# Database on alternative gene splicing in glioma cell cultures

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*Motivation and Aim*: Fundamental biomedical research in oncology, the search for new markers of tumor development, modern post-genomic studies of gene expression on cell cultures need transcriptome profiling and analysis of gene expression and isoforms. Such experiments, in turn, require development of new computer tools and database for analysis of bulk sequencing data. The aim of our study is a computer search for genes and gene isoforms, the difference of their expression is associated with the development of glioblastoma [1].

*Methods and Algorithms*: The work is based on modern high-throughput sequencing technologies and international biomedical data banks analysis. RNA-seq data on glioma cell cultures were obtained at ICG SB RAS. The search for candidate genes in tumors for therapeutic treatment, including individual gene isoforms, is very relevant in healthcare and modern high-tech medicine.

*Results*: This work presents the bioinformatics problems related to the development of computer pipelines for the processing of transcriptomic data, the revealing of the differentially expressed genes, the analysis of alternative splicing, and the description of the gene ontologies categories for the genes sets found. The tasks of automatic search and description of gene functions in connection with cancer diseases, visualization of results and development of biomedical databases are considered. A prototype database of differential alternative splicing of genes is presented, "Differential Alternative Splicing of Human Genes in Secondary Glioblastoma (DASGG)", with the ability to work through a website, to search for expression levels of individual isoforms in tumor cells.

*Conclusion*: Problem of databases development for cancer studies are of great importance for personalized medicine. The results could be applied for fundamental research on glioma stem cells, search for new diagnostic markers.

*References*
1. Kovalev S.S., Lieberfarb E.Y., Gubanova N.V., Bragin A.O., Galieva A.G., Tsukanov A.V., Babenko V.N., Orlov Y.L. Computer analysis of gene alternative splicing in glioma cell cultures by RNA-seq data. *Vestnik NSU. Series: Information Technologies*. 2018;16(3):22-36. DOI 10.25205/1818-7900-2018-16-3-22-36 (in Russian).