

# Package ‘SPACO’

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**Title** Spatial Component Analysis for Spatial Sequencing Data

**Version** 1.0.1

**Description** Spatial components offer tools for dimension reduction and spatially variable gene detection for high dimensional spatial transcriptomics data. Construction of a projection onto low-dimensional feature space of spatially dependent metagenes offers pre-processing to clustering, testing for spatial variability and denoising of spatial expression patterns. For more details, see Koehler et al. (2026) <[doi:10.1093/bioinformatics/btag052](https://doi.org/10.1093/bioinformatics/btag052)>.

**Encoding** UTF-8

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**LinkingTo** Rcpp, RcppEigen

**Depends** R (>= 4.2.3)

**Imports** ggplot2, Seurat (>= 5.3.0), tibble, ggforce, methods, rARPACK, tidy, mgcv, scales, Matrix (>= 1.5)

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**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**NeedsCompilation** yes

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create\_SpaCoObject\_from\_KNN  
*create\_SpaCoObject\_from\_KNN*

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### Description

create\_SpaCoObject\_from\_KNN

### Usage

```
create_SpaCoObject_from_KNN(SeuratObject, n = 10)
```

### Arguments

SeuratObject    Seurat object to export kNN-graph from.  
n                Number of neighbors to consider.

### Value

Returns a SPaCoObject with the SCT data and the kNN-graph as neighborhood matrix.

---

denoised\_projection\_plot  
*Plot denoised gene expression*

---

### Description

Plot denoised gene expression

### Usage

```
denoised_projection_plot(SpaCoObject, feature = NULL)
```

**Arguments**

SpaCoObject	SpacoObject with computed projections
feature	Gene for which to plot denoised projection

**Value**

returns a ggplot object with the denoised gene expression.

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denoise_profiles	<i>computes smoothed gene profiles of genes present in the data.</i>
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---

**Description**

computes smoothed gene profiles of genes present in the data.

**Usage**

```
denoise_profiles(SpaCoObject)
```

**Arguments**

SpaCoObject	Spaco object to compute profiles of.
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**Value**

smoothed gene profiles in the SpaCoObject.

---

eigenMapMatMult	<i>Multiply two matrices using Eigen library</i>
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**Description**

This function multiplies two matrices using the Eigen library, which provides fast linear algebra operations.

**Usage**

```
eigenMapMatMult(A, B)
```

**Arguments**

A	a matrix
B	a matrix

**Value**

the product of A and B

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feature_plot	<i>Plot gene expression</i>
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**Description**

Plot gene expression

**Usage**

```
feature_plot(SpaCoObject, feature)
```

**Arguments**

SpaCoObject	SpacoObject with computed projections
feature	Gene to plot

**Value**

returns a ggplot object with gene expression.

---

read_10x_for_spaco	<i>Read in 10x Visium spatial transcriptomics data</i>
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**Description**

Read in 10x Visium spatial transcriptomics data

**Usage**

```
read_10x_for_spaco(
  data_dir,
  slice,
  filename,
  variable_features_n = variable_features_n,
  spatial_file = spatial_file,
  vars_to_regress = NULL
)
```

**Arguments**

data_dir	Directory containing the H5 file specified by file name and the image data in a sub directory called spatial
slice	Name for the stored image of the tissue slice
filename	Filename of data to be read

variable\_features\_n      Number of most variable features to keep.  
 spatial\_file      Name of csv file from which to read tissue positions.  
 vars\_to\_regress      Names of features to be regressed against using [PercentageFeatureSet](#)

**Value**

Returns a ready to run SPaCoObject.

---

set\_projection      *Set projections of Spaco Object*

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**Description**

Set projections of Spaco Object

**Usage**

```
set_projection(SpaCoObject, data, neighborhood = SpaCoObject@neighbours)
```

**Arguments**

SpaCoObject      Fitted object of class SpaCoObject as returned from [SpaCo] on which to update the projection slot with new data.  
 data      gene expression data matrix; p genes as columns, n loci as rows  
 neighborhood      neighborhood matrix of the new data. Must be of dimension n times n, where n is the number of columns of data

**Value**

Returns the SpaCoObject with the updated data, neighborhood matrix, and projection matrix.

---

seurat\_to\_spaco      *Wrapper to transform existing Seurat object into an SpacoObject.*

---

**Description**

Wrapper to transform existing Seurat object into an SpacoObject.

