

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.