

# Package ‘SpatialCPie’

May 8, 2024

**Title** Cluster analysis of Spatial Transcriptomics data

**Version** 1.20.0

**Description** SpatialCPie is an R package designed to facilitate cluster evaluation for spatial transcriptomics data by providing intuitive visualizations that display the relationships between clusters in order to guide the user during cluster identification and other downstream applications.

The package is built around a shiny ``gadget" to allow the exploration of the data with multiple plots in parallel and an interactive UI. The user can easily toggle between different cluster resolutions in order to choose the most appropriate visual cues.

**biocViews** Transcriptomics, Clustering, RNASeq, Software

**Depends** R (>= 3.6)

**Imports** colorspace (>= 1.3-2), data.table (>= 1.12.2), digest (>= 0.6.21), dplyr (>= 0.7.6), ggforce (>= 0.3.0), ggiraph (>= 0.5.0), ggplot2 (>= 3.0.0), ggrepel (>= 0.8.0), grid (>= 3.5.1), igraph (>= 1.2.2), lpSolve (>= 5.6.13), methods (>= 3.5.0), purrr (>= 0.2.5), readr (>= 1.1.1), rlang (>= 0.2.2), shiny (>= 1.1.0), shinycssloaders (>= 0.2.0), shinyjs (>= 1.0), shinyWidgets (>= 0.4.8), stats (>= 3.6.0), SummarizedExperiment (>= 1.10.1), tibble (>= 1.4.2), tidyr (>= 0.8.1), tidyselect (>= 0.2.4), tools (>= 3.6.0), utils (>= 3.5.0), zeallot (>= 0.1.0)

**Suggests** BiocStyle (>= 2.8.2), jpeg (>= 0.1-8), knitr (>= 1.20), rmarkdown (>= 1.10), testthat (>= 2.0.0)

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**Author** Joseph Bergenstraahle [aut, cre]

**Maintainer** Joseph Bergenstraahle <joseph.bergenstrahle@gmail.com>

## Contents

|                                 |    |
|---------------------------------|----|
| SpatialCPie-package . . . . .   | 2  |
| .arrayPlot . . . . .            | 3  |
| .clusterGraph . . . . .         | 3  |
| .computeClusterColors . . . . . | 4  |
| .likeness . . . . .             | 5  |
| .logsumexp . . . . .            | 5  |
| .makeApp . . . . .              | 6  |
| .makeServer . . . . .           | 6  |
| .makeUI . . . . .               | 7  |
| .maximizeOverlap . . . . .      | 7  |
| .preprocessData . . . . .       | 8  |
| .SVGBarplot . . . . .           | 9  |
| .tidyAssignments . . . . .      | 9  |
| .zscore . . . . .               | 10 |
| parseSpotFile . . . . .         | 10 |
| runCPie . . . . .               | 11 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>13</b> |
|--------------|-----------|

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SpatialCPie-package     *SpatialCPie: Cluster analysis of Spatial Transcriptomics data*

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## Description

SpatialCPie is an R package designed to facilitate cluster evaluation for spatial transcriptomics data by providing intuitive visualizations that display the relationships between clusters in order to guide the user during cluster identification and other downstream applications. The package is built around a shiny "gadget" to allow the exploration of the data with multiple plots in parallel and an interactive UI. The user can easily toggle between different cluster resolutions in order to choose the most appropriate visual cues.

## Author(s)

**Maintainer:** Joseph Bergenstraahle <joseph.bergenstrahle@gmail.com>

---

.arrayPlot                      *Array pie plot*

---

**Description**

Array pie plot

**Usage**

```
.arrayPlot(scores, coordinates, counts = NULL, image = NULL,  
          scoreMultiplier = 1, spotScale = 1, spotOpacity = 1,  
          numTopGenes = 5)
```

**Arguments**

scores                      [data.frame](#) with cluster scores for each spot containing the columns "spot", "name", and "score".

coordinates                [data.frame](#) with rownames matching those in scores and columns "x" and "y" specifying the plotting position of each observation.

image                      a [grid.grob](#) to use as background to the plots.

scoreMultiplier            log multiplication factor applied to the score vector.

spotScale                  pie chart size.

spotOpacity                pie chart opacity.

**Value**

[ggplot](#) object of the pie plot.

---

.clusterGraph                *Cluster graph*

---

**Description**

Cluster graph

**Usage**

```
.clusterGraph(assignments, clusterMeans, featureName,  
              transitionProportions = "To", transitionLabels = FALSE,  
              transitionThreshold = 0, numTopFeatures = 10)
```

**Arguments**

- assignments `data.frame` with columns "name", "resolution", and "cluster".
- clusterMeans `data.frame` with columns "name", "resolution", "cluster", featureName, and "mean".
- featureName `character` with the name of the clustered feature.
- transitionProportions  
how to compute the transition proportions. Possible values are:
- "From": based on the total number of assignments in the lower-resolution cluster
  - "To": based on the total number of assignments in the higher-resolution cluster
- transitionLabels  
`logical` specifying whether to show edge labels.
- transitionThreshold  
hide edges with transition proportions below this threshold.
- numTopFeatures `integer` specifying the number of features to show in the hover tooltips.

