Package ‘tidyHeatmap’

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Type Package

Title A Tidy Implementation of Heatmap

Version 1.6.0

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Description This is a tidy implementation for heatmap. At the moment it is based on the (great) package 'ComplexHeatmap'. The goal of this package is to interface a tidy data frame with this powerful tool. Some of the advantages are: Row and/or columns colour annotations are easy to integrate just specifying one parameter (column names). Custom grouping of rows is easy to specify providing a grouped tbl. For example: df %>% group_by(...). Labels size adjusted by row and column total number. Default use of Brewer and Viridis palettes.

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URL https://www.r-project.org,
https://github.com/stemangiola/tidyHeatmap

BugReports https://github.com/stemangiola/tidyHeatmap

Depends R (>= 3.6)

Imports methods,
stats,
utils,
dplyr (>= 0.8.5),
magrittr (>= 1.5),
tidyr (>= 1.0.3),
rlang (>= 0.4.5),
purrr (>= 0.3.3),
tibble,
ComplexHeatmap (>= 2.2.0),
viridis (>= 0.5.1),
circlize (>= 0.4.8),
RColorBrewer (>= 1.1),
grid,
grDevices,
lifecycle (>= 0.2.0),
dendextend,
patchwork

Suggests spelling,
testthat,
vdiffr,
BiocManager,
knitr,
rmarkdown,
qpdf,
covr,
roxygen2,
forcats,
ggplot2

VignetteBuilder knitr

RdMacros lifecycle

Biarch true

biocViews AssayDomain, Infrastructure

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Language en-US

R topics documented:

`add_annotation` *add_annotation*

Description

add_annotation() takes a tbl object and easily produces a ComplexHeatmap plot, with integration with tibble and dplyr frameworks.

Usage

```
add_annotation(
  my_input_heatmap,
  annotation,
  type = rep("tile", length(quo_names(annotation))),
  palette_discrete = list(),
  palette_continuous = list(),
  size = NULL,
  ...
)
```

Arguments

`my_input_heatmap`	A ‘InputHeatmap‘ formatted as | <SAMPLE> | <TRANSCRIPT> | <COUNT> | <...> |
`annotation`	Vector of quotes
`type`	A character vector of the set c(\"tile\", \"point\", \"bar\", \"line\")
`palette_discrete`	A list of character vectors. This is the list of palettes that will be used for horizontal and vertical discrete annotations. The discrete classification of annotations depends on the column type of your input tibble (e.g., character and factor).

`palette_continuous`	A list of character vectors. This is the list of palettes that will be used for horizontal and vertical continuous annotations. The continuous classification of annotations depends on the column type of your input tibble (e.g., integer, numerical, double).
`size`	A grid::unit object, e.g. unit(2, "cm"). This is the height or width of the annotation depending on the orientation.
`...`	The arguments that will be passed to top_annotation or left_annotation of the ComplexHeatmap container

Details

To be added.

Value

A ‘ComplexHeatmap‘ object

`add_attr` *Add attribute to abject*

Description

Add attribute to abject

Usage

```
add_attr(var, attribute, name)
```

Arguments

`var`	A tibble
`attribute`	An object
`name`	A character name of the attribute

Value

A tibble with an additional attribute

add_bar — *Adds a bar annotation layer to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

add_bar() from a ‘InputHeatmap‘ object, adds a bar annotation layer.

