High-throughput alternative splicing detection using dually constrained correspondence analysis (DCCA)

Florent Baty, Dirk Klingbiel, Francesco Zappa & Martin Brutsche

UNASSIGNED

Alternative splicing is an important component of tumorigenesis. Recent advent of exon array technology enables the detection of alternative splicing at a genome-wide scale. The analysis of high-throughput alternative splicing is not yet standard and methodological developments are still needed. We propose a novel statistical approach—Dually Constrained Correspondence Analysis—for the detection of splicing changes in exon array data. Using this methodology, we investigated the genome-wide alteration of alternative splicing in patients with non-small cell lung cancer treated by bevacizumab/erlotinib. Splicing candidates reveal a series of genes related to carcinogenesis (SFTPB), cell adhesion (STAB2, PCDH15, HABP2), tumor aggressiveness (ARNTL2), apoptosis, proliferation and differentiation (PDE4D, FLT3, IL1R2), cell invasion (ETV1), as well as tumor growth (OLFM4, FGF14), tumor necrosis (AFF3) or tumor suppression (TUSC3, CSMD1, RHOBTB2, SERPINB5), with indication of known alternative splicing in a majority of genes. DCCA facilitates the identification of putative biologically relevant alternative splicing events in high-throughput exon array data.

type: journal paper/review (English)
date of publishing: 19-10-2015
journal title: J Biomed Inform
ISSN electronic: 1532-0480