

# Package ‘sosta’

September 4, 2025

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

**Version** 1.1.1

**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 anatomically relevant structures based on molecular features or cell types. It further calculates a range of metrics at the structure level 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`, `SingleCellExperiment`, `dplyr`, `ggplot2`, `patchwork`, `SummarizedExperiment`, `stats`, `rlang`, `parallel`, `EBImage`, `spatstat.random`, `S4Vectors`

**Suggests** `knitr`, `rmarkdown`, `BiocStyle`, `ExperimentHub`, `lme4`, `lmerTest`, `ggfortify`, `tidyr`, `testthat` (>= 3.0.0)

**VignetteBuilder** `knitr`

**Config/testthat/edition** 3

**LazyData** true

**git\_url** <https://git.bioconductor.org/packages/sosta>

**git\_branch** devel

**git\_last\_commit** 9c2fd54

**git\_last\_commit\_date** 2025-07-17

**Repository** Bioconductor 3.22

**Date/Publication** 2025-09-03

**Author** Samuel Gunz [aut, cre] (ORCID: <<https://orcid.org/0000-0002-8909-0932>>),  
Mark D. Robinson [aut, fnd]

**Maintainer** Samuel Gunz <samuel.gunz@uzh.ch>

## Contents

|                                     |    |
|-------------------------------------|----|
| sosta-package                       | 2  |
| .df2ppp                             | 3  |
| .intensityImage                     | 4  |
| .intensityThreshold                 | 4  |
| .SPE2df                             | 5  |
| assingCellsToStructures             | 5  |
| binaryImageToSF                     | 6  |
| cellTypeProportions                 | 7  |
| createPointPatternTissue            | 8  |
| estimateReconstructionParametersSPE | 9  |
| findIntensityThreshold              | 10 |
| getDimXY                            | 10 |
| meanShapeMetrics                    | 11 |
| minBoundaryDistances                | 12 |
| normalizeCoordinates                | 13 |
| reconstructShapeDensity             | 14 |
| reconstructShapeDensityImage        | 14 |
| reconstructShapeDensitySPE          | 15 |
| shapeIntensityImage                 | 16 |
| shapeMetrics                        | 17 |
| simulateTissueBlobs                 | 18 |
| sostaSPE                            | 19 |
| spatialCoords2SF                    | 19 |
| SPE2ppp                             | 20 |
| stCalculateCurvature                | 20 |
| stCalculateShapeCurl                | 21 |
| stFeatureAxes                       | 22 |
| totalShapeMetrics                   | 23 |
| xyCoordinates                       | 23 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>25</b> |
|--------------|-----------|

---

|               |                                                                                                |
|---------------|------------------------------------------------------------------------------------------------|
| 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 anatomically relevant structures based on molecular features or cell types. It further calculates a range of metrics at the structure level to quantitatively describe tissue architecture. The package is designed to integrate with other packages for the analysis of spatial omics data.

**Author(s)**

**Maintainer:** Samuel Gunz <samuel.gunz@uzh.ch> ([ORCID](#))

Authors:

- Mark D. Robinson <mark.robinson@mls.uzh.ch> [funder]

**See Also**

Useful links:

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

---

`.df2ppp`*Function to convert data.frame to ppp object*

---

**Description**

Assumes that the `data.frame` is the output of `.SPE2df()`. Column order is important!

**Usage**

```
.df2ppp(df, xName, yName, marks = NULL)
```

**Arguments**

|                    |                                                                             |
|--------------------|-----------------------------------------------------------------------------|
| <code>df</code>    | data.frame; with x, y coordinates, image, and categorical mark information. |
| <code>xName</code> | character; column name of x coordinate                                      |
| <code>yName</code> | character; column name of y coordinate                                      |
| <code>marks</code> | character; column name of the mark variable                                 |

**Value**

ppp; object of type ppp

**See Also**

[.SPE2df](#), [as.ppp](#)

**Examples**

```
data(sostaSPE)
df <- .SPE2df(sostaSPE, marks = "cellType", imageCol = "imageName")
ppp <- .df2ppp(df, xName = "x", yName = "y", marks = "cellType")
```

