

# Package: spatialdataR (via r-universe)

June 1, 2026

**Title** Representation of Python's spatialdata in R

**Depends** R (>= 4.5)

**Version** 0.99.41

**Description** R interface to Python/scverse's 'spatialdata' framework for unified spatial omics data handling. Adheres to OME-NGFF standards, providing lazy, on-disk representations for multiscale images and labels (ZarrArray), as well as points and shapes (DuckDB-backed tables). Includes handling of coordinate transformation systems and spatial utilities for cropping, masking, and querying. Integrates tabular annotations as 'SingleCellExperiment's (via 'anndataR'), enabling interoperable spatial omics workflows across R and Python.

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**biocViews** DataImport, DataRepresentation, Infrastructure, ImmunoOncology, GeneExpression, Transcriptomics, SingleCell, Spatial

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blobs	<i>'SpatialData' .zarr toy datasets</i>
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### Description

data were retrieved on Nov. 11th, 2024, from [here](#).

### Value

zarr store.

### Examples

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
(x <- readSpatialData(x))
```

---

centroids	<i>Spatial element centroids</i>
-----------	----------------------------------

---

## Description

Spatial element centroids

## Usage

```
## S4 method for signature 'ANY'  
centroids(x, ...)  
  
## S4 method for signature 'SpatialDataLabel'  
centroids(x, as = c("data.frame", "matrix"))  
  
## S4 method for signature 'SpatialDataShape'  
centroids(x, as = c("data.frame", "matrix", "list"))  
  
## S4 method for signature 'SpatialDataPoint'  
centroids(x, as = c("data.frame", "list"))
```

## Arguments

x	a SpatialData element (any but image).
...	ignored.
as	character string; how results should be returned.

## Value

A table (data.frame or matrix) of spatial coordinates (if as="list", split by instance (shapes) or features (points)).

## Examples

```
x <- file.path("extdata", "blobs.zarr")  
x <- system.file(x, package="spatialdataR")  
x <- readSpatialData(x, tables=FALSE)  
  
centroids(label(x))  
centroids(shape(x))  
  
head(centroids(point(x)))  
xy <- centroids(point(x), "list")  
plot(xy$gene_a, col=a <- "red")  
points(xy$gene_b, col=b <- "blue")  
legend("topright", legend=names(xy), col=c(a, b), pch=21)
```

---

combine	<i>Combine two SpatialData objects</i>
---------	--

---

## Description

Combine two SpatialData objects

## Usage

```
## S4 method for signature 'list,missing'  
combine(x, y, ...)  
  
## S4 method for signature 'SpatialData,SpatialData'  
combine(x, y, ...)
```

## Arguments

x, y	SpatialData objects to combine.
...	ignored.

## Value

A SpatialData objects containing all elements from x and y with names made unique.

## Examples

```
x <- file.path("extdata", "blobs.zarr")  
x <- system.file(x, package="spatialdataR")  
x <- readSpatialData(x)  
  
y <- combine(x, x)  
imageNames(y)  
region(table(y, 1))  
region(table(y, 2))  
  
y <- combine(list(Alpha=x, x, Omega=x))  
shapeNames(y)
```

---

crop	<i>spatial cropping</i>
------	-------------------------

---

### Description

crop subsets `SpatialData` elements according to a rectangular bounding box or arbitrary polygonal shapes.

For `SpatialData` objects, crop propagates the operation across all layers that share the coordinate space `j`.

For `SpatialDataFrames` (points and shapes), cropping relies on `sf::st_intersects` (i.e., instances that intersect the query region in any way are kept). For circle shapes, radii are currently ignored (i.e., a circle is kept if its centroid intersects the query region).

For `SpatialDataArrays` (images and labels), only bounding box cropping is supported. The requested spatial bounding box is projected into pixel coordinates, and the underlying array is sliced accordingly. The `wh` metadata is updated to reflect the new spatial extent.

### Usage

