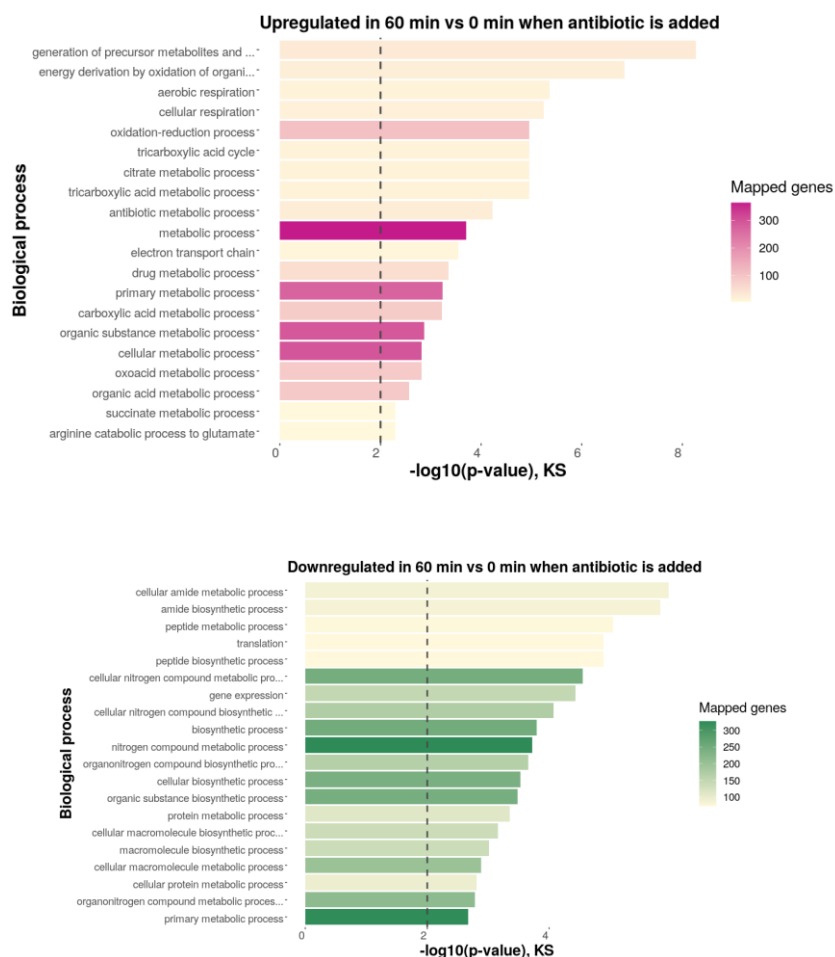Example of plots which can be obtained by using scripts in this repository

Enrichment_analysis_TopGO.r

Ggplot R package and standard bar plot were used for visualisation of GO-enrichment data. Horisontal bars indicate -log10(pvalue) for Kolmogorov- Smirnov test results (This value also can be interpreted as Enrichment score.


Clusterization.R

Ggplot package also was used for visualization of mean expression dinamics of genes within clusters which was extracted based on their expression dinamics at different time points. Usual geom_point plot and geom_line for connection of dots were used for this visualization.

