

Package ‘MultiAssaySpatialExperiment’

September 18, 2026

Version 0.99.12

Date 2026-08-30

Title Multi-Assay Experiment with Spatial Context

Description Extends MultiAssayExperiment with spatial context elements (images, labels, points, shapes) for integrative analysis of spatially resolved multi-omics data. Supports coercion to and from SpatialExperiment and SpatialFeatureExperiment.

License MIT + file LICENSE

URL <https://github.com/Genentech/MultiAssaySpatialExperiment>

BugReports <https://github.com/Genentech/MultiAssaySpatialExperiment/issues>

Encoding UTF-8

Depends R (>= 4.6.0), methods, MultiAssayExperiment

Imports tools, BiocGenerics, BiocParallel, S4Vectors, MatrixGenerics, SummarizedExperiment, SingleCellExperiment, SpatialExperiment, sf

Suggests knitr, rmarkdown, BiocStyle, testthat, arrow, DropletUtils, jsonlite, sfarrow, terra, ggplot2, Matrix, RBioFormats, SpatialFeatureExperiment, spdep, zellkonverter

biocViews Infrastructure, DataRepresentation, Spatial

VignetteBuilder knitr

Collate 'SpatialGenerics.R' 'SpatialLayerList-class.R'
'MultiAssaySpatialExperiment-class.R'
'MultiAssaySpatialExperiment-SpatialExperiment.R'
'MultiAssaySpatialExperiment-SpatialFeatureExperiment.R'
'MultiAssaySpatialExperiment-combine.R'
'MultiAssaySpatialExperiment-spatialMap.R'
'MultiAssaySpatialExperiment-helpers.R'
'MultiAssaySpatialExperiment-package.R'
'MultiAssaySpatialExperiment-read-components.R'
'MultiAssaySpatialExperiment-read-config.R'
'MultiAssaySpatialExperiment-read-cosmx.R'
'MultiAssaySpatialExperiment-read-generics.R'
'MultiAssaySpatialExperiment-read-helpers.R'
'MultiAssaySpatialExperiment-read-merscope.R'
'MultiAssaySpatialExperiment-read-visium.R'

'MultiAssaySpatialExperiment-read-visiumhd.R'
 'MultiAssaySpatialExperiment-read-xenium.R'
 'MultiAssaySpatialExperiment-subset.R' 'spatial-aggregate.R'
 'spatial-annotate.R' 'spatial-operations.R'
 'spatial-raster-convert.R' 'zzz.R'

Config/roxygen2/version 8.1.0

git_url <https://git.bioconductor.org/packages/MultiAssaySpatialExperiment>

git_branch devel

git_last_commit 02ad073

git_last_commit_date 2026-08-30

Repository Bioconductor 3.24

Date/Publication 2026-09-17

Author Patrick Aboyoun [aut, cre],
 Genentech, Inc. [cph]

Maintainer Patrick Aboyoun <aboyounp@gene.com>

Contents

MultiAssaySpatialExperiment-package	3
aggregateByRegion	3
annotateWithRegions	5
buildSpatialMap	6
checkSpatialMap	7
labelsToShapes	8
MultiAssaySpatialExperiment-class	9
MultiAssaySpatialExperiment-combine	12
MultiAssaySpatialExperiment-SpatialExperiment	13
MultiAssaySpatialExperiment-subset	14
prepMASE	16
readCosMxMASE	17
readCSVForMASE	18
readGeoJSONForMASE	19
readGeoParquetForMASE	20
readHDF5ForMASE	20
readMERSCOPEMASE	21
readParquetForMASE	22
readVisiumHDMASE	23
readVisiumMASE	24
readXeniumMASE	25
shapesToLabels	26
spatial-accessors	27
spatialJoin	29
SpatialLayerList-class	30
spatialMatch	31
spatialOverlaps	32

Index

34

MultiAssaySpatialExperiment-package

MultiAssaySpatialExperiment: Multi-Assay Experiment with Spatial Context

Description

Extends MultiAssayExperiment with spatial context elements (images, labels, points, shapes) for integrative analysis of spatially resolved multi-omics data. Supports coercion to and from SpatialExperiment and SpatialFeatureExperiment.

Author(s)

Maintainer: Patrick Aboyoun <aboyounp@gene.com>

Authors:

- Patrick Aboyoun <aboyounp@gene.com>

Other contributors:

- Genentech, Inc. [copyright holder]

See Also

Useful links:

- <https://github.com/Genentech/MultiAssaySpatialExperiment>
- Report bugs at <https://github.com/Genentech/MultiAssaySpatialExperiment/issues>

aggregateByRegion

Aggregate assay values by shape region

Description

Aggregate assay values (e.g., counts, expression) by shape region. Each assay column is linked to a point via spatialMap; the annotation column (from [annotateWithRegions](#)) links points to shapes. Values are aggregated within each shape.

Usage

```
aggregateByRegion(x, by, assays = NULL, FUN = "sum")
```

Arguments

x	A MultiAssaySpatialExperiment .
by	Character. Name of the region column in spatialMap that holds the shape instance IDs (the regionCol from annotateWithRegions , default is the shapes layer name).
assays	Character. Assay names to aggregate (default: all assays in spatialMap).
FUN	Character or function. For character values, one of "sum", "mean", or "count". For "count", returns the number of points per shape; for "sum" and "mean", aggregates assay values. When a function, it is applied to each feature-by-observation submatrix (features as rows, observations in the same shape as columns) and must return a numeric vector of length nrow(submatrix).

Details

Run [annotateWithRegions](#) first to add the by column to spatialMap. Rows with NA in by are dropped.

For "sum" and "mean", the assay matrix (features x columns) is grouped by shape: columns that map to the same shape are aggregated. The result is a list of matrices (one per assay), each with features as rows and shape instance IDs as columns.

Value

A list of matrices (or for FUN = "count" a single DataFrame with columns by and count), one element per assay. Each matrix has features (rows) and shape instance IDs (columns).

Polymorphism

Uses S3/S4 generics only. Table-like elements (spatialMap, experiments) use nrow, colnames, rownames, [[, [, unique, and split. Assay data use [assay](#) for SummarizedExperiment-like objects; plain matrices are passed through. Layer lists use names. Consistent with [annotateWithRegions](#) and [subsetByPolygon](#); see vignette *Working with MultiAssaySpatialExperiment*.

Author(s)

Patrick Aboyoun

Examples

```
pts <- S4Vectors::DataFrame(
  x = c(1.5, 2.5, 3.5),
  y = c(1.5, 2.5, 3.5),
  instance_id = c("A", "B", "C"))
shp_df <- S4Vectors::DataFrame(
  instance_id = c("cell1", "cell2", "cell3"),
  geometry = sf::st_sfc(
    sf::st_polygon(list(matrix(c(1,1,2,1,2,2,1,2,1,1), ncol=2, byrow=TRUE))),
    sf::st_polygon(list(matrix(c(2,1,3,1,3,2,2,2,2,1), ncol=2, byrow=TRUE))),
    sf::st_polygon(list(matrix(c(2,2,3,2,3,3,2,3,2,2), ncol=2, byrow=TRUE)))))
mase <- MultiAssaySpatialExperiment(
  experiments = ExperimentList(assay1 = matrix(1:9, 3, 3,
    dimnames = list(paste0("G", 1:3), c("A", "B", "C")))),
  colData = S4Vectors::DataFrame(row.names = "s1"),
  sampleMap = S4Vectors::DataFrame(
```

```

    assay = "assay1", primary = "s1", colname = c("A", "B", "C")),
  points = PointsLayerList(centroids = pts),
  shapes = ShapesLayerList(cells = shp_df),
  spatialMap = S4Vectors::DataFrame(
    assay = "assay1", colname = c("A", "B", "C"),
    element_type = "points", region = "centroids", instance_id = c("A", "B", "C")))
mase <- annotateWithRegions(mase, points = "centroids", shapes = "cells")
agg <- aggregateByRegion(mase, by = "cells", FUN = "sum")
agg[["assay1"]]

```

annotateWithRegions *Annotate points with shape regions*

Description

Perform a spatial join between a points layer and a shapes layer. For each point, the matched shape's `instance_id` is recorded. This annotation is added to `spatialMap` and enables [aggregateByRegion](#).