Usage

```
add_bar(.data, .column, palette = NULL, size = NULL, ...)

## S4 method for signature 'InputHeatmap'
add_bar(.data, .column, palette = NULL, size = NULL, ...)
```

Arguments

`.data`	A ‘tbl_df‘ formatted as | <ELEMENT> | <FEATURE> | <VALUE> | <...> |
`.column`	Vector of quotes
`palette`	A character vector of colors This is the list of palettes that will be used for horizontal and vertical discrete annotations. The discrete classification of annotations depends on the column type of your input tibble (e.g., character and factor).
`size`	A grid::unit object, e.g. unit(2, "cm"). This is the height or width of the annotation depending on the orientation.
`...`	The arguments that will be passed to top_annotation or left_annotation of the ComplexHeatmap container

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)
```

```
hm %>% add_bar()
```

`add_class` *Add class to abject*

Description

Add class to abject

Usage

```
add_class(var, name)
```

Arguments

`var`	A tibble
`name`	A character name of the attribute

Value

A tibble with an additional attribute

`add_line` *Adds a line annotation layer to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

add_line() from a ‘InputHeatmap‘ object, adds a line annotation layer.

Usage

```
add_line(.data, .column, palette = NULL, size = NULL, ...)

## S4 method for signature 'InputHeatmap'
add_line(.data, .column, palette = NULL, size = NULL, ...)
```

Arguments

`.data`	A ‘tbl_df‘ formatted as | <ELEMENT> | <FEATURE> | <VALUE> | <...> |
`.column`	Vector of quotes
`palette`	A character vector of colors This is the list of palettes that will be used for horizontal and vertical discrete annotations. The discrete classification of annotations depends on the column type of your input tibble (e.g., character and factor).
`size`	A grid::unit object, e.g. unit(2, "cm"). This is the height or width of the annotation depending on the orientation.
`...`	The arguments that will be passed to top_annotation or left_annotation of the ComplexHeatmap container

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% add_line()
```

add_point *Adds a point annotation layer to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

add_point() from a ‘InputHeatmap‘ object, adds a point annotation layer.

Usage

```
add_point(.data, .column, palette = NULL, size = NULL, ...)

## S4 method for signature 'InputHeatmap'
add_point(.data, .column, palette = NULL, size = NULL, ...)
```

Arguments

`.data`	A ‘tbl_df‘ formatted as | <ELEMENT> | <FEATURE> | <VALUE> | <...> |
`.column`	Vector of quotes
`palette`	A character vector of colors This is the list of palettes that will be used for horizontal and vertical discrete annotations. The discrete classification of annotations depends on the column type of your input tibble (e.g., character and factor).
`size`	A grid::unit object, e.g. unit(2, "cm"). This is the height or width of the annotation depending on the orientation.
`...`	The arguments that will be passed to top_annotation or left_annotation of the ComplexHeatmap container

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% add_point()
```

`add_tile` *Adds a tile annotation layer to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

add_tile() from a ‘InputHeatmap‘ object, adds a tile annotation layer.

Usage

```
add_tile(.data, .column, palette = NULL, size = NULL, ...)

## S4 method for signature 'InputHeatmap'
add_tile(.data, .column, palette = NULL, size = NULL, ...)
```

Arguments

`.data`	A ‘tbl_df‘ formatted as | <ELEMENT> | <FEATURE> | <VALUE> | <...> |
`.column`	Vector of quotes
`palette`	A character vector of colors This is the list of palettes that will be used for horizontal and vertical discrete annotations. The discrete classification of annotations depends on the column type of your input tibble (e.g., character and factor).
`size`	A grid::unit object, e.g. unit(2, "cm"). This is the height or width of the annotation depending on the orientation.
`...`	The arguments that will be passed to top_annotation or left_annotation of the ComplexHeatmap container

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% add_tile(CAPRA_TOTAL)
```

`annot_to_list` *annot_to_list*

Description

annot_to_list

Usage

```
annot_to_list(.data)
```

Arguments

`.data`	A data frame

Value

A list

`as_matrix` *Get matrix from tibble*

Description

Get matrix from tibble

Usage

```
as_matrix(tbl, rownames = NULL, do_check = TRUE)
```

Arguments

`tbl`	A tibble
`rownames`	A character string of the rownames
`do_check`	A boolean

Value

A matrix

`check_if_counts_is_na` *Check whether there are NA counts*

Description

Check whether there are NA counts

Usage

```
check_if_counts_is_na(.data, .abundance)
```

Arguments

`.data`	A tibble of read counts
`.abundance`	A character name of the read count column