```
## S4 method for signature 'SpatialDataArray'
crop(x, y, j = 1, ...)
```

```
## S4 method for signature 'SpatialDataFrame'
crop(x, y, j = 1, ...)
```

```
## S4 method for signature 'SpatialData'
crop(x, y, j = 1, ...)
```

### Arguments

<code>x</code>	<code>SpatialData</code> object or element.
<code>y</code>	query specification; bounding box: length-4 numeric list with names 'xmin/xmax/ymin/ymax', or an <code>st_bbox</code> ; polygon: numeric matrix with 2 columns (= xy-coordinates), or an <code>st_polygon</code> ( <code>sfg</code> ) or <code>sfc/sf</code> object.
<code>j</code>	character string specifying a coordinate system.
<code>...</code>	optional arguments passed to and from other methods.

### Value

same as input

### Examples

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")
sd <- readSpatialData(zs, tables=FALSE)
```



j	character string; name of target coordinate space.
g	base R graph; extracted with CTgraph.
cex	scalar numeric; controls fontsize of node labels.
fac, max	scalar numeric; node labels with nchar>max are split and hyphenated at position floor(nchar/fac)

### Value

- CTgraph: graph::graphAM object with nodes for each element and coordinate space, and edges for each transformation (if specified)
- CTpath: list of transformations from i to j; length > 1 if type is "sequential", length-1 otherwise; each element specifies type and data of the transformation
- CTplot: visualizes the element-coordinate space graph with Rgraphviz

### Examples

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x, tables=FALSE)

# object-wide
g <- CTgraph(x)
CTplot(g)

# one element
y <- label(x)
g <- CTgraph(y)
CTplot(g)

# retrieve transformation(s)
# from element to target space
CTpath(x, "blobs_labels", "sequence")
```

---

CTutils

*Coord. trans. utilities*

---

### Description

Coord. trans. utilities

### Usage

```
## S4 method for signature 'SpatialDataAttrs'
axes(x, ...)

## S4 method for signature 'SpatialDataAttrs'
CTlist(x, ...)
```

```

## S4 method for signature 'SpatialDataAttrs'
CTdata(x, i = 1, ...)

## S4 method for signature 'SpatialDataAttrs'
CTtype(x, ...)

## S4 method for signature 'SpatialDataAttrs'
CTname(x, ...)

## S4 method for signature 'SpatialDataElement'
axes(x, ...)

## S4 method for signature 'SpatialDataElement'
CTlist(x, ...)

## S4 method for signature 'SpatialDataElement'
CTtype(x, ...)

## S4 method for signature 'SpatialDataElement'
CTname(x, ...)

## S4 method for signature 'SpatialDataElement'
CTdata(x, i = 1, ...)

## S4 method for signature 'SpatialData'
CTname(x, ...)

## S4 method for signature 'SpatialDataElement'
rmvCT(x, i)

## S4 method for signature 'SpatialDataAttrs'
rmvCT(x, i)

## S4 method for signature 'SpatialDataElement'
addCT(x, name, type = "identity", data = NULL)

## S4 method for signature 'SpatialDataAttrs'
addCT(x, name, type = "identity", data = NULL)

```

### Arguments

x	SpatialData, an element, or SpatialDataAttrs.
...	option arguments passed to and from other methods.
i	for CTpath, source node label; else, string or scalar integer giving the name or index of a coordinate space.
name	character(1); name of coordinate space
type	character(1); type of transformation

data transformation data; size and shape depend on transformation and element type (e.g., numeric(1) for rotation, numeric(2) for scaling in 2D)

### Value

- CTname: character string; transformation name (e.g., "global")
- CTtype: character string; transformation type (e.g., "affine")
- CTdata: list; transformation data (e.g., scalar numeric for rotation)
- CTlist: list; list of transformation specifications per OME-NGFF spec
- add/rmvCT: SpatialDataElement or SpatialDataAttrs with transformation(s) added/removed
- axes: list; each element is a character string (name), or list with axis name and type (e.g., "space" or "channel")

### Examples

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x, tables=FALSE)

# view available target coordinate systems
CTname(z <- meta(label(x)))

# add
addCT(z, "scale", "scale", c(12, 34)) # overwrite
CTname(addCT(z, "new", "translation", c(12, 34)))

# rmv
CTname(rmvCT(z, 2)) # by index
CTname(rmvCT(z, "scale")) # by name
CTname(rmvCT(z, "global")) # identity is protected
```

---

extent	<i>Spatial element extent</i>
--------	-------------------------------

---

### Description

Spatial element extent

### Usage

```
## S4 method for signature 'SpatialData'
extent(x, i = 1)

## S4 method for signature 'SpatialDataArray'
extent(x, i = 1)

## S4 method for signature 'SpatialDataFrame'
extent(x, i = 1)
```

**Arguments**

`x` a SpatialData element (any but table).  
`i` scalar integer or string; target coordinate space.