Usage

```

annotateWithRegions(
  x,
  points,
  shapes,
  spatialCoordsNames = c("x", "y"),
  regionCol = NULL,
  join = st_intersects
)

```

Arguments

<code>x</code>	A MultiAssaySpatialExperiment .
<code>points</code>	Character. Name of the points layer (in <code>spatialPoints(x)</code>).
<code>shapes</code>	Character. Name of the shapes layer (in <code>spatialShapes(x)</code>).
<code>spatialCoordsNames</code>	Character vector. Names of the x and y coordinate columns in the points layer (default <code>c("x", "y")</code>).
<code>regionCol</code>	Character or NULL. Name of the column to add to <code>spatialMap</code> with the shape instance IDs. Default is the shapes name.
<code>join</code>	Function. Spatial join to use, matching st_join . Default st_intersects (point-in-polygon). Use st_nearest_feature to assign each point to the nearest shape when no shape contains it.

Details

For each row in the points layer, `join` determines which shape (if any) matches. The shape's `instance_id` is written to a new column in `spatialMap`. Only `spatialMap` rows that reference the given points layer are updated; other rows get NA for the new column.

With `join = st_intersects` (default), points not falling within any shape receive NA. With `join = st_nearest_feature`, every point is assigned to its nearest shape. The user is responsible for ensuring `instance_id` types match between points and shapes (no coercion).

Value

x with spatialMap updated to include the new annotation column. If spatialMap is NULL or the required layers are missing, x is returned unchanged.

Polymorphism

Uses S3/S4 generics only. Table-like elements (spatialMap, points, shapes) use nrow, colnames, [[, and [. Spatial operations use the supplied join function and `st_as_sfc`. Layer lists use names. Consistent with `subsetByPolygon`; see vignette *Working with MultiAssaySpatialExperiment*.

Author(s)

Patrick Aboyoun

Examples

```
pts <- S4Vectors::DataFrame(
  x = c(1.5, 2.5, 3.5),
  y = c(1.5, 2.5, 3.5),
  instance_id = c("A", "B", "C"))
shp_df <- S4Vectors::DataFrame(
  instance_id = c("cell1", "cell2", "cell3"),
  geometry = sf::st_sfc(
    sf::st_polygon(list(matrix(c(1,1,2,1,2,2,1,2,1,1), ncol=2, byrow=TRUE))),
    sf::st_polygon(list(matrix(c(2,1,3,1,3,2,2,2,2,1), ncol=2, byrow=TRUE))),
    sf::st_polygon(list(matrix(c(2,2,3,2,3,3,2,3,2,2), ncol=2, byrow=TRUE)))))
mase <- MultiAssaySpatialExperiment(
  experiments = ExperimentList(assay1 = matrix(1:9, 3, 3,
    dimnames = list(NULL, c("A", "B", "C")))),
  colData = S4Vectors::DataFrame(row.names = "s1"),
  sampleMap = S4Vectors::DataFrame(
    assay = "assay1", primary = "s1", colname = c("A", "B", "C")),
  points = PointsLayerList(centroids = pts),
  shapes = ShapesLayerList(cells = shp_df),
  spatialMap = S4Vectors::DataFrame(
    assay = "assay1", colname = c("A", "B", "C"),
    element_type = "points", region = "centroids", instance_id = c("A", "B", "C")))
mase <- annotateWithRegions(mase, points = "centroids", shapes = "cells")
spatialMap(mase)
```

buildSpatialMap

Build a spatialMap table from sampleMap

Description

Assemble a spatialMap [DataFrame](#) linking assay observations to spatial layer instances, analogous to [listToMap](#) for sampleMap.

Usage

```
buildSpatialMap(
  sampleMap,
  region,
  element_type = c("points", "shapes"),
  assays = NULL,
  instance_from = "colname"
)
```

Arguments

sampleMap	A DataFrame with MAE columns assay, primary, and colname.
region	Character. Name of the points or shapes layer (must match a name in spatialPoints or spatialShapes when the object is constructed).
element_type	Character. "points" or "shapes".
assays	Optional character vector limiting which assays from sampleMap are included.
instance_from	Character. Column of sampleMap used for instance_id values (default "colname", i.e. observation id equals spatial instance id).

Value

A [DataFrame](#) with columns assay, colname, element_type, region, and instance_id.

See Also

[prepMASE](#), [listToMap](#)

Examples

```
sm <- S4Vectors::DataFrame(
  assay = factor(rep("rna", 3), "rna"),
  primary = c("S1", "S1", "S2"),
  colname = paste0("spot", 1:3))
buildSpatialMap(sm, region = "tissue1", element_type = "points")
```

checkSpatialMap	<i>Check spatialMap consistency</i>
-----------------	-------------------------------------

Description

Run spatialMap diagnostics without constructing a [MultiAssaySpatialExperiment](#). Returns a character vector of problems (empty if valid).

Usage

```
checkSpatialMap(
  spatialMap,
  sampleMap,
  points = PointsLayerList(),
  shapes = ShapesLayerList()
)
```

Arguments

spatialMap	A spatialMap DataFrame or NULL.
sampleMap	A MAE sampleMap DataFrame .
points	A PointsLayerList or named list of point layers.
shapes	A ShapesLayerList or named list of shape layers.

Value

Character vector of error messages (length zero if no problems).

Examples

```
sm <- S4Vectors::DataFrame(
  assay = factor("rna", "rna"),
  primary = "S1",
  colname = "spot1")
spmap <- buildSpatialMap(sm, "coords", "points")
spmap[["instance_id"]] <- "missing"
checkSpatialMap(spmap, sm, points = PointsLayerList(
  coords = S4Vectors::DataFrame(
    x = 1, y = 1, instance_id = "spot1")))
```

labelsToShapes	<i>Convert label rasters to polygon shapes</i>
----------------	--

Description

Dissolve contiguous cells with the same label value into polygons. Thin wrapper around [terra::as.polygons](#) for segmentation masks stored in [spatialLabels\(\)](#) or vendor TIFFs.

Usage

```
labelsToShapes(x, dissolve = TRUE, ...)
```

Arguments

x	A SpatRaster , 2-D matrix/array, or a single element from a RasterLayerList .
dissolve	Logical; dissolve adjacent cells with the same value (default TRUE).
...	Additional arguments passed to terra::as.polygons .

Value

An [sf](#) object with dissolved label polygons.

See Also

[shapesToLabels](#), [spatialLabels](#)

Examples

```
if (requireNamespace("terra", quietly = TRUE)) {
  mat <- matrix(c(1L, 1L, 2L, 2L), 2, 2)
  labelsToShapes(mat)
}
```

MultiAssaySpatialExperiment-class

MultiAssaySpatialExperiment objects

Description

The MultiAssaySpatialExperiment class extends [MultiAssayExperiment](#) with spatial context: raster data (images, labels), points, and shapes.

Details

MultiAssaySpatialExperiment provides slots for spatial layers that complement the ExperimentList. The sampleMap links experiment columns to primary identifiers; the optional spatialMap provides instance-level mapping (assay, colname, element_type, region, instance_id) linking experiment columns to rows in the spatial point or shape layers via explicit foreign key.

Terminology: a *specimen* is a row in colData (sampleMap\$primary); an *observation* is a column in an assay (sampleMap\$colname).

Value

The MultiAssaySpatialExperiment() constructor returns a [MultiAssaySpatialExperiment](#). The layer accessors return the corresponding container: spatialImages() / spatialLabels() a [RasterLayerList](#), spatialPoints() a [PointsLayerList](#), and spatialShapes() a [ShapesLayerList](#); the single-layer accessors (spatialImage(), spatialPoint(), and so on) return one layer, and the *Names() accessors a character vector. imgData() and spatialMap() return a DataFrame or NULL. Replacement methods (the <- forms) return the updated object, and show() returns NULL invisibly.

Slots

ExperimentList, colData, sampleMap, drops Inherited from [MultiAssayExperiment](#).

images A [RasterLayerList](#) of user-attached image rasters (not the same as imgData, which stores specimen-level image metadata from vendor readers).

labels A [RasterLayerList](#) of label/mask layers.

points A [PointsLayerList](#) of point layers.

shapes A [ShapesLayerList](#) of shape layers.

imgData Optional DataFrame linking specimens to images (same structure as SpatialExperiment, including sample_id, image_id, and scaleFactor). Populated by vendor readers; distinct from spatialImages() raster layers.

spatialMap Optional DataFrame for instance-level mapping with required columns:

assay Experiment name (factor; must be in names(experiments))

colname Column identifier within that experiment

element_type Spatial slot discriminator; one of "points" or "shapes"
 region Layer name within that element type (e.g., "cells", "nuclei")
 instance_id Row identifier in that layer (character or integer; no NAs)

The element_type column disambiguates spatial layers with the same name in different slots (e.g., points\$cells vs. shapes\$cells). This explicit routing eliminates ambiguity and enables robust foreign key validation.

