

# Package ‘SpaceMarkers’

July 23, 2025

**Type** Package

**Title** Spatial Interaction Markers

**Version** 1.5.0

**BugReports** <https://github.com/DeshpandeLab/SpaceMarkers/issues>

**URL** <https://github.com/DeshpandeLab/SpaceMarkers>

**Description** Spatial transcriptomic technologies have helped to resolve the connection between gene expression and the 2D orientation of tissues relative to each other. However, the limited single-cell resolution makes it difficult to highlight the most important molecular interactions in these tissues. SpaceMarkers, R/Bioconductor software, can help to find molecular interactions, by identifying genes associated with latent space interactions in spatial transcriptomics.

**Depends** R (>= 4.4.0)

**biocViews** SingleCell, GeneExpression, Software, Spatial,  
Transcriptomics

**Imports** matrixStats, matrixTests, rstatix, spatstat.explore,  
spatstat.geom, ape, hdf5r, nanoparquet, jsonlite, Matrix,  
qvalue, stats, utils, methods, ggplot2, reshape2

**Suggests** data.table, devtools, dplyr, hrbrthemes, knitr, RColorBrewer,  
cowplot, readbitmap, rjson, rmarkdown, BiocStyle, testthat (>=  
3.0.0), viridis, CoGAPS

**Enhances** BiocParallel

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Encoding** UTF-8

**LazyData** false

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**License** MIT + file LICENSE

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

**git\_branch** devel

**git\_last\_commit** 61501f8

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-07-22

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|                  |                                                       |
|------------------|-------------------------------------------------------|
| .getBTMEfeatures | <i>.getBTMEfeatures Load features BayesTME object</i> |
|------------------|-------------------------------------------------------|

---

Description

.getBTMEfeatures Load features BayesTME object

Usage

.getBTMEfeatures(hf)

---

|                                 |                                                                    |
|---------------------------------|--------------------------------------------------------------------|
| <code>.getCogapsFeatures</code> | <i><code>.getCogapsFeatures</code> Load features CoGAPS object</i> |
|---------------------------------|--------------------------------------------------------------------|

---

### Description

`.getCogapsFeatures` Load features CoGAPS object

### Usage

`.getCogapsFeatures(obj)`

---

|                              |                                                                  |
|------------------------------|------------------------------------------------------------------|
| <code>.getCSVfeatures</code> | <i><code>.getCSVFeatures</code> Load features from dataframe</i> |
|------------------------------|------------------------------------------------------------------|

---

### Description

`.getCSVFeatures` Load features from dataframe

### Usage

`.getCSVfeatures(obj)`

---

|                                 |                                                                    |
|---------------------------------|--------------------------------------------------------------------|
| <code>.getSeuratFeatures</code> | <i><code>.getSeuratFeatures</code> Load features Seurat object</i> |
|---------------------------------|--------------------------------------------------------------------|

---

### Description

`.getSeuratFeatures` Load features Seurat object

### Usage

`.getSeuratFeatures(obj)`

---

|                           |                                                                                  |
|---------------------------|----------------------------------------------------------------------------------|
| <code>.inferMethod</code> | <i><code>inferMethod</code> Infer the method used to obtain spatial features</i> |
|---------------------------|----------------------------------------------------------------------------------|

---

### Description

`inferMethod` Infer the method used to obtain spatial features

### Usage

`.inferMethod(spObject, method)`

---

|                          |                                                   |
|--------------------------|---------------------------------------------------|
| <code>.readFormat</code> | <i>readFormat Reads a format into an R object</i> |
|--------------------------|---------------------------------------------------|

---

### Description

`readFormat` Reads a format into an R object

### Usage

```
.readFormat(path)
```

---

|                            |                                           |
|----------------------------|-------------------------------------------|
| <code>curated_genes</code> | <i>Curated Genes for example purposes</i> |
|----------------------------|-------------------------------------------|

---

### Description

A vector with genes selected based on previous runs of SpaceMarkers on the Visium 10x breast ductal carcinoma spatial transcriptomics dataset

