

# Package ‘spARI’

May 2, 2026

**Type** Package

**Title** Spatially Aware Adjusted Rand Index for Evaluating Spatial  
Transcriptomics Clustering

**Version** 1.3.0

**Description** The R package used in the manuscript “Spatially Aware Adjusted Rand  
Index for Evaluating Spatial Transcriptomics Clustering”.

**License** GPL (>= 2)

**Encoding** UTF-8

**Depends** R (>= 4.1.0)

**Imports** Rcpp, stats, Matrix, SpatialExperiment, SummarizedExperiment,  
BiocParallel (>= 1.0)

**LinkingTo** Rcpp

**LazyData** false

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**Suggests** FNN, knitr, rmarkdown, BiocStyle, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**biocViews** Clustering, DataImport, GeneExpression, Transcriptomics,  
Spatial, Software

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## Contents

generate_gs_pairs_int . . . . .	2
generate_sg_pairs_int . . . . .	2
perm_test . . . . .	3
spARI . . . . .	4
spARI_example_data . . . . .	6

<b>Index</b>	<b>7</b>
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generate\_gs\_pairs\_int *Generate object pairs (gs pairs)*

---

### Description

This function identifies all object pairs that belong to the same group in the reference partition but different clusters in the clustering partition

### Arguments

`c_labels`      An integer vector of clustering labels.  
`r_labels`      An integer vector of reference labels.

### Value

An integer matrix with two columns, where each row is a pair of object indices.

### Examples

```
c_labels <- c(1,1,2,2,2,3,3)
r_labels <- c(1,1,1,2,2,3,1)
generate_gs_pairs_int(c_labels, r_labels)
```

---

generate\_sg\_pairs\_int *Generate object pairs (sg pairs)*

---

### Description

This function identifies all object pairs that belong to the same cluster in the clustering partition but different groups in the reference partition

### Arguments

`c_labels`      An integer vector of clustering labels.  
`r_labels`      An integer vector of reference labels.

### Value

An integer matrix with two columns, where each row is a pair of object indices.

**Examples**

```
c_labels <- c(1,1,2,2,2,3,3)
r_labels <- c(1,1,1,2,2,3,1)
generate_sg_pairs_int(c_labels, r_labels)
```

perm\_test

*The function perm\_test is the main function to carry out the hypothesis test procedure proposed in the paper.*

**Description**

The function perm\_test is the main function to carry out the hypothesis test procedure proposed in the paper.

**Usage**

```
perm_test(
  r_labels,
  c_labels,
  coords = NULL,
  dist_mat = NULL,
  f_func_input = NULL,
  h_func_input = NULL,
  alpha_val = 0.8,
  use_parallel = TRUE,
  replicate_times = 100,
  random_seed = 42,
  spe = NULL
)
```

**Arguments**

r_labels	Annotated labels of all spots/cells. Can be numeric vector or character vector.
c_labels	Estimated labels obtained by a certain spatial clustering method.
coords	Spatial coordinates (2 columns). 1st column: first dimension coordinate. 2nd column: second dimension coordinate. Default is NULL.
dist_mat	Distance matrix provided by users. If both coords and dist_mat are provided, we will directly use the distance matrix. Default is NULL. Please notice that if dist_mat is sparse, the weight function for object pairs without recorded distances degenerates to the setting used in the classical Rand index.
f_func_input	R function; function f provided by users.
h_func_input	R function; function h provided by users.
alpha_val	Parameter in the default functions f and h, which belongs to the open interval (0, 1) to keep a positive gap between the maximal weight of the disagreement pair and the weight one of the agreement pair. Default is 0.8.
use_parallel	Logical; if TRUE, use parallel code to permute the two partitions. Default is TRUE.

replicate_times	Number of permutations for both the reference and clustering partitions. Default is 100.
random_seed	Random seed for reproducibility. Default is 42.
spe	SpatialExperiment object; stores various components of spatial transcriptomics data, including spatialCoords: A matrix containing the spatial coordinates; colData\$cell_type: Annotated cell type labels for each spot or cell; colData\$cluster: Clustering labels for each spot or cell. Default is NULL.

