Package ‘SpatialCPie’

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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.

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SpatialCPie-package

SpatialCPie: Cluster analysis of Spatial Transcriptomics data

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)

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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.

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**

```r
.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**

```r
.logsumexp(xs)
```

**Arguments**

- `xs`: input vector

**Value**

log of summed exponentials
.makeApp  

**SpacialCPie App**

**Description**

SpacialCPie App

**Usage**

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

**Arguments**

- **image**: background image.
- **...**: arguments passed to `.preprocessData`. 

**Value**

SpacialCPie `shinyApp` object.

---

.makeServer  

**SpatialCPie server**

**Description**

SpatialCPie server

**Usage**

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

**Arguments**

- **assignments**: `data.frame` 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).
- **clusterMeans**: `data.frame` with columns "name", "resolution", "cluster", `featureName`, and "mean".
- **scores**: `data.frame` with cluster scores for each spot in each resolution containing the columns "spot", "resolution", "cluster", "name", and "score".
- **colors**: vector of colors for each cluster. Names should match the "name" columns of the assignments and scores.
- **image**: background image for the array plots, passed to `grid.raster`.
- **coordinates**: `data.frame` with rownames matching the `names` in `scores` and columns "x" and "y" specifying the plotting position of each observation.
- **featureName**: `character` with the name of the clustered feature.
Value

server function, to be passed to shinyApp.

Description

SpatialCPie UI

Usage

.makeUI()

Value

SpatialCPie UI, to be passed to shinyApp.

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

counts count matrix. rownames should correspond to genes and colnames should correspond to spot coordinates.

margin which margin of the count matrix to cluster. Valid values are c("spot", "sample", "gene", "feature").

resolutions vector of resolutions to cluster.

assignmentFunction function to compute cluster assignments. The function should have the following signature: integer (number of clusters) -> (m, n) feature matrix -> m-length vector (cluster assignment of each data point).

coordinates optional data.frame with pixel coordinates for each spot. rownames should correspond to the colnames of counts and the columns x and y 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)
SVG Barplot

Description
SVG barplot

Usage
.SVGBarplot(xs)

Arguments
xs named vector with observations

Value
character SVG barplot

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.
parseSpotFile

Parse spot detector output

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

```r
## 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**

```r
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 `SummarizedExperiment-class` object containing count values.
- `image`: image to be used as background to the plot.
- `spotCoordinates`: `data.frame` with pixel coordinates. The rows should correspond to the columns (spatial areas) in the count file.
- `margin`: which margin to cluster.
- `resolutions`: numeric vector specifying the clustering resolutions.
- `assignmentFunction`: function to compute cluster assignments.
- `view`: `viewer` 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

```r
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) / 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)
}
```
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