

Package ‘TockyLocus’

November 17, 2024

Title Quantitative Method for Fluorescent Timer Reporters

Version 0.1.0

Author Masahiro Ono [aut, cre]

Maintainer Masahiro Ono <monotockylab@gmail.com>

Description This package provides quantitative analysis methods for Fluorescent Timer data obtained by flow cytometry. Specifically it provides the quantitative analysis methods for trigonometric transformed data, Timer Angle.

Depends R (>= 4.2.0), utils, stats, graphics, grDevices, methods

Imports TockyPrep, ggplot2, ggridges, viridis, RColorBrewer, rlang

Suggests knitr, rmarkdown, KernSmooth

VignetteBuilder knitr

License Apache License 2.0

URL <https://github.com/MonoTockyLab/TockyLocus>, <https://MonoTockyLab.github.io/TockyLocus>

BugReports <https://github.com/MonoTockyLab/TockyLocus/issues>

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Contents

GetStatsTockyLocus	2
Locus_to_colour	3
plotAngleDensity	3
plotTockyLocus	4
plotTockyLocusLegend	5
plot_tocky_locus	5
TockyLocus	6
TockyLocusLegend	7
Index	8

GetStatsTockyLocus	<i>Perform Statistical Tests for Tocky Locus Analysis</i>
--------------------	---

Description

This function performs statistical tests on Tocky Locus data, allowing for different methods and p-value adjustments.

Usage

```
GetStatsTockyLocus(
  x,
  percentTimer = FALSE,
  p_adjust_method = "BH",
  method = "ASR",
  verbose = TRUE
)
```

Arguments

x	A TockyPrepData object containing Tocky Locus data.
percentTimer	Logical. If TRUE, the percentages of Timer-positive cells will be used; if FALSE, percentages of parent cells will be used.
p_adjust_method	Character string specifying the method for p-value adjustment in multiple testing. Default is 'BH' (Benjamini-Hochberg). Other methods available in p.adjust , such as 'holm' or 'bonferroni', can also be used.
method	Character string specifying the statistical test method to use. Options are: 'Wilcox' Mann-Whitney U test (Wilcoxon rank sum test) without data transformation. 'ASR' Arcsine Square Root Transformation, followed by a normality test and t-test. 'Logit' Logit Transformation, followed by a normality test and t-test.
verbose	Logical indicating whether to print progress messages and outputs. Default is TRUE.

Value

A TockyPrepData object containing the statistical outputs for Tocky Locus Analysis, stored in `x@Tocky$TockyLocusStats`.

Examples

```
## Not run:
x <- GetStatsTockyLocus(x, method = 'ASR')

## End(Not run)
```

Locus_to_colour	<i>Convert Timer Angle Data into color code</i>
-----------------	---

Description

This function assigns colors to different ranges of angle values, with an option to use colorblind-friendly colors from the viridis palette.

Usage

```
Locus_to_colour(x, viridis = FALSE)
```

Arguments

x	Angle numeric vector.
viridis	Logical, whether to use the viridis color palette.

Value

a character vector for color code.

Examples

```
## Not run:
col <- Locus_to_colour(x = c(0, 25, 45, 65, 90), viridis = TRUE)

## End(Not run)
```

plotAngleDensity	<i>Plot Density of Angles by Group Using Ridge Plots</i>
------------------	--

Description

This function takes a TockyPrepData object, which should have been previously processed using the timer_transform function, and creates a ridge plot showing the density distribution of angles for each group defined in the dataset.

Usage

```
plotAngleDensity(x, alpha = 0.3, group_order = NULL, scale = 2, legend = FALSE)
```

Arguments

x	A TockyPrepData object that has been processed with the timer_transform function.
alpha	A number between 0 and 1 to be used by ggridges.
group_order	Optional. A character vector to define the order of group
scale	A scaling factor to scale the height of the ridgelines. Used by ggridges.
legend	Logical. If TRUE, legend is included.

Value

A ggplot object showing the density distribution of angles by group.

