DARTS: Deep Learning Augmented RNA-seq Analysis of Transcript Splicing

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SUMMARY

Researchers led by Yi Xing have developed a novel deep learning algorithm to detect alternative splicing patterns in RNA-seq data

BACKGROUND

Development of genetic sequencing tools like RNA-seq has ushered in an age of big data in genomics and transcriptomics. Collective efforts like ENCODE and the Roadmap Epigenomics Project (REP) have accelerated the accumulation of RNA-seq data and provide an unprecedented resource for uncovering transcriptional and post-transcriptional gene regulation. Currently, there are no techniques that can detect alternative splicing in lowly or moderately expressed genes. Splicing is the editing of newly made precursor mRNA (pre-mRNA) into mature mRNA, and each pre-mRNA can be alternatively spliced in different ways that allow a single pre-mRNA to code for many proteins. The ability to detect these alternative splicing patterns can expand the extracted information in the ENCODE and REP datasets and facilitate the discovery of novel biomarkers and therapeutic strategies.

INNOVATION

Researchers led by Xing Yi have developed a novel deep learning algorithm to detect alternative splicing patterns in RNA-seq data. Their innovation, called DARTS, is the only known algorithm that leverages deep learning to augment alternative splicing detection algorithms in lowly and moderately expressed genes. Previous algorithms were unable to do this. In a proof of concept, DARTS was trained on ENCODE and REP datasets and showed an increase in accuracy in detecting differential splicing patterns in low-coverage RNA-seq data. Additionally, DARTS was able to predict splicing changes in lowly expressed genes from data in a cellular model of epithelial-mesenchymal transition that conventional RNA-seq analysis was unable to detect.

APPLICATIONS

- Genomics
- Transcriptomics
- Genetic sequencing
- Biomarker discovery

ADVANTAGES

- Sensitive
- More accurate
- Scalable

PATENT STATUS

Country	Type	Number	Dated	Case
Patent Cooperation Treaty	Reference for National Filings	WO2020/150666	07/23/2020	2018-728

Patent Pending

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INVENTORS

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OTHER INFORMATION

KEYWORDS

big data, machine learning, deep learning, RNA, genomics, transcriptomics, RNA-seq, detection, prediction, bioinformatics, software

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Genomics
- **Computer**
  - Software
- **Medical**
  - Research Tools
  - Screening
  - Software
- **Research Tools**
  - Bioinformatics
  - Expression System
  - Nucleic Acids/DNA/RNA

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