Value

A tbl

`check_if_duplicated_genes` *Check whether there are duplicated genes/transcripts*

Description

Check whether there are duplicated genes/transcripts

Usage

```
check_if_duplicated_genes(.data, .sample, .transcript, .abundance)
```

Arguments

`.data`	A tibble of read counts
`.sample`	A character name of the sample column
`.transcript`	A character name of the transcript/gene column
`.abundance`	A character name of the read count column

Value

A tbl

`check_if_wrong_input` *Check whether there are NA counts*

Description

Check whether there are NA counts

Usage

```
check_if_wrong_input(.data, list_input, expected_type)
```

Arguments

`.data`	A tibble of read counts
`list_input`	A list
`expected_type`	A character string

Value

A tbl

`drop_class` *Remove class to abject*

Description

Remove class to abject

Usage

```
drop_class(var, name)
```

Arguments

`var`	A tibble
`name`	A character name of the class

Value

A tibble with an additional attribute

`error_if_log_transformed` *Check whether a numeric vector has been log transformed*

Description

Check whether a numeric vector has been log transformed

Usage

```
error_if_log_transformed(x, .abundance)
```

Arguments

`x`	A numeric vector
`.abundance`	A character name of the transcript/gene abundance column

Value

NA

`get_abundance_norm_if_exists` *Get column names either from user or from attributes*

Description

Get column names either from user or from attributes

Usage

```
get_abundance_norm_if_exists(.data, .abundance)
```

Arguments

`.data`	A tibble
`.abundance`	A character name of the abundance column

Value

A list of column enquo or error

`get_elements` *Get column names either from user or from attributes*

Description

Get column names either from user or from attributes

Usage

```
get_elements(.data, .element, of_samples = TRUE)
```

Arguments

`.data`	A tibble
`.element`	A character name of the sample column
`of_samples`	A boolean

Value

A list of column enquo or error

`get_elements_features`

Get column names either from user or from attributes

Description

Get column names either from user or from attributes

Usage

```
get_elements_features(.data, .element, .feature, of_samples = TRUE)
```

Arguments

`.data`	A tibble
`.element`	A character name of the sample column
`.feature`	A character name of the transcript/gene column
`of_samples`	A boolean

Value

A list of column enquo or error

`get_elements_features_abundance`

Get column names either from user or from attributes

Description

Get column names either from user or from attributes

Usage

```
get_elements_features_abundance(
  .data,
  .element,
  .feature,
  .abundance,
  of_samples = TRUE
)
```

Arguments

`.data`	A tibble
`.element`	A character name of the sample column
`.feature`	A character name of the transcript/gene column
`.abundance`	A character name of the read count column
`of_samples`	A boolean

Value

A list of column enquo or error

`get_sample_counts` *Get column names either from user or from attributes*

Description

Get column names either from user or from attributes

Usage

```
get_sample_counts(.data, .sample, .abundance)
```

Arguments

`.data`	A tibble
`.sample`	A character name of the sample column
`.abundance`	A character name of the read count column

Value

A list of column enquo or error

`get_sample_transcript` *Get column names either from user or from attributes*

Description

Get column names either from user or from attributes

Usage

```
get_sample_transcript(.data, .sample, .transcript)
```

Arguments

`.data`	A tibble
`.sample`	A character name of the sample column
`.transcript`	A character name of the transcript/gene column

Value

A list of column enquo or error

`get_sample_transcript_counts` *Get column names either from user or from attributes*

Description

Get column names either from user or from attributes

Usage

```
get_sample_transcript_counts(.data, .sample, .transcript, .abundance)
```

Arguments

`.data`	A tibble
`.sample`	A character name of the sample column
`.transcript`	A character name of the transcript/gene column
`.abundance`	A character name of the read count column