### Format

A vector with 114 pre-selected genes

### Value

a vector of genes

---

|                              |                                               |
|------------------------------|-----------------------------------------------|
| <code>findAllHotspots</code> | <i>Find hotSpots for all spatial patterns</i> |
|------------------------------|-----------------------------------------------|

---

### Description

Convenience function to find hotspots for all spatial patterns

### Usage

```
findAllHotspots(
  spPatterns,
  params = NULL,
  outlier = "positive",
  nullSamples = 1000,
  includeSelf = TRUE,
  ...
)
```

**Arguments**

|             |                                                                                                                                                                                                                             |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| spPatterns  | A data frame that contains the spatial coordinates and metrics for spatial features (cell types/cell processes). The column names must include 'x' and 'y' as well as the spatially varying features.                       |
| params      | a named vector of the optimal sigma and threshold for a given spatial pattern. The names should be 'sigmaOpt' and 'threshOpt'. The default value is NULL.                                                                   |
| outlier     | a character string specifying whether to apply the outlier threshold to the kernel density distribution in a one-sided manner (specify 'positive' the default) or in a two sided manner (specify 'two.sided').              |
| nullSamples | a numeric values specifying the number of spatial patterns to randomly sample for a null distribution.                                                                                                                      |
| includeSelf | a logic value specifying whether to consider the spatial influence the pattern has on surrounding regions only (set to FALSE), or whether to also consider the influence of the pattern itself (set to TRUE , the default). |
| ...         | Arguments passed to methods                                                                                                                                                                                                 |

---

|                     |                                                                                                                                                                                                                                                                                                                                                                                   |
|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| findGenesOfInterest | <i>findGenesOfInterest Identify genes associated with pattern interaction. This function identifies genes exhibiting significantly higher values of testMat in the Interaction region of the two patterns compared to regions with exclusive influence from either pattern. It uses Kruskal-Wallis test followed by posthoc analysis using Dunn's Test to identify the genes.</i> |
|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

findGenesOfInterest Identify genes associated with pattern interaction. This function identifies genes exhibiting significantly higher values of testMat in the Interaction region of the two patterns compared to regions with exclusive influence from either pattern. It uses Kruskal-Wallis test followed by posthoc analysis using Dunn's Test to identify the genes.

**Usage**

```
findGenesOfInterest(testMat, goodGenes, region, fdr.level=0.05,
  analysis=c("enrichment", "overlap"),...)
```

**Arguments**

|           |                                                                                                                                          |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------|
| testMat   | A matrix of counts with cells as columns and genes as rows                                                                               |
| goodGenes | A vector of user specified genes expected to interact a priori. The default for this is NULL as the function can find these genes itself |
| region    | A data frame of the reference pattern regions that overlap with the other patterns                                                       |
| fdr.level | False Discovery Rate. The default value is 0.05.                                                                                         |
| analysis  | a character string that specifies the type of analysis to carry out, whether overlap or enrichment.                                      |
| ...       | Additional arguments to be passed to lower level functions                                                                               |

**Value**

a list of genes exhibiting significantly higher values of testMat in the Interaction region of the two #' patterns compared to regions with exclusive influence from either pattern.

---

|                     |                                                       |
|---------------------|-------------------------------------------------------|
| findPatternHotspots | <i>Identify hotspots of spatial pattern influence</i> |
|---------------------|-------------------------------------------------------|

---

**Description**

This function calculates 'hotspots' which are regions of high spatial influence based on an outlier threshold from a null distribution.

**Usage**

```
findPatternHotspots(
  spPatterns,
  params = NULL,
  patternName = "Pattern_1",
  outlier = "positive",
  nullSamples = 1000,
  includeSelf = TRUE,
  ...
)
```

**Arguments**

|             |                                                                                                                                                                                                                             |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| spPatterns  | A data frame that contains the spatial coordinates and metrics for spatial features (cell types/cell processes). The column names must include 'x' and 'y' as well as the spatially varying features.                       |
| params      | a named vector of the optimal sigma and threshold for a given spatial pattern. The names are should be 'sigmaOpt' and 'threshOpt'. The default value is NULL.                                                               |
| patternName | a character string that specifies the pattern of interest                                                                                                                                                                   |
| outlier     | a character string specifying whether to apply the outlier threshold to the kernel density distribution in a one-sided manner (specify 'positive' the default) or in a two sided manner (specify 'two.sided').              |
| nullSamples | a numeric values specifying the number of spatial patterns to randomly sample for a null distribution.                                                                                                                      |
| includeSelf | a logic value specifying whether to consider the spatial influence the pattern has on surrounding regions only (set to FALSE), or whether to also consider the influence of the pattern itself (set to TRUE , the default). |
| ...         | Arguments passed to methods                                                                                                                                                                                                 |