**Value**

`ggplot` object of the cluster graph.

---

`.computeClusterColors` *Compute cluster colors*

---

**Description**

Computes colors so that dissimilar clusters are far away in color space.

**Usage**

```
.computeClusterColors(clusterMeans)
```

**Arguments**

clusterMeans matrix of size (n, K) representing the n feature means for each of the K clusters.

**Value**

vector of cluster colors.

---

.likeness                      *Likeness score*

---

**Description**

Likeness score

**Usage**

.likeness(d, c = 1)

**Arguments**

d                      distance vector.  
c                      log multiplier.

**Value**

vector of scores.

---

.logsumexp                      *Logsumexp*

---

**Description**

Adapted from <https://stat.ethz.ch/pipermail/r-help/2011-February/269205.html>

**Usage**

.logsumexp(xs)

**Arguments**

xs                      input vector

**Value**

log of summed exponentials

---

`.makeApp`                      *SpatialCPie App*

---

### Description

SpatialCPie App

### Usage

```
.makeApp(image, ...)
```

### Arguments

|                    |  |
|--------------------|--|
| <code>image</code> | background image.                                  |
| <code>...</code>   | arguments passed to <code>.preprocessData</code> . |

### Value

SpatialCPie [shinyApp](#) object.

---

`.makeServer`                      *SpatialCPie server*

---

### Description

SpatialCPie server

### Usage

```
.makeServer(assignments, clusterMeans, counts, scores, colors, image,
             coordinates, featureName)
```

### Arguments

|                           |   |
|---------------------------|---|
| <code>assignments</code>  | <a href="#">data.frame</a> with cluster assignments containing the columns "unit" (name of the observational unit; either a gene name or a spot name), "resolution", "cluster", and "name" (a unique identifier of the (resolution, cluster) pair). |
| <code>clusterMeans</code> | <a href="#">data.frame</a> with columns "name", "resolution", "cluster", <code>featureName</code> , and "mean".   |
| <code>scores</code>       | <a href="#">data.frame</a> with cluster scores for each spot in each resolution containing the columns "spot", "resolution", "cluster", "name", and "score".  |
| <code>colors</code>       | vector of colors for each cluster. Names should match the "name" columns of the assignments and scores.   |
| <code>image</code>        | background image for the array plots, passed to <a href="#">grid.raster</a> .   |
| <code>coordinates</code>  | <a href="#">data.frame</a> with rownames matching the <a href="#">names</a> in scores and columns "x" and "y" specifying the plotting position of each observation.   |
| <code>featureName</code>  | <a href="#">character</a> with the name of the clustered feature.   |

**Value**

server function, to be passed to [shinyApp](#).

---

*.makeUI*                      *SpatialCPie UI*

---

**Description**

SpatialCPie UI

**Usage**

`.makeUI()`

**Value**

SpatialCPie UI, to be passed to [shinyApp](#).

---

*.maximizeOverlap*            *Maximize overlap*

---

**Description**

Maximize overlap

**Usage**

`.maximizeOverlap(xss)`

**Arguments**

`xss`                      list of lists of labels.

**Value**

`xss`, relabeled so as to maximize the overlap between labels in consecutive label lists.

---

`.preprocessData`      *Preprocess data*

---

### Description

Preprocesses input data for `.makeServer`.

### Usage

```
.preprocessData(counts, margin, resolutions, assignmentFunction,
  coordinates = NULL)
```

### Arguments

|                                 |  |
|---------------------------------|--|
| <code>counts</code>             | count matrix. rownames should correspond to genes and colnames should correspond to spot coordinates.  |
| <code>margin</code>             | which margin of the count matrix to cluster. Valid values are <code>c("spot", "sample", "gene", "feature")</code> .  |
| <code>resolutions</code>        | vector of resolutions to cluster.  |
| <code>assignmentFunction</code> | function to compute cluster assignments. The function should have the following signature: <code>integer (number of clusters) -&gt; (m, n) feature matrix -&gt; m-length vector (cluster assignment of each data point)</code> . |
| <code>coordinates</code>        | optional <code>data.frame</code> with pixel coordinates for each spot. rownames should correspond to the colnames of counts and the columns <code>x</code> and <code>y</code> should specify the pixel coordinates of the spots. |

### Value

list with the following elements:

- `$assignments`: tidy assignments
- `$means`: cluster means
- `$scores`: cluster scores for each spot in each resolution
- `$colors`: cluster colors
- `$coordinates`: spot coordinates, either from `coordinates` or parsed from assignments
- `$featureName`: name of the clustered feature (the "opposite" of `margin`)



---

.SVGBarplot            *SVG barplot*

---

**Description**

SVG barplot

**Usage**

.SVGBarplot(xs)

**Arguments**

xs                    named vector with observations

**Value**

character SVG barplot

---

.tidyAssignments        *Tidy assignments*

---

**Description**

Tidy assignments

**Usage**

.tidyAssignments(assignments)

**Arguments**

assignments        list of assignment vectors.

