

Package ‘SpatialExperiment’

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Type Package

Title S4 Class for Spatial Experiments handling

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Description Defines S4 classes for storing data for spatial experiments.
Main examples are reported by using seqFISH and 10x-Visium Spatial Gene Expression data.
This includes specialized methods for storing, retrieving spatial coordinates, 10x dedicated parameters and their handling.

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BugReports <https://github.com/drighelli/SpatialExperiment/issues>

Encoding UTF-8

LazyData true

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Depends R (>= 4.0.0), methods, SingleCellExperiment

Imports S4Vectors

Suggests testthat, knitr, rjson, Matrix

VignetteBuilder knitr

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`imagePaths, VisiumExperiment-method`
imagePaths-getter

Description

getter for the list of `imagePaths` stored into the `VisiumExperiment` class object.

Usage

```
## S4 method for signature 'VisiumExperiment'
imagePaths(x)
```

Arguments

`x` a `VisiumExperiment` class object

Value

a list of paths of 10x Visium images

Examples

```
example(VisiumExperiment)
imagePaths <- list.files(system.file(file.path("extdata", "10x_visium",
                                             "images"),
                                   package="SpatialExperiment"), full.names=TRUE)
imagePaths(ve)
```

imagePaths<- ,VisiumExperiment-method
imagePaths-setter

Description

sets the list of image paths for the VisiumExperiment class object.

Usage

```
## S4 replacement method for signature 'VisiumExperiment'  
imagePaths(x) <- value
```

Arguments

x	a VisiumExperiment class object
value	a list within the paths of the images of a 10x Visium experiment

Value

none

Examples

```
example(VisiumExperiment)  
imagePaths <- list.files(system.file(file.path("extdata", "10x_visium",  
                                         "images"),  
                             package="SpatialExperiment"), full.names=TRUE)  
imagePaths(ve) <- imagePaths
```

isInTissue,VisiumExperiment-method
isInTissue

Description

returns a mask of TRUE/FALSE Barcodes spots, indicating which ones are in tissue and which ones are not.

Usage

```
## S4 method for signature 'VisiumExperiment'  
isInTissue(x)
```

Arguments

x	a VisiumExperiment class object.
---	----------------------------------

Value

a TRUE/FALSE mask.

Examples

```
ve <- readRDS(file=system.file(file.path("extdata", "10x_visium",
                                     "ve.RDS"), package="SpatialExperiment"))
isInTissue(ve)
sum(isInTissue(ve))
```

scaleFactors, *VisiumExperiment*-method
scaleFactors-getter

Description

gets the scale factors from a *VisiumExperiment* class object.

Usage

```
## S4 method for signature 'VisiumExperiment'
scaleFactors(x)
```

Arguments

x a *VisiumExperiment* class object.

Value

a *DataFrame* with the 10x *Visium* scale factors.

Examples

```
ve <- readRDS(file=system.file(file.path("extdata", "10x_visium",
                                     "ve.RDS"), package="SpatialExperiment"))
scaleFactors(ve)
```

scaleFactors<-, *VisiumExperiment*-method
scaleFactors-setter

Description

sets the scale factors in a *VisiumExperiment* class object.

Usage

```
## S4 replacement method for signature 'VisiumExperiment'
scaleFactors(x) <- value
```

Arguments

x a *VisiumExperiment* class object.
value a list of 10x *Visium* scale factors.

Value

a VisiumExperiment class object.

Examples

```
example(VisiumExperiment)
```

show,SpatialExperiment-method
SpatialExperiment show method

Description

a method for showing the SpatialExperiment

Usage

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

Arguments

object a SpatialExperiment object instance

Value

none

Examples

```
example(SpatialExperiment, echo=FALSE) # using class example  
show(se)
```

show,VisiumExperiment-method
VisiumExperiment show method

Description

a method for showing the VisiumExperiment

Usage

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

Arguments

object a VisiumExperiment object instance

Value

none

Examples

```
example(VisiumExperiment, echo=FALSE) #using class example
show(ve)
```

spatialCoords, *SpatialExperiment*-method
spatialCoords-getter

Description

a getter method which returns the spatial coordinates previously stored in a *SpatialExperiment* class object.