**Value**

a character vector with the spatial feature name if the spatial influence exceeded the threshold for that spot/cell, and NA otherwise

**See Also**

Other getIntGenes: [getInteractingGenes\(\)](#), [getPairwiseInteractingGenes\(\)](#)

**Examples**

```
library(SpaceMarkers)
#Visium data links
urls <- read.csv(system.file("extdata","visium_data.txt",
                             package="SpaceMarkers",mustWork = TRUE))
sp_url <- urls[["visium_url"]][2]
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
#Obtaining CoGAPS Patterns i.e Spatial Features
cogaps_result <- readRDS(system.file("extdata","CoGAPS_result.rds",
                                     package="SpaceMarkers",mustWork = TRUE))
spFeatures <- slot(cogaps_result,"sampleFactors")
#Obtaining Spatial Coordinates
download.file(sp_url, basename(sp_url), mode = "wb")
untar(basename(sp_url))
spCoords <- load10XCoords(visiumDir = ".", version = "1.0")
rownames(spCoords) <- spCoords$barcode
#Match Dimensions
barcodes <- intersect(rownames(spFeatures),spCoords$barcode)
spCoords <- spCoords[barcodes,]
spFeatures <- spFeatures[barcodes,]
spPatterns <- cbind(spCoords,spFeatures[barcodes,])
spPatterns<-spPatterns[c("barcode","y","x","Pattern_1","Pattern_5")]
data("optParams")
hotspots <- findPatternHotspots(
  spPatterns = spPatterns,
  patternName = "Pattern_1",
  params = optParams[, "Pattern_1"],
  outlier = "positive",nullSamples = 1000,includeSelf = TRUE)
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
```

---

getIMScores

---

*getIMScores*


---

**Description**

Get the interaction scores for SpaceMarkers

**Usage**

```
getIMScores(SpaceMarkers)
```

**Arguments**

SpaceMarkers      A list of SpaceMarkers objects

**Value**

A data frame with columns Gene and SpaceMarkersMetric

**Examples**

```
example(getPairwiseInteractingGenes)
getIMScores(SpaceMarkers)
```

---

|                     |                                                           |
|---------------------|-----------------------------------------------------------|
| getInteractingGenes | <i>Calculate Interaction Regions and Associated Genes</i> |
|---------------------|-----------------------------------------------------------|

---

**Description**

This function calculates statistically significant genes using a non-parametric Kruskal-Wallis test for genes in any one region of influence and a post hoc Dunn's test is used for analysis of genes between regions.

**Usage**

```
getInteractingGenes(
  data,
  spPatterns,
  refPattern = "Pattern_1",
  mode = c("DE", "residual"),
  optParams = NULL,
  reconstruction = NULL,
  hotspots = NULL,
  analysis = c("enrichment", "overlap"),
  minOverlap = 50,
  ...
)
```

**Arguments**

|                |                                                                                                                                                                                                                                                                                                                                 |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data           | original spatial data matrix.                                                                                                                                                                                                                                                                                                   |
| spPatterns     | A data frame that contains the spatial coordinates and metrics for spatial features (cell types/cell processes). The column names must include 'x' and 'y' as well as the spatially varying features.                                                                                                                           |
| refPattern     | a character string that specifies the pattern whose "interaction" with every other pattern we want to study. The default value is "Pattern_1".                                                                                                                                                                                  |
| mode           | SpaceMarkers mode of operation. Possible values are "DE" (the default) or "residual".                                                                                                                                                                                                                                           |
| optParams      | a matrix with dimensions 2 X N, where N is the number of spatial patterns with optimal parameters. The first row contains the kernel width 'sigmaOpt' for each pattern, and the second row is the threshOpt (outlier threshold) for each pattern. Users can also input their preferred param values. The default value is NULL. |
| reconstruction | reconstruction of the data matrix from latent spaces. Required for "residual" mode.                                                                                                                                                                                                                                             |