Terminology and spatialdata alignment

MASE adopts terminology from Python spatialdata where practical while following Bioconductor S4 conventions:

- **element_type:** Matches spatialdata's element type discriminator (values: "points", "shapes", "images", "labels"). Currently only "points" and "shapes" are supported in spatialMap linkage; images and labels are reference layers accessed via spatialImages() and spatialLabels().
- **region:** Corresponds to spatialdata's region (layer name within an element type).
- **instance_id:** Matches spatialdata's instance identifier (row ID within a region). Recommended types: integer, character, or factor. Must be unique within each (element_type, region) combination.
- **Class naming:** MASE uses "Layer" suffix (PointsLayerList, ShapesLayerList) rather than "Element" to avoid R naming collisions. See ?SpatialLayerList for details.
- **Accessor naming:** MASE uses spatialPoints(), spatialShapes() (with "spatial" prefix) as S4 generics, while spatialdata uses bare attribute access (sdata.points, sdata.shapes). This follows Bioconductor conventions and avoids conflicts with base R functions.

Constructor

MultiAssaySpatialExperiment(experiments = ExperimentList(), colData = DataFrame(), sampleMap = DataFrame())
 Creates a MultiAssaySpatialExperiment object.

experiments An [ExperimentList](#) or list of experiments.

colData A [DataFrame](#) of specimen-level metadata (one row per primary identifier in sampleMap\$primary).

sampleMap A [DataFrame](#) with columns assay, primary, colname.

metadata, drops Additional [MultiAssayExperiment](#) arguments.

images, labels [RasterLayerList](#) of user-attached raster layers (distinct from imgData, which vendor readers use for image metadata).

points, shapes [PointsLayerList](#) and [ShapesLayerList](#) of spatial layers.

imgData Optional [DataFrame](#) linking specimens to images (populated by vendor readers; use getImg() for SPE-compatible access).

spatialMap Optional [DataFrame](#) for instance-level mapping.

Accessors

In the code snippets below, x is a MultiAssaySpatialExperiment object:

spatialImages(x), spatialImages(x) <- value: Get or set the full [RasterLayerList](#) of image layers.

spatialLabels(x), spatialLabels(x) <- value: Get or set the full [RasterLayerList](#) of label layers.

spatialPoints(x), spatialPoints(x) <- value: Get or set the full [PointsLayerList](#) of point layers.

`spatialShapes(x)`, `spatialShapes(x) <- value`: Get or set the full [ShapesLayerList](#) of shape layers.

`spatialImage(x, i)`, `spatialImage(x, i) <- value`: Get or set a single image layer by index `i` (character or integer).

`spatialLabel(x, i)`, `spatialLabel(x, i) <- value`: Get or set a single label layer by index `i`.

`spatialPoint(x, i)`, `spatialPoint(x, i) <- value`: Get or set a single point layer by index `i`.

`spatialShape(x, i)`, `spatialShape(x, i) <- value`: Get or set a single shape layer by index `i`.

`spatialImageNames(x)`, `spatialLabelNames(x)`, `spatialPointNames(x)`, `spatialShapeNames(x)`: Get the names of the image, label, point, and shape layers, respectively.

`imgData(x)`, `imgData(x) <- value`: Get or set the optional `DataFrame` linking specimens to images (SpatialExperiment-compatible columns such as `sample_id`, `image_id`, and `scaleFactor`).

`spatialMap(x)`, `spatialMap(x) <- value`: Get or set the optional `DataFrame` for instance-level mapping.

Displaying

The `show()` method prints the inherited `MultiAssayExperiment` summary followed by counts of spatial images, labels, points, shapes, and whether `imgData` and `spatialMap` are present.

Author(s)

Patrick Aboyoun

See Also

- [MultiAssaySpatialExperiment-subset](#) for subsetting methods
- [MultiAssaySpatialExperiment-combine](#) for combining methods
- [RasterLayerList](#), [PointsLayerList](#), [ShapesLayerList](#) for spatial layer containers

Examples

```
mat <- matrix(rnorm(20), 5, 4,
  dimnames = list(paste0("G", 1:5), paste0("obs", 1:4)))
pts <- S4Vectors::DataFrame(
  x = 1:4, y = 1:4, instance_id = paste0("obs", 1:4))
mase <- MultiAssaySpatialExperiment(
  experiments = ExperimentList(rna = mat),
  colData = S4Vectors::DataFrame(
    tissue = c("core", "margin"),
    row.names = c("specimen_A", "specimen_B")),
  sampleMap = S4Vectors::DataFrame(
    assay = factor(rep("rna", 4), "rna"),
    primary = rep(c("specimen_A", "specimen_B"), each = 2),
    colname = paste0("obs", 1:4)),
  points = PointsLayerList(coords = pts),
  spatialMap = S4Vectors::DataFrame(
    assay = factor(rep("rna", 4), "rna"),
    colname = paste0("obs", 1:4),
    element_type = "points",
    region = "coords",
    instance_id = paste0("obs", 1:4))
)
```

```
mase
spatialPointNames(mase)
mase[, "specimen_A"]
```

MultiAssaySpatialExperiment-combine

MultiAssaySpatialExperiment combining

Description

Methods for combining [MultiAssaySpatialExperiment](#) objects. `c` merges two MASE objects (adding assays); `cbind` combines along columns (adding specimens); `complete.cases` identifies specimens with data in all assays.

Value

`c()` and `cbind()` return a combined [MultiAssaySpatialExperiment](#); `complete.cases()` returns a logical vector flagging specimens (primaries) present in all assays.

Combining

`c(x, ..., sampleMap = NULL, mapFrom = NULL)`: When ... is a single [MultiAssaySpatialExperiment](#), merges the two objects (experiments, colData, sampleMap, spatial layers, imgData, spatialMap). Experiment and spatial layer names must be unique across objects. Otherwise delegates to [c, MultiAssayExperiment-method](#).

`cbind(..., deparse.level = 1)`: Combines MASE objects column-wise (same assay names, adds specimens). Spatial layers with the same name are row-bound; imgData and spatialMap are row-bound.

`complete.cases(x)`: Returns a logical vector indicating which specimens (primaries) have data in all assays. Delegates to [complete.cases, MultiAssayExperiment-method](#).

Author(s)

Patrick Aboyoun

See Also

- [MultiAssaySpatialExperiment](#) for the main class
- [MultiAssaySpatialExperiment-subset](#) for subsetting methods

Examples

```
mat1 <- matrix(rnorm(20), 5, 4,
  dimnames = list(paste0("G", 1:5), paste0("S", 1:4)))
mat2 <- matrix(rnorm(20), 5, 4,
  dimnames = list(paste0("G", 1:5), paste0("S", 1:4)))
sm1 <- S4Vectors::DataFrame(
  assay = factor(rep("assay1", 4), "assay1"),
  primary = paste0("S", 1:4),
  colname = paste0("S", 1:4))
sm2 <- S4Vectors::DataFrame(
```

```

    assay = factor(rep("assay2", 4), "assay2"),
    primary = paste0("S", 1:4),
    colname = paste0("S", 1:4))
cd <- S4Vectors::DataFrame(row.names = paste0("S", 1:4))
mase1 <- MultiAssaySpatialExperiment(
  ExperimentList(assay1 = mat1), cd, sm1)
mase2 <- MultiAssaySpatialExperiment(
  ExperimentList(assay2 = mat2), cd, sm2)
c(mase1, mase2)
complete.cases(mase1)

```

MultiAssaySpatialExperiment-SpatialExperiment

MultiAssaySpatialExperiment - SpatialExperiment integration

Description

Coercion between [SpatialExperiment](#) and [MultiAssaySpatialExperiment](#), plus methods for `spatialCoords`, `imgData`, `scaleFactors`, `getImg`, `addImg`, `rmvImg`, and related `SpatialExperiment`-derived functionality.

Value

Coercion returns the requested object: a [MultiAssaySpatialExperiment](#) from a [SpatialExperiment](#), or a [SpatialExperiment](#) from a MASE. `spatialCoords()` returns a numeric coordinate matrix and `scaleFactors()` a numeric vector. The image methods return image data (`getImg()`) or an updated MASE for the modifying methods (such as `addImg()`). `molecules()` returns the molecule data of the first assay, or `NULL`.

Coercion

`as(spe, "MultiAssaySpatialExperiment")`: Stores the assay data as a plain [SingleCellExperiment](#) (the [SpatialExperiment](#) class itself is not retained); `spatialCoords` are copied to `points` (with a matching `spatialMap`), and `imgData` is passed through. This keeps all spatial content in MASE's own layers, which is what `writeParquet()` understands.

