

Homework due Thursday 6pm

-> you are welcome to turn it in early

Friday -> Quiz (midterm)

open note

open Google

learned general data visualization analysis approaches

- normalization

- dimensionality reduction

- clustering

- differential testing

-> rest of the class -> applications to different single cell and spatial omics technologies/data

-> examples of application

- reflection cards: if you have any questions that you'd like us to review together prior to the quiz

-> an hour

Today: RNA velocity

-> slides

Limitations :



Imaging:

- how well are we able to figure out what is cytoplasm vs nucleus
- targeted, what happens if I just don't happen to profile dynamic genes
- assumed all RNAs moving from nucleus to cytoplasm
 - > if we had other biological processes that lead to nuclear retention
 - > trafficking back into nucleus

Sequencing:

- how well are we able to distinguish unspliced vs. spliced
 - > maybe there are introns that are not annotated, working with organism where annotations aren't very good
- to get a robust quantification of intronic reads, we would long (full transcript coverage ideal)
 - assuming RNAs are moving from unspliced to spliced
 - > intronic retention

Both:

- assuming constant rates (might not be true)
- > different populations of cells may have different rates

- what happens if we apply RNA velocity to noise?