Motivation
Currently, biotechnology research is focused on applying microorganisms in the biorefinery. Such research relies heavily on computational bioinformatics analysis using genomic data. The Clostridium beijerinckii NRRL B-598 is a bacterium that is known as a producer of butanol. Its wider utilization can lead to a revolutionary solution for ecology. Unfortunately, we are missing its comprehensive functional annotation that would help to establish an economically viable process.

Overview of experiment
Pre-processing data
Operon inference
The first co-expression networks for C. beijerinckii NRRL B-598 were created by algorithms which are based on Pearson’s correlation coefficient and mutual information.

The gene regulatory networks were created by algorithms that are based on bootstrap, random forest, and differential equation analysis. The final result was inferred using unification gene regulatory networks that were created from different approaches and penetration of gene regulatory networks which were created from different datasets using Cytoscape platform.

Conclusion
The main accomplished aims of the thesis:
✓ Toolbox for pre-processing raw RNA-Seq
✓ The innovated pipeline and toolbox for infer operon dataset
✓ Inference of gene co-express networks
✓ Inference of gene regulatory networks
✓ Created the first gene regulation network for C. beijerinckii NRRL B-598 with 8787 edges (gene regulations).