To do list

12 October, 2021

To do

- Learn about `spatialExperiment`
  - Go through this textbook
  - 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
- Data
  - TNBC MIBI data
  - 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
- CRAN task view on single cell imaging data
  - http://bioconductor.org/packages/release/bioc/html/pRoloc.html
  - https://cran.r-project.org/web/packages/spatialTIME/index.html

Recently completed

- Learn about `spatialExperiment`
  - Go through this textbook
  - Chapter 1

  - Chapter 2
  - Chapter 3
  - Chapter 4
  - Chapter 5
  - Chapter 6

Ideas

- `MultiplexUtils` package to store the multiplex conversion functions?
- Call multiplex data package MIexampleData

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?
  - Contains Visium and seqFISH data
- 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?
- What is the purpose of the `DropletUtils` package? What is Droplet data?

About spatial transcriptomics

- Can `VistoSeg` be used to count/summarize the pixels in a cell?
- 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?

About read10xVisium.R

- Is it ok for the image data argument to be empty?
- Does it all the types of files at once?
  - Can you explain the expected file structure a little bit?

Angie questions

- What is the file structure for typical Vectra data after Inform processing?
- How challenging is it to get the .tiff images?
- How are file names / ids set up for the Vectra instrument?
- What image preprocessing occurs before Inform?
- Data dictionary somewhere?
  - What is the "Confidence" column for Vectra data?
  - What are the TMA Sector/Row/Column/Field variables?
  - Are column names consistent for each analysis?