Package: SpatialCPie (via r-universe)

November 25, 2026

Title Cluster analysis of Spatial Transcriptomics data

Version 1.30.0

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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Roxygen list(markdown = TRUE)

RoxygenNote 6.1.1

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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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`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

```
## 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 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

```
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)
}
```

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