`as(mase, "SpatialExperiment")`: Requires exactly one assay. Builds a [SpatialExperiment](#) from that assay's data plus `spatialCoords` resolved from `points(mase)` and `imgData(mase)`.

spatialCoords and scaleFactors

`spatialCoords(x, assay = 1L)`: Returns spatial coordinates from the assay (if a `SpatialExperiment`) or from `spatialPoints(x)`.

`spatialCoordsNames(x)`: Returns coordinate column names from the first assay or `points` layer.

`scaleFactors(x, sample_id = TRUE, image_id = TRUE)`: Returns scale factors from `imgData`.

imgData methods

`getImg(x, sample_id = NULL, image_id = NULL)`: Retrieves image(s) from `imgData`.

`addImg(x, imageSource, scaleFactor, sample_id, image_id, load = TRUE)`: Adds an image to `imgData`.

`rmvImg(x, sample_id = NULL, image_id = NULL)`: Removes image(s) from `imgData`.

`imgSource(x, sample_id = NULL, image_id = NULL, path = FALSE)`: Returns image source path(s).

`imgRaster(x, sample_id = NULL, image_id = NULL)`: Returns raster image(s).

`rotateImg(x, sample_id = NULL, image_id = NULL, degrees = 90)`: Rotates image(s) in place.

`mirrorImg(x, sample_id = NULL, image_id = NULL, axis = c("h", "v"))`: Mirrors image(s) in place.

molecules

`molecules(x, ...)`: Returns molecule data from the first assay if it is a `SpatialExperiment` with a `molecules` assay; otherwise `NULL`.

Author(s)

Patrick Aboyoun

See Also

- [MultiAssaySpatialExperiment](#) for the main class
- [SpatialExperiment](#) for single-assay spatial data

Examples

```
mat <- matrix(1:12, 3, 4,
  dimnames = list(paste0("G", 1:3), paste0("cell", 1:4)))
spe <- SpatialExperiment::SpatialExperiment(
  assays = list(counts = mat),
  spatialCoords = matrix(c(1:4, 1:4), 4, 2))
mase <- as(spe, "MultiAssaySpatialExperiment")
names(mase)
spatialCoords(mase)
as(mase, "SpatialExperiment")
```

MultiAssaySpatialExperiment-subset

MultiAssaySpatialExperiment subsetting

Description

Methods for subsetting a [MultiAssaySpatialExperiment](#). They extend [subsetBy](#) with propagation to spatial slots.

Value

`subsetByColData()` and `subsetByRow()` return a [MultiAssaySpatialExperiment](#) restricted to the selected specimens or rows; the linked spatial layers, `imgData`, and `spatialMap` are subset accordingly.

Subsetting

In the snippets below, `x` is a [MultiAssaySpatialExperiment](#):

`subsetByColData(x, y)`: Subset by primary identifiers (specimens). `spatialMap`, `imgData`, and linked points, shapes, images, and labels are filtered to retained specimens (via `sampleMap` and `spatialMap`).

`subsetByRow(x, y, i = TRUE, ...)`: Subset rows of experiments. Spatial layers are assay-level and unchanged.

`subsetByColumn(x, y)`: Subset assay columns (observations). When `y` is a list (one element per assay), each element may be column names, indices, or a logical vector — the usual [subsetByColumn](#) interface. `spatialMap`, `imgData`, and linked points, shapes, images, and labels are filtered to retained columns. To subset by assay `colData`, build a logical vector or column names and pass a list, e.g. `subsetByColumn(mase, list(rna = colData(experiments(mase)[["rna"]])$ == "tumor"))`.

`subsetByAssay(x, y)`: Subset assays. Points, shapes, images, labels, `spatialMap`, and `imgData` are filtered to layers and rows linked to retained assays via `spatialMap`. Auxiliary shape layers not referenced in `spatialMap` are dropped.

`x[i, j, k, ..., drop = FALSE]`: Subset by row (`i`), column (`j`), and assay (`k`) indices. Equivalent to composing `subsetByColData`, `subsetByColumn`, `subsetByRow`, and `subsetByAssay`. If `drop = TRUE`, empty assays are removed.

`subsetByBoundingBox(x, xmin, xmax, ymin, ymax, ...)`: Subset by bounding box. Filters points and shapes within the rectangle; propagates to assays via `spatialMap` when present. When `crop_rasters = TRUE` (default), `spatialImages` and `spatialLabels` are cropped to the same bounding box (single-scale, pixel coordinates for matrix rasters; **terra** extent for `SpatRaster` layers).

`subsetByPolygon(x, polygon, ...)`: Subset by polygon. Filters points and shapes within or intersecting the `sf` geometry; propagates to assays via `spatialMap` when present. Raster layers are cropped to the polygon bounding box when `crop_rasters = TRUE`.

Polymorphism

All subsetting uses S3/S4 generics only. Table-like elements (`spatialMap`, `sampleMap`, `imgData`, points, shapes) use `nrow`, `colnames`, `[[`, `[`, `unique`, and `split` (from **BiocGenerics**). Layer lists use names and length. Spatial filtering additionally requires `sf::st_intersects` (and `st_as_sf`, `st_bbox` for shapes / polygon). For spatial filtering, `instance_id` in points, shapes, and `spatialMap` must have matching types (no coercion). See vignette *Working with MultiAssaySpatialExperiment* for a per-operation propagation table.

Author(s)

Patrick Aboyoun

See Also

- [MultiAssaySpatialExperiment](#) for the main class
- [MultiAssaySpatialExperiment-combine](#) for combining methods

Examples

```
mat <- matrix(rnorm(20), 5, 4,
  dimnames = list(paste0("G", 1:5), paste0("obs", 1:4)))
pts <- S4Vectors::DataFrame(
  x = 1:4, y = 1:4, instance_id = paste0("obs", 1:4))
sm <- S4Vectors::DataFrame(
  assay = factor(rep("rna", 4), "rna"),
  primary = rep(c("specimen_A", "specimen_B"), each = 2),
  colname = paste0("obs", 1:4))
mase <- MultiAssaySpatialExperiment(
  experiments = ExperimentList(rna = mat),
  colData = S4Vectors::DataFrame(row.names = c("specimen_A", "specimen_B")),
  sampleMap = sm,
  points = PointsLayerList(coords = pts),
  spatialMap = buildSpatialMap(sm, "coords", "points"))
subsetByColData(mase, "specimen_A")
subsetByBoundingBox(mase, xmin = 1.5, xmax = 3.5, ymin = 1.5, ymax = 3.5)
```

```
prepMASE
```

Prepare components for a MultiAssaySpatialExperiment

Description

Wraps [prepMultiAssay](#) and harmonizes spatial slots. Returns a list suitable for [MultiAssaySpatialExperiment](#) or `do.call`.

Usage

```
prepMASE(
  ExperimentList,
  colData,
  sampleMap,
  points = PointsLayerList(),
  shapes = ShapesLayerList(),
  images = RasterLayerList(),
  labels = RasterLayerList(),
  imgData = NULL,
  spatialMap = NULL,
  ...
)
```

Arguments

<code>ExperimentList</code>	A ExperimentList or named list of assays passed to prepMultiAssay .
<code>colData</code>	A DataFrame of specimen-level metadata (one row per <code>sampleMap\$primary</code>), passed to prepMultiAssay .
<code>sampleMap</code>	A DataFrame with MAE columns <code>assay</code> , <code>primary</code> , and <code>colname</code> , passed to prepMultiAssay .
<code>points</code>	A PointsLayerList or named list of point layers.
<code>shapes</code>	A ShapesLayerList or named list of shape layers.

images	A RasterLayerList of image layers (default empty).
labels	A RasterLayerList of label layers (default empty).
imgData	Optional specimen-level image metadata DataFrame .
spatialMap	Optional instance-level mapping DataFrame .
...	Additional arguments passed to <code>prepMultiAssay</code> (metadata, drops).

Value

A list with elements `experiments`, `colData`, `sampleMap`, `metadata`, `drops`, and `spatial slot components`.

See Also

[buildSpatialMap](#), [prepMultiAssay](#)

Examples

```
mat <- matrix(1:6, 2, 3, dimnames = list(c("G1", "G2"), paste0("spot", 1:3)))
sm <- S4Vectors::DataFrame(
  assay = factor(rep("rna", 3), "rna"),
  primary = c("S1", "S1", "S2"),
  colname = paste0("spot", 1:3))
pts <- S4Vectors::DataFrame(
  x = 1:3, y = 1:3, instance_id = paste0("spot", 1:3))
prepared <- prepMASE(
  ExperimentList(rna = mat),
  S4Vectors::DataFrame(row.names = c("S1", "S2")),
  sm,
  points = PointsLayerList(tissue1 = pts),
  spatialMap = buildSpatialMap(sm, "tissue1", "points"))
do.call(MultiAssaySpatialExperiment, prepared)
```

readCosMxMASE

Read NanoString CosMx SMI Spatial Data

Description

Load a NanoString CosMx output directory into a [MultiAssaySpatialExperiment](#).

