

After DEG:

- [Enrichment Analysis](#) (Implemented for up and down-regulated genes in separate files in the folder. In the results folder the images are there.)
 - [Pathway Analysis](#) (Implemented for up and down-regulated genes in separate files in the folder. In the results folder the images are there.)
1. [Gene co-expression network analysis](#) (found top 100 genes)
 2. [PPI Network Construction using STRING website](#) (from previous 100 found 88 genes here)
 3. Using Cytoscape and cytoHubba plugin selected top 10, 20, 30, 40 genes for ranking algorithms: Closeness, MCC, MNC (Implemented with Desktop app CytoScape)
 - a. [Graph for top 10 Closeness](#)
 - b. [Graph for top 20 Closeness](#)
 - c. [Graph for top 30 Closeness](#)
 - d. [Graph for top 40 Closeness](#)
 - e. [Graph for top 10 MCC](#)
 - f. [Graph for top 20 MCC](#)
 - g. [Graph for top 30 MCC](#)
 - h. [Graph for top 40 MCC](#)
 - i. [Graph for top 10 MNC](#)
 - j. [Graph for top 20 MNC](#)
 - k. [Graph for top 30 MNC](#)
 - l. [Graph for top 40 MNC](#)
 - m. [CSV for top 10 Closeness](#)
 - n. [CSV for top 20 Closeness](#)
 - o. [CSV for top 30 Closeness](#)
 - p. [CSV for top 40 Closeness](#)
 - q. [CSV for top 10 MCC](#)
 - r. [CSV for top 20 MCC](#)
 - s. [CSV for top 30 MCC](#)
 - t. [CSV for top 40 MCC](#)
 - u. [CSV for top 10 MNC](#)
 - v. [CSV for top 20 MNC](#)

- w. [CSV for top 30 MNC](#)
 - x. [CSV for top 40 MNC](#)
4. [Intersect top 10 Hub Genes for closeness, MCC, MNC](#) (10, 20, 40 intersect are in in 1 file, so for 5 and 7 same link)
 5. [Intersect top 20 Hub Genes for closeness, MCC, MNC](#)
 6. [Intersect top 30 Hub Genes for closeness, MCC, MNC](#) (final as give high performance than 10, 20, 40)
 7. [Intersect top 40 Hub Genes for closeness, MCC, MNC](#)
 8. Related CSV files and other processing files are in [this](#) folder
 9. Evaluation was implemented with catboost and previous models, that file is in the folder mentioned above.