Package 'xenLite'

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Title Simple classes and methods for managing Xenium datasets

Version 1.7.0

Description Define a relatively light class for managing Xenium data using Bioconductor. Address use of parquet for coordinates, SpatialExperiment for assay and sample data. Address serialization and use of cloud storage.

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Encoding UTF-8

Depends R (>= 4.1)

Suggests knitr, testthat, BiocStyle, yesno, terra, SpatialFeatureExperiment, SFEData, tiff

Imports SpatialExperiment, BiocFileCache, Matrix, S4Vectors, SummarizedExperiment, methods, utils, EBImage, shiny, HDF5Array, arrow, ggplot2, SingleCellExperiment, TENxIO, dplyr, graphics, stats

VignetteBuilder knitr

biocViews Infrastructure

RoxygenNote 7.3.2

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BugReports https://github.com/vjcitn/xenLite/issues

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`cacheMtif` *cache and/or retrieve path to an ome.tif file for demonstration*

Description

cache and/or retrieve path to an ome.tif file for demonstration

Usage

```
cacheMtif(
  cache = BiocFileCache::BiocFileCache(),
  url =
   "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenData/morphology_focus_0001.ome.tif"
)
```

Arguments

cache	defaults to BiocFileCache::BiocFileCache()
url	location where tiff file can be retrieved

Value

path to cached resource

Note

The tiff file was retrieved after running SFEData::XeniumOutput("v2"), and depicts a pancreas tissue sample.

Examples

```
pa <- cacheMtif()
if (!requireNamespace("tiff")) stop("install tiff package to run this example")
x <- tiff::readTIFF(pa)
plot(0, xlim = c(0, 1000), ylim = c(0, 1000), xlab = " ", ylab = " ")
rasterImage(x * 5.5, 0, 0, 1000, 1000)
```

---

cacheSfeLungNtx *cache and/or retrieve path to an SFE of V1 lung demo data from 10x*

Description

cache and/or retrieve path to an SFE of V1 lung demo data from 10x

Usage

```
cacheSfeLungNtx(
  cache = BiocFileCache::BiocFileCache(),
  url = "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenData/sfeLung.zip"
)
```

Arguments

cache	defaults to BiocFileCache::BiocFileCache()
url	location where zip file can be retrieved

Value

path to cached resource

Note

Lacks transcript coordinates

cacheXenLuad *cache and/or retrieve path to Xenium Lung Adenocarcinoma example data, zipped SPEP accompanied by parquet*

Description

cache and/or retrieve path to Xenium Lung Adenocarcinoma example data, zipped SPEP accompanied by parquet

Usage

```
cacheXenLuad(
  cache = BiocFileCache::BiocFileCache(),
 url = "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenData/luad_lite.zip"
)
```

Arguments

cache	defaults to BiocFileCache::BiocFileCache()
url	location where zip file can be retrieved

Value

path to cached resource

Examples

```
if (interactive()) {
  pa <- cacheXenLuad()
  luad <- restoreZipXenSPEP(pa)
  print(luad)
  print(slot(luad, "cellbounds_path"))
  viewSeg(luad, xlim = c(4000, 4500), ylim = c(2000, 2500))
}
```

cacheXenPdmelLite *counts-in-memory version of melanoma 5k dataset*

Description

counts-in-memory version of melanoma 5k dataset

Usage

```
cacheXenPdmelLite(
  cache = BiocFileCache::BiocFileCache(),
 url = "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenData/pdmel_lite.zip"
)
```

Arguments

cache	defaults to BiocFileCache::BiocFileCache()
url	location where zip file can be retrieved

Value

path to cached resource

Examples

```
if (interactive()) {
  pa <- cacheXenPdmelLite()
  pdmel_lite <- restoreZipXenSPEP(pa)
  print(pdmel_lite)
}
```

---

cacheXenProstLite *counts-in-memory version of prostate 5k dataset*

Description

counts-in-memory version of prostate 5k dataset

Usage

```
cacheXenProstLite(
  cache = BiocFileCache::BiocFileCache(),
  url = "https://mghp.osn.xsede.org/bir190004-bucket01/BiocXenData/prost_lite.zip"
)
```

