

Package: *sosta* (via r-universe)

January 20, 2025

Title A package for the analysis of anatomical tissue structures in spatial omics data

Version 0.99.3

Description ``sosta`` (Spatial Omics SStructure Analysis) is a package for analyzing spatial omics data to explore tissue organization at the anatomical structure level. It reconstructs morphologically relevant structures based on molecular features or cell types. It further calculates a range of structural and shape metrics to quantitatively describe tissue architecture. The package is designed to integrate with other packages for the analysis of spatial (omics) data.

License GPL (>= 3) + file LICENSE

Encoding UTF-8

Depends R (>= 4.4.0)

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

URL <https://github.com/sgunz/sosta>, <https://sgunz.github.io/sosta/>

BugReports <https://github.com/sgunz/sosta/issues>

biocViews Software, Spatial, Transcriptomics, Visualization

Imports terra, sf, smoothr, spatstat.explore, spatstat.geom, SpatialExperiment, dplyr, ggplot2, patchwork, SummarizedExperiment, stats, rlang, parallel

Suggests knitr, rmarkdown, ggspavis, BiocStyle, imcdatasets, ggfortify, tidyr, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs libgdal-dev gdal-bin libgeos-dev libmagick++-dev gsfonts libicu-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/sosta>

RemoteRef HEAD

RemoteSha 225afd3a78fef6111c11dfd4575915da50060e30

Contents

.intensityImage	2
.intensityThreshold	3
binaryImageToSF	3
estimateReconstructionParametersSPE	4
findIntensityThreshold	5
getDimXY	6
meanShapeMetrics	7
normalizeCoordinates	7
reconstructShapeDensity	8
reconstructShapeDensityImage	9
reconstructShapeDensitySPE	10
shapeIntensityImage	11
shapeMetrics	12
SPE2ppp	13
st_calculateCurvature	13
st_calculateShapeCurl	14
st_feature_axes	15
totalShapeMetrics	16
xyCoordinates	16
Index	18

.intensityImage	<i>Function to estimate the intensity image of a point pattern</i>
-----------------	--

Description

Function to estimate the intensity image of a point pattern

Usage

```
.intensityImage(ppp, mark_select = NULL, bndw = NULL, dim)
```

Arguments

ppp	point pattern object of class ppp
mark_select	character; name of mark that is to be selected for the reconstruction
bndw	bandwidth of kernel density estimator
dim	numeric; x dimension of the final reconstruction.

Value

list; list with the intensity image and the bandwidth and dimension parameters

.intensityThreshold *Function to estimate the intensity threshold for the reconstruction of spatial structures*

Description

Function to estimate the intensity threshold for the reconstruction of spatial structures

Usage

```
.intensityThreshold(density_image, steps = 250)
```

Arguments

`density_image` real-valued pixel image; output from the function `.intensityImage`
`steps` numeric; value used to filter the density estimates, where only densities greater than the maximum value divided by threshold are considered. Default is 250.

Value

numeric; estimated threshold

`binaryImageToSF` *Converts a binary matrix to an sf polygon*

Description

Converts a binary matrix to an sf polygon

Usage

```
binaryImageToSF(binaryMatrix, xmin, xmax, ymin, ymax)
```

Arguments

`binaryMatrix` matrix; binary matrix
`xmin` integer; minimum x coordinate of the coordinate system
`xmax` integer; maximum x coordinate of the coordinate system
`ymin` integer; minimum y coordinate of the coordinate system
`ymax` integer; maximum y coordinate of the coordinate system

Value

sf object

Examples

```
matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
poly_R <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
plot(poly_R)
```

estimateReconstructionParametersSPE

Estimate reconstruction parameters from a set of images

Description

Estimate reconstruction parameters from a set of images

Usage

```
estimateReconstructionParametersSPE(
  spe,
  marks,
  image_col,
  mark_select = NULL,
  nimages = NULL,
  fun = "bw.diggle",
  dim = 500,
  ncores = 1,
  plot_hist = TRUE
)
```

