

## Streszczenie i słowa kluczowe po angielsku (Summary and keywords in English)

The dissertation entitled „Time series gene expression analysis based on transcriptome and translome sequencing data” presents methods for analyzing data derived from two sequencing technologies - RNAseq and RIBOseq. These technologies, which are important tools in molecular biology research, open up possibilities for gene identification and expression analysis at the transcriptome and translome levels. The work focuses on the development of an integrated approach for data analysis of both techniques, allowing the study of gene expression in time courses. An R language library has been implemented that enables the use of data from parallel RNAseq and RIBOseq experiments to identify gene expression patterns over time. In addition, by applying appropriate normalizations and calculating translation efficiency, the library provides a more accurate view of the translation process compared to other currently available tools.

The results section discusses the preliminary stages of data analysis, such as quality control, data cleaning, mapping to a reference genome, and read counting, to prepare data for use in the „TimeSeqR” library and to perform initial analysis.

The key element of the work is the implementation of the „TimeSeqR” library in the R language, which allows the analysis of RNAseq and RIBOseq data in time courses. This library enables data normalization, differential gene expression analysis over time, clustering of genes with similar expression, and functional analysis of groups of genes. The thesis presents installation instructions and environment configuration, implementation details of the library, as well as a description of the programming interface and how to use the program through a graphical interface.

At the end of the dissertation, examples of the use of the library „TimeSeqR” on data from the organism *Bacillus subtilis*, literature data from the organism *Saccharomyces cerevisiae*, and simulated data are presented, along with their processing. The

results obtained are also discussed in comparison with other tools for the analysis of similar data.

Keywords: sequencing, RNAseq, RIBOseq, data analysis, time courses.