**Value**

Length-2 list with numeric x and y ranges.

**Examples**

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x, tables=FALSE)

# object-wide
extent(x)

# element-wise
extent(image(x))
extent(point(x))
extent(shape(x))

# with transformation(s)
extent(label(x), "scale")
extent(label(x), "translation")
```

---

mask

*Aggregate data across layers*


---

**Description**

Masking operations serve to aggregate data across layers, e.g., counting points in shapes, averaging image channels by labels, etc. For added flexibility, these may be carried out directly between elements, or using an input SpatialData object and specifying element names.

**Usage**

```
## S4 method for signature 'SpatialData'
mask(
  x,
  i,
  j,
  k,
  how = NULL,
  name = function(i, j) sprintf("%s_by_%s", i, j),
  ...
)
```

**Arguments**

x	<a href="#">SpatialData</a> object.
i, j	character string; names of elements to mask, specifically, i will be masked by j, adding a table for j in x.
k	string or scalar integer; specifies target coordinate space (defaults to first common coordinate space between i and j)
how	character string; statistic to use for masking.
name	function use to generate the new table's name.
...	optional arguments passed to and from other methods.

**Value**

Input [SpatialData](#) object x with an additional table.

**Examples**

```
library(SingleCellExperiment)
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x, tables=FALSE)

# count points in shapes
y <- mask(x, "blobs_points", "blobs_circles")
tail(tables(y), 1)

# average image channels by labels
y <- mask(x, "blobs_image", "blobs_labels")
tail(tables(y), 1)

# TODO: shape,shape example
```

---

misc

*Miscellaneous 'SpatialData' methods*

---

**Description**

Miscellaneous methods (e.g., `show`) for the [SpatialData](#) class and its elements.

**Usage**

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

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

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

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

### Arguments

object            [SpatialData](#) object or one of its elements, i.e., a [SpatialDataImage/Label/Point/Shape](#).

### Value

NULL

### Examples

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")
(sd <- readSpatialData(zs))

# show element
image(sd)
label(sd)
point(sd)
shape(sd)

# show .zattrs
meta(label(sd))
meta(image(sd, 2))
```

---

path

*Retrieve SpatialData on-disk paths*

---

### Description

Retrieve [SpatialData](#) on-disk paths

### Usage

```
## S4 method for signature 'SpatialDataArray'
path(object, ...)
```

```
## S4 method for signature 'SpatialDataFrame'
path(object, ...)
```

```
## S4 method for signature 'SingleCellExperiment'
path(object, ...)
```

```
## S4 method for signature 'SpatialData'
path(object, simplify = TRUE, ...)
```

**Arguments**

object            [SpatialData](#) object or one of its elements.  
 ...                ignored.  
 simplify         logical scalar; whether to flatten paths into a tibble.

**Value**

for single elements, a character string; for [SpatialData](#) objects, if `simplify=TRUE` (default), a tibble where rows=elements and columns=layers/elements/paths. if `simplify=FALSE`, a depth-3 list where levels=layers/elements/paths.