Value

A list of column enquo or error

`get_x_y_annotation_columns` *get_x_y_annotation_columns*

Description

get_x_y_annotation_columns

Usage

```
get_x_y_annotation_columns(.data, .column, .row, .abundance)
```

Arguments

`.data`	A ‘tbl‘ formatted as | <SAMPLE> | <TRANSCRIPT> | <COUNT> | <...> |
`.column`	The name of the column horizontally presented in the heatmap
`.row`	The name of the column vertically presented in the heatmap
`.abundance`	The name of the transcript/gene abundance column

Value

A list

`heatmap` *Creates a 'InputHeatmap' object from 'tbl_df' on evaluation creates a 'ComplexHeatmap'*

Description

heatmap() takes a tbl object and easily produces a ComplexHeatmap plot, with integration with tibble and dplyr frameworks.

Usage

```
heatmap(
  .data,
  .row,
  .column,
  .value,
  transform = NULL,
  .scale = "row",
  palette_value = c("#440154FF", "#21908CFF", "#fefada"),
  palette_grouping = list(),
  annotation = NULL,
  type = rep("tile", length(quo_names(annotation))),
  palette_discrete = list(),
  palette_continuous = list(),
  ...
)

heatmap_(
  .data,
  .row,
  .column,
  .value,
  transform = NULL,
  .scale = "row",
  palette_value = c("#440154FF", "#21908CFF", "#fefada"),
  palette_grouping = list(),
  annotation = NULL,
  type = rep("tile", length(quo_names(annotation))),
  palette_discrete = list(),
  palette_continuous = list(),
  ...
)

## S4 method for signature 'tbl'
heatmap(
  .data,
  .row,
  .column,
  .value,
  transform = NULL,
  .scale = "row",
  palette_value = c("#440154FF", "#21908CFF", "#fefada"),
  palette_grouping = list(),
  annotation = NULL,
  type = rep("tile", length(quo_names(annotation))),
  palette_discrete = list(),
  palette_continuous = list(),
  ...
)

## S4 method for signature 'tbl_df'
heatmap(
  .data,
  .row,
  .column,
  .value,
  transform = NULL,
  .scale = "row",
  palette_value = c("#440154FF", "#21908CFF", "#fefada"),
  palette_grouping = list(),
  annotation = NULL,
  type = rep("tile", length(quo_names(annotation))),
  palette_discrete = list(),
  palette_continuous = list(),
  ...
)
```

Arguments

`.data`	A ‘tbl_df‘ formatted as | <ELEMENT> | <FEATURE> | <VALUE> | <...> |
`.row`	The name of the column vertically presented in the heatmap
`.column`	The name of the column horizontally presented in the heatmap
`.value`	The name of the column for the value of the element/feature pair
`transform`	A function, used to transform .value row-wise (e.g., transform = log1p)
`.scale`	A character string. Possible values are c(\"none\", \"row\", \"column\", \"both\")
`palette_value`	A character vector This is the palette that will be used as gradient for .value. For example c("red", "white", "blue"). For higher flexibility you can use circlize::colorRamp2\(c\(-2, -1, 0, 1, 2\), viridis::magma\(5\)\)
`palette_grouping`	A list of character vectors. This is the list of palettes that will be used for grouping. For example list(RColorBrewer::brewer.pal(8, "Accent")) or list(c("#B3E2CD", "#FDCDAC", "#CBD5E8")) or list(c("black", "red"))
`annotation`	DEPRECATED. please use the annotation functions add_* function \(* one of tile, point, bar, line \).
`type`	DEPRECATED. please use the annotation functions add_* function \(* one of tile, point, bar, line \).
`palette_discrete`	DEPRECATED. please use the annotation functions add_* function \(* one of tile, point, bar, line \).

`palette_continuous`
: DEPRECATED. please use the annotation functions add_* function \(* one of tile, point, bar, line \).