Usage

```
readCosMxMASE(
  data_dir,
  sample_id = NULL,
  fov_ids = NULL,
  load_transcripts = FALSE,
  images = TRUE,
  load_images = FALSE,
  min_area = NULL
)
```

Arguments

<code>data_dir</code>	Character. Path to CosMx output directory.
<code>sample_id</code>	Character. Optional sample identifier (default: directory name).
<code>fov_ids</code>	Character vector or NULL. FOV IDs to load (default: NULL loads all).
<code>load_transcripts</code>	Logical. Whether to load transcript data (default: FALSE).
<code>images</code>	Logical. Whether to load image metadata (default: TRUE).
<code>load_images</code>	Logical. Whether to load image data (default: FALSE).
<code>min_area</code>	Numeric. Minimum polygon area for filtering (default: NULL).

Details

Supports multi-FOV datasets. Use `fov_ids` to load specific fields of view, or NULL to load all FOVs into one object. Transcript coordinates are optional (`load_transcripts`).

Value

A [MultiAssaySpatialExperiment](#) object.

See Also

[readMERSCOPEMASE](#), [readXeniumMASE](#)

Examples

```
## A minimal mock CosMx output directory is bundled for a runnable example;
## in practice, point 'data_dir' at a real CosMx output directory.
dir <- system.file("extdata", "cosmx_mock",
  package = "MultiAssaySpatialExperiment")
mase <- readCosMxMASE(dir, images = FALSE, load_transcripts = FALSE)
names(mase)
```

<code>readCSVForMASE</code>	<i>Read CSV Files for MASE</i>
-----------------------------	--------------------------------

Description

Read a CSV file into a [DataFrame](#) for MASE component assembly.

Usage

```
readCSVForMASE(file_path, ...)

## S4 method for signature 'character'
readCSVForMASE(file_path, ...)
```

Arguments

<code>file_path</code>	Character path to CSV file
<code>...</code>	Additional arguments passed to format-specific methods

Value

DataFrame

Examples

```
tmp <- tempfile(fileext = ".csv")
df <- data.frame(
  cell_id = paste0("C", 1:3),
  x_centroid = 1:3,
  y_centroid = 1:3)
write.csv(df, tmp, row.names = FALSE)
readCSVForMASE(tmp)
unlink(tmp)
```

readGeoJSONForMASE	<i>Read GeoJSON Files for MASE</i>
--------------------	------------------------------------

Description

Read a GeoJSON file via **sf** for shape layers in MASE readers.

Usage

```
readGeoJSONForMASE(file_path, ...)

## S4 method for signature 'character'
readGeoJSONForMASE(file_path, quiet = TRUE, ...)
```

Arguments

<code>file_path</code>	Character path to GeoJSON file
<code>...</code>	Additional arguments passed to format-specific methods
<code>quiet</code>	Logical, suppress sf reading messages

Value

sf or equivalent object

Examples

```
tmp <- tempfile(fileext = ".geojson")
pt <- sf::st_point(c(10, 20))
sf_obj <- sf::st_sf(id = "C1", geometry = sf::st_sfc(pt))
sf::st_write(sf_obj, tmp, quiet = TRUE, delete_dsn = TRUE)
readGeoJSONForMASE(tmp, quiet = TRUE)
unlink(tmp)
```

readGeoParquetForMASE *Read GeoParquet Files for MASE*

Description

Read a GeoParquet file via **sfarrow** for geometry layers in MASE readers.

Usage

```
readGeoParquetForMASE(file_path, ...)

## S4 method for signature 'character'
readGeoParquetForMASE(file_path, ...)
```

Arguments

file_path	Character path to GeoParquet file
...	Additional arguments passed to format-specific methods

Value

sf object or equivalent object

Examples

```
if (requireNamespace("sfarrow", quietly = TRUE) &&
    requireNamespace("sf", quietly = TRUE)) {
  tmp <- tempfile(fileext = ".parquet")
  pt <- sf::st_sfc(sf::st_point(c(1, 2)))
  sf_obj <- sf::st_sf(id = 1L, geometry = pt)
  sfarrow::st_write_parquet(sf_obj, tmp)
  readGeoParquetForMASE(tmp)
  unlink(tmp)
}
```

readHDF5ForMASE *Read HDF5 Files for MASE*

Description

Read an HDF5 matrix file (10x or AnnData/h5ad) into a [SummarizedExperiment](#) for MASE assembly.

Usage

```
readHDF5ForMASE(file_path, type = c("10x", "anndata"), ...)

## S4 method for signature 'character,character'
readHDF5ForMASE(file_path, type = c("10x", "anndata"), ...)
```

Arguments

file_path	Character path to HDF5 file
type	Character: "10x" for 10x HDF5, "anndata" for h5ad
...	Additional arguments passed to format-specific methods

Value

SummarizedExperiment

Examples

```
## Requires DropletUtils and a 10x filtered_feature_bc_matrix.h5 file
readHDF5ForMASE("filtered_feature_bc_matrix.h5", type = "10x")
```

readMERSCOPEMASE	<i>Read Vizgen MERSCOPE Spatial Data</i>
------------------	--

Description

Load a Vizgen MERSCOPE (MERFISH) output directory into a [MultiAssaySpatialExperiment](#).

Usage

```
readMERSCOPEMASE(
  data_dir,
  sample_id = NULL,
  fov_ids = NULL,
  segmentation = c("cellpose", "watershed", "both"),
  load_transcripts = FALSE,
  images = TRUE,
  load_images = FALSE,
  min_area = NULL,
  min_qv = 20
)
```

Arguments

data_dir	Character. Path to MERSCOPE output directory.
sample_id	Character. Optional sample identifier (default: directory name).
fov_ids	Character vector or NULL. FOV IDs to load (default: NULL loads all).
segmentation	Character. Segmentation method: "cellpose", "watershed", or "both" (default: "cellpose").
load_transcripts	Logical. Whether to load transcript data (default: FALSE).
images	Logical. Whether to load image metadata (default: TRUE).
load_images	Logical. Whether to load image data (default: FALSE).
min_area	Numeric. Minimum polygon area for filtering (default: NULL).
min_qv	Numeric. Minimum quality value for transcripts (default: 20).

Details

Supports multi-FOV datasets and multiple segmentation methods (segmentation: "cellpose", "watershed", or "both"). Transcript coordinates are optional (load_transcripts).

Value

A [MultiAssaySpatialExperiment](#) object.

See Also

[readCosMxMASE](#), [readXeniumMASE](#)

Examples

```
## A minimal mock MERSCOPE output directory is bundled for a runnable
## example; in practice, point 'data_dir' at a real MERSCOPE region directory.
dir <- system.file("extdata", "merscope_mock",
                  package = "MultiAssaySpatialExperiment")
mase <- readMERSCOPEMASE(dir, segmentation = "cellpose",
                        images = FALSE, load_transcripts = FALSE)
names(mase)
```

readParquetForMASE	<i>Read Parquet Files for MASE</i>
--------------------	------------------------------------

Description

Read a Parquet file into a [DataFrame](#) for use in MASE component assembly or custom readers.

Usage

```
readParquetForMASE(file_path, ...)

## S4 method for signature 'character'
readParquetForMASE(file_path, col_select = NULL, ...)
```

Arguments

file_path	Character path to Parquet file
...	Additional arguments passed to format-specific methods
col_select	Optional character vector of column names to select

Value

DataFrame

Examples

```
if (requireNamespace("arrow", quietly = TRUE)) {
  tmp <- tempfile(fileext = ".parquet")
  df <- data.frame(cell_id = paste0("C", 1:3), x = 1:3, y = 1:3)
  arrow::write_parquet(df, tmp)
  readParquetForMASE(tmp)
  unlink(tmp)
}
```

readVisiumHDMASE	<i>Read 10x Genomics Visium HD Spatial Data</i>
------------------	---

Description

Load a 10x Genomics Visium HD Space Ranger output directory into a [MultiAssaySpatialExperiment](#).