**Examples**

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")
sd <- readSpatialData(zs)

# element-wise
path(shape(sd))

# object-wide
path(sd)
path(sd, FALSE)$labels
```

---

 query

*queries*


---

**Description**

`query` provides a interface for table-based subsetting of [SpatialData](#) objects. It filters a specified table using `dplyr::filter` logic and propagates the result to all associated spatial elements (i.e., only instances present in the filtered table are kept).

For spatial cropping, see [crop](#).

**Usage**

```
## S4 method for signature 'SpatialData'
query(x, ..., i = 1)
```

**Arguments**

x                 [SpatialData](#) object.  
 ...                logic passed to `dplyr::filter`.  
 i                 index or name of table to query.

**Value**

SpatialData object

**Examples**

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")
sd <- readSpatialData(zs)

# filter by 'region' and propagate to shapes/points
t <- table(sd)
query(sd, i=1, region == region(t))
```

---

readSpatialData	<i>Reading 'SpatialData'</i>
-----------------	------------------------------

---

**Description**

Reading 'SpatialData'

**Usage**

```
readImage(x, ...)
readLabel(x, ...)
readPoint(x, ...)
readShape(x, ...)
readTable(x)
readSpatialData(
  x,
  images = TRUE,
  labels = TRUE,
  points = TRUE,
  shapes = TRUE,
  tables = TRUE
)
```

**Arguments**

x	For readImage/Label/Point/Shape/Table, path to a SpatialData element. For readSpatialData, path to a SpatialData-.zarr store.
...	option arguments passed to and from other methods.

images, labels, points, shapes, tables

Control which elements should be read for each layer. The default, NULL, reads all elements; alternatively, may be FALSE to skip a layer, or a integer vector specifying which elements to read.

### Value

- For readSpatialData, a SpatialData.,
- For element readers, a SpatialDataImage/Label/Point/Shape or SingleCellExperiment.

### Examples

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")

# read complete Zarr store
(sd <- readSpatialData(zs))

# helper that gets path to last element in layer '1'
fn <- \(.) tail(list.files(file.path(zs, .), full.names=TRUE), 1)

# read individual elements
(i <- readImage(fn("images")))
channels(i)

(p <- readPoint(fn("points")))
as.data.frame(head(p))

(s <- readShape(fn("shapes")))
data(s)
```

---

SpatialData-class      *The 'SpatialData' class*

---

### Description

SpatialData provides an R interface to Python's spatialdata, which enables the representation of diverse spatial omics datasets using the OME-NGFF (Next Generation File Format) standard. In R,

- images and labels are ZarrArrays (Rarr package).
- points and shapes are managed using duckspatial tables.
- tables are SingleCellExperiments (read with anndataR).

**Usage**

```
SpatialData(  
  images = list(),  
  labels = list(),  
  points = list(),  
  shapes = list(),  
  tables = list()  
)  
  