`...`
: The arguments that will be passed to the Heatmap function of ComplexHeatmap backend

Details

[Maturing]

This function takes a tbl as an input and creates a ‘ComplexHeatmap‘ plot. The information is stored in a ‘InputHeatmap‘ object that is updated along the pipe statement, for example adding annotation layers.

Value

A ‘InputHeatmap‘ objects that gets evaluated to a ‘ComplexHeatmap‘ object

A ‘InputHeatmap‘ object

A ‘InputHeatmap‘ object

A ‘InputHeatmap‘ object

Examples

```
library(dplyr)

tidyHeatmap::N52 %>%
group_by( `Cell type`) %>%
tidyHeatmap::heatmap(
 .row = symbol_ct,
 .column = UBR,
 .value = `read count normalised log`,
)
```

`ifelse2_pipe` *This is a generalisation of ifelse that accepts an object and return an objects*

Description

This is a generalisation of ifelse that accepts an object and return an objects

Usage

```
ifelse2_pipe(.x, .p1, .p2, .f1, .f2, .f3 = NULL)
```

Arguments

`.x`	A tibble
`.p1`	A boolean
`.p2`	ELSE IF condition
`.f1`	A function
`.f2`	A function
`.f3`	A function

Value

A tibble

`ifelse_pipe` *This is a generalisation of ifelse that accepts an object and return an objects*

Description

This is a generalisation of ifelse that accepts an object and return an objects

Usage

```
ifelse_pipe(.x, .p, .f1, .f2 = NULL)
```

Arguments

`.x`	A tibble
`.p`	A boolean
`.f1`	A function
`.f2`	A function

Value

A tibble

`input_heatmap` *input_heatmap*

Description

input_heatmap() takes a tbl object and easily produces a ComplexHeatmap plot, with integration with tibble and dplyr frameworks.

Usage

```
input_heatmap(
  .data,
  .horizontal,
  .vertical,
  .abundance,
  transform = NULL,
  .scale = "row",
  palette_value = c("#440154FF", "#21908CFF", "#fefada"),
  palette_grouping = list(),
  ...
)
```

Arguments

`.data`	A ‘tbl‘ formatted as | <SAMPLE> | <TRANSCRIPT> | <COUNT> | <...> |
`.horizontal`	The name of the column horizontally presented in the heatmap
`.vertical`	The name of the column vertically presented in the heatmap
`.abundance`	The name of the transcript/gene abundance column
`transform`	A function, used to transform .value, for example log1p
`.scale`	A character string. Possible values are c(\"none\", \"row\", \"column\", \"both\")
`palette_value`	A character vector, or a function for higher customisation (colorRamp2). This is the palette that will be used as gradient for abundance. If palette_value is a vector of hexadecimal colours, it should have 3 values. If you want more customisation, you can pass to palette_value a function, that is derived as for example ‘colorRamp2(c(-2, 0, 2), palette_value)‘
`palette_grouping`	A list of character vectors. This is the list of palettes that will be used for grouping
`...`	Further arguments to be passed to ComplexHeatmap::Heatmap

Details

To be added.

Value

A ‘ComplexHeatmap‘ object

layer_arrow_down *Adds a layers of symbols above the heatmap tiles to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

layer_arrow_down() from a ‘InputHeatmap‘ object, adds a bar annotation layer.

Usage

```
layer_arrow_down(.data, ...)

## S4 method for signature 'InputHeatmap'
layer_arrow_down(.data, ...)
```

Arguments

`.data`	A ‘InputHeatmap‘
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% layer_arrow_down()
```

`layer_arrow_up` *Adds a layers of symbols above the heatmap tiles to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

layer_arrow_up() from a ‘InputHeatmap‘ object, adds a bar annotation layer.

Usage

```
layer_arrow_up(.data, ...)

## S4 method for signature 'InputHeatmap'
layer_arrow_up(.data, ...)
```

Arguments

`.data`	A ‘InputHeatmap‘
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% layer_arrow_up()
```

`layer_diamond` *Adds a layers of symbols above the heatmap tiles to a 'InputHeatmap', that on evaluation creates a 'ComplexHeatmap'*

Description

layer_diamond() from a 'InputHeatmap' object, adds a bar annotation layer.

