

## GIANT TROUBLESHOOTING

### GALAXY CONFIGURATION

1. [JAVA script] HTML pages generated by GIANT tools require execution of javascript modules. To allow such scripts to be executed, add the corresponding tools to the whitelist through the galaxy administrator interface.

### DEPENDENCIES

2. [Heatmap and Clustering tool] When using *Heatmap and Clustering* tool option : "Reorder sample based on a factors file". Error can occur depending on the **sort** linux program version installed. The **sort** program have to deal with '-V' and '-k' options.

### IDENTIFIED BUGS

3. [*Differential expression* tool][*Volcano plot* tool] *Differential expression* and *Volcano plot* tools use *BiomaRt* R package to collect biological information on genes/probes when option "Add gene/probe information" is selected. This option requires direct connection to web databases, this connection can fail due to multiple reasons, thus provoking the tool failure with error messages as `curl::curl_fetch_memory(url, handle = handle)`. In this situation, try to re-run the tool or search for any internet connection limitations. If the error remains, please unselect the "Add gene/probe information" option until the connection is restored.
4. [*GSEA formatting* tool] When formatting expression file for further GSEA analysis with the GSEA formatting tool, the user has to pay attention to row names of expression file (1st column). If the expression file row names are already official gene symbols, no remap step is necessary during GSEA analysis. On the contrary, if the expression file row names are probeset identifiers (e.g. probeset level normalization), the user has to select "*Collapse/Remap*" GSEA software option and to precise the corresponding Chip platform.

### ADVICES

5. [*Differential expression* tool] Even if several filtering options are embedded in the *Differential expression* tool, user can apply the native Galaxy *Filter* tool on the differential results file to try several cutoff values without rerunning the full differential analysis. In this case, the user has to remove the first two lines of the differential results file (containing non-numeric values) before applying the *Filter* tool.