Arguments

cache	defaults to BiocFileCache::BiocFileCache()
url	location where zip file can be retrieved

Value

path to cached resource

Examples

```
if (interactive()) {
  pa <- cacheXenProstLite()
  prost_lite <- restoreZipXenSPEP(pa)
  print(prost_lite)
}
```

clipRect *restrict XenSPEP to cells with centroids in specified rectangle, also restrict boundary and transcript location features*

Description

restrict XenSPEP to cells with centroids in specified rectangle, also restrict boundary and transcript location features

Usage

```
clipRect(xsce, xlim, ylim)
```

Arguments

xsce	XenSPEP instance
xlim	numeric(2)
ylim	numeric(2)

Value

XenSPEP instance

Note

Could be too RAM-hungry.

Examples

```
args(clipRect)
```

demoapp *simple app to explore an image*

Description

simple app to explore an image

Usage

```
demoapp(simple = FALSE)
```

Arguments

simple	logical(1) if TRUE, use a cached tiff for illustration

Value

No value returned, run for side effect of app initiation.

Note

Navigate file input control to location of tiffs

Examples

```
if (interactive()) demoapp(simple = TRUE)
```

`e2sym` *helper function to map ENS ids to symbols*

Description

helper function to map ENS ids to symbols

Usage

```
e2sym(x)
```

Arguments

`x`	character() mix of Ensembl Ids and other strings; the latter are left unchanged

Value

a vector like x with gene symbols from v79 mapping substituted where possible

Examples

```
e2sym(c("ABC", "ENSG00000213088", "ENSG00000107796", "ENSG00000163017"))
```

`e79sym` *mapping from ENSG to symbols based on EnsDb.Hsapiens.v79*

Description

mapping from ENSG to symbols based on EnsDb.Hsapiens.v79

Usage

```
e79sym
```

Format

character()

Value

character vector

Note

named character vector with values gene symbols, name ENSG ids

Examples

```
data(e79sym)
head(e79sym)
```

`getCellBoundaries` *method for cell boundary extraction*

Description

method for cell boundary extraction

Usage

```
getCellBoundaries(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

Examples

```
showMethods("getCellBoundaries")
```

`getCellBoundaries,XenSPEP-method`
method for cell boundary extraction

Description

method for cell boundary extraction

Usage

```
## S4 method for signature 'XenSPEP'
getCellBoundaries(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

getNucleusBoundaries *method for nucleus boundary extraction*

Description

method for nucleus boundary extraction

Usage

```
getNucleusBoundaries(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

Examples

```
showMethods("getNucleusBoundaries")
```

getNucleusBoundaries,XenSPEP-method *method for nucleus boundary extraction*

Description

method for nucleus boundary extraction

Usage

```
## S4 method for signature 'XenSPEP'
getNucleusBoundaries(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

getTranscripts *method for transcript extraction*

Description

method for transcript extraction

Usage

```
getTranscripts(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

Examples

```
showMethods("getTranscripts")
```

getTranscripts,XenSPEP-method *method for transcript extraction*

Description

method for transcript extraction

Usage

```
## S4 method for signature 'XenSPEP'
getTranscripts(x)
```

Arguments

x	instance of XenSPEP

Value

reference to ingested parquet

Examples

```
showMethods("getTranscripts")
```

ggprepSeg *prepare a XenSPEP for ggplot2 visualization*

Description

prepare a XenSPEP for ggplot2 visualization

Usage

```
ggprepSeg(xsce, xlim = c(5800, 6200), ylim = c(6300, 6700))
```

Arguments

xsce	XenSPEP instance
xlim	numeric(2)
ylim	numeric(2)

Value

a list with components 'bounds' (data.frame including relevant colData rows (all colData variables) and cell boundary coordinates) and 'txdata', a filtered arrow Table.

Note

This is idiosyncratic. Quintiles of cell_area (values in 'sizq') are produced, and transcript locations are filtered. A more general approach that allows selection of coloring of cells by feature characteristics is needed.

Examples

