Package 'XeniumIO'

February 28, 2026

Type Package

Title Import and represent Xenium data from the 10X Xenium Analyzer

Version 1.2.0

Description The package allows users to readily import spatial data
obtained from the 10X Xenium Analyzer pipeline. Supported formats include
'parquet', 'h5', and 'mtx' files. The package mainly represents data
as SpatialExperiment objects.

License Artistic-2.0

Depends TENxIO, R (>= 4.5.0)

Imports BiocBaseUtils, BiocGenerics, BiocIO, jsonlite, methods,
S4Vectors, SingleCellExperiment, SpatialExperiment,
SummarizedExperiment, VisiumIO

Suggests arrow, BiocFileCache, BiocStyle, knitr, rmarkdown, tinytest

biocViews Software, Infrastructure, DataImport, SingleCell, Spatial

VignetteBuilder knitr

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

BugReports https://github.com/waldronlab/XeniumIO/issues

URL https://github.com/waldronlab/XeniumIO

Collate 'XeniumFile.R' 'TENxXenium-class.R' 'XeniumIO-package.R'
'utilities.R'

Date 2025-04-04

git_url https://git.bioconductor.org/packages/XeniumIO

git_branch RELEASE_3_22

git_last_commit 727bab9

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-27

Author Marcel Ramos [aut, cre] (ORCID:
<https://orcid.org/0000-0002-3242-0582>),
Dario Righelli [ctb],
Estella Dong [ctb]

Maintainer Marcel Ramos <marcel.ramos@sph.cuny.edu>

Contents

XeniumIO-package   *XeniumIO: Import and represent Xenium data from the 10X Xenium Analyzer*

Description

The package allows users to readily import spatial data obtained from the 10X Xenium Analyzer pipeline. Supported formats include 'parquet', 'h5', and 'mtx' files. The package mainly represents data as SpatialExperiment objects.

Author(s)

Maintainer: Marcel Ramos <marcel.ramos@sph.cuny.edu> (ORCID)

Other contributors:

- Dario Righelli [contributor]

- Estella Dong [contributor]

See Also

Useful links:

- https://github.com/waldronlab/XeniumIO

- Report bugs at https://github.com/waldronlab/XeniumIO/issues

---

TENxXenium-class   *A class to represent Xenium output data*

Description

This class is a composed class of TENxFileList which can contain a list of TENxFile objects for the cell-feature matrix. It is meant to handle a single Xenium sample from 10X Genomics.

Usage

```
TENxXenium(
  resources,
  xeniumOut,
  sample_id = "sample01",
  format = c("mtx", "h5"),
  boundaries_format = c("parquet", "csv.gz"),
  spatialCoordsNames = c("x_centroid", "y_centroid"),
  ...
)

## S4 method for signature 'TENxXenium,ANY,ANY'
import(con, format, text, ...)
```

Arguments

resources	A [TENxFileList](#) object or a file path to the tarball containing the matrix / assay data resources.
xeniumOut	character(1) The path to the Xenium output directory.
sample_id	character(1) A single string specifying the sample ID.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of [BiocFile](#).
boundaries_format	
	character(1) Either "parquet" or "csv.gz" to specify the file extension of the boundaries file. Default is "parquet".
spatialCoordsNames	
	character() A vector of strings specifying the names of the columns in the spatial data containing the spatial coordinates.
...	In the constructor, additional arguments passed to [TENxFileList](#); otherwise, not used.
con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a [BiocFile](#) derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
text	If con is missing, this can be a character vector directly providing the string data to import.

Details

Note that one can provide a ref argument to import method which will get passed to the internal splitAltExps operation. This allows one to set a mainExpName in the output object.

Value

A [SpatialExperiment](#) object

Functions

- import(con = TENxXenium, format = ANY, text = ANY): Import Xenium Analyzer data

Slots

resources A [TENxFileList](#) or [TENxH5](#) object containing the cell feature matrix.

boundaries Either a [TENxSpatialParquet](#) or [TENxSpatialCSV](#) object containing the spatial boundaries data.

coordNames character() A vector specifying the names of the columns in the spatial data containing the spatial coordinates.

sampleId character(1) A scalar specifying the sample identifier.

colData TENxSpatialParquet A [TENxSpatialParquet](#) object containing the spatial coordinates data.

metadata XeniumFile A [XeniumFile](#) object containing the metadata information.

See Also

https://www.10xgenomics.com/support/software/xenium-onboard-analysis/latest/analysis/xoa-output-understanding-outputs

Examples

```
showClass("TENxXenium")

zipfile <- paste0(
    "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenDemo/",
    "Xenium_Prime_MultiCellSeg_Mouse_Ileum_tiny_outs.zip"
)
destfile <- XeniumIO:::.cache_url_file(zipfile)
outfold <- file.path(
    tempdir(), tools::file_path_sans_ext(basename(zipfile))
)
if (!dir.exists(outfold))
    dir.create(outfold, recursive = TRUE)
unzip(
    zipfile = destfile, exdir = outfold, overwrite = FALSE
)
TENxXenium(xeniumOut = outfold) |>
    import(ref = "Gene Expression")
```

XeniumFile-class   *A minimal class to represent Xenium metadata*

Description

This class is a minimal class to represent Xenium metadata. It is dedicated to importing experiment.xenium metadata files. It uses the jsonlite package to import the metadata.

Usage

```
XeniumFile(resource)

## S4 method for signature 'XeniumFile,ANY,ANY'
import(con, format, text, ...)
```

Arguments

resource	character(1) The path to the Xenium metadata file.
con	The connection from which data is loaded or to which data is saved. If this is a character vector, it is assumed to be a file name and a corresponding file connection is created and then closed after exporting the object. If it is a [BiocFile](#) derivative, the data is loaded from or saved to the underlying resource. If missing, the function will return the output as a character vector, rather than writing to a connection.
format	The format of the output. If missing and con is a file name, the format is derived from the file extension. This argument is unnecessary when con is a derivative of [BiocFile](#).
text	If con is missing, this can be a character vector directly providing the string data to import.
...	Parameters to pass to the format-specific method.

Value

A [XeniumFile](#) object

Functions

- import(con = XeniumFile, format = ANY, text = ANY): Import Xenium metadata

Examples

```
showClass("XeniumFile")
```

Index