BITS :: Call for Abstracts 2021 - Oral communication

Type	Oral communication
Session	Algorithms for Bioinformatics
Title	MET exon 14 skipping: a case study for the detection of genetic variants in cancer driver genes by deep learning.
All Authors	Nosi V (1), Alessandri L. (1) and Calogero RA (1)

Affiliation

Department of Molecular Biotechnology and Health Sciences, University of Torino, Torino

Motivation

Disruption of alternative splicing (AS) is frequently observed in cancer and it might represent an important signature for tumor progression and therapy. Exon skipping (ES) represents one of the most frequent AS events and in non-small cell lung cancer (NSCLC) MET exon 14 skipping was shown to be targetable.

Methods

We constructed neural networks (NN/CNN) specifically designed to detect MET exon 14 skipping events using RNAseq data. Furthermore, for discovery purpose we also developed a sparsely connected autoencoder to identify uncharacterized MET isoforms.

Results

The neural networks had Met exon 14 skipping detection rate greater than 94%, when tested on a manually curated set of 690 TCGA bronchus and lung samples. When globally applied to 2605 TCGA samples, we observed that the majority of false positives was characterized by a blurry coverage of exon 14, but interesting they share a common coverage peak in the second intron and we speculate that this event could be the transcription signature of a LINE1 (Long Interspersed Nuclear Element 1)-MET (Mesenchymal Epithelial Transition receptor tyrosine kinase) fusion.
Taken together our results indicate that neural networks can be an effective tool to provide a quick classification of pathological transcription events and sparsely connected autoencoders could represent the basis for the development of an effective discovery tool.

Info	
-	
Figure	
-	
Availability	https://github.com/kendomaniac/metObservatory

Corresponding Author

Name, Surname	Raffaele , Calogero
Email	raffaele.calogero@unito.it
Submitted on	15.04.2021