EMBO Practical Course on Analysis and Informatics of Microarray Data
Exercise sheet for BIIT tools

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 (default is 0.29)
5) Try out cloud tags of datasets' annotations (mouse-overing on the dendogram)
6) Enable show cell tooltips from Output options to see more information on the output
7) Input a set of genes to compare their similarity to your one query gene using Gene filters option
8) Select few datasets of interest and look expression profiles using ExpressView link
9) Send output to g:Profiler for functional profiling using GO annotations link
10) Make a query of a gene from mouse and human platforms. Compare the output gene lists and their respective g:Profiler results.

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

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

VisHiC (http://biit.cs.ut.ee/vishic)

17) Upload your own dataset using Soft or tab-separated files by creating a folder or alternatively check out the example datasets provided
18) Search for your favourite gene(s) from the clusters using search box above the dendogram
19) Look for cluster having unique annotations (marked with asterix in the first column of the Cluster statistics table)
20) Adjust the cluster size limits and additional threshold to make the output more compact