Arguments

spe	SpatialExperiment; a object of class SpatialExperiment
marks	character; name of column in colData that will correspond to the ppp marks
image_col	character; name of a column in colData that corresponds to the image
mark_select	character; name of mark that is to be selected for the reconstruction

nimages	integer; number of images for the estimation. Will be randomly sampled
fun	character; function to estimate the kernel density. Default bw.diggle.
dim	numeric; x dimension of the final reconstruction. A lower resolution speed up computation but lead to less exact reconstruction. Default = 500
ncores	numeric; number of cores for parallel processing using mclapply. Default = 1
plot_hist	logical; if histogram of estimated densities and thresholds should be plotted. Default = TRUE

Value

tibble; tibble with estimated intensities and thresholds

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
spe_sel <- spe[, spe[["image_name"]] %in% c("E02", "E03", "E04")]
estimateReconstructionParametersSPE(spe_sel,
  marks = "cell_category",
  image_col = "image_name", mark_select = "islet", plot_hist = TRUE
)
```

findIntensityThreshold

Estimate the intensity threshold for the reconstruction of spatial structures

Description

Estimate the intensity threshold for the reconstruction of spatial structures

Usage

```
findIntensityThreshold(ppp, mark_select = NULL, bndw = NULL, dim, steps = 250)
```

Arguments

ppp	point pattern object of class ppp
mark_select	character; name of mark that is to be selected for the reconstruction
bndw	numeric; bandwidth of the sigma parameter in the density estimation, if no value is given the bandwidth is estimated using cross validation with the bw.diggle function.
dim	numeric; x dimension of the final reconstruction.
steps	numeric; value used to filter the density estimates, where only densities greater than the maximum value divided by threshold are considered. Default is 250.

Value

numeric; estimated intensity threshold

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
ppp <- SPE2ppp(spe, marks = "cell_category", image_col = "image_name", image_id = "E04")
findIntensityThreshold(ppp, mark_select = "islet", dim = 250)
```

getDimXY

Function to get the dimension based on dim of y axis

Description

Function to get the dimension based on dim of y axis

Usage

```
getDimXY(ppp, ydim)
```

Arguments

ppp	point pattern object of class ppp
ydim	dimension of y axis

Value

vector; vector with x and y dimension

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
ppp <- SPE2ppp(spe,
  marks = "cell_category", image_col = "image_name",
  image_id = "E04"
)
getDimXY(ppp, 500)
```

meanShapeMetrics	<i>Calculate mean shape metrics of a set of polygons</i>
------------------	--

Description

Calculate mean shape metrics of a set of polygons

Usage

```
meanShapeMetrics(totalShapeMetricMatrix)
```

Arguments

```
totalShapeMetricMatrix  
matrix of shape metrics
```

Value

matrix; matrix of mean shape metrics

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)  
islet_poly <- reconstructShapeDensityImage(spe,  
  marks = "cell_category",  
  image_col = "image_name", image_id = "E04", mark_select = "islet", dim = 500  
)  
shape_metrics <- totalShapeMetrics(islet_poly)  
meanShapeMetrics(shape_metrics)
```

normalizeCoordinates	<i>Function to normalize coordinates between zero and one while keep scaling</i>
----------------------	--

Description

Function to normalize coordinates between zero and one while keep scaling

Usage

```
normalizeCoordinates(coords)
```

Arguments

```
coords          matrix; matrix with coordinates
```

Value

matrix; coordinates scaled between 0 and 1

Examples

```
matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
coords <- xyCoordinates(matrix_R)
normalizeCoordinates(coords)
```

reconstructShapeDensity

Reconstruct polygon from point pattern density

Description

This function estimates the density of a spatial point pattern (ppp), thresholds the density to create a binary image, and then converts it to a valid sf object (polygons).

Usage

```
reconstructShapeDensity(
  ppp,
  mark_select = NULL,
  bndw = NULL,
  thres = NULL,
  dim
)
```

Arguments

ppp	point pattern object of class ppp
mark_select	character; name of mark that is to be selected for the reconstruction
bndw	bandwidth of kernel density estimator
thres	intensity threshold for the reconstruction
dim	numeric; x dimension of the final reconstruction.