|            |                                                                                                                                                                                                                                                                                                                                           |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| hotspots   | a vector that specifies the patterns to compare to the 'refPattern'. The default is NULL which indicates that all patterns would be compared to the 'refPattern'.                                                                                                                                                                         |
| analysis   | a character string that specifies the type of downstream analysis to be performed. Possible values are "enrichment" (default) and "overlap". In enrichment mode, all genes are returned, ranked by the SpaceMarkers metric. In overlap mode, only the genes which are significantly overexpressed in the interaction region are returned. |
| minOverlap | a number that specifies the minimum overlap between genes in two patterns to be considered for the statistical tests. The default is 50.                                                                                                                                                                                                  |
| ...        | Arguments passed to methods                                                                                                                                                                                                                                                                                                               |

### Value

a list of data frames with information about the interacting genes of the refPattern and each latent feature pattern matrix (interacting\_genes object). There is also a data frame with all of the regions of influence for any two of patterns (the hotspots object).

### See Also

Other getIntGenes: [findPatternHotspots\(\)](#), [getPairwiseInteractingGenes\(\)](#)

### Examples

```
library(SpaceMarkers)
#Visium data links
urls <- read.csv(system.file("extdata","visium_data.txt",
package="SpaceMarkers",mustWork = TRUE))
counts_url <- urls[["visium_url"]][1]
sp_url <- urls[["visium_url"]][2]
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
files <- list.files(".")[grepl(basename(counts_url),list.files("."))]
unlink(files)
download.file(counts_url,basename(counts_url), mode = "wb")
counts_matrix<-load10XExpr(visiumDir=".",h5filename = basename(counts_url))
#Obtaining CoGAPS Patterns
cogaps_result <- readRDS(system.file("extdata","CoGAPS_result.rds",
package="SpaceMarkers",mustWork = TRUE))
features <- intersect(rownames(counts_matrix),rownames(
  slot(cogaps_result,"featureLoadings")))
barcodes <- intersect(colnames(counts_matrix),rownames(
  slot(cogaps_result,"sampleFactors")))
counts_matrix <- counts_matrix[features,barcodes]
cogaps_matrix <- slot(cogaps_result,"featureLoadings")[features,]%*%
  t(slot(cogaps_result,"sampleFactors")[barcodes,])
#Obtaining Spatial Coordinates
download.file(sp_url, basename(sp_url), mode = "wb")
untar(basename(sp_url))
spCoords <- load10XCoords(visiumDir = ".", version = "1.0")
rownames(spCoords) <- spCoords$barcode
spCoords <- spCoords[barcodes,]
spPatterns <- cbind(spCoords,slot(cogaps_result,
"sampleFactors")[barcodes,])
data("curated_genes")
```

```

spPatterns<-spPatterns[c("barcode","y","x","Pattern_1","Pattern_5")]
counts_matrix <- counts_matrix[curated_genes,]
cogaps_matrix <- cogaps_matrix[curated_genes, ]
data("optParams")
SpaceMarkersMode <- "DE"
ref_Pattern <- "Pattern_1"
SpaceMarkers_test <- getInteractingGenes(
  data=counts_matrix,reconstruction=NULL,
  optParams = optParams,
  spPatterns = spPatterns,
  refPattern = "Pattern_1",
  mode="DE",analysis="overlap")
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
files <- list.files(".")[grepl(basename(counts_url),list.files("."))]
unlink(files)

```

---

getOverlapScores

*getOverlapScores*


---

## Description

Calculate the overlap scores between patterns in hotspots

## Usage

```
getOverlapScores(hotspots, patternList = NULL)
```

## Arguments

|             |                                                                     |
|-------------|---------------------------------------------------------------------|
| hotspots    | A data frame with columns x, y, barcode and pattern names           |
| patternList | A character vector of pattern names to calculate overlap scores for |

## Value

A data frame with columns pattern1, pattern2 and overlapScore

## Examples

```

hotspots <- data.frame(x = c(1,2,3,4,5),
  y = c(1,2,3,4,5),
  barcode = c("A","B","C","D","E"),
  pattern1 = c(1,0,1,0,1),
  pattern2 = c(1,1,0,0,1))
getOverlapScores(hotspots)
getOverlapScores(hotspots, c("pattern1","pattern2"))

```

---

```
getPairwiseInteractingGenes
      getPairwiseInteractingGenes
```

---

## Description

Performs pairwise analysis to find genes associated with spatial interaction between pairs of spatially varying patterns.