## S4 method for signature 'SpatialData'  
x$name  
  
## S4 replacement method for signature 'SpatialData'  
x$name <- value  
  
## S4 method for signature 'SpatialData,numeric,ANY'  
x[[i, j, ...]]  
  
## S4 method for signature 'SpatialData,character,ANY'  
x[[i, j, ...]]  
  
## S4 method for signature 'SpatialDataElement'  
data(x, k = 1, ...)  
  
## S4 method for signature 'SpatialDataElement'  
meta(x)  
  
## S4 method for signature 'SpatialData,ANY,ANY,ANY'  
x[i, j, ..., drop = FALSE]  
  
## S4 method for signature 'SpatialData'  
rownames(x)  
  
## S4 method for signature 'SpatialData'  
colnames(x)  
  
## S4 method for signature 'SpatialData,character'  
layer(x, i)  
  
## S4 method for signature 'SpatialData,ANY'  
layer(x, i)  
  
## S4 method for signature 'SpatialData,character'  
element(x, i)  
  
## S4 method for signature 'SpatialData,numeric'  
element(x, i)
```

```

## S4 method for signature 'SpatialData,missing'
element(x, i)

## S4 method for signature 'SpatialData,ANY'
element(x, i)

## S4 replacement method for signature 'SpatialData,character'
element(x, i) <- value

## S4 method for signature 'SpatialData'
images(x)

## S4 method for signature 'SpatialData'
labels(object)

## S4 method for signature 'SpatialData'
points(x)

## S4 method for signature 'SpatialData'
shapes(x)

## S4 method for signature 'SpatialData'
tables(x)

## S4 replacement method for signature 'SpatialData,character,ANY'
x[[i]] <- value

## S4 replacement method for signature 'SpatialData,numeric,ANY'
x[[i]] <- value

## S4 replacement method for signature 'SpatialData,ANY,ANY'
x[[i]] <- value

```

### Arguments

images	list of <a href="#">SpatialDataImages</a>
labels	list of <a href="#">SpatialDataLabels</a>
points	list of <a href="#">SpatialDataPoints</a>
shapes	list of <a href="#">SpatialDataShapes</a>
tables	list of <a href="#">SingleCellExperiments</a>
x, object	<a href="#">SpatialData</a> object.
name	character string for extraction (see <code>?base::`\$`</code> ).
value	(list of) element(s) with layer-compliant object(s), or <code>NULL</code> / <code>list()</code> to remove an element/layer completely; for <code>element&lt;-</code> , a single <a href="#">SpatialDataElement</a> of the same class as <code>element(x, i)</code> .
i, j	character string, scalar or vector of indices specifying the element to extract from a given layer.

...	optional arguments passed to and from other methods.
k	scalar index specifying which scale to use; Inf to use lowest available resolution.
drop	ignored.

**Value**

SpatialData

**Examples**

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
(x <- readSpatialData(x))

# subsetting
# layers are taken in order of appearance
# (images, labels, points, shapes, tables)
x[-4] # drop layer
x[4, -2] # drop element
x["shapes", c(1, 3)] # subset layer
x[c(1, 2), list(1, c(1, 2))] # multiple
```

---

SpatialDataArray	SpatialDataArray
------------------	------------------

---

**Description**

The `SpatialDataImage` and `-Label` classes represent elements from a `SpatialData`'s images/ and labels/ layers, respectively. In both cases, these are represented as a `ZarrArray` (data slot), and associated with `.zattrs` represented as `SpatialDataAttrs` (meta slot); a list of metadata stores other arbitrary info.

Currently defined methods (here, `x` is a `SpatialDataArray`):

- `data/meta(x)` access underlying `data/.zattrs`
- `data_type(x)` gets the underlying data type (e.g., `float64`)
- `channels(x)` gets channel names (applies to images only)
- `dim(x)` returns the dimensions of `data(x)`
- `length(x)` returns the length of `data(x)`

**Usage**

```

SpatialDataImage(
  data = list(),
  meta = SpatialDataAttrs(),
  metadata = list(),
  ...
)

SpatialDataLabel(
  data = list(),
  meta = SpatialDataAttrs(),
  metadata = list(),
  ...
)

## S4 method for signature 'SpatialDataArray'
dim(x)

## S4 method for signature 'SpatialDataArray'
length(x)

## S4 method for signature 'SpatialDataArray'
data_type(x)

## S4 method for signature 'DelayedArray'
data_type(x)

## S4 method for signature 'SpatialDataAttrs'
channels(x, ...)

## S4 method for signature 'SpatialDataImage'
channels(x, ...)

## S4 method for signature 'SpatialDataElement'
channels(x, ...)

## S4 method for signature 'SpatialDataImage,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]

## S4 method for signature 'SpatialDataLabel,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

```

**Arguments**

data	list of ZarrArrays
meta	<a href="#">SpatialDataAttrs</a>
metadata	optional list of arbitrary additional content.

... option arguments passed to and from other methods.  
 x SpatialDataArray  
 i, j, k indices specifying elements/slices to extract.  
 drop ignored.

**Value**

SpatialDataArray

**Examples**

```
zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")

# get path to 'i'th element in layer 'l'
fn <- \(l, i=1) list.dirs(file.path(zs, l), recursive=FALSE)[i]

# label
(x <- readLabel(fn("labels")))
x[1:10, 1:10]
meta(x)

# image
readImage(fn("images"))

# multi-scale
(x <- readImage(fn("images", 2)))

channels(x)
dim(data(x, 1)) # highest res.
dim(data(x, Inf)) # lowest res.

# RGB visual
rgb <- apply(
  data(x, 1), c(2, 3),
  \(.) rgb(.[1], .[2], .[3]))
plot(
  row(rgb), col(rgb), col=rgb,
  pch=15, asp=1, ylim=c(ncol(rgb), 0))
```