---

|                              |                                                                    |
|------------------------------|--------------------------------------------------------------------|
| <code>.intensityImage</code> | <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, markSelect = NULL, bndw = NULL, dim)
```

**Arguments**

|                         |                                                                       |
|-------------------------|-----------------------------------------------------------------------|
| <code>ppp</code>        | point pattern object of class <code>ppp</code>                        |
| <code>markSelect</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

---

|                                  |                                                                                                  |
|----------------------------------|--------------------------------------------------------------------------------------------------|
| <code>.intensityThreshold</code> | <i>Function to estimate the intensity threshold for the reconstruction of spatial structures</i> |
|----------------------------------|--------------------------------------------------------------------------------------------------|

---

**Description**

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

**Usage**

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

**Arguments**

|                           |                                                                                                                                                               |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>densityImage</code> | real-valued pixel image; output from the function <code>.intensityImage</code>                                                                                |
| <code>steps</code>        | 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

---

.SPE2df*Function to convert SpatialExperiment object to a data frame*

---

**Description**

Function to convert SpatialExperiment object to a data frame

**Usage**

```
.SPE2df(spe, imageCol = NULL, marks = NULL, colNames = FALSE)
```

**Arguments**

|          |                                                                      |
|----------|----------------------------------------------------------------------|
| spe      | SpatialExperiment; a object of class SpatialExperiment               |
| imageCol | character; name of a column in colData that corresponds to the image |
| marks    | character; name of column in colData with categorical marks          |
| colNames | logical; extract colnames from SpatialExperiment                     |

**Value**

data.frame with x, y coordinates, image, and categorical mark information

**Examples**

```
data(sostaSPE)
.SPE2df(sostaSPE, marks = "cellType", imageCol = "imageName") |> head()
```

---

assingCellsToStructures*Function to assign points / coordinates to structures*

---

**Description**

This function assigns each spatial coordinate in a SpatialExperiment object (spe) to the first intersecting structure from a given set of spatial structures.

**Usage**

```
assingCellsToStructures(
  spe,
  allStructs,
  imageCol,
  uniqueId = "structID",
  nCores = 1
)
```

**Arguments**

|            |                                                                                                                                                                               |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| spe        | SpatialExperiment; An object of class SpatialExperiment containing spatial point data. Must contain colnames for correct assignment.                                          |
| allStructs | sf; A simple feature collection (sf object) representing spatial structures. Must contain a column which contains a unique identifier for each structure. Default = structID. |
| imageCol   | character; The column name in spe and allStructs that identifies the corresponding image.                                                                                     |
| uniqueId   | character; The column name in the simple feature collection for which to compute the assignment.                                                                              |
| nCores     | integer; The number of cores to use for parallel processing (default is 1).                                                                                                   |

**Value**

A named list with structure assignments for each spatial point in spe. Points that do not overlap with any structure are assigned NA. Names correspond to colnames of the SpatialExperiment input object.

**Examples**

```
library("SpatialExperiment")
data("sostaSPE")
allStructs <- reconstructShapeDensitySPE(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  markSelect = "A", bndw = 3.5, thres = 0.045
)
# The function `assingCellsToStructures` needs colnames so we create them here
colnames(sostaSPE) <- paste0("cell_", c(1:dim(sostaSPE)[2]))

res <- assingCellsToStructures(
  spe = sostaSPE, allStructs = allStructs, imageCol = "imageName"
)
# Assign the structure assignment in the order of the columns in the `SpatialExperiment` object
colData(sostaSPE)$structAssign <- res[colnames(sostaSPE)]

if (require("ggplot2")) {
  cbind(
    colData(sostaSPE[, sostaSPE[["imageName"]] == "image1"]),
    spatialCoords(sostaSPE[, sostaSPE[["imageName"]] == "image1"])
  ) |>
  as.data.frame() |>
  ggplot(aes(x = x, y = y, color = structAssign)) +
  geom_point(size = 0.25) +
  coord_equal()
}
```

---

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**

```
matrixR <- 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)
polyR <- binaryImageToSF(matrixR, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
plot(polyR)
```

---

|                     |                                                                             |
|---------------------|-----------------------------------------------------------------------------|
| cellTypeProportions | <i>Calculate the proportion of each cell type within spatial structures</i> |
|---------------------|-----------------------------------------------------------------------------|

---

**Description**

Calculate the proportion of each cell type within spatial structures

**Usage**