Usage

```
layer_diamond(.data, ...)

## S4 method for signature 'InputHeatmap'
layer_diamond(.data, ...)
```

Arguments

`.data`	A 'InputHeatmap'
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Details

[Maturing]

It uses 'ComplexHeatmap' as visualisation tool.

Value

A 'InputHeatmap' object that gets evaluated to a 'ComplexHeatmap'

A 'InputHeatmap' object that gets evaluated to a 'ComplexHeatmap'

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% layer_diamond()
```

`layer_point` *Adds a layers of symbols above the heatmap tiles to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

layer_point() from a ‘InputHeatmap‘ object, adds a bar annotation layer.

Usage

```
layer_point(.data, ...)

## S4 method for signature 'InputHeatmap'
layer_point(.data, ...)
```

Arguments

`.data`	A ‘InputHeatmap‘
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% layer_point()
```

layer_square — *Adds a layers of symbols above the heatmap tiles to a ‘InputHeatmap‘, that on evaluation creates a ‘ComplexHeatmap‘*

Description

layer_square() from a ‘InputHeatmap‘ object, adds a bar annotation layer.

Usage

```
layer_square(.data, ...)

## S4 method for signature 'InputHeatmap'
layer_square(.data, ...)
```

Arguments

`.data`	A ‘InputHeatmap‘
`...`	Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```
library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% layer_square()
```

`N52` *Example data set N52*

Description

Example data set N52

Usage

```
N52
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 520 rows and 15 columns.

`parse_formula` *.formula parser*

Description

.formula parser

Usage

```
parse_formula(fm)
```

Arguments

`fm`	a formula

Value

A character vector

`pasilla` *Example data set Pasilla*

Description

Example data set Pasilla

Usage

```
pasilla
```

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 504 rows and 8 columns.

`prepend` *From rlang deprecated*

Description

From rlang deprecated

Usage

```
prepend(x, values, before = 1)
```

Arguments

`x`	An array
`values`	An array
`before`	A boolean

Value

An array

`quo_names` *Convert array of quosure (e.g. c(col_a, col_b)) into character vector*

Description

Convert array of quosure (e.g. c(col_a, col_b)) into character vector

Usage

```
quo_names(v)
```

Arguments

`v`	A array of quosures (e.g. c(col_a, col_b))

Value

A character vector

`save_pdf` *Save plot on PDF file*

Description

save_pdf() takes as input a Heatmap from ComplexHeatmap and save it to PDF file

Usage

```
save_pdf(
  .heatmap,
  filename,
  width = NULL,
  height = NULL,
  units = c("in", "cm", "mm")
)
```

Arguments

`.heatmap`	A ‘Heatmap‘
`filename`	A character string. The name of the output file/path
`width`	A ‘double‘. Plot width
`height`	A ‘double‘. Plot height
`units`	A character string. units ("in", "cm", or "mm")

Details

[Maturing]

It simply save an ‘Heatmap‘ to a PDF file use pdf() function in the back end

Value

NA

Examples

```
library(dplyr)
tidyHeatmap::heatmap(
  dplyr::group_by(tidyHeatmap::pasilla,location, type),
  .column = sample,
  .row = symbol,
  .value = `count normalised adjusted`,
 ) %>%
 save_pdf(tempfile())
```

---

save_pdf,Heatmap-method *save_pdf*

Description

save_pdf

Usage

```
## S4 method for signature 'Heatmap'
save_pdf(
  .heatmap,
  filename,
  width = NULL,
  height = NULL,
  units = c("in", "cm", "mm")
)
```

Arguments

`.heatmap`	A ‘Heatmap‘
`filename`	A character string. The name of the output file/path
`width`	A ‘double‘. Plot width
`height`	A ‘double‘. Plot height
`units`	A character string. units ("in", "cm", or "mm")