Examples

```
## Not run:
plotAngleDensity(x)

## End(Not run)
```

plotTockyLocus	<i>Produce scatter plots of percentages of cells in each Tocky Locus.</i>
----------------	---

Description

Produce scatter plots of percentages of cells in each Tocky Locus.

Usage

```
plotTockyLocus(
  x,
  percentTimer = FALSE,
  group_order = NULL,
  locus_colours = NULL,
  group_colors = NULL,
  group_by = TRUE,
  p_adjust_method = "fdr",
  ylim = NULL,
  stats = TRUE,
  verbose = TRUE
)
```

Arguments

x	A TockyPrepData object
percentTimer	A logical value for whether Percent Timer data is produced. Default is FALSE and produces Percent Parent data.
group_order	The order of groups (optional).
locus_colours	(optional) to choose colours for Tocky Loci.
group_colors	(optional) to choose colours for groups.
group_by	A logical value for whether different groups are plotted in different panels.
p_adjust_method	A method for p-value adjustment in statistical tests.
ylim	(Optional) the range of y values to be displayed.
stats	A logical value for whether to produce statistical outputs. This is effective only for two-group analysis.
verbose	Logical indicating whether to print Tocky Locus stats. Default is TRUE.

Value

A ggplot object

Examples

```
## Not run:
plotTockyLocus(x)

## End(Not run)
```

plotTockyLocusLegend *Plot Coloured Tocky Locus Legend*

Description

Plot Coloured Tocky Locus Legend

Usage

```
plotTockyLocusLegend(mar_par = c(4, 4, 10, 4))
```

Arguments

mar_par parameters for the function mar. The default is c(4, 4, 10, 4)

Value

A plot with colored rectangles and labels.

Examples

```
## Not run:
plotTockyLocusLegend()

## End(Not run)
```

plot_tocky_locus *Generate basic QC plots for Tocky data (Timer-Blue vs Timer-Red 2d plots)*

Description

This function creates quick control plots for the TockyPrepData object analyzing fluorescence changes over time in cellular activities.

Usage

```
plot_tocky_locus(
  x,
  file = "PlotTockyLocus",
  n = 3,
  max_cell_number = 20000,
  viridis = FALSE,
  interactive = FALSE
)
```

Arguments

<code>x</code>	A TockyPrepData object produced by the function <code>prep_tocky</code> .
<code>file</code>	The name of the output file.
<code>n</code>	The number of plots per row and column in the output grid.
<code>max_cell_number</code>	The maximum number of cells to be displayed per panel.
<code>viridis</code>	(Optional). If TRUE, a colour-blind friendly colour set is used.
<code>interactive</code>	(Optional). If TRUE, an interactive session is used to trim plot area.

Value

An unchanged TockyPrepData object, primarily for consistency in pipeline usage.

Examples

```
## Not run:
plot_tocky_locus(data)

## End(Not run)
```

TockyLocus

Calculate Tocky Locus using Timer Angle

Description

Calculate Tocky Locus using Timer Angle

Usage

```
TockyLocus(x)
```

Arguments

<code>x</code>	A data.frame object or a TockyPrepData object
----------------	---

Value

Input data frame object including Tocky Locus data.

Examples

```
## Not run:  
x <- TockyLocus(x)  
  
## End(Not run)
```

TockyLocusLegend*Generate Tocky Locus Legend For a Plot*

Description

Generate Tocky Locus Legend For a Plot

Usage

```
TockyLocusLegend(legend = TRUE, cex = 1, viridis = FALSE)
```

Arguments

legend	A logical argument.
cex	A numeric value for the text size.
viridis	(Optional). If TRUE, a colour-blind friendly colour set is used.

Examples

```
## Not run:  
TockyLocusLegend()  
  
## End(Not run)
```

Index

GetStatsTockyLocus, [2](#)

Locus_to_colour, [3](#)

p.adjust, [2](#)

plot_tocky_locus, [5](#)

plotAngleDensity, [3](#)

plotTockyLocus, [4](#)

plotTockyLocusLegend, [5](#)

TockyLocus, [6](#)

TockyLocusLegend, [7](#)