Title  Unified multi-dimensional visualizations with Gestalt principles
Version  1.4.0
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, hexbin
VignetteBuilder  knitr
git_url  https://git.bioconductor.org/packages/escheR
git_branch  RELEASE_3_19
.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, ...)
add_fill_bin(p, var, bins = 30, point_size = 2.8, fun = sum, ...)
```

**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.
- **bins**
  - numeric vector giving number of bins in both vertical and horizontal directions. Set to 30 by default.
- **fun**
  - function for summary. See more detail in `stat_summary_hex`
- **...**
  - Reserved for future arguments.

**Value**

an ggplot object.

**Examples**

```
library(STexampleData)

spe <- Visium_humanDLPCF()

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

```r
add_ground(p, var, stroke = 0.5, point_size = 2, ...)
add_ground_bin(p, var, bins = 30, stroke = 1, point_size = 3, ...)
```

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.
- `bins` numeric vector giving number of bins in both vertical and horizontal directions. Set to 30 by default.

Value

an ggplot object.

Examples

```r
library(STexampleData)
spe <- Visium_humanDLPFC()
make_escheR(spe) |> 
  add_ground(var = "ground_truth")
```
**add_symbol**  

*Adding symbols to each spot in the spatial map*

**Description**

Adding symbols to each spot in the spatial map

**Usage**

```
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**

```r
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)
```

**make_escheR**  

*Create a new spatial map for spatial transcriptomics data*

**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

**Value**

an ggplot object that contains the spatial transcriptomics data.

**References**


**Examples**

```
library(STexampleData)  
# SpatialExperiment Object
spe <- Visium_humanDLtPFC()  
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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