

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 *ordrered 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