**Usage**

```
seurat_to_spaco(SeuratObject, assay = "SCT", n_image = 1, layer = "scale.data")
```

**Arguments**

SeuratObject	Seurat object to export
assay	Assay to export from the Seurat object. Default is SCT assay.
n_image	Number of the image to export from Seurat object. Only relevant if Seurat object contains multiple images. Default is 1.
layer	Which layer to export data from. Default is scale.data.

**Value**

Returns a SpaCoObject with all slots filled necessary to perform the spatial component analysis.

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SpaCo	<i>SpaCo</i>
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**Description**

SpaCo

**Usage**

```
SpaCo(
  SpaCoObject,
  PC_criterion = "percent",
  PC_value = 0.95,
  set_nspacs = NULL,
  nSim = 1000,
  nSpacQuantile = 0.05,
  reducedSpots = FALSE,
  nReduce = 1000
)
```

**Arguments**

SpaCoObject	Object of class SpaCoObject as generated from [SpaCoObject] on which to perform SCA.
PC_criterion	criterion on which to select number of principal components for initial covariance matrix reconstruction; either "number" to select a number of PCs or "percent" to select number of PCs to explain specified amount of data variance
PC_value	Value to specify number of PCs or desired level of explained variance, see "PC_criterion"
set_nspacs	Boolean if number of relevant spacs is to be computed. Increases run time significantly
nSim	Number of simulations for computation of spac number
nSpacQuantile	Quantile to use as cutoff for spac number
reducedSpots	Should algorithm be run on a subset of spots? Default = FALSE
nReduce	Number of spots to sample to run algorithm on subset if reducedSpots==TRUE. Ignored if reducedSpots==FALSE

**Value**

Returns a SpaCoObject filled with the result of the spatial component analysis.

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SpaCoObject	<i>Create a constructor function that creates an object of class SpaCoObject</i>
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**Description**

Create a constructor function that creates an object of class SpaCoObject

**Usage**

```
SpaCoObject(neighbours, data, coordinates)
```

**Arguments**

neighbours	Binary matrix with weights describing if cells are to be considered neighbours or not depending on the defined distance.
data	Matrix with normalized and scaled gene counts. Rows as cells and genes as columns
coordinates	Matri with the cell coordinates on the slides. Rows and Columns in the 10x Visium case.

**Value**

Returns a SpaCoObject with the given slots filled

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Spaco_plot	<i>Plot SPaCo meta genes.</i>
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**Description**

Plot SPaCo meta genes.

**Usage**

```
Spaco_plot(SpaCoObject, spac = 1)
```

**Arguments**

SpaCoObject	SpacoObject with computed projections
spac	component to plot

**Value**

returns a ggplot object with the meta gene expression.

---

spacs\_to\_seurat      *transfer computed spatial components to existing Seurat object.*

---

**Description**

transfer computed spatial components to existing Seurat object.

**Usage**

```
spacs_to_seurat(SpaCoObject, SeuratObject, nSpacs = SpaCoObject@nSpacs)
```

**Arguments**

SpaCoObject	SpaCoObject to export spatial components from.
SeuratObject	Seurat object to add spatial components to.
nSpacs	Number of Spacs which are to be projected on for dimension reduction

**Value**

Returns a Seurat Object with the spatial components projections in the dimensional reduction slot.

---

subset\_non\_neighbour\_cells  
*Filtering function to remove cells without neighbours in defined distance from existing Seurat object to be conformable with existing SpaCoObject.*

---

**Description**

Filtering function to remove cells without neighbours in defined distance from existing Seurat object to be conformable with existing SpaCoObject.

**Usage**

```
subset_non_neighbour_cells(SpaCoObject, SeuratObject)
```

**Arguments**

SpaCoObject	SpaCoObject to integrate into Seurat object.
SeuratObject	Seurat object to be filtered.

**Value**

Returns a Seurat object with cells filtered to match SpaCoObject.



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SVGTest	<i>Compute the spatial variable genes of a SpaCoObject after running runSCA</i>
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**Description**

Compute the spatial variable genes of a SpaCoObject after running runSCA

**Usage**

```
SVGTest(SpaCoObject, adjustMethod = "holm")
```

**Arguments**

SpaCoObject SpaCoObject to compute spatially variable genes of.  
adjustMethod method for p-value adjustment. See p.adjust function.

**Value**

returns a data frame of spatial variable genes and their p-Values.

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