Usage

```
## S4 method for signature 'SpatialExperiment'
spatialCoords(x)
```

Arguments

x A *SpatialExperiment* class object.

Value

a *DataFrame* within the spatial coordinates.

Examples

```
example(SpatialExperiment)
spatialCoords(se)
```

spatialCoords<-, *SpatialExperiment*-method
spatialCoords-setter

Description

a setter method which sets/replaces the spatial coordinate in a *SpatialExperiment* class object.

Usage

```
## S4 replacement method for signature 'SpatialExperiment'
spatialCoords(x) <- value
```

Arguments

x a SpatialExperiment class object
value a DataFrame with the new spatial coordinates to set.

Value

none

Examples

```
example(SpatialExperiment)
fakeFishCoords <- cbind(fishCoordinates[,c(1:3)], fishCoordinates[,3])
                  colnames(fakeFishCoords) <- c("MyCell_ID", "Irrelevant", "x", "y")
spatialCoords(se) <- fakeFishCoords
spatialCoords(se)
```

spatialCoordsNames, SpatialExperiment-method
spatialCoordsNames-getter

Description

getter method for the spatial coordinates names in a SpatialExperiment class object.

Usage

```
## S4 method for signature 'SpatialExperiment'
spatialCoordsNames(x)
```

Arguments

x a SpatialExperiment class object.

Value

a vector with the colnames of the spatial coordinates.

Examples

```
example(SpatialExperiment)
spatialCoordsNames(se)
```

 SpatialExperiment-class

The SpatialExperiment class

Description

The SpatialExperiment class is designed to represent 10x Visium spatial Gene Expression data. It inherits from the [SingleCellExperiment](#) class and is used in the same manner. In addition, the class supports the integration with 10x Visium spatial coordinates and its scale factors.

Usage

```
SpatialExperiment(..., spatialCoords = data.frame())
```

Arguments

...	arguments to be passed to the SingleCellExperiment constructor to fill the slots of the base class.
spatialCoords	the spatial coordinates

Value

none

Author(s)

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Examples

```
## building random seqFISH data coordinates
fishCoordinates <- data.frame(Cell_ID=paste0("cell",c(1:30)),
                             Irrelevant=100,
                             x=sample(c(-4000:4000), size=30, replace=TRUE),
                             y=sample(c(-4000:4000), size=30, replace=TRUE))
## building random seqFISH cell labels
fishCellLabels <- data.frame(Cell_ID=paste0("cell",c(1:30)),
                             class="neuron",
                             classID=sample(c(0:5), size=30, replace=TRUE))
## building random seqFISH count matrix
fishCounts <- matrix(sample(0:100, size=(30*30), replace=TRUE),
                    nrow=30, ncol=30,
                    dimnames=list(paste0("gene",c(1:30)),
                                   paste0("cell",c(1:30))))
## creating SpatialExperiment object
se <- SpatialExperiment(rowData=rownames(fishCounts),
                       colData=fishCellLabels,
                       assays=SimpleList(counts=as.matrix(fishCounts)),
                       spatialCoords=fishCoordinates)
```



```
                                package="SpatialExperiment")
tissPosEx <- read.csv(posFile,
                     sep="\t", header=FALSE,
                     col.names=c("Barcodes", "in_tissue",
                                   "array_row", "array_col",
                                   "pxl_col_in_fullres", "pxl_row_in_fullres"))
scaleFile <- system.file(file.path("extdata", "10x_visium",
                                   "scalefactors_json.json"),
                         package="SpatialExperiment")

scalefactors <- rjson::fromJSON(file=scaleFile)
imagePaths <- list.files(system.file(file.path("extdata", "10x_visium",
                                             "images"),
                                   package="SpatialExperiment"), full.names=TRUE)

ve <- VisiumExperiment(rowData=featuresEx, colData=barcodesEx,
                      assays=c(counts=countsEx),
                      spatialCoords=tissPosEx,
                      scaleFactors=scalefactors,
                      imagePaths=imagePaths)

ve
```

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