

# To do list

07 October, 2021

## To do

- Learn about `spatialExperiment`
  - Go through this textbook
  - 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

- Learn about `spatialExperiment`
  - Go through this textbook

- Chapter 1
- Chapter 2
- Chapter 3

## 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?
- Why is `spatialCoords` its own slot rather than being a `colData` variable? is this because it was built on top of `singleCellExperiment`? Does having its own slot add functionality?
- Did you (Lukas) right the whole spatial transcriptomics book yourself?
  - Including the preprocessing steps section?

## About spatial transcriptomics

- What is a molecule?
- How many genes are there typically in an ST experiment?
- 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?