## Usage

```
getPairwiseInteractingGenes(
  data,
  spPatterns,
  mode = c("DE", "residual"),
  optParams = NULL,
  reconstruction = NULL,
  hotspots = NULL,
  minOverlap = 50,
  analysis = c("enrichment", "overlap"),
  patternPairs = NULL,
  ...,
  workers = NULL
)
```

## Arguments

|                             |                                                                                                                                                                                                                                                                                                                                           |
|-----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>           | original spatial data matrix.                                                                                                                                                                                                                                                                                                             |
| <code>spPatterns</code>     | A data frame that contains the spatial coordinates and metrics for spatial features (cell types/cell processes). The column names must include 'x' and 'y' as well as the spatially varying features.                                                                                                                                     |
| <code>mode</code>           | SpaceMarkers mode of operation. Possible values are "DE" (the default) or "residual".                                                                                                                                                                                                                                                     |
| <code>optParams</code>      | a matrix with dimensions 2 X N, where N is the number of spatial patterns with optimal parameters. The first row contains the kernel width 'sigmaOpt' for each pattern, and the second row is the threshOpt (outlier threshold) for each pattern. Users can also input their preferred param values. The default value is NULL.           |
| <code>reconstruction</code> | reconstruction of the data matrix from latent spaces. Required for "residual" mode.                                                                                                                                                                                                                                                       |
| <code>hotspots</code>       | a vector that specifies the patterns to compare to the 'refPattern'. The default is NULL which indicates that all patterns would be compared to the 'refPattern'.                                                                                                                                                                         |
| <code>minOverlap</code>     | a number that specifies the minimum overlap between genes in two patterns to be considered for the statistical tests. The default is 50.                                                                                                                                                                                                  |
| <code>analysis</code>       | a character string that specifies the type of downstream analysis to be performed. Possible values are "enrichment" (default) and "overlap". In enrichment mode, all genes are returned, ranked by the SpaceMarkers metric. In overlap mode, only the genes which are significantly overexpressed in the interaction region are returned. |

patternPairs     A matrix of pattern pairs to be analyzed. Default is  
 ...               Arguments passed to methods  
 workers           (optional) Number of workers to be used for parallel processing.

## Details

=====

## Value

a list of data frames for each pattern with 1) names of the patterns (patterns object) 2) data frame with the hotspots of influence for the two patterns (the hotspots object). 3) data frame with the genes associated with the interaction between the two patterns (interacting genes object, empty if insufficient interaction).

## See Also

Other getIntGenes: [findPatternHotspots\(\)](#), [getInteractingGenes\(\)](#)