---

SpatialDataAttrs

*The 'SpatialDataAttrs' class*

---

**Description**

The 'SpatialDataAttrs' class

**Usage**

```
SpatialDataAttrs(  
  x,  
  type = c("array", "frame"),  
  label = FALSE,  
  trans = NULL,  
  ver = "0.4",  
  nch = 3,  
  ...  
)  
  
## S4 method for signature 'SpatialDataAttrs'  
x$name  
  
## S4 method for signature 'SpatialDataPoint'  
feature_key(x)  
  
## S4 method for signature 'SpatialDataAttrs'  
feature_key(x)  
  
## S4 replacement method for signature 'SpatialDataAttrs,character'  
feature_key(x) <- value  
  
## S4 method for signature 'SingleCellExperiment'  
region_key(x)  
  
## S4 method for signature 'SingleCellExperiment'  
region(x)  
  
## S4 method for signature 'SingleCellExperiment'  
regions(x)  
  
## S4 replacement method for signature 'SingleCellExperiment,character'  
regions(x) <- value  
  
## S4 replacement method for signature 'SingleCellExperiment,NULL'  
regions(x) <- value  
  
## S4 method for signature 'list'  
instance_key(x)  
  
## S4 method for signature 'SingleCellExperiment'  
instance_key(x)  
  
## S4 method for signature 'SpatialDataFrame'  
instance_key(x)  
  
## S4 method for signature 'SpatialDataLabel'
```

```

instance_key(x)

## S4 replacement method for signature 'SpatialDataAttrs,character'
instance_key(x) <- value

## S4 replacement method for signature 'SingleCellExperiment,character'
instance_key(x) <- value

## S4 method for signature 'SpatialDataLabel'
instances(x)

## S4 method for signature 'SpatialDataPoint'
instances(x)

## S4 method for signature 'SpatialDataShape'
instances(x)

## S4 method for signature 'SingleCellExperiment'
instances(x)

## S4 replacement method for signature 'SingleCellExperiment'
instances(x) <- value

```

### Arguments

x	element or list extracted from a OME-NGFF compliant .zattrs file.
type	character string; either "array" (image/label) or "frame" (point/shape).
label	flag; when type="frame", should attributes be for a label?
trans	list of coordinate transformations; defaults to identity only.
ver	character string; specified the .zarr version to comply with.
nch	scalar integer; how many channels should there be? (ignored unless type="frame" and label=FALSE).
...	additional attributes (e.g., version, feature_key).
name	character string for extraction (see ?base::'\$').
value	character string (for one region and _keys), or vector (for many regions, instances and regions).

### Details

When x is a spatial element, the following applies: SpatialDataFrame: feature/instance\_key, SingleCellExperiment: region, region/instance\_key.

When missing x, SpatialDataAttrs will generate a valid object with default axes (array: cyx, frame: xy) and transformations (identify) according to the specified type.

### Value

character string

**Examples**

```

x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x)

# tables
region(table(x))
region_key(table(x))

# points
instance_key(point(x))
fk <- feature_key(point(x))
base::table(point(x)[[fk]])

# transformations
(z <- meta(label(x)))
CTname(z)
CTtype(z)
CTdata(z, "scale")

# constructor
SpatialDataAttrs(type="frame")
SpatialDataAttrs(type="array")
SpatialDataAttrs(type="array", nch=7)
SpatialDataAttrs(type="array", label=TRUE)

```

---

SpatialDataFrame

SpatialDataFrame

---

**Description**

The `SpatialDataPoint` and `-Shape` classes represent elements from a `SpatialData`'s points/ and shapes/ layers, respectively. In both cases, these are represented as a `duckspatial_df` (data slot), and associated with `.zattrs` represented as `SpatialDataAttrs` (meta slot); a list of metadata stores other arbitrary info.

