

# Package ‘xenLite’

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**Title** Simple classes and methods for managing Xenium datasets

**Version** 1.1.0

**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.

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.1)

**Suggests** knitr, testthat, BiocStyle, yesno, terra,  
SpatialFeatureExperiment, SFEDData, 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

**URL** <https://github.com/vjcitn/xenLite>

**BugReports** <https://github.com/vjcitn/xenLite/issues>

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## Contents

cacheMtif . . . . .	2
cacheSfeLungNtx . . . . .	3
cacheXenLuad . . . . .	4
cacheXenPdmelLite . . . . .	4
cacheXenProstLite . . . . .	5
clipRect . . . . .	6
demoapp . . . . .	6
e2sym . . . . .	7
e79sym . . . . .	8
getCellBoundaries . . . . .	8
getCellBoundaries,XenSPEP-method . . . . .	9
getNucleusBoundaries . . . . .	9
getNucleusBoundaries,XenSPEP-method . . . . .	10
getTranscripts . . . . .	10
getTranscripts,XenSPEP-method . . . . .	11
ggprepSeg . . . . .	11
ingest_xen . . . . .	12
loadGeometry . . . . .	13
loadGeometry,XenSPEP-method . . . . .	13
plotXenGgprep . . . . .	14
printXenGgprep . . . . .	14
resetParqPaths . . . . .	15
restoreZipXenSPEP . . . . .	15
show,XenSPEP-method . . . . .	16
viewSeg . . . . .	16
viewSegG2 . . . . .	17
XenSPEP . . . . .	18
XenSPEP-class . . . . .	18
zipXenSPEP . . . . .	19
[,XenSPEP,ANY,ANY,ANY-method . . . . .	19
<b>Index</b>	<b>21</b>

---

cacheMtif	<i>cache and/or retrieve path to an ome.tif file for demonstration</i>
-----------	--

---

### Description

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

### Usage

```
cacheMtif(
  cache = BiocFileCache::BiocFileCache(),
  url =
    "https://mgph.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 VI lung demo data from 10x*

---

**Description**

cache and/or retrieve path to an SFE of VI 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	<i>cache and/or retrieve path to Xenium Lung Adenocarcinoma example data, zipped SPEP accompanied by parquet</i>
--------------	--

---

**Description**

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

**Usage**

```
cacheXenLuad(
  cache = BiocFileCache::BiocFileCache(),
  url = "https://mgdp.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	<i>counts-in-memory version of melanoma 5k dataset</i>
-------------------	--

---

**Description**

counts-in-memory version of melanoma 5k dataset

**Usage**

```
cacheXenPdmelLite(
  cache = BiocFileCache::BiocFileCache(),
  url = "https://mgdp.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**

<code>xsce</code>	XenSPEP instance
<code>xlim</code>	numeric(2)
<code>ylim</code>	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**

<code>simple</code>	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	<i>helper function to map ENS ids to symbols</i>
-------	--

---

**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	<i>produce a pre-loaded XenSPEP (SpatialExperiment with parquet references)</i>
------------	---

---

**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	<i>read and bind parquet data to XenSPEP</i>
--------------	--

---

**Description**

read and bind parquet data to XenSPEP

**Usage**

```
loadGeometry(x)
```

**Arguments**

x                   instance of XenSPEP

**Value**

instance of XenSPEP

---

loadGeometry, XenSPEP-method
<i>read and bind parquet data to XenSPEP</i>

---

**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	<i>utility for dealing with cached Xen_SPEP in temp folder</i>
----------------	--

---

**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	<i>use unzip, readRDS, and loadGeometry to restore a XenSPEP</i>
-------------------	--

---

**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	<i>naive polygon viewer, will indicate presence of transcripts for two genes in cells</i>
-----------	---

---

**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	<i>serialize the collection of XenSPEP and parquet with zip</i>
------------	---

---

**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	<i>formal bracket definition, that leaves parquet geometry information alone.</i>
------------------------------	---

---

**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.

# Index

- \* **datasets**
  - e79sym, [8](#)
  - [,XenSPEP,ANY,ANY,ANY-method, [19](#)
- cacheMtif, [2](#)
- cacheSfeLungNtx, [3](#)
- cacheXenLuad, [4](#)
- cacheXenPdmellite, [4](#)
- cacheXenProstLite, [5](#)
- clipRect, [6](#)
- demoapp, [6](#)
- e2sym, [7](#)
- e79sym, [8](#)
- getCellBoundaries, [8](#)
- getCellBoundaries,XenSPEP-method, [9](#)
- getNucleusBoundaries, [9](#)
- getNucleusBoundaries,XenSPEP-method, [10](#)
- getTranscripts, [10](#)
- getTranscripts,XenSPEP-method, [11](#)
- ggprepSeg, [11](#)
- ingest\_xen, [12](#)
- loadGeometry, [13](#)
- loadGeometry,XenSPEP-method, [13](#)
- plotXenGgprep, [14](#)
- printXenGgprep, [14](#)
- resetParqPaths, [15](#)
- restoreZipXenSPEP, [15](#)
- show,XenSPEP-method, [16](#)
- viewSeg, [16](#)
- viewSegG2, [17](#)
- XenSPEP, [18](#)
- XenSPEP-class, [18](#)
- zipXenSPEP, [19](#)