```
cellTypeProportions(spe, structColumn, cellTypeColumn, nCores = 1)
```

**Arguments**

|                |                                                                             |
|----------------|-----------------------------------------------------------------------------|
| spe            | SpatialExperiment object                                                    |
| structColumn   | character; name of the colData column specifying the structure assignments  |
| cellTypeColumn | character; name of the colData column specifying cell types                 |
| nCores         | integer; The number of cores to use for parallel processing (default is 1). |

**Value**

A data frame where rows correspond to unique structures and columns correspond to cell types, containing the proportion of each cell type within each structure.

**Examples**

```
library("SpatialExperiment")
data("sostaSPE")
allStructs <- reconstructShapeDensitySPE(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  markSelect = "A", bndw = 3.5, thres = 0.045
)
# The function `assingCellsToStructures` needs colnames so we create them here
colnames(sostaSPE) <- paste0("cell_", c(1:dim(sostaSPE)[2]))
# Assign the structure assignment in the order of the columns in the `SpatialExperiment` object
colData(sostaSPE)$structAssign <- assingCellsToStructures(
  spe = sostaSPE, allStructs = allStructs, imageCol = "imageName"
)[colnames(sostaSPE)]
cellTypeProportions(sostaSPE, "structAssign", "cellType")
```

---

```
createPointPatternTissue
```

*Create a Point Pattern on a Simulated Tissue Image*

---

**Description**

This function generates a spatial point pattern with different types of points (A, B, C) distributed over the simulated tissue structure.

**Usage**

```
createPointPatternTissue(tissueImage, intA, intB, intCInA, intCInB)
```

**Arguments**

|             |                                                                                     |
|-------------|-------------------------------------------------------------------------------------|
| tissueImage | Matrix; A binary matrix representing the simulated tissue.                          |
| intA        | Numeric; Intensity of type "A" points (points per unit area) on tissue regions.     |
| intB        | Numeric; Intensity of type "B" points (points per unit area) on non-tissue regions. |
| intCInA     | Numeric; Intensity of type "C" points placed in extended regions around tissue.     |
| intCInB     | Numeric; Intensity of type "C" points placed within tissue.                         |

**Value**

A ppp object representing the spatial point pattern.

**Examples**

```
tissueImage <- simulateTissueBlobs(128, 100, 7)
createPointPatternTissue(tissueImage, 0.1, 0.1, 0.005, 0.005)
```



---

estimateReconstructionParametersSPE

*Estimate reconstruction parameters from a set of images*


---

## Description

Estimate reconstruction parameters from a set of images

## Usage

```
estimateReconstructionParametersSPE(
  spe,
  marks,
  imageCol,
  markSelect = NULL,
  nImages = NULL,
  fun = "bw.diggle",
  dim = 500,
  nCores = 1,
  plotHist = TRUE
)
```

## Arguments

|            |                                                                                                                                                |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| spe        | SpatialExperiment; a object of class SpatialExperiment                                                                                         |
| marks      | character; name of column in colData that will correspond to the ppp marks                                                                     |
| imageCol   | character; name of a column in colData that corresponds to the image                                                                           |
| markSelect | 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                                                                   |
| plotHist   | logical; if histogram of estimated densities and thresholds should be plotted. Default = TRUE                                                  |

## Value

tibble; tibble with estimated intensities and thresholds

## Examples

```
data("sostaSPE")
estimateReconstructionParametersSPE(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  markSelect = "A", plotHist = 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, markSelect = NULL, bndw = NULL, dim, steps = 250)
```

### Arguments

|            |                                                                                                                                                                                       |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ppp        | point pattern object of class ppp                                                                                                                                                     |
| markSelect | 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

```
data(sostaSPE)
ppp <- SPE2ppp(sostaSPE, marks = "cellType", imageCol = "imageName", imageId = "image1")
findIntensityThreshold(ppp, markSelect = "A", 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**

```
data(sostaSPE)
pp <- SPE2ppp(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  imageId = "image1"
)
getDimXY(pp, 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**

```
totalShapeMetricMatrix
  matrix of shape metrics
```

**Value**

matrix; matrix of mean shape metrics

**Examples**

