

You are asked to implement your algorithms in Java and to give us a runnable jar of your algorithms so that we can test it on new pathways.

Your program should work on either linux or windows. In addition, currently the school has only Java 6 on its computers so please use Java 6 and not Java 7.

The runnable jar usage should be:

Java -jar XXX.jar pathway.txt genesToRank.txt where pathway.txt is the list of genes in the pathway (the query), and genesToRank is the list of genes that should be ranked by their closeness to the pathway.

Remarks:

1. To ease running, in all stages you can assume that the data files would be in the executing directory (that is, instead of giving it as input in the command line you can open it directly from your main).
2. You can add additional parameters to this execution command, as long as you explain clearly how to use your software.
3. Both pathway.txt and genesToRank.txt are simple files with one gene id in each line. The genesToRank list may contain some of the pathway genes - they should not be ranked in your final output.

Example of pathway.txt:

```
AT1G09780
AT1G12900
AT1G13440
AT1G18270
AT1G22170
AT1G32060
AT1G42970
AT1G43670
AT1G56190
AT1G74030
AT1G79550
```

4. The output is the 1000 top ranked genes, from the best candidate to the last, one gene per row followed by a tab and the gene's score. Example:

```
AT3G08590 0.904511
AT3G26650 0.885222
AT2G01140 0.88173
AT4G26530 0.851136
AT2G29560 0.795132
AT3G04120 0.693785
AT4G24620 0.441438
AT3G12780 0.402785
AT2G36530 0.314698
```

AT3G52930	0.281915
AT2G36460	0.279486
AT3G54050	0.061068
AT4G37870	0.05635
AT3G62410	0.049744
AT2G21330	0.043797

....