TODO

Format with bioconductor vignette requirements.

SpatialUtils

R package with convenience functions for molecule-based spatial transcriptomics data analysis (xenium by 10x, cosmx SMI by nanostring, and merscope by vizgen). Introduces a new class to store ST data: MoleculeExperiment class.

Why the MoleculeExperiment class?

1) Enable easy analysis of spatial transcriptomics data at the molecule level, rather than the cell level.
2) Standardisation of molecule-based ST data across vendors, to hopefully facilitate comparison of different data sources.

The ME object

Constructing an ME object

- instructions on how to use readMolecules() correctly
- highlight benefits of how readMolecules() works e.g., readMolecules enables the user to decide if they want to keep all the data that is vendor-specific (e.g., qv in xenium).

ME object structure

- what are the slots? for now @molecules

- what information does each slot contain? highlight how this enables standardisation of ST data across different vendors.

- what is the format in which the information is stored? for now the list format

- why is information stored like this? performance reasons? (e.g., enabling minimal copying and thus less memory intensive?)

Methods to work with an ME object

- Briefly introduce all methods that can be used to access and manipulate data in the @molecules slot.
- Then explain each method in detail, and compare their performance when used on the ME implementation (list) or the naive implementation (df) of the data. Show microbenchmarking results in R code chunks
    - summarisation functions
    - getters (data reading)
    - setters (data manipulation)
    - plotting functions