

Package ‘sosta’

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

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Description `sosta` (Spatial Omics STructure 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.

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| sosta-package | <i>sosta: A package for the analysis of anatomical tissue structures in spatial omics data</i> |
|---------------|--|

Description

‘sosta’ (Spatial Omics STructure 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.

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See Also

Useful links:

- <https://github.com/sgunz/sosta>
- <https://sgunz.github.io/sosta/>
- Report bugs at <https://github.com/sgunz/sosta/issues>

.intensityImage *Function to estimate the intensity image of a point pattern*

Description

Function to estimate the intensity image of a point pattern

Usage

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

Arguments

| | |
|--------------------------|---|
| <code>ppp</code> | point pattern object of class <code>ppp</code> |
| <code>mark_select</code> | character; name of mark that is to be selected for the reconstruction |
| <code>bndw</code> | bandwidth of kernel density estimator |
| <code>dim</code> | 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

| | |
|--------------------------|--|
| <code>spe</code> | SpatialExperiment; a object of class SpatialExperiment |
| <code>marks</code> | character; name of column in <code>colData</code> that will correspond to the ppp marks |
| <code>image_col</code> | character; name of a column in <code>colData</code> that corresponds to the image |
| <code>mark_select</code> | character; name of mark that is to be selected for the reconstruction |
| <code>nimages</code> | integer; number of images for the estimation. Will be randomly sampled |
| <code>fun</code> | character; function to estimate the kernel density. Default <code>bw.diggle</code> . |
| <code>dim</code> | numeric; x dimension of the final reconstruction. A lower resolution speed up computation but lead to less exact reconstruction. Default = 500 |
| <code>ncores</code> | numeric; number of cores for parallel processing using <code>mclapply</code> . Default = 1 |
| <code>plot_hist</code> | 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 <code>bw.diggle</code> 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

| | |
|-------------------|-----------------------------------|
| <code>ppp</code> | point pattern object of class ppp |
| <code>ydim</code> | 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`*Calculate mean shape metrics of a set of polygons*

Description

Calculate mean shape metrics of a set of polygons

Usage

```
meanShapeMetrics(totalShapeMetricMatrix)
```

Arguments

| | |
|-------------------------------------|-------------------------|
| <code>totalShapeMetricMatrix</code> | 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 *Function to normalize coordinates between zero and one while keep scaling*

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

| | |
|--------------------------|---|
| <code>ppp</code> | point pattern object of class ppp |
| <code>mark_select</code> | character; name of mark that is to be selected for the reconstruction |
| <code>bndw</code> | bandwidth of kernel density estimator |
| <code>thres</code> | intensity threshold for the reconstruction |
| <code>dim</code> | 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 *Calculate a set of shape metrics of a set of polygons*

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 *Function to extract x y coordinates from binary image*

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)
```

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