Whole transcriptome RNA sequencing data from blood leukocytes derived from Parkinson's disease patients prior to and following deep brain stimulation treatment

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Abstract:

Recent evidence demonstrates the power of RNA sequencing (RNA-Seq) for identifying valuable and urgently needed blood biomarkers and advancing both early and accurate detection of neurological diseases, and in particular Parkinson's disease (PD). RNA sequencing technology enables non-biased, high throughput, probe-independent inspection of expression data and high coverage and both quantification of global transcript levels as well as the detection of expressed exons and junctions given a sufficient sequencing depth (coverage). However, the analysis of sequencing data frequently presents a bottleneck. Tools for quantification of alternative splicing from sequenced libraries hardly exist at the present time, and methods that support multiple sequencing platforms are especially lacking. Here, we describe in details a whole RNA-Seq transcriptome dataset produced from PD patient's blood leukocytes. The samples were taken prior to, and following deep brain stimulation (DBS) treatment while being on stimulation and following 1 h of complete electrical stimulation cessation and from healthy control volunteers. We describe in detail the methodology applied for analyzing the RNA-Seq data including differential expression of long noncoding RNAs (lncRNAs). We also provide details of the corresponding analysis of in-depth splice isoform data from junction and exon reads, with the use of the software AltAnalyze. Both the RNA-Seq raw (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42608) and analyzed data (https://www.synapse.org/#!Synapse:syn2805267) may be found valuable towards detection of novel blood biomarkers for PD.

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