### **Distance Metrics**

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# Expression profiling pipelines



## RnaSeq pipelines

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

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

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• Think about appropriate inputs and outputs for your functions

Adding data to a list:

mylist = [] mylist.append(3) mylist += [4,5,6] Adding data to a list:

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Lists of lists:

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### open("supp2data.csv")



### open("supp2data.csv").next()



### open("supp2data.csv").read()



#### csv.reader(open("supp2data.csv")).next()



# csv.reader(urlopen( "http://example.com/csv" )).next()



- Write a function to calculate all pairwise Pearson correlations for the yeast expression pro les.
- Save the results of your pairwise correlation calculation in the CDT format described in the JavaTreeView manual.
- Read PNAS 95:14863
- Try the rst 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.