Package: OSTA.data (via r-universe)

March 12, 2025

Title OSTA book data

Depends R (>= 4.4)

Version 0.99.2

Description 'OSTA.data' is a companion package for the ``Orchestrating Spatial Transcriptomics Analysis'' (OSTA) with Bioconductor online book. Throughout OSTA, we rely on a set of publicly available datasets that cover different sequencing- and imaging-based platforms, such as Visium, Visium HD, Xenium (10x Genomics) and CosMx (NanoString). In addition, we rely on scRNA-seq (Chromium) data for tasks, e.g., spot deconvolution and label transfer (i.e., supervised clustering). These data been deposited in an Open Storage Framework (OSF) repository, and can be queried and downloaded using functions from the 'osfr' package. For convenience, we have implemented 'OSTA.data' to query and retrieve data from our OSF node, and cache retrieved Zip archives using 'BiocFileCache'.

Imports osfr, utils, BiocFileCache

Suggests BiocStyle, DropletUtils, knitr, VisiumIO, SpatialExperimentIO

biocViews DataImport, DataRepresentation, ExperimentHubSoftware, Infrastructure, ImmunoOncology, GeneExpression, Transcriptomics, SingleCell, Spatial

Encoding UTF-8

RoxygenNote 7.3.2

License Artistic-2.0

VignetteBuilder knitr

URL `https://github.com/estellad/OSTA.data`

BugReports `https://github.com/estellad/OSTA.data`

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/OSTA.data

RemoteRef HEAD

RemoteSha d82e4e6eba6070d3804115f0622205617901a45c

Contents

`OSTA.data` *Datasets used in OSTA*

Description

Datasets used in OSTA

Usage

```
OSTA.data_list(url = "https://osf.io/5n4q3")

OSTA.data_load(
  id,
  bfc = BiocFileCache(),
  url = "https://osf.io/5n4q3",
  pol = TRUE,
  mol = TRUE
)
```

Arguments

`url`	character string; an OSF identifier (passed to `osf_retrieve_node`)
`id`	character string; dataset identifier (see `OSTA.data_list` for valid options)
`bfc`	`BiocFileCache` instance giving the location of files stored on disk
`pol, mol`	logical scalar; specifies whether or not to retrieve boundaries and molecules, respectively

Details

The following datasets are currently available:

- Janesick *et al.*: Visium, Visium HD, Xenium and Chromium data on human colorectal cancer; source: 10x Genomics
- Oliveira *et al.*: Visium, Xenium and Chromium data on human breast cancer; source: GSE243280
- 1k-plex CosMx data on 2 mouse brain sections (coronal hippocampus and cortex, coronal hemisphere) source: NanoString
- 6k-plex CosMx data on human brain (frontal cortex); source: NanoString

Value

- `OSTA.data_list` returns a character vector of currently available datasets
- `OSTA.data_load` return a character string; the path to a Zip archive

References

Oliveira *et al.* Characterization of immune cell populations in the tumor microenvironment of colorectal cancer using high definition spatial profiling. *bioRxiv* 2024.06.04.597233 (2024).

Janesick *et al.* High resolution mapping of the tumor microenvironment using integrated single-cell, spatial and in situ analysis. *Nature Communications* 14:8353 (2023).

Examples

```
# view available datasets
OSTA.data_list()

# retrieve 10x Xenium data from Oliveira et al.
id <- "Xenium_HumanColon_Oliveira"
pa <- OSTA.data_load(id)

# unpack & view contents
td <- tempfile()
dir.create(td)
unzip(pa, exdir=td)
list.files(td)

# read into 'SpatialExperiment'
library(SpatialExperimentIO)
(spe <- readXeniumSXE(td))
```

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