## Examples

```
library(SpaceMarkers)
#Visium data links
urls <- read.csv(system.file("extdata","visium_data.txt",
package="SpaceMarkers",mustWork = TRUE))
counts_url <- urls[["visium_url"]][1]
sp_url <- urls[["visium_url"]][2]
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
files <- list.files(".")[grepl(basename(counts_url),list.files("."))]
unlink(files)
download.file(counts_url,basename(counts_url), mode = "wb")
counts_matrix<-load10XExpr(visiumDir=".",
h5filename = basename(counts_url))
#Obtaining CoGAPS Patterns
cogaps_result <- readRDS(system.file("extdata","CoGAPS_result.rds",
package="SpaceMarkers",mustWork = TRUE))
features <- intersect(rownames(counts_matrix),rownames(
  slot(cogaps_result,"featureLoadings")))
barcodes <- intersect(colnames(counts_matrix),rownames(
  slot(cogaps_result,"sampleFactors")))
counts_matrix <- counts_matrix[features,barcodes]
cogaps_matrix <- slot(cogaps_result,"featureLoadings")[features,]%*%
  t(slot(cogaps_result,"sampleFactors")[barcodes,])
#Obtaining Spatial Coordinates
download.file(sp_url, basename(sp_url), mode = "wb")
untar(basename(sp_url))
spCoords <- load10XCoords(visiumDir = ".", version = "1.0")
rownames(spCoords) <- spCoords$barcode
spCoords <- spCoords[barcodes,]
spPatterns <- cbind(spCoords,
slot(cogaps_result,"sampleFactors")[barcodes,])
data("curated_genes")
spPatterns<-spPatterns[c("barcode","y","x","Pattern_1",
"Pattern_3","Pattern_5")]
```

```

counts_matrix <- counts_matrix[curated_genes,]
cogaps_matrix <- cogaps_matrix[curated_genes, ]
optParams <- matrix(c(6, 2, 6, 2, 6, 2), nrow = 2)
rownames(optParams) <- c("sigmaOpt", "threshOpt")
colnames(optParams) <- c("Pattern_1", "Pattern_3", "Pattern_5")
SpaceMarkersMode <- "DE"
patternPairs <- matrix(c("Pattern_1", "Pattern_1",
                        "Pattern_3", "Pattern_5"), nrow=2)
SpaceMarkers <- getPairwiseInteractingGenes(
  data=counts_matrix, reconstruction=NULL,
  optParams = optParams,
  spPatterns = spPatterns,
  mode="DE", analysis="enrichment", patternPairs=patternPairs)
#Remove present Directories if any
unlink(basename(sp_url))
unlink("spatial", recursive = TRUE)
files <- list.files(".")[grepl(basename(counts_url), list.files("."))]
unlink(files)

```

---

|                    |                              |
|--------------------|------------------------------|
| getSpatialFeatures | <i>Load spatial features</i> |
|--------------------|------------------------------|

---

## Description

This function loads spatial features from a file containing spatial features

## Usage

```
getSpatialFeatures(filePath, method = NULL, featureNames = ".")
```

## Arguments

|              |                                                                                                                                                                                               |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| filePath     | A string path to the location of the file containing the spatial features.                                                                                                                    |
| method       | A string specifying the type of object to obtain spatial feature from. Default NULL, where the method is inferred based on object type. Other methods are: "CoGAPS", "Seurat", or "BayesTME". |
| featureNames | An array of strings specifying the column names corresponding to the feature names or a regex string. In the case of Seurat, all metadata columns with "_Feature" suffix are selected.        |

## Value

a matrix of spatial features with barcodes associated with individual coordinates

## Examples

```

library(SpaceMarkers)
#CoGAPS data filePath
filePath <- system.file("extdata", "CoGAPS_result.rds",
package = "SpaceMarkers", mustWork = TRUE)
spFeatures <- getSpatialFeatures(filePath, method = "CoGAPS")
head(spFeatures)

```

---

`getSpatialParameters`    *Read optimal parameters for spatial kernel density from user input or .json file*

---

## Description

This function obtains the width of a spatial kernel density ( $\sigma$ ) from either the user input or from a scale factors .json file. The outlier threshold around the set of spots (threshold) for each pattern is specified by the user (default is 4).

## Usage

```
getSpatialParameters(
  spatialPatterns,
  visiumDir = ".",
  spatialDir = "spatial",
  pattern = "scalefactors_json.json",
  sigma = NULL,
  threshold = 4,
  resolution = c("lowres", "hires", "fullres"),
  ...
)
```

## Arguments

|                              |                                                                                                                                                                                |
|------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>spatialPatterns</code> | A data frame that contains the spatial coordinates for each cell type. The column names must include 'x' and 'y' as well as a set of numbered columns named 'Pattern_1.....N'. |
| <code>visiumDir</code>       | A string path specifying the location of the 10xVisium directory                                                                                                               |
| <code>spatialDir</code>      | A string path specifying the location of the spatial folder containing the .json file of the spot characteristics                                                              |
| <code>pattern</code>         | A string specifying the name of the .json file                                                                                                                                 |
| <code>sigma</code>           | A numeric value specifying the width of the kernel density estimate to be used for smoothing                                                                                   |
| <code>threshold</code>       | A numeric value specifying how many standard deviations above the mean of a null distribution to use an outlier threshold for identifying 'hotspots'                           |
| <code>resolution</code>      | A string specifying image resolution                                                                                                                                           |
| <code>...</code>             | Arguments passed to methods                                                                                                                                                    |