Cluster Expression by Time with novobiocin treatment
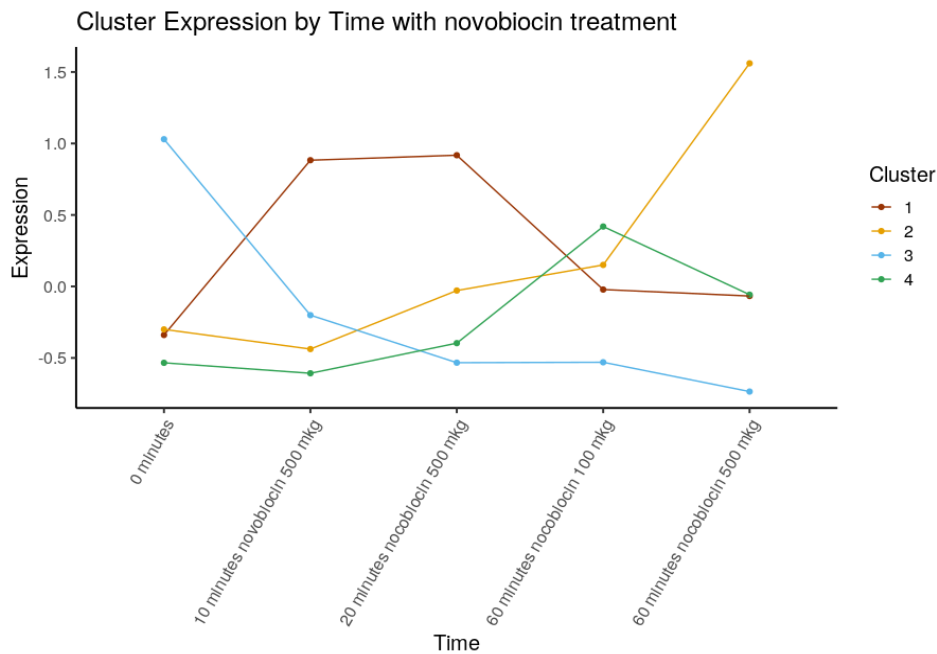
We also performed hyperheometric test to test hypothesis if converging (><) or diverging (<>) genes are enriched by genes within different clusters. For visualization of test results heatmap plot where p-value was used as value for cell colors was implemented.


Results of Hyperheometric test for overpresentation of clusters in converging and diverging genes
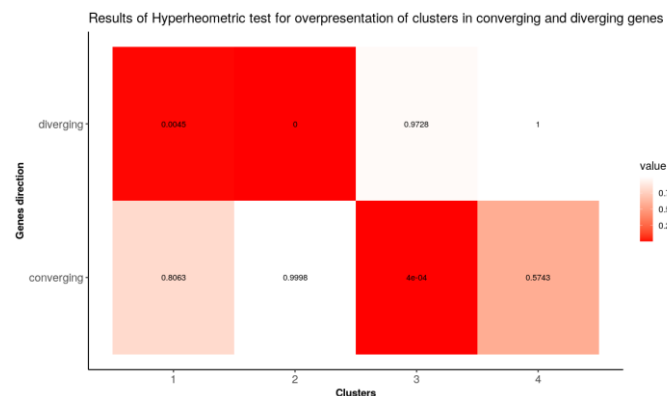
FGSEA.r

For representation of GSEA analysis results the standard code of function *plotEnrichment* from fgsea R package was slightly changed and new function *plotEnr* was created.

Default line color was changed from green. At the example picture you can see it as blue, but you can change it in script and also you can change text size or vertical bar color if you want (Relevant comments can be found in this part of FGSEA.r script)

Diverging genes forward (>)
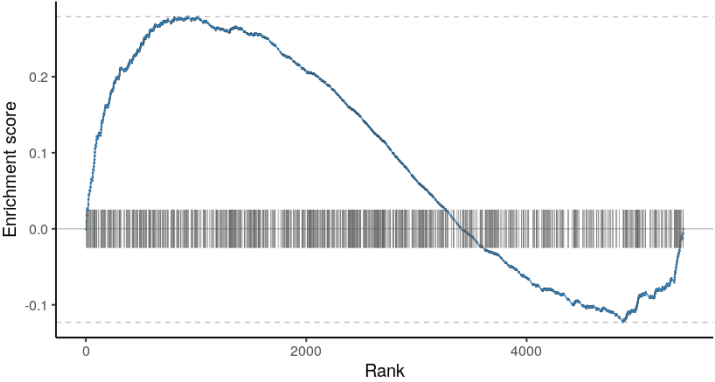
Expression dinamics of leucine operon genes