```
data(sostaSPE)
struct <- reconstructShapeDensityImage(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  imageId = "image1", markSelect = "A", dim = 500
)
shapeMetrics <- totalShapeMetrics(struct)
meanShapeMetrics(shapeMetrics)
```

---

|                      |                                                                                                   |
|----------------------|---------------------------------------------------------------------------------------------------|
| minBoundaryDistances | <i>Compute minimum boundary distances for each cell within its corresponding image structures</i> |
|----------------------|---------------------------------------------------------------------------------------------------|

---

### Description

Compute minimum boundary distances for each cell within its corresponding image structures

### Usage

```
minBoundaryDistances(spe, imageCol, structColumn, allStructs, nCores = 1)
```

### Arguments

|              |                                                                             |
|--------------|-----------------------------------------------------------------------------|
| spe          | SpatialExperiment object                                                    |
| imageCol     | character; name of the colData column specifying the image name             |
| structColumn | character; name of the colData column specifying structure assignments      |
| allStructs   | sf object; contains spatial structures with corresponding image names       |
| nCores       | integer; The number of cores to use for parallel processing (default is 1). |

### Value

A named list containing the minimum distances between cells and structure boundaries, values within structures have negative values. Names correspond to colnames of the SpatialExperiment input object.

### Examples

```
library("SpatialExperiment")
data("sostaSPE")

allStructs <- reconstructShapeDensitySPE(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  markSelect = "A", bndw = 3.5, thres = 0.045
)
# The function `assingCellsToStructures` needs colnames so we create them here
colnames(sostaSPE) <- paste0("cell_", c(1:dim(sostaSPE)[2]))
# Assign the structure assignment in the order of the columns in the `SpatialExperiment` object
colData(sostaSPE)$structAssign <- assingCellsToStructures(
  spe = sostaSPE, allStructs = allStructs, imageCol = "imageName"
)[colnames(sostaSPE)]

res <- minBoundaryDistances(
  spe = sostaSPE, imageCol = "imageName", structColumn = "structAssign",
  allStructs = allStructs
)

colData(sostaSPE)$minDist <- res[colnames(sostaSPE)]

if (require("ggplot2")) {
  cbind(colData(sostaSPE), spatialCoords(sostaSPE)) |>
    as.data.frame() |>
```

```

    ggplot(aes(x = x, y = y, color = minDist)) +
    geom_point(size = 0.25) +
    scale_colour_gradient2() +
    geom_sf(data = allStructs, fill = NA, inherit.aes = FALSE) +
    facet_wrap(~imageName)
}

```

---

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

```

matrixR <- 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(matrixR)
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, markSelect = NULL, bndw = NULL, thres = NULL, dim)
```

### Arguments

|            |                                                                       |
|------------|-----------------------------------------------------------------------|
| ppp        | point pattern object of class ppp                                     |
| markSelect | 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

```
data("sostaSPE")
ppp <- SPE2ppp(sostaSPE, marks = "cellType", imageCol = "imageName", imageId = "image1")
thres <- findIntensityThreshold(ppp, markSelect = "A", dim = 500)
struct <- reconstructShapeDensity(ppp, markSelect = "A", thres = thres, dim = 500)
plot(struct)
```

---

reconstructShapeDensityImage

*Reconstruct structure from spe object with given image id*


---

### Description

Reconstruct structure from spe object with given image id

**Usage**

```
reconstructShapeDensityImage(
  spe,
  marks,
  imageCol,
  imageId,
  markSelect,
  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                                                                                                                                                  |
| imageCol   | character; name of a column in colData that corresponds to the image                                                                                                                                                        |
| imageId    | character; image id, must be present in imageCol                                                                                                                                                                            |
| markSelect | 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; smoothing bandwidth in the density estimation, corresponds to the sigma parameter in the density.ppp function, if no value is given the bandwidth is estimated using cross validation with the bw.diggle function. |
| thres      | numeric; intensity threshold for the reconstruction; if NULL the threshold is set as the mean between the mode of the pixel intensity distributions                                                                         |

**Value**

sf object of class POLYGON

**Examples**

```
data("sostaSPE")
struct <- reconstructShapeDensityImage(sostaSPE,
  marks = "cellType", imageCol = "imageName", imageId = "image1",
  markSelect = "A", dim = 500
)
plot(struct)
```