```
pa <- cacheXenLuad()
luad <- restoreZipXenSPEP(pa)
hh <- ggprepSeg(luad, c(4000, 4500), c(2000, 2500))
ggplot2::ggplot(hh$bounds, ggplot2::aes(
  x = vertex_x, y = vertex_y, group = cell_id,
  colour = sizq, fill = sizq
)) +
  ggplot2::geom_polygon(alpha = .5)
```

ingest_xen *produce a pre-loaded XenSPEP (SpatialExperiment with parquet references)*

Description

produce a pre-loaded XenSPEP (SpatialExperiment with parquet references)

Usage

```
ingest_xen(folder)
```

Arguments

folder	character(1) 'standard' Xenium output folder

Value

instance of XenSPEP

Examples

```
chkns <- function(pkstring) {
  if (!requireNamespace(pkstring)) {
    message(sprintf("install %s to use this feature; returning NULL", pkstring))
    return(NULL)
  }
}
chkns("SFEData")
chkns("HDF5Array")
chkns("SingleCellExperiment")
if (requireNamespace("SFEData")) {
  td <- tempdir()
  z <- SFEData::XeniumOutput("v2", td)
  ii <- ingest_xen(file.path(td, "xenium2"))
  print(validObject(ii))
  plot(SpatialExperiment::spatialCoords(ii), pch = ".")
}
```

---

loadGeometry *read and bind parquet data to XenSPEP*

Description

read and bind parquet data to XenSPEP

Usage

```
loadGeometry(x)
```

Arguments

x	instance of XenSPEP

Value

instance of XenSPEP

loadGeometry,XenSPEP-method *read and bind parquet data to XenSPEP*

Description

read and bind parquet data to XenSPEP

Usage

```
## S4 method for signature 'XenSPEP'
loadGeometry(x)
```

Arguments

x	instance of XenSPEP

Value

instance of XenSPEP

plotXenGgprep *plot method for ggplot2-prepared XenSPEP*

Description

plot method for ggplot2-prepared XenSPEP

Usage

```
plotXenGgprep(x, y, ...)
```

Arguments

x	instance of S3 class ‘xen_ggprep‘
y	not used
...	not used

Value

ggplot

Note

roxygen had problems with this

Examples

```
pa <- cacheXenLuad()
luad <- restoreZipXenSPEP(pa)
hh <- ggprepSeg(luad, c(4000, 4500), c(2000, 2500))
plotXenGgprep(hh)
```

printXenGgprep *print method for ggplot2-prepared XenSPEP*

Description

print method for ggplot2-prepared XenSPEP

Usage

```
printXenGgprep(x, ...)
```

Arguments

x	instance of S3 class ‘xen_ggprep‘
...	not used

Value

operates with cat()

resetParqPaths *utility for dealing with cached Xen_SPEP in temp folder*

Description

utility for dealing with cached Xen_SPEP in temp folder

Usage

```
resetParqPaths(xsp, base)
```

Arguments

xsp	instance of XenSPEP
base	folder path where parquet files are found

Value

XenSPEP instance

Note

Will prepend current folder path to parquet-oriented slot values.

restoreZipXenSPEP *use unzip, readRDS, and loadGeometry to restore a XenSPEP*

Description

use unzip, readRDS, and loadGeometry to restore a XenSPEP

Usage

```
restoreZipXenSPEP(zipf, exdir = tempdir())
```

Arguments

zipf	character(1) path to zip file created with 'zipXenSPEP'
exdir	character(1) defaults to tempdir(), where contents are unpacked

Value

instance of XenSPEP

Note

Session folder position will change with setwd(), on.exit ensures return to position when started.

Examples

```
# used implicitly
if (interactive()) {
  example(cacheXenLuad)
}
```

show,XenSPEP-method *display aspects of XenSPEP*

Description

display aspects of XenSPEP

Usage

