0.33, −0.17,  0.04, −0.07, −0.09, ...],
  [−0.64, −0.38, −0.32, −0.29, −0.22, ...],
  [−0.23,  0.19, −0.36,  0.14, −0.40, ...],
  ...]
]
```

Fun with logarithms

In log space, multiplication and division become addition and subtraction:

$$\begin{aligned} \log(xy) &= \log(x) + \log(y) \\ \log(x/y) &= \log(x) - \log(y) \end{aligned}$$

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Also, we can change of the base of a logarithm like so:

$$\log_A(x) = \log(x)/\log(A)$$

Pearson distances

Pearson similarity

$$s(x,y) = \frac{1}{N}\sum_{i}^{N}\left(\frac{x_i - x_{offset}}{\phi_x}\right)\left(\frac{y_i - y_{offset}}{\phi_y}\right)$$

$$\phi_G = \sqrt{\sum_{i}^{N}\frac{(G_i - G_{offset})^2}{N}}$$

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

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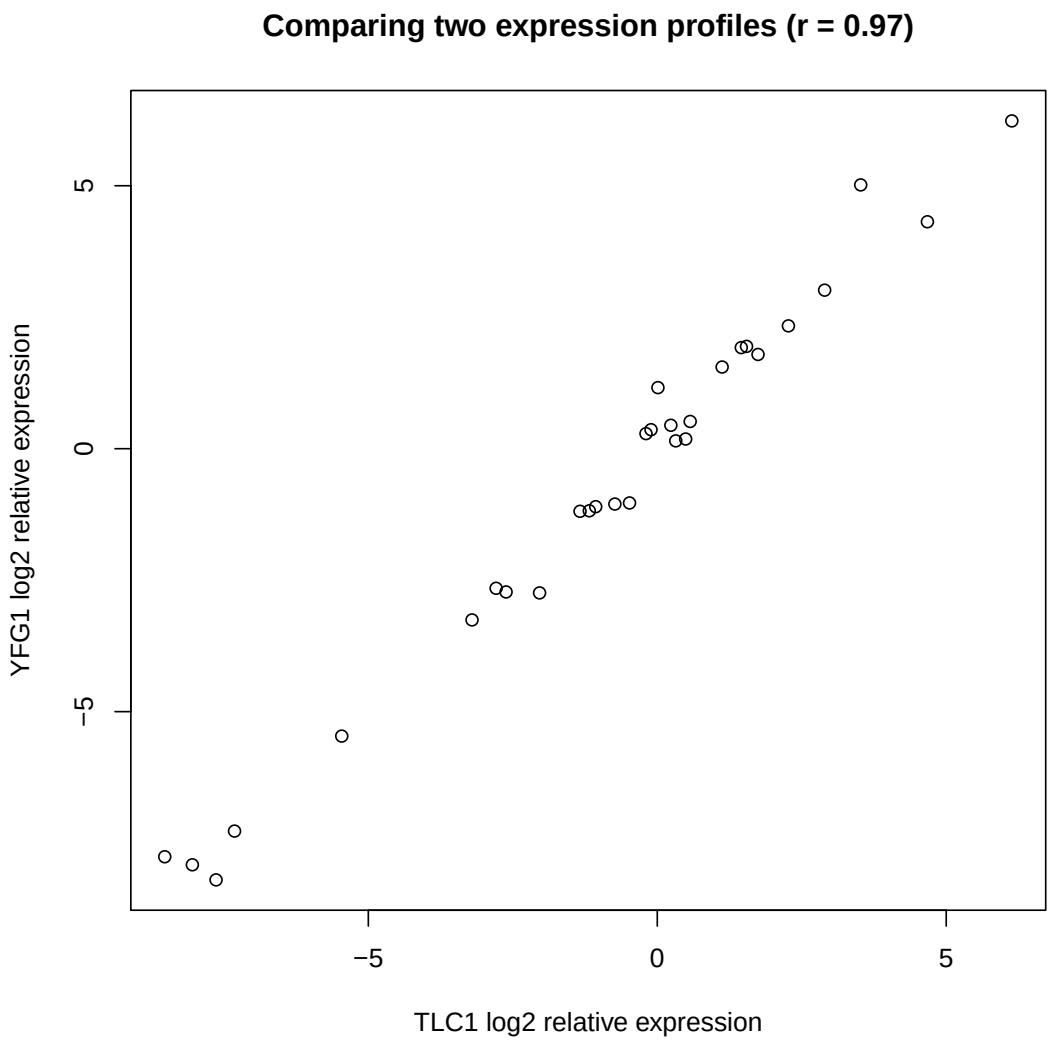
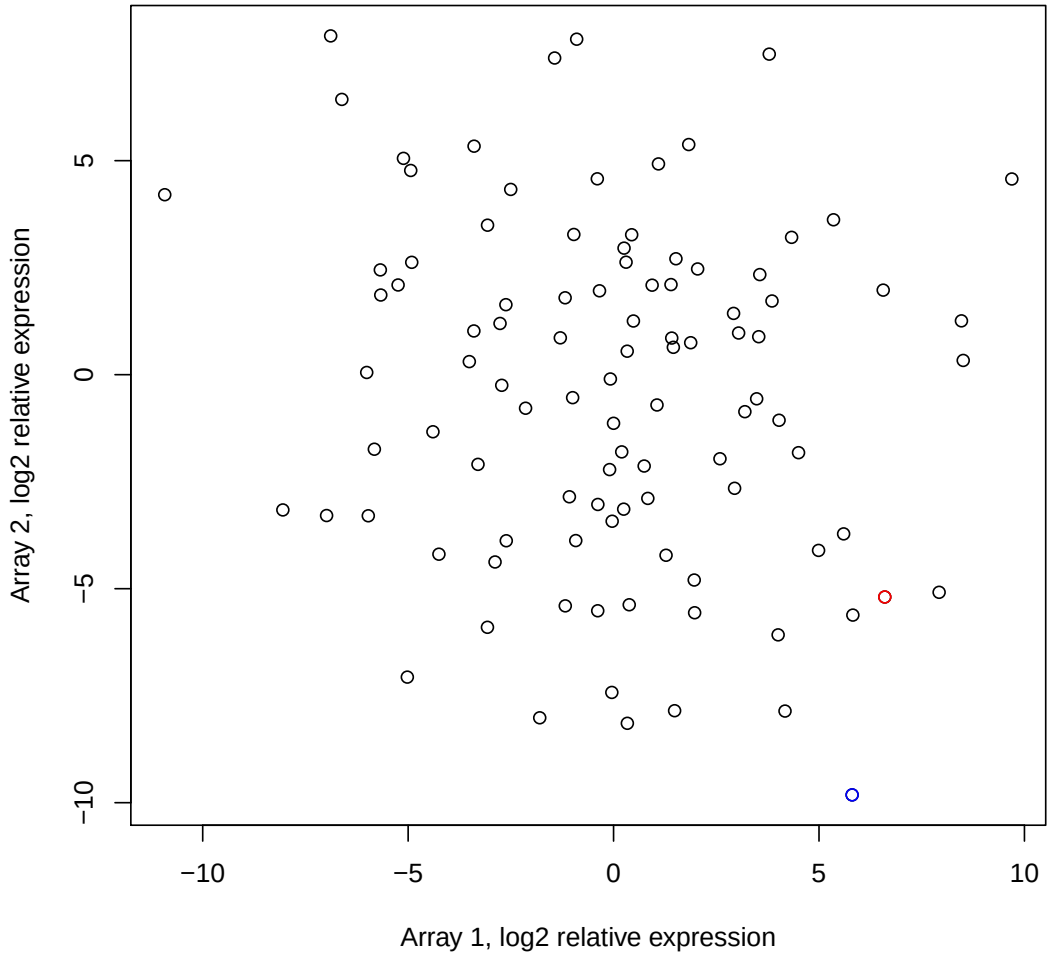
Euclidean distance

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

Comparing all measurements for two genes



Comparing all genes for two measurements



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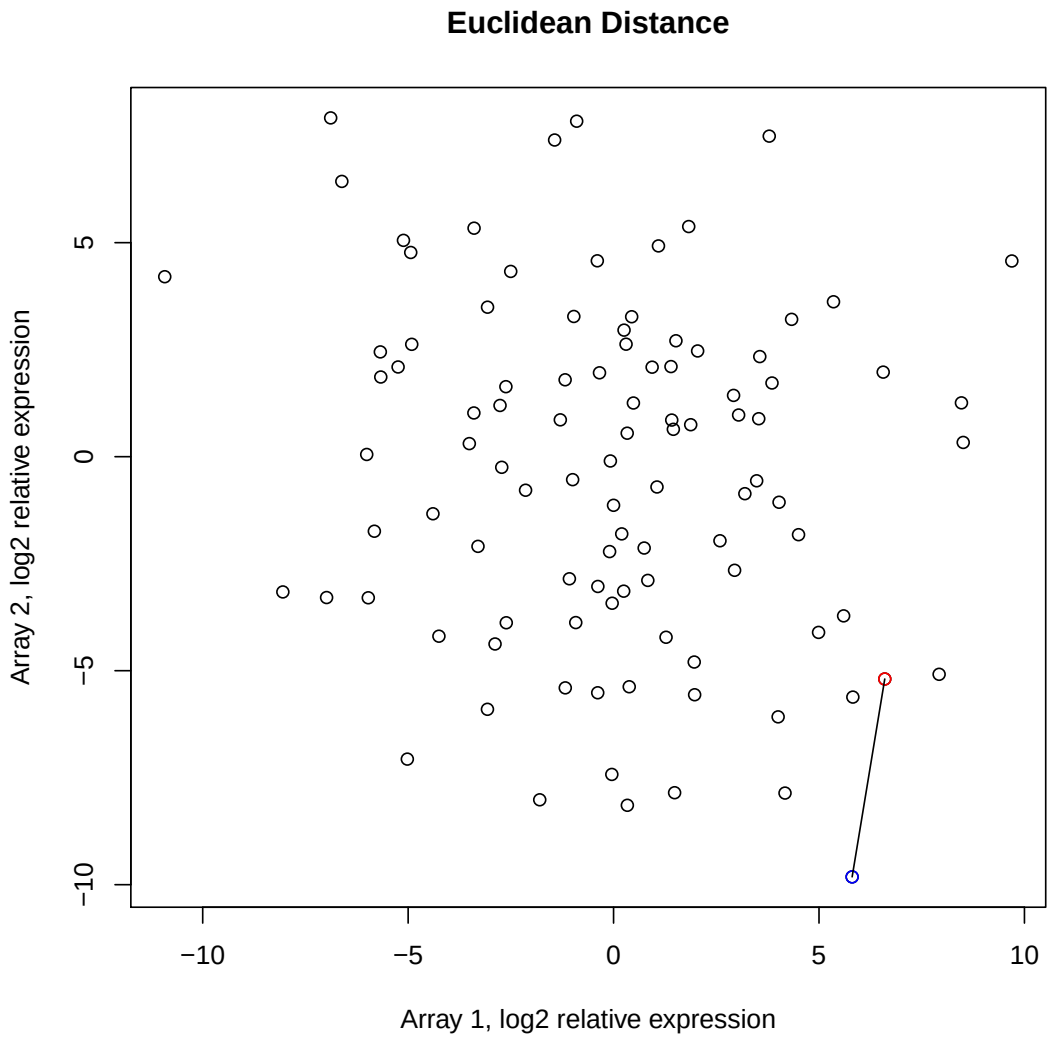