---

reconstructShapeDensitySPE

*Reconstruct structure from spatial experiment object per image id*

---

**Description**

Reconstruct structure from spatial experiment object per image id

**Usage**

```
reconstructShapeDensitySPE(
  spe,
  marks,
  imageCol,
  markSelect,
  dim = 500,
  bndw = NULL,
  thres = NULL,
  nCores = 1
)
```

**Arguments**

|            |                                                                                                                                                                                                      |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| spe        | SpatialExperiment; a object of class SpatialExperiment                                                                                                                                               |
| marks      | character; name of column in colData that will correspond to the ppp marks                                                                                                                           |
| imageCol   | character; name of a column in colData that corresponds to the image                                                                                                                                 |
| markSelect | 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 for each image individually. |
| thres      | numeric; intensity threshold for the reconstruction; if NULL the threshold is set as the mean between the mode of the pixel intensity distributions estimated for each image individual              |
| nCores     | numeric; number of cores for parallel processing using mclapply. Default = 1                                                                                                                         |

**Value**

simple feature collection

**Examples**

```
data("sostaSPE")
allStructs <- reconstructShapeDensitySPE(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  markSelect = "A", bndw = 3.5, thres = 0.005
)
allStructs
```

---

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,
  imageCol,
  imageId,
  markSelect,
  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                                                                                                                                                  |
| imageCol   | character; name of a column in colData that corresponds to the image                                                                                                                                                        |
| imageId    | character; image id, must be present in imageCol                                                                                                                                                                            |
| markSelect | character; name of mark that is to be selected for the reconstruction                                                                                                                                                       |
| bndw       | numeric; smoothing bandwidth in the density estimation, corresponds to the sigma parameter in the density.ppp function, 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**

```
data("sostaSPE")
shapeIntensityImage(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  imageId = "image1", markSelect = "A"
)
```

---

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)
polyR <- binaryImageToSF(matrix_R, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
shapeMetrics(polyR)
```

---

|                     |                              |
|---------------------|------------------------------|
| simulateTissueBlobs | <i>Simulate Tissue Blobs</i> |
|---------------------|------------------------------|

---

**Description**

This function generates a simulated tissue-like structure using a Gaussian blur technique.

**Usage**

```
simulateTissueBlobs(size, seedNumber, clumpSize)
```

**Arguments**

|            |                                                                                                 |
|------------|-------------------------------------------------------------------------------------------------|
| size       | Integer; The size (width and height) of the simulated tissue image.                             |
| seedNumber | Integer; The number of random seed points used to generate tissue blobs.                        |
| clumpSize  | Numeric; The standard deviation (sigma) of the Gaussian blur applied to generate tissue clumps. |

**Value**

A binary matrix representing the simulated tissue structure.

**Examples**

```
tissueImage <- simulateTissueBlobs(128, 100, 7)
image(tissueImage)
```

---

|          |                                                                                         |
|----------|-----------------------------------------------------------------------------------------|
| sostaSPE | <i>Example SpatialExperiment Object with Simulated Tissue Images and Point Patterns</i> |
|----------|-----------------------------------------------------------------------------------------|

---

### Description

This dataset contains a simulated `SpatialExperiment` object (`sostaSPE`) representing three tissue images, each with a corresponding spatial point pattern. The point patterns contain different cell types (A, B, and C), distributed according to simulated tissue structures.

### Usage

```
sostaSPE
```

### Format

A `SpatialExperiment` object with the following structure:

**x** Numeric; x-coordinate of each point (cell location).

**y** Numeric; y-coordinate of each point (cell location).

**cell\_type** Factor; Cell type assigned to each point (A, B, or C).

**image\_name** Factor; Identifier for the tissue image (`image1`, `image2`, or `image3`).

### Details

The dataset was generated as follows:

- Three tissue images were simulated using `simulateTissueBlobs()`.
- Spatial point patterns were created for each tissue using `createPointPatternTissue()`.
- The point pattern data was converted into a `SpatialExperiment` object with spatial coordinates.

---

|                               |                                                          |
|-------------------------------|----------------------------------------------------------|
| <code>spatialCoords2SF</code> | <i>Function to convert spatialCoords to an sf object</i> |
|-------------------------------|----------------------------------------------------------|

---

### Description

Function to convert `spatialCoords` to an `sf` object

### Usage

