

Package ‘escheR’

June 6, 2023

Title Unified multi-dimensional visualizations with Gestalt principles

Version 1.1.1

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.

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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), rlang, SummarizedExperiment

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

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

Suggests STexampleData, knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

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

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add_fill	<i>Adding fill to highlight the figure in the spatial map</i>
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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

```
library(STexampleData)

spe <- Visium_humanDLPFC()

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

add_ground	<i>Adding border to highlight the ground in the spatial map</i>
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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 <code>make_escher()</code> , with or without other layers of aesthetics.
var	A <code>character(1)</code> with the name of the <code>colData(spe)</code> column that has the values to be used as the background.
stroke	A <code>numeric(1)</code> specifying the thickness of the border.
point_size	A <code>numeric(1)</code> specifying the size of the spot in the ggplot. Defaults to 2.
...	Reserved for future arguments.

Value

an ggplot object.

Examples

```
library(STexampleData)

spe <- Visium_humanDLPFC()

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

add_symbol	<i>Adding symbols to each spot in the spatial map</i>
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Description

Adding symbols to each spot in the spatial map

Usage

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

Arguments

<code>p</code>	a spatial map created by <code>make_escheR()</code> , with or without other layers of aesthetics.
<code>var</code>	A <code>character(1)</code> with the name of the <code>colData(spe)</code> column that has the values to be used as the background.
<code>size</code>	A <code>numeric(1)</code> specifying the size of the symbols in the <code>ggplot</code> . Defaults to 1.
<code>...</code>	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)
```

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 'SpatialExperiment'
make_escheR(object, spot_size = 2, y_reverse = TRUE, ...)
```

Arguments

object	a data object that contains the spatial transcriptomics data. Currently only working for spatial transcriptomics data as <code>SpatialExperiment</code> objects.
spot_size	A numeric(1) specifying the size of the spot in the ggplot. Defaults to 2.
...	Reserved for future arguments.
y_reverse	(logical) Whether to reverse y coordinates, which is often required for 10x Genomics Visium data. Default = TRUE.

Value

an ggplot object that contains the spatial transcriptomics data.

References

Guo B & Hicks SC (2023). escheR: Unified multi-dimensional visualizations with Gestalt principles. *bioRxiv*, doi: 10.1101/2023.03.18.533302

Examples

```
library(STexampleData)

spe <- Visium_humanDLPFC()

make_escheR(spe)
```

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