Usage

```
readVisiumHDMASE(
  data_dir,
  sample_id = NULL,
  bin_size = c("008", "002", "016"),
  load_boundaries = FALSE,
  images = TRUE,
  load_images = FALSE,
  min_area = NULL
)
```

Arguments

<code>data_dir</code>	Character. Path to Space Ranger output directory.
<code>sample_id</code>	Character. Optional sample identifier (default: directory name).
<code>bin_size</code>	Character vector. Bin sizes to load: "002", "008", "016" (default: "008").
<code>load_boundaries</code>	Logical. Whether to load cell segmentation boundaries (default: FALSE).
<code>images</code>	Logical. Whether to load image metadata (default: TRUE).
<code>load_images</code>	Logical. Whether to load image data (default: FALSE).
<code>min_area</code>	Numeric. Minimum polygon area for filtering (default: NULL).

Details

Visium HD provides binned expression at 2 μm , 8 μm , and 16 μm resolution (codes "002", "008", "016"). Each requested bin size becomes a separate assay in the returned object.

Value

A [MultiAssaySpatialExperiment](#) with one experiment per requested bin size.

See Also

[readVisiumMASE](#), [readXeniumMASE](#)

Examples

```
## Requires a Visium HD Space Ranger output directory
mase <- readVisiumHDMASE("path/to/visium_hd", bin_size = "008")
names(mase)
```

readVisiumMASE	<i>Read 10x Genomics Visium Spatial Data</i>
----------------	--

Description

Load a 10x Genomics Visium Space Ranger output directory into a [MultiAssaySpatialExperiment](#).

Usage

```
readVisiumMASE(
  data_dir,
  sample_id = NULL,
  type = c("HDF5", "sparse"),
  data = c("filtered", "raw"),
  images = TRUE,
  load_images = FALSE,
  unit = c("pixel", "micron"),
  min_area = NULL,
  block_size = NULL
)
```

Arguments

<code>data_dir</code>	Character. Path to Space Ranger output directory.
<code>sample_id</code>	Character. Optional sample identifier (default: directory name).
<code>type</code>	Character. Matrix format: "HDF5" or "sparse" (default: "HDF5").
<code>data</code>	Character. Data type: "filtered" or "raw" (default: "filtered").
<code>images</code>	Logical. Whether to load image metadata (default: TRUE).
<code>load_images</code>	Logical. Whether to load image data (default: FALSE).
<code>unit</code>	Character. Coordinate units: "pixel" or "micron" (default: "pixel").
<code>min_area</code>	Numeric. Minimum polygon area for filtering (default: NULL).
<code>block_size</code>	Numeric. Block size for chunked reading (default: 100MB).

Details

Reads spot-by-gene counts, tissue positions, spot geometries, and optional H&E image metadata (images). Coordinates may be returned in pixels or microns (`unit`). For Visium HD data, use [readVisiumHDMASE](#).

Value

A [MultiAssaySpatialExperiment](#) object.

See Also

[readVisiumHDMASE](#), [readXeniumMASE](#)

Examples

```
## Requires a Space Ranger output directory (see package tests for mock layout)
mase <- readVisiumMASE("path/to/visium")
names(mase)
```

readXeniumMASE	<i>Read 10x Genomics Xenium Spatial Data</i>
----------------	--

Description

Load a 10x Genomics Xenium output directory into a [MultiAssaySpatialExperiment](#).

Usage

```
readXeniumMASE(
  data_dir,
  sample_id = NULL,
  segmentations = c("cell", "nucleus", "both"),
  images = TRUE,
  load_images = FALSE,
  add_transcripts = FALSE,
  min_area = NULL,
  min_phred = 20,
  block_size = NULL
)
```

Arguments

data_dir	Character. Path to Xenium output directory.
sample_id	Character. Optional sample identifier (default: directory name).
segmentations	Character. Segmentation type: "cell", "nucleus", or "both" (default: "cell").
images	Logical. Whether to load image metadata (default: TRUE).
load_images	Logical. Whether to load image data (default: FALSE).
add_transcripts	Logical. Whether to include transcript data (default: FALSE).
min_area	Numeric. Minimum polygon area for filtering (default: NULL).
min_phred	Integer. Minimum phred score for transcripts (default: 20).
block_size	Numeric. Block size for chunked reading (default: 100MB).

Details

Reads cell-by-gene counts, cell coordinates, optional segmentation polygons (segmentations), and optionally transcript-level coordinates (add_transcripts). Image metadata is included when images = TRUE; set load_images = TRUE to load raster data.

Value

A [MultiAssaySpatialExperiment](#) object with expression, coordinates, optional shapes, and spatialMap linkage.

See Also

[readVisiumMASE](#), [readVisiumHDMASE](#), [readCosMxMASE](#), [readMERSCOPEMASE](#)

Examples

```
## Requires a Xenium output directory (see package tests for mock layout)
mase <- readXeniumMASE("path/to/xenium")
names(mase)
```

shapesToLabels

Rasterize polygon shapes to a label image

Description

Burn shape geometries into a label raster. When template is NULL, an empty raster is created from the bounding box of x.

Usage

```
shapesToLabels(x, template = NULL, field = "instance_id", background = NA, ...)
```

Arguments

x	An sf object or data.frame with polygon geometries.
template	Optional SpatRaster defining extent and resolution.
field	Character; attribute column used as label values (default "instance_id").
background	Numeric background value (default NA).
...	Additional arguments passed to terra::rasterize.

Value

A SpatRaster label image.

See Also

[labelsToShapes](#), [spatialShapes](#)

Examples

```
if (requireNamespace("terra", quietly = TRUE)) {
  mat <- matrix(c(1L, 1L, 2L, 2L), 2, 2)
  polys <- labelsToShapes(mat)
  polys$instance_id <- polys[["lyr.1"]]
  shapesToLabels(polys, field = "instance_id", background = 0L)
}
```

spatial-accessors	<i>Access spatial element slots</i>
-------------------	-------------------------------------

Description

Generic functions to access `spatialImages`, `spatialLabels`, `spatialPoints`, `spatialShapes`, and `spatialMap` slots of [MultiAssaySpatialExperiment](#). The `imgData` generic is imported from **Spatial-Experiment**.

Usage

```
spatialImages(x)

spatialLabels(x)

spatialPoints(x)

spatialShapes(x)

spatialMap(x)

spatialImages(x) <- value

spatialLabels(x) <- value

spatialPoints(x) <- value

spatialShapes(x) <- value

spatialMap(x) <- value

spatialImage(x, i)

spatialLabel(x, i)

spatialPoint(x, i)

spatialShape(x, i)

spatialImageNames(x)

spatialLabelNames(x)
```

```

spatialPointNames(x)

spatialShapeNames(x)

spatialImage(x, i) <- value

spatialLabel(x, i) <- value

spatialPoint(x, i) <- value

spatialShape(x, i) <- value

```

Arguments

<code>x</code>	A MultiAssaySpatialExperiment object
<code>value</code>	Replacement value for the element
<code>i</code>	Index (character or integer) for the element name

Details

Slot accessors (`spatialImages`, `spatialLabels`, etc.) return the full element list. Single-element accessors (`spatialImage`, `spatialLabel`, etc.) take an index `i` (character or integer) and return the element. Name accessors return character vectors of element names. Replacement functions for slots take a full list; single- element replacements take an index and the new value.

For single-element accessors, a character index with no matching name (e.g., `spatialImage(x, "nonexistent")`) returns `NULL`. Integer indices that are out of bounds raise an error.

Value

For accessors: the slot or element contents. For replacement functions: the modified object.

Author(s)

Patrick Aboyoun

See Also

[MultiAssaySpatialExperiment](#), [RasterLayerList](#), [PointsLayerList](#), [ShapesLayerList](#)

Examples

```

mat <- matrix(rnorm(20), 5, 4, dimnames = list(paste0("G", 1:5), paste0("obs", 1:4)))
explist <- ExperimentList(rna = mat)
cd <- S4Vectors::DataFrame(sample = "specimen_1", row.names = "specimen_1")
sm <- S4Vectors::DataFrame(
  assay = factor(rep("rna", 4), "rna"),
  primary = rep("specimen_1", 4),
  colname = paste0("obs", 1:4))
mase <- MultiAssaySpatialExperiment(
  experiments = explist,
  colData = cd,
  sampleMap = sm,
  images = RasterLayerList(brightfield = matrix(1:12, 3, 4))

```

```

)
spatialImageNames(mase)
spatialImage(mase, 1L)
spatialImage(mase, "brightfield")
spatialImages(mase) <- RasterLayerList(fluorescent = matrix(20:31, 3, 4))
spatialImageNames(mase)

```

spatialJoin

Spatial join between spatial layer tables

Description

Join two spatial [DataFrame](#) layers on a spatial predicate. The `DataFrame` method uses `sf` attribute joins via `st_join`.