```
## S4 method for signature 'XenSPEP'
show(object)
```

Arguments

object	instance of XenSPEP

Value

operates with cat()

viewSeg *naive polygon viewer*

Description

naive polygon viewer

Usage

```
viewSeg(x, xlim, ylim, show_tx = FALSE, ...)
```

Arguments

x	instance of XenSPEP
xlim	numeric(2) ordered vector of max and min on x
ylim	numeric(2) ordered vector of max and min on y
show_tx	logical(1) display transcript locations if TRUE, defaults to FALSE.
...	passed to polygon()

Value

run for side effect of plotting

Note

This is more RAM-sparing than clipRect followed by view.

Examples

```
luad <- cacheXenLuad()
pa <- cacheXenLuad()
luad <- restoreZipXenSPEP(pa)
rownames(luad) <- make.names(SummarizedExperiment:::rowData(luad)$Symbol, unique = TRUE)
out <- viewSeg(luad, c(5800, 6300), c(1300, 1800), lwd = .5)
out$ncells
```

viewSegG2 *naive polygon viewer, will indicate presence of transcripts for two genes in cells*

Description

naive polygon viewer, will indicate presence of transcripts for two genes in cells

Usage

```
viewSegG2(x, xlim, ylim, gene1, gene2, show_tx = FALSE, ...)
```

Arguments

x	instance of XenSPEP
xlim	numeric(2) ordered vector of max and min on x
ylim	numeric(2) ordered vector of max and min on y
gene1	character(1) gene to be checked, cell polygon will be filled if gene has non-zero count
gene2	character(1) gene to be checked, cell polygon will be filled if gene has non-zero count
show_tx	logical(1) display transcript locations if TRUE, defaults to FALSE.
...	passed to polygon()

Value

Primarily for plotting. A list is invisibly returned with elements polys, ncells and call.

Note

This is more RAM-sparing than clipRect followed by view. Colors are pre-assigned for individual and joint occupancies in this draft of this visualizer.

Examples

```
luad <- cacheXenLuad()
pa <- cacheXenLuad()
luad <- restoreZipXenSPEP(pa)
rownames(luad) <- make.names(SummarizedExperiment:::rowData(luad)$Symbol, unique = TRUE)
out <- viewSegG2(luad, c(5800, 6300), c(1300, 1800), lwd = .5, gene1 = "CD4", gene2 = "EPCAM")
legend(5800, 1370, fill = c("purple", "cyan", "pink"), legend = c("CD4", "EPCAM", "both"))
out$ncells
```

XenSPEP *XenSPEP (SpatialExperiment with parquet references) constructor*

Description

XenSPEP (SpatialExperiment with parquet references) constructor

Usage

```
XenSPEP(folder)
```

Arguments

folder	character(1) 'standard' Xenium output folder

Value

instance of XenSPEP

Examples

```
# is not used yet
args(XenSPEP)
```

XenSPEP-class *manage SpatialExperiment with parquet references*

Description

manage SpatialExperiment with parquet references

zipXenSPEP *serialize the collection of XenSPEP and parquet with zip*

Description

serialize the collection of XenSPEP and parquet with zip

Usage

```
zipXenSPEP(xsp, targetfile)
```

Arguments

xsp	instance of XenSPEP with geometry loaded
targetfile	character(1) destination of zip process

Value

output of zip()

Note

a .rds and three parquet files are zipped together for restoration by ‘restoreZipXenSPEP‘. The outcome is ‘paste0(targetfile, ".zip")‘.

Examples

```
zipXenSPEP
```

`[,XenSPEP,ANY,ANY,ANY-method` *formal bracket definition, that leaves parquet geometry information alone.*

Description

formal bracket definition, that leaves parquet geometry information alone.

Usage

```
## S4 method for signature 'XenSPEP,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

Arguments

`x`	instance of XenSPEP
`i`	feature selection
`j`	cell selection
`...`	passed to SpatialExperiment methods
`drop`	logical(1)

Value

XenSPEP instance

Note

Gives a message and calls callNextMethod.

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