## Value

a numeric matrix of `sigmaOpt` - the optimal width of the gaussian distribution, and the `threshOpt` - outlier threshold around the set of spots for each pattern

**Examples**

```
library(SpaceMarkers)
# Create test data
cells <- c()
test_num <- 500
for(i in 1:test_num){
  cells[length(cells)+1] <- paste0("cell_",i)
}
spPatterns <- data.frame(barcode = cells,
y = runif(test_num, min=0, max=test_num),
x = runif(test_num, min=0, max=test_num),
Pattern_1 = runif(test_num, min=0, max=1),
Pattern_2 = runif(test_num, min=0, max=1) )
# Call the getSpatialParameters function with the test data
optParams <- getSpatialParameters(spPatterns, sigma = 10)
```

---

getSpatialParamsMoransI

*Calculate the optimal parameters from spatial kernel density for cell-cell interactions*

---

**Description**

This function uses Morans.I to calculate the optimal width of the kernel density (sigmaOpt) as well as the outlier threshold around the set of spots (threshOpt) for a null distribution.

**Usage**

```
getSpatialParamsMoransI(spatialPatterns, ...)
```

**Arguments**

spatialPatterns

A data frame that contains the spatial coordinates for each cell type. The column names must include 'x' and 'y' as well as a set of numbered columns named 'Pattern\_1.....N'.

... Arguments passed to methods

**Value**

a numeric matrix of sigmaOpts - the optimal width of the gaussian distribution, and the threshOpt - outlier threshold around the set of spots for each pattern

**Examples**

```
library(SpaceMarkers)
# Create test data
cells <- c()
test_num <- 500
for(i in 1:test_num){
  cells[length(cells)+1] <- paste0("cell_",i)
}
```

```

spPatterns <- data.frame(barcode = cells,
y = runif(test_num, min=0, max=test_num),
x = runif(test_num, min=0, max=test_num),
Pattern_1 = runif(test_num, min=0, max=1),
Pattern_2 = runif(test_num, min=0, max=1) )
# Call the getSpatialParamsMoransI function with the test data
optParams <- getSpatialParamsMoransI(spPatterns)

```

---

load10XCoords

*Load 10x Visium Spatial Coordinates*


---

## Description

This function loads spatial coordinates for each cell from a 10X Visium spatial folder.

## Usage

```
load10XCoords(visiumDir, resolution = "lowres", version = NULL)
```

## Arguments

|            |                                                                                                                                                                                                                       |
|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| visiumDir  | A string path to the location of the folder containing the spatial coordinates. The folder in your visiumDir must be named 'spatial' and must contain files 'scalefactors_json.json' and 'tissue_positions_list.csv.' |
| resolution | A string specifying which values to look for in the .json object. Can be either lowres or highres.                                                                                                                    |
| version    | A string specifying the version of the spaceranger data.                                                                                                                                                              |

## Value

a data frame of the spatial coordinates ( x and y) for each spot/cell

## Examples

```

library(SpaceMarkers)
#Visium data links
urls <- read.csv(system.file("extdata","visium_data.txt",
package = "SpaceMarkers",mustWork = TRUE))
sp_url <- urls[["visium_url"]][2]
# Spatial Coordinates
download.file(sp_url, basename(sp_url), mode = "wb")
untar(basename(sp_url))
spCoords <- load10XCoords(visiumDir = ".", version = "1.0")
unlink("spatial", recursive = TRUE)
unlink("Visium_Human_Breast_Cancer_spatial.tar.gz")

```



---

|             |                                        |
|-------------|----------------------------------------|
| load10XExpr | <i>Load 10X Visium Expression Data</i> |
|-------------|----------------------------------------|

---

### Description

This loads log-transformed 10X Visium expression data from standard 10X Visium folder.