Value

sf object of class POLYGON

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
ppp <- SPE2ppp(spe, marks = "cell_category", image_col = "image_name", image_id = "E04")
thres <- findIntensityThreshold(ppp, mark_select = "islet", dim = 500)
islet_poly <- reconstructShapeDensity(ppp, mark_select = "islet", thres = thres, dim = 500)
plot(islet_poly)
```

reconstructShapeDensityImage

Reconstruct structure from spe object with given image id

Description

Reconstruct structure from spe object with given image id

Usage

```
reconstructShapeDensityImage(
  spe,
  marks,
  image_col,
  image_id,
  mark_select,
  dim = 500,
  bndw = NULL,
  thres = NULL
)
```

Arguments

spe	SpatialExperiment; a object of class SpatialExperiment
marks	character; name of column in colData that will correspond to the ppp marks
image_col	character; name of a column in colData that corresponds to the image
image_id	character; image id, must be present in image_col
mark_select	character; name of mark that is to be selected for the reconstruction
dim	numeric; x dimension of the final reconstruction. A lower resolution speed up computation but lead to less exact reconstruction. Default = 500
bndw	numeric; bandwidth of the sigma parameter in the density estimation, if no value is given the bandwidth is estimated using cross validation with the bw.diggle function.
thres	numeric; intensity threshold for the reconstruction

Value

sf object of class POLYGON

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
islet_poly <- reconstructShapeDensityImage(spe,
  marks = "cell_category",
  image_col = "image_name", image_id = "E04", mark_select = "islet", dim = 500
)
plot(islet_poly)
```

reconstructShapeDensitySPE

Reconstruct structure from spatial experiment object per image id

Description

Reconstruct structure from spatial experiment object per image id

Usage

```
reconstructShapeDensitySPE(
  spe,
  marks,
  image_col,
  mark_select,
  dim = 500,
  bndw = NULL,
  thres,
  ncores = 1
)
```

Arguments

spe	SpatialExperiment; a object of class SpatialExperiment
marks	character; name of column in colData that will correspond to the ppp marks
image_col	character; name of a column in colData that corresponds to the image
mark_select	character; name of mark that is to be selected for the reconstruction
dim	numeric; x dimension of the final reconstruction. A lower resolution speed up computation but lead to less exact reconstruction. Default = 500
bndw	numeric; bandwidth of the sigma parameter in the density estimation, if no value is given the bandwidth is estimated using cross validation with the bw.diggle function.
thres	numeric; intensity threshold for the reconstruction
ncores	numeric; number of cores for parallel processing using mclapply. Default = 1

Value

simple feature collection

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
spe_sel <- spe[, spe[["image_name"]] %in% c("E02", "E03", "E04")]
all_islets <- reconstructShapeDensitySPE(spe_sel,
  marks = "cell_category",
  image_col = "image_name", mark_select = "islet", bndw = sigma, thres = 0.0025
)
all_islets
```

shapeIntensityImage *Intensity plot*

Description

This function plots the intensity of a point pattern image and displays a histogram of the intensity values. Note that intensities less than largest intensity value divided by 250 are not displayed in the histogram.

Usage

```
shapeIntensityImage(
  spe,
  marks,
  image_col,
  image_id,
  mark_select,
  bndw = NULL,
  dim = 500
)
```

Arguments

spe	SpatialExperiment; a object of class SpatialExperiment
marks	character; name of column in colData that will correspond to the ppp marks
image_col	character; name of a column in colData that corresponds to the image
image_id	character; image id, must be present in image_col
mark_select	character; name of mark that is to be selected for the reconstruction
bndw	numeric; bandwidth of the sigma parameter in the density estimation, if no value is given the bandwidth is estimated using cross validation with the bw.diggle function.
dim	numeric; x dimension of the final reconstruction. A lower resolution speeds up computation but lead to less exact reconstruction. Default = 500

Value

ggplot object with intensity image and histogram

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
shapeIntensityImage(spe,
  marks = "cell_category", image_col = "image_name",
  image_id = "E04", mark_select = "islet"
)
```

 shapeMetrics

Calculate a set of shape metrics of a polygon

Description

Calculate a set of shape metrics of a polygon

Usage

```
shapeMetrics(sfPoly)
```

Arguments

sfPoly POLYGON of class sfc

Value

list; list of shape metrics

Examples

```
matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
poly_R <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
shapeMetrics(poly_R)
```

SPE2ppp	<i>Function to convert spatial coordinates of a SpatialExperiment object to a ppp object</i>
---------	--

Description

Function to convert spatial coordinates of a SpatialExperiment object to a ppp object

