

Bioinformatics

Lab 7. MicroArray Data Analysis

Please use data in the following site for testing:

http://proteomics.yvu.edu/courses/BIOL4800_6900/LAB/micro_array/

Software tools needed:

Cluster3 and javatree view

download: <https://sourceforge.net/projects/jtreeview/>

<http://bonsai.hgc.jp/%7Emdehoon/software/cluster/software.htm#ctv>

Manual:

<http://bonsai.hgc.jp/~mdehoon/software/cluster/manual/>

<http://jtreeview.sourceforge.net/docs/JTVUserManual/index.html>

<http://www.boneandcancer.org/MOLab%20protocols%20since%202011-2005/G14%20Custer3%20Manual.pdf>

Examples:

<http://jtreeview.sourceforge.net/examples/>

Tutorial:

<http://homer.ucsd.edu/homer/basicTutorial/clustering.html>

Steps for testing:

Open the downloaded file in Excel;

Copy the first 6 columns data - you may copy a part of data (i. e. 100 genes).

Then only keep the gene symbols, and the average values of the two treatments (column B, E, F). Save the file in “.txt”.

Start Cluster 3.0 program, then open the data file, you can filter the data or do some type of transformation, then choose “Hierarchical” to do clustering.

A file “.cdt” will be saved automatically.

The clustered file can then be viewed using Java Treeview.