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SR splicing, splicing-ratio based splicing detection method

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Through alternative splicing, most human genes express multiple isoforms that often differ in function. To infer isoform regulation from high-throughput sequencing of cDNA fragments (RNA-seq), a pipeline is developed to detect differential alternative splicing events between RNA-Seq samples of treatment and control conditions. It is based on a metric defined as splicing ratio (SR) which was used in some splicing related studies (SRSplicing is flexible to handle different types of study design. Either control group or treatment group can have single or replicated/pooled samples. It can analyze all major types of alternative splicing patterns and use RNA-Seq reads and use RNA-Seq reads mapped to splice junctions. By comparing with other commonly used software, the performance of SRSplicing is evaluated from three aspects: sensitivity, accuracy, and validation. SRSplicing has comparable sensitivity and higher accuracy. Experimental validation using qRT-PCR (quantitative real time polymerase chain reaction) confirmed a selected set of splicing events that are significantly changed in Pten knock out data of the mouse MEF cell line, demonstrating the utility of the approach applied on experimental biological data sets. SRSplicing used different statistics and less filtering to return a list of significantly changed splicing events, with associated p values and false discovery corrections. It includes detailed information on the detected splicing differences such as which exon/junctions are involved, alternative splice type (skipped exon, mutually exclusive exons, retained intron, alternative 5' splice site, and alternative 3' splice site), magnitude of difference, and coverage.

Recent Publications

1. Huang Tao et al. (2016) SNHG8 is identified as a key regulator of epstein-barr virus(EBV)-associated gastric cancer by an integrative analysis of IncRNA and mRNA expression. Oncotarget. 7(49):80990-81002. Doi:10.18632/Oncotarget.13167.
2. Shao Ming Shen et al. (2018) Nuclear PTEN safeguards pre-mRNA splicing to link Golgi apparatus for its tumor suppressive role. Nature Communications. 9(1):2392. Doi:10.1038/s41467-018-04760-1.

Biography

Yan Ji obtained his PhD Degree in Bioinformatics from Shanghai Institutes for Biological Science of the Chinese Academy of Sciences, P R China. Before May 2015, he worked as a Translational Researcher at the Innovation Center of China, AstraZeneca (a pharmaceutical company). Since June 2015, he has been an Assistant Professor in Shanghai Institutes for Biological Science of the Chinese Academy of Sciences, P R China and studied some tumour types which are prevalent in China by using high-throughput data analysis from different perspectives including splicing and long non-coding RNAs. He has published more than 8 papers in reputed journals. In this conference, he will present a novel method detecting splicing events which has been successfully used to discover PTEN-regulated splicing events.

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