Currently defined methods (here, `x` is an `SpatialDataFrame`):

- `data/meta(x)` access underlying data/.zattrs
- `geom_type(x)` get the shape's type (e.g., POLYGON)
- `names(x)` returns the underlying table's column names
- `dim(x)` returns the dimensions of `data(x)`
- ``$``, ``[[`` directly access columns of `data(x)`
- `filter`, `select` to subset rows/columns à la `dplyr`
- `as.data.frame` to coerce `x` to a `data.frame`

**Usage**

```
SpatialDataPoint(  
  data = NULL,  
  meta = SpatialDataAttrs(type = "frame"),  
  metadata = list(),  
  ik = NULL,  
  fk = NULL,  
  ...  
)  
  
SpatialDataShape(  
  data = NULL,  
  meta = SpatialDataAttrs(type = "frame"),  
  metadata = list(),  
  ...  
)  
  
## S4 method for signature 'SpatialDataFrame'  
length(x)  
  
## S4 method for signature 'SpatialDataFrame'  
dim(x)  
  
## S4 method for signature 'SpatialDataFrame'  
names(x)  
  
## S4 method for signature 'SpatialDataFrame'  
as.data.frame(x)  
  
## S4 method for signature 'SpatialDataShape'  
geom_type(x)  
  
## S3 method for class 'SpatialDataFrame'  
pull(.data, ...)  
  
## S3 method for class 'SpatialDataFrame'  
select(.data, ...)  
  
## S3 method for class 'SpatialDataFrame'  
mutate(.data, ...)  
  
## S3 method for class 'SpatialDataFrame'  
filter(.data, ...)  
  
## S4 method for signature 'SpatialDataFrame,ANY,ANY'  
x[[i, j, ...]]  
  
## S4 method for signature 'SpatialDataPoint'
```

```

x$name

## S3 method for class 'SpatialDataShape'
.DollarNames(x, pattern = "")

## S4 method for signature 'SpatialDataShape'
x$name

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

```

### Arguments

data	duckspatial_df for on-disk representation, or a data.frame to be converted.
meta	<a href="#">SpatialDataAttrs</a>
metadata	optional list of arbitrary content describing the overall object.
ik, fk	character string specifying "instance_/feature_key" of the spatialdata_attrs; used to match observations/features.
...	optional arguments passed to and from other methods.
x, .data	SpatialDataFrame
i, j	indices for subsetting (see ?base::Extract).
name	character string for extraction (see ?base::`\$`).
drop, pattern	ignored.

### Value

SpatialDataFrame

### Examples

```

zs <- file.path("extdata", "blobs.zarr")
zs <- system.file(zs, package="spatialdataR")

# points
pa <- list.dirs(
  file.path(zs, "points"),
  recursive=FALSE, full.names=TRUE)
(x <- readPoint(pa))

y <- filter(x,
  genes == "gene_b",
  instance_id == 7)
head(as.data.frame(y))

# shapes
pa <- list.dirs(
  file.path(zs, "shapes"),
  recursive=FALSE, full.names=TRUE)

```

```

# circles
(x <- readShape(pa[1]))
length(x)
x$radius

# polygons
(y <- readShape(pa[2]))
df <- as.data.frame(y)
plot(df, col=seq(nrow(df)))

# multi-polygons
(z <- readShape(pa[3]))
df <- as.data.frame(z)
plot(df, col=seq(nrow(df)))

```

---

table-utils

SpatialData *annotations*


---

## Description

SpatialData annotations

## Usage

```

## S4 method for signature 'SingleCellExperiment'
meta(x)

## S4 method for signature 'SpatialData,ANY'
hasTable(x, i)

## S4 method for signature 'SpatialData,character'
hasTable(x, i, name = FALSE)

## S4 method for signature 'SpatialData,ANY'
getTable(x, i, j, assay = 1, drop = TRUE)

## S4 method for signature 'SpatialData,character'
getTable(x, i, j, assay = 1, drop = TRUE)

## S4 method for signature 'SpatialData,ANY'
setTable(x, i, ..., name = NULL, rk = "rk", ik = "ik")

## S4 method for signature 'SpatialData,character'
setTable(x, i, y, name = NULL, rk = "region", ik = "instance_id")

```

**Arguments**

x	<code>SpatialData</code> object.
i	character string; name of the element for which to get/set a table.
name	logical; should the table name be returned instead of TRUE/FALSE?
j	character string; colData column, or row name to retrieve assay data.
assay	character string or scalar integer; specifies which assay to use when j is a row name.
drop	logical; should observations (columns) that don't belong to i be filtered out?
...	option arguments passed to and from other methods.
rk, ik	character string; region and instance key (the latter will be ignored if an instance key is already specified within element i).
y	<code>SingleCellExperiment</code> containing annotations for i.

