ENFIN-EMBRACE workshop
Exercise sheet for Microarray analysis

MEM (http://biit.cs.ut.ee/mem)

1) Input your favourite gene (e.g. Nanog).
2) Pick one probeset to start with.
3) Start with one platform, e.g U133 for human.
4) Apply dataset filters to standard deviation.
5) Try out cloud tags describing datasets.
6) Enable mouse-over information from options to see.
7) Select few datasets of interest and look expression using ExpressView link
8) Send output to g:Profiler for functional profiling using GO annotations link
9) Query from mouse and human platforms the same gene. Compare the gene lists and g:Profiler results.

g:Profiler (http://biit.cs.ut.ee/gprofiler)

10) Convert mouse genes to human using g:Orth from previous step (MEM output).
   Compare annotations for these lists using g:Cocoa
11) If you have your favourite dataset in hand then pick most highly expressed genes and use them as input while selecting ordered list query option.
12) If you have certain chromosome location of interest then input it to g:Profiler to see what genes are located there and if some GO annotation, pathway or regulatory motif comes up as significant

KEGGAnim (http://biit.cs.ut.ee/kegganim)

13) Either upload your own dataset by creating a folder or pick one of the existing datasets
14) Choose a pathway of interest by your previous knowledge or select a pathway with many mapping probes. Start Animation.
15) Create a picture with most interesting datapoints for presentation using CineFilm
16) Try out Pathway components selection menu and edit Condition titles

GraphWeb (http://biit.cs.ut.ee/graphweb)

17) Select one or more datasets of interest from the server files or upload your own network file. Look for highly connected components (subset of the graph having many edges) using Strongly connected components or Markov Chain Clustering (MCL).
18) Choose a network and input your favourite gene set. Use network neighbourhood to find edges between your genes from the selected dataset (e.g. Human combined protein interactions)
19) Modify network settings by assigning more weight to smaller networks or selecting only large modules for output.