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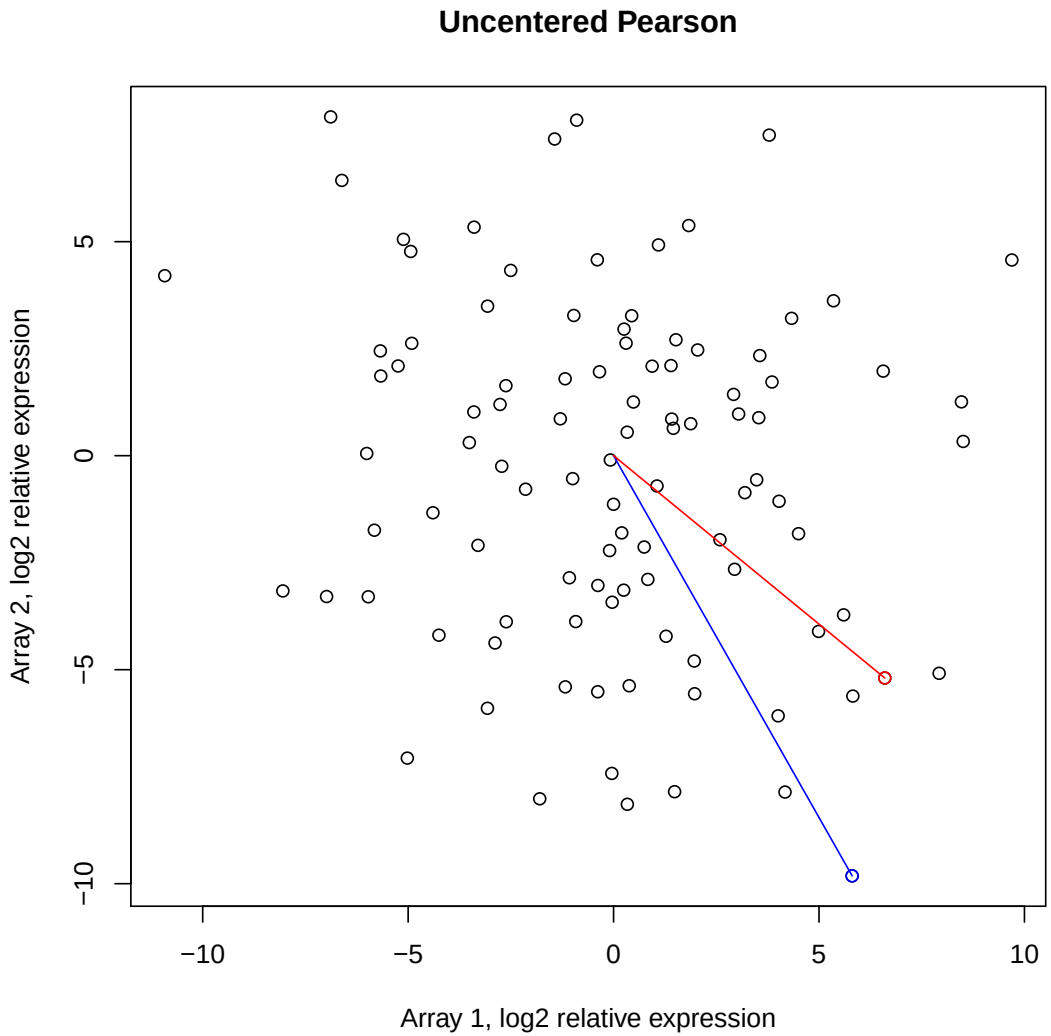
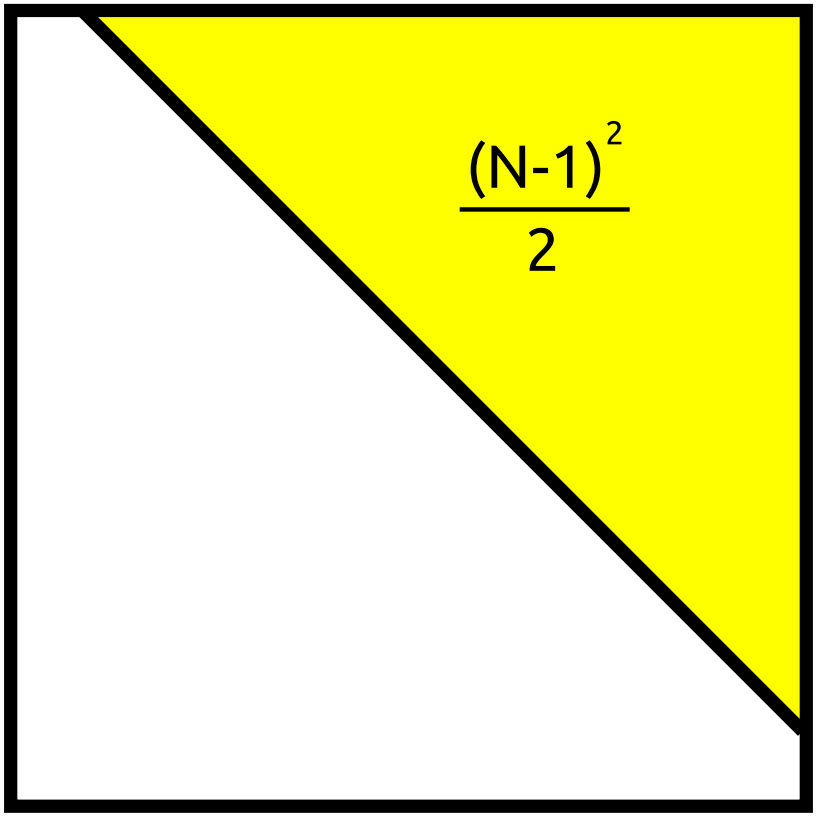
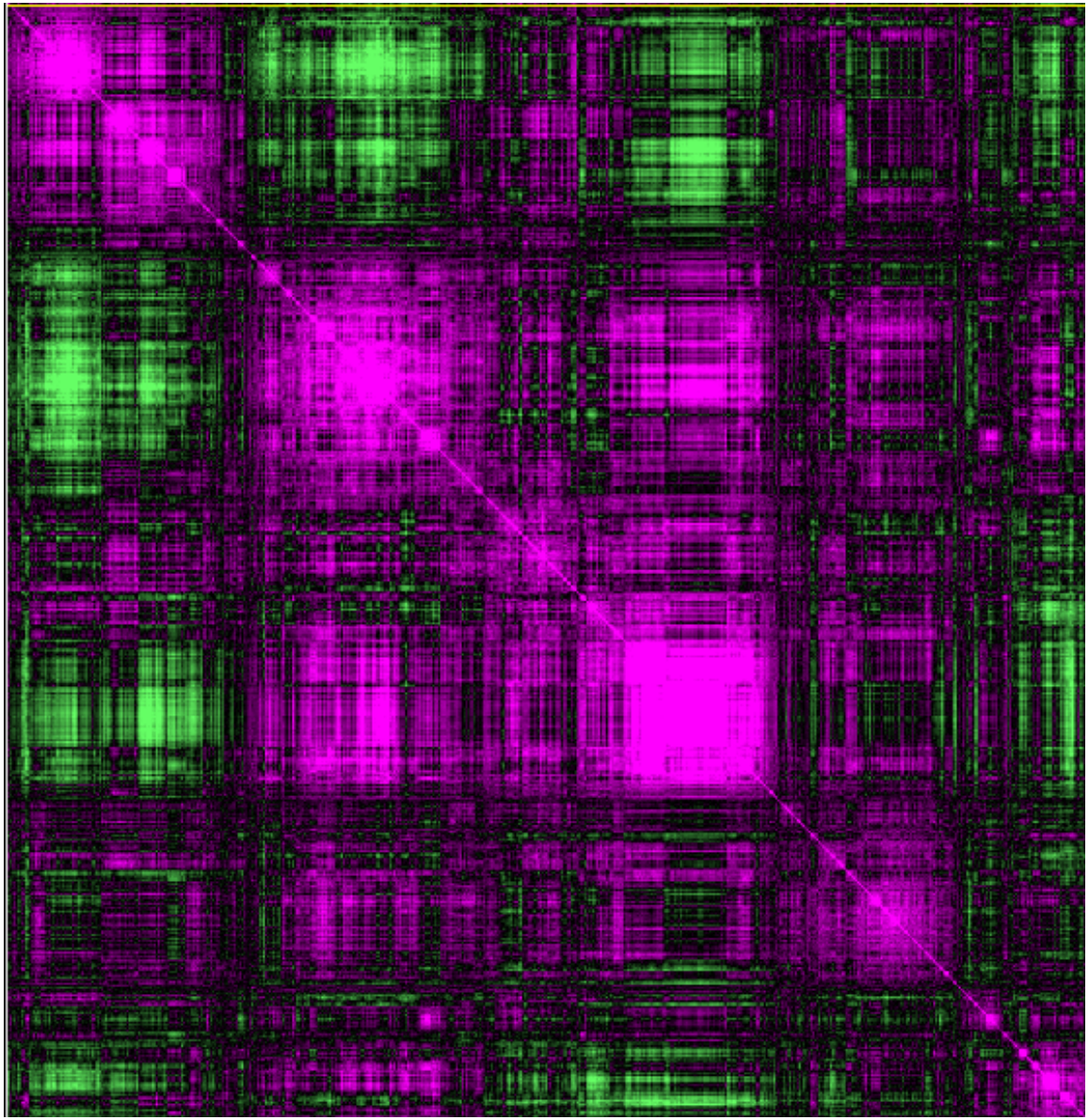


Measure all pairwise distances under distance metric



Clustering exercises – Visualizing the distance matrix



Homework

1. Write a function to calculate all pairwise Pearson correlations for the yeast expression profiles.
2. Save the results of your pairwise correlation calculation in the CDT format described in the JavaTreeView manual.
3. Read PNAS 95:14863
4. Try the first two problems, replacing the Pearson correlation with the distance metric from the PNAS paper or with one of the distance metrics from the Cluster3 manual.