**Value**

a [data.frame](#) containing the assignments, with the data relabeled so that the overlap between consecutive assignment vectors is maximized. Additionally, a "root" resolution is added.

---

|                      |                |
|----------------------|----------------|
| <code>.zscore</code> | <i>Z-score</i> |
|----------------------|----------------|

---

**Description**

Z-score

**Usage**

```
.zscore(xs)
```

**Arguments**

`xs` vector of observations

**Value**

`xs`, z-normalized. if all elements of `xs` are equal, a vector of zeros will be returned instead.

---

|                            |                                   |
|----------------------------|-----------------------------------|
| <code>parseSpotFile</code> | <i>Parse spot detector output</i> |
|----------------------------|-----------------------------------|

---

**Description**

Parses the output from the ST spot detector tool for use with SpatialCPie.

**Usage**

```
parseSpotFile(file)
```

**Arguments**

`file` spot file

**Value**

`data.frame` with columns "x" and "y" specifying the pixel coordinates of each spot

**Examples**

```
## Create spot file
data <- rbind(
  c(7, 18, 7.00, 18.07, 563.2, 947.0),
  c(8, 11, 8.00, 11.04, 612.5, 627.7)
)
filename <- tempfile()
write.table(
  data,
  file = filename,
  sep = "\t",
  quote = FALSE,
  col.names = c("x", "y", "new_x", "new_y", "pixel_x", "pixel_y")
)

## Parse spot file
parseSpotFile(filename)

## Delete spot file
unlink(filename)
```

runCPie

*Run SpatialCPie***Description**

Runs the SpatialCPie gadget.

**Usage**

```
runCPie(counts, image = NULL, spotCoordinates = NULL,
  margin = "spot", resolutions = 2:4,
  assignmentFunction = function(k, x) kmeans(x, centers = k)$cluster,
  view = NULL)
```

**Arguments**

|                    |   |
|--------------------|---|
| counts             | gene count matrix or a <a href="#">SummarizedExperiment-class</a> object containing count values.                               |
| image              | image to be used as background to the plot.   |
| spotCoordinates    | <a href="#">data.frame</a> with pixel coordinates. The rows should correspond to the columns (spatial areas) in the count file. |
| margin             | which margin to cluster.  |
| resolutions        | <a href="#">numeric</a> vector specifying the clustering resolutions.   |
| assignmentFunction | function to compute cluster assignments.  |
| view               | <a href="#">viewer</a> object.  |

**Value**

a list with the following items:

- "clusters": Cluster assignments (may differ from assignments)
- "clusterGraph": The cluster tree ggplot object
- "arrayPlot": The pie plot ggplot objects

**Examples**

```
if (interactive()) {
  options(device.ask.default = FALSE)

  ## Set up coordinate system
  coordinates <- as.matrix(expand.grid(1:10, 1:10))

  ## Generate data set with three distinct genes generated by three
  ## distinct cell types
  profiles <- diag(rep(1, 3)) + runif(9)
  centers <- cbind(c(5, 2), c(2, 8), c(8, 2))
  mixes <- apply(coordinates, 1, function(x) {
    x <- exp(-colSums((centers - x) ^ 2) / 50)
    x / sum(x)
  })
  means <- 100 * profiles %*% mixes
  counts <- matrix(rpois(prod(dim(means)), means), nrow = nrow(profiles))
  colnames(counts) <- apply(
    coordinates,
    1,
    function(x) do.call(paste, c(as.list(x), list(sep = "x"))))
  )
  rownames(counts) <- paste("gene", 1:nrow(counts))

  ## Run SpatialCPie
  runCPie(counts)
}
```

# Index

## \* **internal**

- .SVGBarplot, 9
- .arrayPlot, 3
- .clusterGraph, 3
- .computeClusterColors, 4
- .likeness, 5
- .logsumexp, 5
- .makeApp, 6
- .makeServer, 6
- .makeUI, 7
- .maximizeOverlap, 7
- .preprocessData, 8
- .tidyAssignments, 9
- .zscore, 10

- .SVGBarplot, 9
- .arrayPlot, 3
- .clusterGraph, 3
- .computeClusterColors, 4
- .likeness, 5
- .logsumexp, 5
- .makeApp, 6
- .makeServer, 6, 8
- .makeUI, 7
- .maximizeOverlap, 7
- .preprocessData, 6, 8
- .tidyAssignments, 9
- .zscore, 10

character, 4, 6, 9

data.frame, 3, 4, 6, 8–11

ggplot, 3, 4

grid.grob, 3

grid.raster, 6

integer, 4

logical, 4

names, 6

numeric, 11

parseSpotFile, 10

runCPie, 11

shinyApp, 6, 7

SpatialCPie (SpatialCPie-package), 2

SpatialCPie-package, 2

viewer, 11