```
spatialCoords2SF(spe)
```

### Arguments

`spe` `SpatialExperiment`; a object of class `SpatialExperiment`

### Value

`sf`; Simple feature collection of geometry type POINT

**Examples**

```
data(sostaSPE)
speSel <- sostaSPE[, sostaSPE[["imageName"]] == "image1"]
spatialCoords2SF(speSel)
```

---

|         |                                                                                              |
|---------|----------------------------------------------------------------------------------------------|
| 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 = NULL, imageCol = NULL, imageId = NULL)
```

**Arguments**

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

**Value**

ppp; object of type ppp

**Examples**

```
data(sostaSPE)
SPE2ppp(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  imageId = "image1"
)
```

---

|                      |                                         |
|----------------------|-----------------------------------------|
| stCalculateCurvature | <i>Calculate curvature of sf object</i> |
|----------------------|-----------------------------------------|

---

**Description**

Calculate curvature of sf object

**Usage**

```
stCalculateCurvature(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**

```
matrixR <- 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)
polyR <- binaryImageToSF(matrixR, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
stCalculateCurvature(polyR)
```

---

stCalculateShapeCurl    *Calculate curl of a polygon*

---

**Description**

Calculate curl of a polygon

**Usage**

```
stCalculateShapeCurl(sfPoly)
```

**Arguments**

|        |                     |
|--------|---------------------|
| sfPoly | POLYGON of class sf |
|--------|---------------------|

**Value**

numeric; the curl of the polygon

**Examples**

```
matrixR <- 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)
polyR <- binaryImageToSF(matrixR, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
stCalculateShapeCurl(polyR)
```

stFeatureAxes

*Calculate the length of feature axes of an sf polygon***Description**

Calculate the length of feature axes of an sf polygon

**Usage**

```
stFeatureAxes(sfPoly)
```

**Arguments**

sfPoly                      POLYGON of class sf

**Value**

list; list containing the major and minor axis lengths

**Examples**

```
matrixR <- 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)
polyR <- binaryImageToSF(matrixR, xmin = 0, xmax = 1, ymin = 0, ymax = 1)
stFeatureAxes(polyR)
```

---

|                   |                                                              |
|-------------------|--------------------------------------------------------------|
| 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**

```
data(sostaSPE)
struct <- reconstructShapeDensityImage(sostaSPE,
  marks = "cellType", imageCol = "imageName",
  imageId = "image1", markSelect = "A", dim = 500
)
totalShapeMetrics(struct)
```

---

|               |                                                              |
|---------------|--------------------------------------------------------------|
| 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**

```
matrixR <- 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(matrixR)
```



# Index

- \* **datasets**
  - sostaSPE, [19](#)
- \* **internal**
  - sosta-package, [2](#)
  - .SPE2df, [3](#), [5](#)
  - .df2ppp, [3](#)
  - .intensityImage, [4](#)
  - .intensityThreshold, [4](#)
- as.ppp, [3](#)
- assingCellsToStructures, [5](#)
- binaryImageToSF, [6](#)
- cellTypeProportions, [7](#)
- createPointPatternTissue, [8](#)
- estimateReconstructionParametersSPE, [9](#)
- findIntensityThreshold, [10](#)
- getDimXY, [10](#)
- meanShapeMetrics, [11](#)
- minBoundaryDistances, [12](#)
- normalizeCoordinates, [13](#)
- reconstructShapeDensity, [14](#)
- reconstructShapeDensityImage, [14](#)
- reconstructShapeDensitySPE, [15](#)
- shapeIntensityImage, [16](#)
- shapeMetrics, [17](#)
- simulateTissueBlobs, [18](#)
- sosta (sosta-package), [2](#)
- sosta-package, [2](#)
- sostaSPE, [19](#)
- spatialCoords2SF, [19](#)
- SPE2ppp, [20](#)
- stCalculateCurvature, [20](#)
- stCalculateShapeCurl, [21](#)
- stFeatureAxes, [22](#)
- totalShapeMetrics, [23](#)
- xyCoordinates, [23](#)