

# Package ‘SpatialExperiment’

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**Type** Package

**Title** S4 Class for Spatial Experiments handling

**Version** 1.0.0

**Date** 2020-07-21

**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.

**License** GPL-3

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

**Encoding** UTF-8

**LazyData** true

**biocViews** DataRepresentation, DataImport, Infrastructure, SingleCell, ImmunoOncology

**Depends** R (>= 4.0.0), methods, SingleCellExperiment

**Imports** S4Vectors

**Suggests** testthat, knitr, rjson, Matrix

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

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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)
```



**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)

Dario Righelli

## 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)

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