---

save_pdf,InputHeatmap-method *save_pdf*

Description

save_pdf

Usage

```
## S4 method for signature 'InputHeatmap'
save_pdf(
  .heatmap,
  filename,
  width = NULL,
  height = NULL,
  units = c("in", "cm", "mm")
)
```

Arguments

`.heatmap`	A ‘Heatmap‘
`filename`	A character string. The name of the output file/path
`width`	A ‘double‘. Plot width
`height`	A ‘double‘. Plot height
`units`	A character string. units ("in", "cm", or "mm")

`scale_design` *Scale design matrix*

Description

Scale design matrix

Usage

```
scale_design(df, .formula)
```

Arguments

`df`	A tibble
`.formula`	a formula

Value

A tibble

`scale_robust` *Scale counts in a robust way against sd == 0*

Description

Scale counts in a robust way against sd == 0

Usage

```
scale_robust(y)
```

Arguments

`y`	A numerical array

Value

A scaled and centred numerical array

`select_closest_pairs` *Sub function of remove_redundancy_elements_though_reduced_dimensions*

Description

Sub function of remove_redundancy_elements_though_reduced_dimensions

Usage

```
select_closest_pairs(df)
```

Arguments

`df`	A tibble

Value

A tibble with pairs to drop

`split_rows` *Split the heatmap row-wise depending on the biggest branches in the cladogram.*

Description

split_rows() from a ‘InputHeatmap‘ object, split the row cladogram.

split_columns() from a ‘InputHeatmap‘ object, split the column cladogram.

Usage

```
split_rows(.data, number_of_groups)

## S4 method for signature 'InputHeatmap'
split_rows(.data, number_of_groups)

split_columns(.data, number_of_groups)

## S4 method for signature 'InputHeatmap'
split_columns(.data, number_of_groups)
```

Arguments

`.data`	A ‘InputHeatmap‘
`number_of_groups`	An integer. The number of groups to split the cladogram into.

Details

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

[Maturing]

It uses ‘ComplexHeatmap‘ as visualisation tool.

Value

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

A ‘InputHeatmap‘ object that gets evaluated to a ‘ComplexHeatmap‘

Examples

```

library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% split_rows(2)


library(dplyr)

hm =
  tidyHeatmap::N52 %>%
  tidyHeatmap::heatmap(
    .row = symbol_ct,
    .column = UBR,
    .value = `read count normalised log`
)

hm %>% split_columns(2)
```

`wrap_heatmap` *Wrap tidyHeatmap (ComplexHeatmap) in a patchwork-compliant patch*

Description

In order to add tidyHeatmap (ComplexHeatmap) element to a patchwork they can be converted to a compliant representation using the ‘wrap_heatmap()‘ function. This allows you to position either grobs, ggplot objects, patchwork objects, or even base graphics (if passed as a formula) in either the full area, the full plotting area (anything between and including the axis label), or the panel area (only the actual area where data is drawn).

Usage

```
wrap_heatmap(
  panel = NULL,
  plot = NULL,
  full = NULL,
  clip = TRUE,
  ignore_tag = FALSE
)

## S4 method for signature 'InputHeatmap'
wrap_heatmap(
  panel = NULL,
  plot = NULL,
  full = NULL,
  clip = TRUE,
  ignore_tag = FALSE
)
```

Arguments

`panel, plot, full`	A grob, ggplot, patchwork, formula, raster, or nativeRaster object to add to the respective area.
`clip`	Should the grobs be clipped if expanding outside its area
`ignore_tag`	Should tags be ignored for this patch. This is relevant when using automatic tagging of plots and the content of the patch does not qualify for a tag.

Value

A wrapped_patch object

A wrapped_patch object

Examples

```
tidyHeatmap::N52 |>
tidyHeatmap::heatmap(
 .row = symbol_ct,
 .column = UBR,
 .value = `read count normalised log`,
) |>
wrap_heatmap()
```

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