Package ‘escheR’

April 3, 2024

Title  Unified multi-dimensional visualizations with Gestalt principles

Version  1.2.0

Description  The creation of effective visualizations is a fundamental component of data analysis. In biomedical research, new challenges are emerging to visualize multi-dimensional data in a 2D space, but current data visualization tools have limited capabilities. To address this problem, we leverage Gestalt principles to improve the design and interpretability of multi-dimensional data in 2D data visualizations, layering aesthetics to display multiple variables. The proposed visualization can be applied to spatially-resolved transcriptomics data, but also broadly to data visualized in 2D space, such as embedding visualizations. We provide this open source R package escheR, which is built off of the state-of-the-art ggplot2 visualization framework and can be seamlessly integrated into genomics toolboxes and workflows.

License  MIT + file LICENSE

Encoding  UTF-8

Roxygen  list(markdown = TRUE)

RoxygenNote  7.2.3

biocViews  Spatial, SingleCell, Transcriptomics, Visualization, Software

Depends  ggplot2, R (>= 4.3)

Imports  SpatialExperiment (>= 1.6.1), SingleCellExperiment, rlang, SummarizedExperiment

BugReports  https://github.com/boyigu01/escheR/issues

URL  https://github.com/boyigu01/escheR

Suggests  STexampleData, BumpyMatrix, knitr, rmarkdown, BiocStyle, ggpubr, scran, scater, scuttle, Seurat

VignetteBuilder  knitr

git_url  https://git.bioconductor.org/packages/escheR

git_branch  RELEASE_3_18
`.contain_reserved_col_name`

Check if rowData(spe) contains reserved name

**Description**

Internal Function

**Usage**

`.contain_reserved_col_name(col_name)`

**Arguments**

- `col_name` - the colnames

**Value**

TRUE when `col_name` contains reserved names, FALSE
add_fill

Adding fill to highlight the figure in the spatial map

Description

Adding fill to highlight the figure in the spatial map

Usage

add_fill(p, var, point_size = 2, ...)

Arguments

- **p**: a spatial map created by `make_escheR()`, with or without other layers of aesthetics.
- **var**: A character(1) with the name of the colData(spe) column that has the values to be used as the background.
- **point_size**: A numeric(1) specifying the size of the spot in the ggplot. Defaults to 2.
- **...**: Reserved for future arguments.

Value

an ggplot object.

Examples

```r
library(STexampleData)

spe <- Visium_humanDLPFC()

make_escheR(spe) |> 
   add_fill(var = "ground_truth")
```

add_ground

Adding border to highlight the ground in the spatial map

Description

Adding border to highlight the ground in the spatial map

Usage

add_ground(p, var, stroke = 0.5, point_size = 2, ...)

Arguments

- **p**: a spatial map created by `make_escheR()`, with or without other layers of aesthetics.
- **var**: A character(1) with the name of the `colData(spe)` column that has the values to be used as the background.
- **stroke**: A numeric(1) specifying the thickness of the border.
- **point_size**: A numeric(1) specifying the size of the spot in the ggplot. Defaults to 2.
- **...**: Reserved for future arguments.

Value

an ggplot object.

Examples

```r
library(STexampleData)

spe <- Visium_humanDLPFC()

make_escheR(spe) |>
  add_ground(var = "ground_truth")
```

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Description

Adding symbols to each spot in the spatial map

Usage

```r
add_symbol(p, var, size = 1, ...)
```

Arguments

- **p**: a spatial map created by `make_escheR()`, with or without other layers of aesthetics.
- **var**: A character(1) with the name of the `colData(spe)` column that has the values to be used as the background.
- **size**: A numeric(1) specifying the size of the symbols in the ggplot. Defaults to 1.
- **...**: Reserved for future arguments.

Value

an ggplot object.
Examples

library(STexampleData)

spe <- Visium_humanDLPFC()

# Convert a continuous variable to categorical
spe$in_tissue <- factor(spe$in_tissue)

make_escheR(spe) |> 
  add_ground(var = "ground_truth") |> 
  add_symbol(var = "in_tissue", size = 0.5)

Description

make_escheR() is a generic function to initialize a ggplot object that contains a spatial map. Because the ggplot object saves the input spatial transcriptomics data, the transcriptomics data will be used in the following layering process to add more aesthetic components in the plot following the grammar of graphics and ggplot2 syntax.

Usage

make_escheR(object, spot_size = 2, ...)

## S3 method for class 'SingleCellExperiment'
make_escheR(object, spot_size = 2, dimred = "PCA", ...)

## S3 method for class 'SpatialExperiment'
make_escheR(object, spot_size = 2, dimred = NULL, y_reverse = TRUE, ...)

## S3 method for class 'data.frame'
make_escheR(object, spot_size = 2, .x, .y, ...)

Arguments

object a data object that contains the spatial transcriptomics data. Currently only working for spatial transcriptomics data as SpatialExperiment objects.

spot_size A numeric(1) specifying the size of the spot in the ggplot. Defaults to 2.

... Reserved for future arguments.

dimred String or integer scalar specifying the existing dimensionality reduction results to use.

y_reverse (logical) Whether to reverse y coordinates, which is often required for 10x Genomics Visium data. Default = TRUE.

.x the X-coordinate

.y the Y-coordinate
make_escheR

Value

an ggplot object that contains the spatial transcriptomics data.

References


Examples

library(STexampleData)
# SpatialExperiment Object
spe <- Visium_humanDLPFC()
make_escheR(spe)

# SingleCellExperiment Object
sce <- SingleCellExperiment(counts(spe))
reducedDims(sce) <- list(
    # Example embedding
    EG = matrix(seq.int(1, ncol(spe)*2), ncol = 2)
)
make_escheR(sce, dimred = "EG")

# data.frame Object
x <- spatialCoords(spe)[,1]
y <- spatialCoords(spe)[,2]
df <- colData(spe) |> data.frame()
make_escheR(object = df, .x = x, .y = y)
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