

**BIOMEDICAL DATA SCIENCE  
PRESENTS:  
BIODS 260  
11/10/22 1:30PM-2:50PM  
MSOB X303 (SEE ZOOM DETAILS BELOW)**

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## **TITLE:**

Revealing patterns of alternative splicing in single cells

## **ABSTRACT:**

Alternative splicing shapes the output of the genome and contributes to each cell's unique identity, but single-cell RNA sequencing has struggled to capture its impact. We have shown that low recovery of mRNAs from single cells can lead to misleading conclusions about alternative splicing and its regulation. To address this, we have developed a method, Psix, to confidently identify splicing that changes across a landscape of single cells, using a probabilistic model that is robust against the data limitations of scRNA-seq. Its autocorrelation-inspired approach finds patterns of alternative splicing that correspond to patterns of cell identity, such as cell type or developmental stage, without the need for explicit cell clustering, labeling, or trajectory inference. Psix reveals cell type-dependent splicing patterns and the wiring of the splicing regulatory networks that control them, enabling scRNA-seq analysis to go beyond transcription to understand the roles of post-transcriptional regulation in determining cell identity.

## **SUGGESTED READINGS:**

CF Buen Abad Najar, N Yosef, LF Lareau. Coverage-dependent bias creates the appearance of binary splicing in single cells. eLife, 2020.

<https://elifesciences.org/articles/54603>

CF Buen Abad Najar, P Burra, N Yosef, LF Lareau. Identifying cell state-associated alternative splicing events and their coregulation. Genome Research, 2022

<https://genome.cshlp.org/content/32/7/1385.short>

Zoom link:

<https://stanford.zoom.us/j/92874055477pwd=aThzNmpmNEQ1L2FjV0E5ZXF5SDR1UT09&from=addon>

Password: 705300