## Package 'SpatialDatasets'

November 7, 2024

Version 1.4.0

Title Collection of spatial omics datasets

Description This is a collection of publically available spatial omics datasets.  Where possible we have curated these datasets as either SpatialExperiments,  MoleculeExperiments or CytoImageLists and included annotations of the sample characteristics.
<pre>URL https://github.com/SydneyBioX/SpatialDatasets</pre>
BugReports https://github.com/SydneyBioX/SpatialDatasets/issues
License GPL-3
Encoding UTF-8
biocViews ExperimentData, ExperimentHub, ReproducibleResearch, SingleCellData, SpatialData, Homo_sapiens_Data, Mus_musculus_Data
Depends ExperimentHub, SpatialExperiment,
Imports utils
VignetteBuilder knitr
Suggests BiocStyle, knitr, rmarkdown
RoxygenNote 7.3.2
git_url https://git.bioconductor.org/packages/SpatialDatasets
git_branch RELEASE_3_20
git_last_commit 25277b8
git_last_commit_date 2024-10-29
Repository Bioconductor 3.20
Date/Publication 2024-11-07
Author Farhan Ameen [aut], Nick Robertson [aut], Alex Qin [aut], Elijah Willie [aut], Ellis Patrick [aut, cre]
Maintainer Ellis Patrick <ellis.patrick@sydney.edu.au></ellis.patrick@sydney.edu.au>
Contents
SpatialDatasets

2 SpatialDatasets

Index 3

SpatialDatasets

A collection of publically available spatial omics datasets.

## **Description**

This is a collection of publically available spatial omics datasets. Where possible we have curated these datasets as either SpatialExperiments, MoleculeExperiments or CytoImageLists and included annotations of the sample characteristics.

## **Details**

The SpatialDatasets package contains a collection of spatially-resolved omics datasets for use in examples, demonstrations, and tutorials.

The datasets are from several different platforms including IMC, MIBI-TOF, CODEX, Xenium, CosMx and MERFISH. They have been sourced from various publicly available sources.

Additional examples and documentation are provided in the package vignette.

Datasets

The SpatialDatasets package contains the following datasets:

- spe\_Keren\_2018 (MIBI-TOF): A study on triple negative breast cancer containing 40 samples measured using MIBI-TOF published by [Keren et al. (2018)](https://doi.org/10.1016/j.cell.2018.08.039).
- Ferguson\_Images (IMC): A study on head and neck cutaneous squamous cell carcinoma containing 44 samples measured using IMC published by [Ferguson et al. (2022)](https://doi.org/10.1158/1078-0432.CCR-22-1332).
- spe\_Ferguson\_2022 (IMC): A study on head and neck cutaneous squamous cell carcinoma containing 44 samples measured using IMC published by [Ferguson et al. (2022)](https://doi.org/10.1158/1078-0432.CCR-22-1332).
- spe\_Schurch\_2020 (CODEX): A study on advanced colorectal cancer containing 140 samples measured using CODEX published by [Schurch et al. (2020)](https://doi.org/10.1016/j.cell.2020.07.005).
- spe\_Ali\_2020 (IMC): A study on breast cancer containing 483 samples measured using IMC published by [Ali et al. (2020)](https://doi.org/10.1038/s43018-020-0026-6).

The datasets will be a SpatialExperiment or MoleculeExperiment.

# load using dataset name spe <- spe\_Keren\_2018() spe

## **Index**

```
Ferguson_Images (SpatialDatasets), 2
SpatialDatasets, 2
spe_Ali_2020 (SpatialDatasets), 2
spe_Ferguson_2022 (SpatialDatasets), 2
spe_Keren_2018 (SpatialDatasets), 2
spe_Schurch_2020 (SpatialDatasets), 2
```