### Usage

```
load10XExpr(visiumDir = NULL, h5filename = "filtered_feature_bc_matrix.h5")
```

### Arguments

|            |                                                           |
|------------|-----------------------------------------------------------|
| visiumDir  | A string path to the h5 file with expression information. |
| h5filename | A string of the name of the h5 file in the directory.     |

### Value

A matrix of class dgeMatrix or Matrix that contains the expression info for each sample (cells) across multiple features (genes)

### Examples

```
library(SpaceMarkers)
#Visium data links
urls <- read.csv(system.file("extdata","visium_data.txt",
package = "SpaceMarkers",mustWork = TRUE))
counts_url <- urls[["visium_url"]][1]
#Remove present Directories if any
files <- list.files(".")[grepl(basename(counts_url),list.files("."))]
unlink(files)
download.file(counts_url,basename(counts_url), mode = "wb")
counts_matrix<-load10XExpr(visiumDir=".",h5filename = basename(counts_url))
files <- list.files(".")[grepl(basename(counts_url),list.files("."))]
unlink(files)
```

---

|           |                                                     |
|-----------|-----------------------------------------------------|
| optParams | <i>Optimal paramters of 5 patterns from CoGAPS.</i> |
|-----------|-----------------------------------------------------|

---

### Description

A dataset with the optimal width of the gaussian distribution (sigmaOpt) and the outlier threshold around the set of spots (thresOpt) for each pattern obtained from CoGAPS. CoGAPS was ran on spatial transcriptomic data from a breast cancer sample.

**Format**

A data frame with 2 rows and 5 columns:

**Pattern\_1** immune cell pattern paramters

**Pattern\_2** Disp.1 parameters

**Pattern\_3** intraductal carcinoma (DCIS) parameters

**Pattern\_4** Disp.2 parameters

**Pattern\_5** invasive carcinoma lesion pattern paramters

**Value**

A matrix of optimal parameters for patterns identified by CoGAPS

---

|              |                     |
|--------------|---------------------|
| plotIMScores | <i>plotIMScores</i> |
|--------------|---------------------|

---

**Description**

Plot the top SpaceMarkers IMScores

**Usage**

```
plotIMScores(
  df,
  interaction,
  cutOff = 0,
  nGenes = 20,
  geneText = 12,
  metricText = 12,
  increments = 1,
  out = NULL
)
```

**Arguments**

|             |                                                       |
|-------------|-------------------------------------------------------|
| df          | A data frame with columns Gene and SpaceMarkersMetric |
| interaction | The interaction to plot                               |
| cutOff      | The cut off value for the plot                        |
| nGenes      | The number of genes to plot                           |
| geneText    | The font size for the gene text                       |
| metricText  | The font size for the metric text                     |
| increments  | The increments for the y-axis                         |
| out         | The output path for the plot                          |

**Examples**

```
example(getPairwiseInteractingGenes)
plotIMScores(getIMScores(SpaceMarkers), "Pattern_1_Pattern_3")
```

---

|                   |                          |
|-------------------|--------------------------|
| plotOverlapScores | <i>plotOverlapScores</i> |
|-------------------|--------------------------|

---

**Description**

Plot the overlap scores between patterns in hotspots

**Usage**

```
plotOverlapScores(  
  df,  
  title = "Spatial Overlap Scores",  
  out = NULL,  
  fontsize = 15  
)
```

**Arguments**

|          |                                                               |
|----------|---------------------------------------------------------------|
| df       | A data frame with columns pattern1, pattern2 and overlapScore |
| title    | The title of the plot                                         |
| out      | The output path for the plot                                  |
| fontsize | The font size of the plot                                     |

**Value**

A ggplot object

**Examples**

```
df <- data.frame(pattern1 = c("pattern1", "pattern1", "pattern2", "pattern2"), pattern2 = c("pattern1", "pattern2", "pattern2", "pattern1"), overlapScore = c(0.5, 0.5, 0.5, 0.5))  
plotOverlapScores(df)  
plotOverlapScores(df, "Overlap Scores", "overlapScores.png", 15)
```

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