### Value

spARI returns an R numeric including the following information.

spARI_obs	numeric, the observed spARI value calculated by r_labels and c_labels
p_value	numeric, the p-value of the hypothesis testing

### Examples

```
library(spARI)
data(spARI_example_data)
true_labels = spARI_example_data$true_labels
c1_labels = spARI_example_data$c1_labels
c2_labels = spARI_example_data$c2_labels
coords = spARI_example_data$coords
test_res1 = perm_test(r_labels=true_labels, c_labels=c1_labels, coords=coords,
  use_parallel=FALSE)
test_res2 = perm_test(r_labels=true_labels, c_labels=c2_labels, coords=coords,
  use_parallel=FALSE)
```

---

spARI

*The function spARI is the main function to calculate spRI and spARI values proposed in the paper.*

---

### Description

The function spARI is the main function to calculate spRI and spARI values proposed in the paper.

### Usage

```
spARI(
  r_labels,
  c_labels,
  coords = NULL,
  dist_mat = NULL,
  f_func_input = NULL,
  h_func_input = NULL,
  alpha_val = 0.8,
  spe = NULL
)
```

**Arguments**

r_labels	Annotated labels of all spots/cells. Can be numeric vector or character vector.
c_labels	Estimated labels obtained by a certain spatial clustering method.
coords	Spatial coordinates (2 columns). 1st column: first dimension coordinate. 2nd column: second dimension coordinate. Default is NULL.
dist_mat	Distance matrix provided by users. If both coords and dist_mat are provided, we will directly use the distance matrix. Default is NULL. Please notice that if dist_mat is sparse, the weight function for object pairs without recorded distances degenerates to the setting used in the classical Rand index.
f_func_input	R function; function f provided by users.
h_func_input	R function; function h provided by users.
alpha_val	Parameter in the default functions f and h, which belongs to the open interval (0, 1) to keep a positive gap between the maximal weight of the disagreement pair and the weight one of the agreement pair. Default is 0.8.
spe	SpatialExperiment object; stores various components of spatial transcriptomics data, including spatialCoords: A matrix containing the spatial coordinates; colData\$cell_type: Annotated cell type labels for each spot or cell; colData\$cluster: Clustering labels for each spot or cell. Default is NULL.

**Value**

spARI returns an R numeric including the following information.

spRI_value	numeric, the spRI value calculated by r_labels and c_labels
spARI_value	numeric, the spARI value calculated by r_labels and c_labels

**Examples**

```
library(spARI)
### --- Import example data --- ###
# (1) true_labels: ground truth of 160 spots (input as r_labels)
# (2) c1_labels: one partition results of these spots (input as c_labels)
# (3) c2_labels: another partition results of these spots (input as c_labels)
# (4) coords: spatial coordinates of these spots (2 columns)
data(spARI_example_data)
true_labels = spARI_example_data$true_labels
c1_labels = spARI_example_data$c1_labels
c2_labels = spARI_example_data$c2_labels
coords = spARI_example_data$coords
### --- Compute spRI and spARI --- ###
res1 = spARI(r_labels=true_labels, c_labels=c1_labels, coords=coords)
res2 = spARI(r_labels=true_labels, c_labels=c2_labels, coords=coords)
cat(paste0("1st: spRI=", round(res1[1], 3), ", spARI=", round(res1[2], 3), "\n"))
cat(paste0("2nd: spRI=", round(res2[1], 3), ", spARI=", round(res2[2], 3), "\n"))
```

---

spARI\_example\_data      *Example data for spARI*

---

### Description

This dataset includes simulated spatial clustering results for demonstration purposes. It contains the following objects:

- `true_labels`: Ground-truth labels of 160 spots.
- `c1_labels`: First clustering result to compare.
- `c2_labels`: Second clustering result to compare.
- `coords`: Spatial coordinates (matrix with 2 columns).

### Usage

```
data(spARI_example_data)
```

### Format

An environment containing 4 objects:

**true\_labels** Numeric or factor vector of length 160.

**c1\_labels** Numeric or factor vector of length 160.

**c2\_labels** Numeric or factor vector of length 160.

**coords** Numeric matrix of size 160x2.

# Index

## \* datasets

spARI\_example\_data, [6](#)

generate\_gs\_pairs\_int, [2](#)

generate\_sg\_pairs\_int, [2](#)

perm\_test, [3](#)

spARI, [4](#)

spARI\_example\_data, [6](#)