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Transcriptomics data analysis: Gene alternative splicing events in glioma cells

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Statement of the Problem: We consider problem of detection of genes responsible for glioma progression in cell cultures by RNA-seq. Diffused gliomas are the most common type of intracranial malignant neoplasm and account for more than 60% of all primary brain tumors. We revealed set of differently expressed genes and alternative splicing events in normal brain and glioma cell cultures.

Methodology & Theoretical Orientation: The primary cell culture samples from normal brain and secondary glioblastoma were processed for RNA extraction. This was followed by RNA-sequencing and filtration of reads (Trimmomatic). For assessment of gene expression level and finding differently expressed genes we used Cufflinks. Set of computer tools were used for sequencing data processing (TopHAt, rMATS).

Conclusion & Significance: The RNA-seq analysis of the cells cultures of normal brain and glioma confirmed association of genes with tumor progression. The results provide an experimental basis for the observation that hypothyroidism induction by administration of propylthiouracil is associated with improved survival in glioblastoma patients. Hypothyroidism may improve survival in animal models of cancer and recent clinical studies of tyrosine kinase inhibitor treatment of renal cell carcinoma patients have suggested that the side effect of hypothyroidism contributes to improved outcomes. Though sequencing technologies (RNA-seq) provide new data on gene expression presented in the databases, large collection of human clinical data keep importance of microarray data analysis, especially in many tissues and organs, including brain (such as BioGPS). We continue integration of transcriptomics data in brain cells using available databases. The work on alternative splicing opens new perspectives for cancer research in glioma continuing studies.

Recent Publications

1. Abnizova I, te Boekhorst R, Orlov Y (2017) Computational Errors and Biases of Short Read Next Generation Sequencing. Journal of Proteomics & Bioinformatics; J Proteomics Bioinform; 10: 1-17.

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Biography

Yuriy L Orlov has wide expertise in bioinformatics and computer genomics. He developed computer programs for analysis of next-generation sequencing data. He is head of Computer Genomics Laboratory at Life Sciences Department, Novosibirsk State University, Russia. His area of interests include neuro-informatics, DNA sequence analysis, integration of genome annotation and expression data, statistical analysis of ChIP (Chromatin ImmunoPrecipitation) sequencing data (ChIP-seq, ChIA-PET) and Hi-C data. He is organizer of international conferences BGRS of series (Bioinformatics of Genome Regulation and Structure) and Young Scientists Schools on systems biology and bioinformatics (SBB series) in Novosibirsk since 1998.

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