Usage

```
spatialJoin(x, y, join = st_intersects, sparse = TRUE, ...)
```

Arguments

<code>x</code>	A DataFrame with spatial data.
<code>y</code>	A spatial table to join against.
<code>join</code>	Spatial predicate function (default st_intersects).
<code>sparse</code>	Logical; when TRUE, request a sparse pair-table result where supported by methods (default TRUE for the generic signature; the <code>DataFrame</code> method materializes via <code>st_join</code>).
<code>...</code>	Additional arguments for methods.

Value

Join result. The `DataFrame` method returns an `sf` object from `st_join`.

Author(s)

Patrick Aboyoun

See Also

[spatialMatch](#) for first-match indexing without attaching attributes.

Examples

```

library(sf)
pts <- S4Vectors::DataFrame(
  spot = c("A", "B"),
  geometry = c("POINT (1 1)", "POINT (5 5)")
)
cells <- S4Vectors::DataFrame(
  cell = c("C1", "C2"),
  geometry = c(
    "POLYGON ((0 0, 3 0, 3 3, 0 3, 0 0))",

```

```
"POLYGON ((4 4, 6 4, 6 6, 4 6, 4 4)))"
spatialJoin(pts, cells)
```

SpatialLayerList-class

Spatial layer list objects

Description

The [SpatialLayerList](#) class is a virtual base extending [SimpleList](#). Concrete subclasses [RasterLayerList](#), [PointsLayerList](#), and [ShapesLayerList](#) provide typed containers for raster data (images, labels), point coordinates, and shape geometries.

Details

All layers must be named and have unique names. Element-type validity is enforced by each concrete class: [RasterLayerList](#) requires `dim()` with length ≥ 2 (e.g., `matrix`, `array`, `DelayedArray`, `StoredSpatialImage`); [PointsLayerList](#) requires `DataFrame` elements with at least 2 columns (typically `x`, `y`) and often an instance identifier; [ShapesLayerList](#) requires `DataFrame` elements (with `sf` a geometry column may be present).

Value

The constructors `RasterLayerList()`, `PointsLayerList()`, and `ShapesLayerList()` return an object of the corresponding class. Coercion via `as()` returns the requested `*LayerList`, and the `show()` method returns `NULL` invisibly.

Constructors

`RasterLayerList(...)`: Creates a [RasterLayerList](#). Accepts named arguments, a single named list, or a single [List](#). Each element must have `dim()` with length ≥ 2 .

`PointsLayerList(...)`: Creates a [PointsLayerList](#). Accepts named `DataFrame` elements or a single list/List. Each element must have at least 2 columns.

`ShapesLayerList(...)`: Creates a [ShapesLayerList](#). Accepts named `DataFrame` or `data.frame` elements (coerced to `DataFrame`); or a single list/List.

Coercion

`as(x, "RasterLayerList")`, `as(x, "PointsLayerList")`, `as(x, "ShapesLayerList")`: Coerce list or [List](#) to the target class. For `ShapesLayerList`, `data.frame` elements are converted to `DataFrame`.

Displaying

The `show()` method prints the class name, length, and for each layer: index, name, element class, and dimensions (raster) or row x col (points/shapes).

Note**Terminology alignment with spatialdata:**

MASE uses the "Layer" suffix (PointsLayerList, ShapesLayerList, RasterLayerList) rather than "Element" to avoid naming collisions with R base classes and Bioconductor conventions. The Python spatialdata package uses "element" as an internal discriminator (e.g., element_type column, sdata.points, sdata.shapes) but does not define List container classes.

MASE's element_type column in spatialMap corresponds to spatialdata's element type discriminator, routing to the appropriate spatial slot: "points" → PointsLayerList, "shapes" → ShapesLayerList. See ?MultiAssaySpatialExperiment for details on the spatialMap linkage model.

Other intentional differences: MASE uses spatialPoints(), spatialShapes(), etc. (with "spatial" prefix) as S4 generic accessors, while spatialdata uses bare attribute access (sdata.points, sdata.shapes). This follows Bioconductor S4 conventions and avoids conflicts with base R functions.

Author(s)

Patrick Aboyoun

See Also

- [MultiAssaySpatialExperiment](#) for usage in multi-assay context
- [SimpleList](#) for the base class

Examples

```
RasterLayerList()
RasterLayerList(img = matrix(1:12, 3, 4))

pts <- S4Vectors::DataFrame(x = c(1, 2), y = c(3, 4))
PointsLayerList(coords = pts)

ShapesLayerList()
df <- S4Vectors::DataFrame(id = 1:2, value = c("a", "b"))
ShapesLayerList(regions = df)
```

spatialMatch

Spatial match for DataFrame

Description

For each row of x, find the first matching row in table based on a spatial relationship. Analogous to match(x, table) from **S4Vectors**: returns an integer vector of positions in table.

Arguments

<code>x</code>	A DataFrame with coordinate columns representing point locations.
<code>table</code>	A DataFrame with a geometry column representing spatial regions.
<code>...</code>	Additional arguments passed to methods. Common arguments: <code>coords</code> Character vector of length 2 naming the coordinate columns in <code>x</code> . <code>geom</code> Character; name of the geometry column in <code>table</code> (default "geometry"). <code>join</code> A spatial join function (default <code>sf::st_intersects</code>). Must accept two geometry arguments and return either an <code>sfg</code> list or an integer vector.

Details

The `DataFrame` method builds point geometries from the coordinate columns of `x`, applies the `join` function against the geometry column of `table`, and returns the first match per row.

Downstream packages can define methods for their own `DataFrame` subclasses to push the spatial join to an alternative backend (e.g., SQL-based spatial joins, Arrow compute, in-memory acceleration).

Value

An integer vector of length `nrow(x)`. Each element is the row position in `table` of the first spatial match, or NA if no match is found.

Author(s)

Patrick Aboyoun

See Also

[spatialOverlaps](#) for the predicate analogue (like `is.na`).

Examples

```
library(sf)
pts <- S4Vectors::DataFrame(x = c(1, 5, 10), y = c(1, 5, 10))
shapes <- S4Vectors::DataFrame(
  geometry = st_as_sfc(c(
    "POLYGON((0 0, 6 0, 6 6, 0 6, 0 0))",
    "POLYGON((7 7, 12 7, 12 12, 7 12, 7 7))"))
spatialMatch(pts, shapes, coords = c("x", "y"))
## 1 1 2
```

spatialOverlaps

Spatial overlap predicate for DataFrame

Description

Test which rows of a [DataFrame](#) spatially intersect a region. Analogous to `is.na` or duplicated from **S4Vectors**: returns a logical vector that can be used for subsetting via `x[spatialOverlaps(x, y, ...), ]`.

Arguments

<code>x</code>	A DataFrame with spatial data (coordinate columns or a geometry column).
<code>y</code>	A spatial region to test against. Typically an <code>sfc</code> , <code>sfg</code> , or similar geometry object from <code>sf</code> .
<code>...</code>	Additional arguments passed to methods. Common arguments: <code>coords</code> Character vector of length 2 naming the coordinate columns in <code>x</code> (e.g., <code>c("x", "y")</code>). When provided, point geometries are constructed from these columns and tested for intersection with <code>y</code>. <code>geom</code> Character; name of the geometry column in <code>x</code> (default <code>"geometry"</code>). Used when <code>coords</code> is not provided.

Details

The `DataFrame` method uses `sf` functions (`st_as_sfc`, `st_intersects`). Downstream packages can define methods for their own `DataFrame` subclasses to use alternative backends (e.g., SQL databases, Arrow, HDF5).

Two modes are supported based on the arguments:

Coordinate mode When `coords` is provided, point geometries are constructed from those columns and tested against `y`.

Geometry mode When `coords` is `NULL` (the default), the column named by `geom` is used directly.

Value

A logical vector of length `nrow(x)`. `TRUE` for rows whose spatial data intersects `y`.

Author(s)

Patrick Aboyoun

See Also

[spatialMatch](#) for the relational analogue (like `match`).