**Value**

- `hasTable`: logical scalar (or character string, if `name=TRUE`); whether or not a table annotating i exists in x
- `getTable`: `SingleCellExperiment`; the table annotating i with optional filtering of matching observations
- `valTable`: vector of values (according to j) from the table annotating i

**Examples**

```
library(SingleCellExperiment)
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x)

# check if element has a 'table'
hasTable(x, "blobs_points")
hasTable(x, "blobs_labels")

# retrieve 'table' for element 'i'
sce <- getTable(x, i="blobs_labels")
head(colData(sce))
meta(sce)

# get values from 'table'
getTable(x,
  i="blobs_labels",
  j="channel_0_sum")

# add 'table' annotating an element 'i'

# labels
y <- x; tables(y) <- list()
mtx <- matrix(0, 1, length(instances(label(y))))
```

```
sce <- SingleCellExperiment(list(counts=mtx))
y <- setTable(y, i <- "blobs_labels", sce)
getTable(y, i)

# shapes
i <- "blobs_circles"
mtx <- matrix(0, 1, nrow(shape(x, i)))
sce <- SingleCellExperiment(list(counts=mtx))
y <- setTable(x, i, sce)
getTable(y, i)
```

---

trans

*Transformations*


---

## Description

Transformations

## Usage

```
## S4 method for signature 'SpatialDataElement'
transform(x, i = 1, ...)

## S4 method for signature 'SpatialDataElement'
sequence(x, t, ..., rev = FALSE)

## S4 method for signature 'SpatialDataArray'
mirror(x, t = c("v", "h"), k = 1, ...)

## S4 method for signature 'SpatialDataArray'
flip(x, k = 1, ...)

## S4 method for signature 'SpatialDataArray'
flop(x, k = 1, ...)

## S4 method for signature 'SpatialDataArray'
rotate(x, t, k = 1, ..., rev = FALSE)

## S4 method for signature 'SpatialDataArray'
scale(x, t, ...)

## S4 method for signature 'SpatialDataArray,numeric'
translation(x, t, ...)

## S4 method for signature 'SpatialDataFrame'
rotate(x, t, ...)

## S4 method for signature 'SpatialDataFrame'
```

```
scale(x, t, ...)

## S4 method for signature 'SpatialDataFrame,numeric'
translation(x, t, ...)
```

### Arguments

x	SpatialData element.
i	scalar integer or string; target coordinate space.
...	option arguments passed to and from other methods.
t	transformation data; exceptions: for <code>mirror</code> , controls whether to perform vertical or horizontal reflection; no data is needed for <code>flip (v)</code> and <code>flop (h)</code> .
rev	flag; should transformation(s) be reversed?
k	scalar index specifying which scale to use; <code>Inf</code> to use lowest available resolution; only applies to <code>SpatialDataArrays</code> (images, labels).

### Value

SpatialData element with transformation(s) applied.

### Examples

```
x <- file.path("extdata", "blobs.zarr")
x <- system.file(x, package="spatialdataR")
x <- readSpatialData(x, tables=FALSE)

# image
y <- x
image(y) <- scale(image(y), c(1, 1, 1/3))
dim(image(x))
dim(image(y))

# point
y <- x
point(y, "rot") <- rotate(point(y), 20)
point(y, "wide") <- scale(point(y), c(1.2, 1))

xy0 <- centroids(point(y))
xy1 <- centroids(point(y, "rot"))
xy2 <- centroids(point(y, "wide"))

plot(xy0[, c(1, 2)], asp=1)
points(xy1[, c(1, 2)], col=2)
points(xy2[, c(1, 2)], col=4)

# shape
y <- x
shape(y, "rot") <- rotate(shape(y), 5)
shape(y, "wide") <- scale(shape(y), c(1.2, 1))
shape(y, "left") <- translation(shape(y), c(-5, 0))
y[,"shapes", c("rot", "wide", "left")]
```

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