Usage

```
SPE2ppp(spe, marks, image_col = NULL, image_id = NULL)
```

Arguments

spe	SpatialExperiment; a object of class SpatialExperiment
marks	character; name of column in colData that will correspond to the ppp marks
image_col	character; name of a column in colData that corresponds to the image
image_id	character; image id, must be present in image_col

Value

ppp; object of type ppp

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
SPE2ppp(spe, marks = "cell_category", image_col = "image_name", image_id = "E04")
```

st_calculateCurvature *Title*

Description

Title

Usage

```
st_calculateCurvature(sfPoly, smoothness = 5)
```

Arguments

sfPoly	POLYGON of class sf
smoothness	list; curvature measures

Value

list; list of curvatures values

References

<https://stackoverflow.com/questions/62250151/calculate-curvature-of-a-closed-object-in-r>

Examples

```
matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
poly_R <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
st_calculateCurvature(poly_R)
```

st_calculateShapeCurl *Calculate curl of a polygon*

Description

Calculate curl of a polygon

Usage

```
st_calculateShapeCurl(sfPoly)
```

Arguments

sfPoly POLYGON of class sf

Value

numeric; the curl of the polygon

Examples

```

matrix_R <- matrix(c(
  1, 1, 1, 1, 1, 0,
  1, 1, 0, 0, 1, 1,
  1, 1, 0, 0, 1, 1,
  1, 1, 1, 1, 1, 0,
  1, 1, 0, 1, 1, 0,
  1, 1, 0, 0, 1, 1,
  1, 1, 0, 0, 1, 1
), nrow = 7, byrow = TRUE)
poly_R <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
st_calculateShapeCurl(poly_R)

```

st_feature_axes	<i>Calculate the length of feature axes of an sf polygon</i>
-----------------	--

Description

Calculate the length of feature axes of an sf polygon

Usage

```
st_feature_axes(sfPoly)
```

Arguments

sfPoly POLYGON of class sf

Value

list; list containing the major and minor axis lengths

Examples

```

matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
poly_R <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
st_feature_axes(poly_R)

```

totalShapeMetrics	<i>Calculate a set of shape metrics of a set of polygons</i>
-------------------	--

Description

Calculate a set of shape metrics of a set of polygons

Usage

```
totalShapeMetrics(sfInput)
```

Arguments

sfInput MULTIPOLYGON of class sf

Details

Calculate a set of shape metrics of a set of polygons. The function calculates all metrics that are implemented in the function shapeMetrics()

Value

matrix; matrix of shape metrics

Examples

```
spe <- imcdatasets::Damond_2019_Pancreas("spe", full_dataset = FALSE)
islet_poly <- reconstructShapeDensityImage(spe,
  marks = "cell_category",
  image_col = "image_name", image_id = "E04", mark_select = "islet", dim = 500
)
totalShapeMetrics(islet_poly)
```

xyCoordinates	<i>Function to extract x y coordinates from binary image</i>
---------------	--

Description

Function to extract x y coordinates from binary image

Usage

```
xyCoordinates(inputMatrix)
```

Arguments

inputMatrix a binary matrix

Value

matrix; matrix with x,y coordinates of the cell of the input matrix

Examples

```
matrix_R <- matrix(c(
  0, 0, 0, 0, 0, 0, 0, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 1, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 1, 1, 0, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 1, 1, 0, 0, 1, 1, 0, 0,
  0, 0, 0, 0, 0, 0, 0, 0, 0
), nrow = 9, byrow = TRUE)
xyCoordinates(matrix_R)
```

Index

.intensityImage, [2](#)
.intensityThreshold, [3](#)
binaryImageToSF, [3](#)
estimateReconstructionParametersSPE, [4](#)
findIntensityThreshold, [5](#)
getDimXY, [6](#)
meanShapeMetrics, [7](#)
normalizeCoordinates, [7](#)
reconstructShapeDensity, [8](#)
reconstructShapeDensityImage, [9](#)
reconstructShapeDensitySPE, [10](#)
shapeIntensityImage, [11](#)
shapeMetrics, [12](#)
SPE2ppp, [13](#)
st_calculateCurvature, [13](#)
st_calculateShapeCurl, [14](#)
st_feature_axes, [15](#)
totalShapeMetrics, [16](#)
xyCoordinates, [16](#)