Examples

```
library(sf)
pts <- S4Vectors::DataFrame(x = c(1, 5, 10), y = c(1, 5, 10))
polygon <- st_as_sfc("POLYGON((0 0, 6 0, 6 6, 0 6, 0 0))")
spatialOverlaps(pts, polygon, coords = c("x", "y"))
## TRUE TRUE FALSE
```

Index

*** classes**
 MultiAssaySpatialExperiment-class, [9](#)
 SpatialLayerList-class, [30](#)
*** internal**
 MultiAssaySpatialExperiment-package, [3](#)
*** methods**
 MultiAssaySpatialExperiment-class, [9](#)
 MultiAssaySpatialExperiment-SpatialExperiment, [13](#)
 MultiAssaySpatialExperiment-subset, [14](#)
 SpatialLayerList-class, [30](#)
 [, MultiAssaySpatialExperiment, ANY, ANY, ANY-method (MultiAssaySpatialExperiment-subset), [14](#)
 coerce, List, RasterLayerList-method (SpatialLayerList-class), [30](#)
 coerce, list, RasterLayerList-method (SpatialLayerList-class), [30](#)
 coerce, List, ShapesLayerList-method (SpatialLayerList-class), [30](#)
 coerce, list, ShapesLayerList-method (SpatialLayerList-class), [30](#)
 coerce, MultiAssaySpatialExperiment, SpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 coerce, SpatialExperiment, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 dataFrame, [6–8](#), [10](#), [16–18](#), [22](#), [29](#), [32](#), [33](#)
 ExperimentList, [10](#), [16](#)
 addImg, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 aggregateByRegion, [3](#), [5](#)
 aggregateByRegion, MultiAssaySpatialExperiment-method (aggregateByRegion), [3](#)
 annotateWithRegions, [3](#), [4](#), [5](#)
 annotateWithRegions, MultiAssaySpatialExperiment-method (annotateWithRegions), [5](#)
 assay, [4](#)
 buildSpatialMap, [6](#), [17](#)
 c, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-combine), [12](#)
 cbind, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-combine), [12](#)
 checkSpatialMap, [7](#)
 coerce, List, PointsLayerList-method (SpatialLayerList-class), [30](#)
 coerce, list, PointsLayerList-method (SpatialLayerList-class), [30](#)
 coerce, List, RasterLayerList-method (SpatialLayerList-class), [30](#)
 coerce, list, RasterLayerList-method (SpatialLayerList-class), [30](#)
 coerce, List, ShapesLayerList-method (SpatialLayerList-class), [30](#)
 coerce, list, ShapesLayerList-method (SpatialLayerList-class), [30](#)
 coerce, MultiAssaySpatialExperiment, SpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 coerce, SpatialExperiment, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 dataFrame, [6–8](#), [10](#), [16–18](#), [22](#), [29](#), [32](#), [33](#)
 ExperimentList, [10](#), [16](#)
 getImg, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 imgData, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), [9](#)
 imgData, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), [9](#)
 imgRaster, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 imgSource, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)
 labelsToShapes, [8](#), [26](#)
 List, [30](#)
 listToMap, [6](#), [7](#)
 mirrorImg, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-SpatialExperiment), [13](#)

- molecules, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- MultiAssayExperiment, 9, 10
- MultiAssaySpatialExperiment, 4, 5, 7, 9, 12–18, 21–28, 31
- MultiAssaySpatialExperiment
(MultiAssaySpatialExperiment-class), 9
- MultiAssaySpatialExperiment-class, 9
- MultiAssaySpatialExperiment-combine, 11, 12, 15
- MultiAssaySpatialExperiment-package, 3
- MultiAssaySpatialExperiment-SpatialExperiment, 13
- MultiAssaySpatialExperiment-subset, 11, 12, 14

- PointsLayerList, 8–11, 16, 28, 30
- PointsLayerList
(SpatialLayerList-class), 30
- PointsLayerList-class
(SpatialLayerList-class), 30
- prepMASE, 7, 16
- prepMultiAssay, 16, 17

- RasterLayerList, 8–11, 17, 28, 30
- RasterLayerList
(SpatialLayerList-class), 30
- RasterLayerList-class
(SpatialLayerList-class), 30
- readCosMxMASE, 17, 22, 26
- readCSVForMASE, 18
- readCSVForMASE, character-method
(readCSVForMASE), 18
- readGeoJSONForMASE, 19
- readGeoJSONForMASE, character-method
(readGeoJSONForMASE), 19
- readGeoParquetForMASE, 20
- readGeoParquetForMASE, character-method
(readGeoParquetForMASE), 20
- readHDF5ForMASE, 20
- readHDF5ForMASE, character, character-method
(readHDF5ForMASE), 20
- readMERSCOPEMASE, 18, 21, 26
- readParquetForMASE, 22
- readParquetForMASE, character-method
(readParquetForMASE), 22
- readVisiumHDMASE, 23, 24–26
- readVisiumMASE, 24, 24, 26
- readXeniumMASE, 18, 22, 24, 25, 25
- rmvImg, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- rmvImg, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- scaleFactors, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- ShapesLayerList, 8–11, 16, 28, 30
- ShapesLayerList
(SpatialLayerList-class), 30
- ShapesLayerList-class
(SpatialLayerList-class), 30
- shapesToLabels, 8, 26
- show, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 9
- show, PointsLayerList-method
(SpatialLayerList-class), 30
- show, RasterLayerList-method
(SpatialLayerList-class), 30
- show, ShapesLayerList-method
(SpatialLayerList-class), 30
- SimpleList, 30, 31
- SingleCellExperiment, 13
- spatial-accessors, 27
- spatialCoords, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- spatialCoordsNames, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-SpatialExperiment), 13
- SpatialExperiment, 13, 14
- spatialImage (spatial-accessors), 27
- spatialImage, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 9
- spatialImage<- (spatial-accessors), 27
- spatialImage<- , MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 9
- spatialImageNames (spatial-accessors), 27
- spatialImageNames, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 9
- spatialImages (spatial-accessors), 27
- spatialImages, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 9
- spatialImages<- (spatial-accessors), 27
- spatialImages<- , MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-class), 27

- 9
- spatialJoin, 29
- spatialJoin, DataFrame, DataFrame-method (spatialJoin), 29
- spatialLabel (spatial-accessors), 27
- spatialLabel, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialLabel<- (spatial-accessors), 27
- spatialLabel<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialLabelNames (spatial-accessors), 27
- spatialLabelNames, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialLabels, 8
- spatialLabels (spatial-accessors), 27
- spatialLabels, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialLabels<- (spatial-accessors), 27
- spatialLabels<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- SpatialLayerList, 30
- SpatialLayerList-class, 30
- spatialMap (spatial-accessors), 27
- spatialMap, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialMap<- (spatial-accessors), 27
- spatialMap<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialMatch, 29, 31, 33
- spatialMatch, DataFrame, DataFrame-method (spatialMatch), 31
- spatialOverlaps, 32, 32
- spatialOverlaps, DataFrame-method (spatialOverlaps), 32
- spatialPoint (spatial-accessors), 27
- spatialPoint, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialPoint<- (spatial-accessors), 27
- spatialPoint<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialPointNames (spatial-accessors), 27
- spatialPointNames, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialPoints (spatial-accessors), 27
- spatialPoints, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialPoints<- (spatial-accessors), 27
- spatialPoints<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialShape (spatial-accessors), 27
- spatialShape, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialShape<- (spatial-accessors), 27
- spatialShape<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialShapeNames (spatial-accessors), 27
- spatialShapeNames, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialShapes, 26
- spatialShapes (spatial-accessors), 27
- spatialShapes, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- spatialShapes<- (spatial-accessors), 27
- spatialShapes<-, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-class), 9
- st_as_sfc, 6
- st_intersects, 5, 29
- st_join, 5, 29
- st_nearest_feature, 5
- subsetBy, 14
- subsetByAssay, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-subset), 14
- subsetByBoundingBox (MultiAssaySpatialExperiment-subset), 14
- subsetByBoundingBox, MultiAssaySpatialExperiment-method (MultiAssaySpatialExperiment-subset), 14
- subsetByColData, MultiAssaySpatialExperiment, ANY-method (MultiAssaySpatialExperiment-subset), 14
- subsetByColData, MultiAssaySpatialExperiment, character-method (MultiAssaySpatialExperiment-subset), 14

14
subsetByColumn, 15
subsetByColumn, MultiAssaySpatialExperiment, ANY-method
(MultiAssaySpatialExperiment-subset),
14
subsetByPolygon, 4, 6
subsetByPolygon
(MultiAssaySpatialExperiment-subset),
14
subsetByPolygon, MultiAssaySpatialExperiment-method
(MultiAssaySpatialExperiment-subset),
14
subsetByRow, MultiAssaySpatialExperiment, ANY-method
(MultiAssaySpatialExperiment-subset),
14
subsetByRow, MultiAssaySpatialExperiment, List-method
(MultiAssaySpatialExperiment-subset),
14
subsetByRow, MultiAssaySpatialExperiment, list-method
(MultiAssaySpatialExperiment-subset),
14
SummarizedExperiment, 20
terra::as.polygons, 8