# To do list

07 October, 2021

## To do

- Learn about `spatialExperiment`
  - Go through this textbook
  - Chapter 1
  - Chapter 2
  - Chapter 3
  - Chapter 4
  - Chapter 5
  - Chapter 6
  - Chapter 7
  - Chapter 8
  - Read bioarxiv paper
  - Check out workshops from last bioconductor conference here, here
- Make Vectra compatible with `spatialExperiment`
  - Check out `read10xVisium()` function, which creates a SpatialExperiment object from the raw input files expected from the 10x Genomics processing software (link)
  - Write function for tabular data
  - Determine slot/structure for adding clinical data
  - Write function for image data
    - Each pixel is a row?
    - If segmentation is defined, write function for extracting cells and putting into table format
- Explore `ExperimentData` packages on Bioconductor
  - Check out ST example data
  - Check out JP's
  - Check out Sean Davis's
  - Check out Stephanie's Visium package
  - Think about which dataset you would want to turn into a package
  - Go through guidelines on how to create ExperimentHub package
- Put Simon's mIF data in `data` folder
  - Do brief exploratory analysis
  - Add this data to datasets document
  - Work towards making this compatible with Spatial Experiment
- Spatial proteomics
  - Look for existing packages
  - http://bioconductor.org/packages/release/bioc/html/pRoloc.html

## Recently completed

## Ongoing questions

- Types of Bioconductor packages include: analysis software packages, annotation packages, data packages, workflow packages, online books
  - What are each of these?
  - Is `spatialExperiment` a workflow package?
- When creating a data package, would it be best to have data from one platform (just Vectra) or from multiple platforms?
- What software do you use to make the pretty figures?

## About spatial transcriptomics

- What is a molecule?
- From a data structure perspective, what are the differences between spatial transcriptomics and multiplex single cell imaging?
  - ST doesn't have single cell masks, right?
  - ST is wayyy more multiplex in the sense that there are hundreds if not thousands of genes
  - ST has counts and MI has continuous marker intensities
    - Are there "intensities" at all for ST?