Package: spARI (via r-universe)

May 30, 2026

Type Package

Title Spatially Aware Adjusted Rand Index for Evaluating Spatial Transcritpomics Clustering

Version 1.2.0

Description The R package used in the manuscript ``Spatially Aware Adjusted Rand Index for Evaluating Spatial Transcritpomics 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

Config/pak/sysreqs libmagick++-dev gsfonts libicu-dev libssl-dev zlib1g-dev

Repository https://bioc-release.r-universe.dev

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Contents

`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.

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