대학원 인공지능학과

Artificial Intelligence Special Lecture

TITLE Alternative poly-Adenylation

- An uncharted territory in gene regulation -

When : 2021.12.08.(WED) P.M.12:00~

Where : Zoom

링크 https://zoom.us/j/97505765134?pwd=LzFVeTVYYlJVTmM2Qk9sTEYyRmtnZz09

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Speaker : Hari Krishna Yalamanchili (Professor, Baylor College of Medicine)

Abstract : Almost 70% of human genes undergo alternative polyadenylation (APA) and generate mRNA transcripts with varying lengths, typically of the 3' untranslated regions (UTR). APA plays an important role in development and cellular differentiation, and its dysregulation can cause neuropsychiatric diseases and increase cancer severity. Increasing awareness of APA's role in human health and disease has propelled the development of several 3' sequencing (3'Seq) techniques that allow for precise identification of APA sites. However, despite the recent data explosion, there are no robust computational tools that are precisely designed to analyze 3'Seq data. Analytical approaches that have been used to analyze these data predominantly use proximal to distal usage. With about 50% of human genes having more than two APA isoforms, current methods fail to capture the entirety of APA changes and do not account for non-proximal to non-distal changes. Addressing these key challenges, this study demonstrates PolyA-miner, an algorithm to accurately detect and assess differential alternative polyadenylation specifically from 3'Seq data. Genes are abstracted as APA matrices, and differential APA usage is inferred using iterative consensus non-negative matrix factorization (NMF) based clustering. PolyA-miner accounts for all non-proximal to non-distal APA switches using vector projections and reflects precise gene-level 3'UTR changes. It can also effectively identify novel APA sites that are otherwise undetected when using reference-based approaches. Evaluation on multiple datasets-first-generation MicroArray Quality Control (MAQC) brain and Universal Human Reference (UHR) PolyA-seq data, recent glioblastoma cell line NUDT21 knockdown Poly(A)-ClickSeq (PAC-seq) data, and our own mouse hippocampal and human stem cell-derived neuron PAC-seq data-strongly supports the value and protocol-independent applicability of PolyA-miner. Strikingly, in the glioblastoma cell line data, PolyA-miner identified more than twice the number of genes with APA changes than initially reported. With the emerging importance of APA in human development and disease, PolyA-miner can significantly improve data analysis and help decode the underlying APA dynamics.

BIO : Dr. Hari Krishna Yalamanchili is an assistant professor at Baylor College of Medicine.He did his bachelor's in Bioinformatics from Jaypee University of Information Technology, India in 2007 and M.S. in Bioinformatics from International Institute of Information Technology-Hyderabad, India in 2009. He received his Ph.D. in Bioinformatics and Computational Genomics from The University of Hong Kong, in 2014. His dissertation was on Computational Approaches for Protein Function and Gene Association Networks" in Dr. Junwen Wang's lab. After doctoral studies, He did his postdoctoral training primarily focusing on computational neurogenomics jointly in the laboratories of Dr. Zhandong Liu and Dr. Huda Zoghbi at the Neurological Research Institute, Baylor College of Medicine.

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