Package 'jamba'

March 10, 2025

Title Just Analysis Methods Base

Version 1.0.2

Description Just analysis methods ('jam') base functions
focused on bioinformatics.
Version- and gene-centric alphanumeric sort,
unique name and version assignment, colorized console and 'HTML' output,
color ramp and palette manipulation,
'Rmarkdown' cache import, styled 'Excel' worksheet import and export,
interpolated raster output from smooth scatter and image plots,
list to delimited vector, efficient list tools.

Depends R (>= 3.0.0)

Imports methods, grDevices, graphics, stats, utils, colorspace,
RColorBrewer, KernSmooth, withr

Suggests crayon, farver, knitr, rmarkdown, testthat (>= 3.0.0)

Enhances ggplot2, ggridges, IRanges, S4Vectors, openxlsx, kableExtra,
matrixStats, viridisLite, ComplexHeatmap, circlize,
GenomicRanges, igraph, pryr, rstudioapi, Matrix,
sparseMatrixStats

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URL https://jmw86069.github.io/jamba/

BugReports https://github.com/jmw86069/jamba/issues

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Contents

`adjustAxisLabelMargins` *Adjust axis label margins*

Description

Adjust axis label margins to accommodate axis labels

Usage

```
adjustAxisLabelMargins(
  x,
  margin = 1,
  maxFig = 1/2,
  cex = graphics::par("cex"),
  cex.axis = graphics::par("cex.axis"),
  prefix = "-- -- ",
  ...
)
```

Arguments

x	character vector of axis labels
margin	integer value indicating which margin to adjust, using the order by graphics::par("mar"), 1=bottom, 2=left, 3=top, 4=right.
maxFig	numeric fraction less than 1, indicating the maximum size of margin relative to the figure size. Setting margins too large results in an error otherwise.
cex	numeric or NULL, default graphics::par("cex"), used as a convenience with cex * cex.axis passed to graphics::strwidth(). However, graphics::axis() itself should use cex.axis when adjusting axis label font size.
cex.axis	numeric, default graphics::par("cex.axis") to define the axis label font size.
prefix	character string to add whitespace around the axis label in order to add a "buffer" of whitespace.
...	additional parameters are ignored.

Details

This function takes a vector of axis labels, and the margin where they will be used, and adjusts the relevant axis margin to accomodate the label size, up to a maximum fraction of the figure size as defined by maxFig.

Labels are assumed to be perpendicular to the axis, for example argument las=2 when using graphics::text().

Note this function does not render labels in the figure, and therefore does not revert axis margins to their original size. That process should be performed separately.

Value

list named "mai" suitable for use in graphics::par() to adjust margin size using in inches.

See Also

Other jam plot functions: coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
xlabs <- paste0("item_", (1:20));
ylabs <- paste0("rownum_", (1:20));

# proper adjustment should be done using withr, for example
x_cex <- 0.8;
y_cex <- 1.2;
withr::with_par(adjustAxisLabelMargins(xlabs, 1, cex.axis=x_cex), {
   withr::local_par(adjustAxisLabelMargins(ylabs, 2, cex.axis=y_cex))
   nullPlot(xlim=c(1,20), ylim=c(1,20), doMargins=FALSE);
   graphics::axis(1, at=1:20, labels=xlabs, las=2, cex.axis=x_cex);
   graphics::axis(2, at=1:20, labels=ylabs, las=2, cex.axis=y_cex);
})

withr::with_par(adjustAxisLabelMargins(xlabs, 3, cex.axis=x_cex), {
   withr::local_par(adjustAxisLabelMargins(ylabs, 4, cex.axis=y_cex))
   nullPlot(xlim=c(1,20), ylim=c(1,20), doMargins=FALSE);
   graphics::axis(3, at=1:20, labels=xlabs, las=2);
   graphics::axis(4, at=1:20, labels=ylabs, las=2);
})

par("mar")
```

`alpha2col` *set R color alpha value*

Description

Define the alpha transparency per R color

Usage

```
alpha2col(x, alpha = 1, maxValue = 1, ...)
```

Arguments

`x`	R compatible color, either a color name, or hex value, or a mixture of the two. Any value compatible with `col2rgb`.
`alpha`	numeric alpha transparency to use per x color. alpha is recycled to length(x) as needed.
`maxValue`	numeric maximum value to return, useful when the downstream alpha range should be 255. By default maxValue=1 is returned.
`...`	Additional arguments are ignored.

Value

`character` vector of R colors, with alpha values.

See Also

Other jam color functions: applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
withr::with_par(list("mfrow"=c(2,2)), {
for (alpha in c(1, 0.8, 0.5, 0.2)) {
   nullPlot(plotAreaTitle=paste0("alpha=", alpha),
      doMargins=FALSE);
   usrBox(fill=alpha2col("yellow",
      alpha=alpha));
}
})
```

`applyCLrange` *Apply CL color range*

Description

Restrict chroma (C) and luminance (L) ranges for a vector of R colors

Usage

```
applyCLrange(
  x,
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  Cgrey = getOption("jam.Cgrey", 5),
  fixYellow = TRUE,
  CLmethod = c("scale", "floor", "expand"),
  fixup = TRUE,
  ...
)
```

Arguments

x	vector of R colors
lightMode	NULL or logical. When lightMode=NULL then Crange and Lrange values are used as-is; when lightMode=TRUE or lightMode=FALSE then default values are used for Crange and Lrange values, where lightMode=TRUE is intended for colors to have contrast against a light/bright/white background, and lightMode=FALSE is intended for colors to have contrast against a dark background.

Crange	NULL or numeric range with minimum and maximum allowed values for the chroma (C) component.
Lrange	NULL or numeric range with minimum and maximum allowed values for the luminance (L) component.
Cgrey	numeric chroma (C) value, which defines grey colors at or below this chroma. Any colors at or below the grey cutoff will have their C values unchanged. This mechanism prevents converting black to red, for example. To disable the effect, set Cgrey=-1.
fixYellow	logical indicating whether to "fix" the darkening of yellow, which otherwise turns to green. Instead, since JAM can, JAM will make the yellow slightly more golden before darkening, which is achieved by calling fixYellowHue().
CLmethod	character string indicating how to alter values outside the respective Crange and Lrange ranges. "scale" will rescale values only if any are outside of range, and will rescale the full range of c(Crange, Cvalues) to c(Crange). In this way, only values outside the range are rescaled. "floor" will apply a fixed cutoff, any values outside the range are set to equal the range boundary itself. "expand" will rescale all values so the range is equal to Crange.
fixup	logical passed to hcl2col() and subsequently to colorspace::hex() when converting colors outside the color gamut (visible range.) When fixup is NULL, the hcl2col() method applies its own aggressive technique to restrict the color range.
...	additional argyments are passed to fixYellowHue() when fixYellow is TRUE.

Details

This function is primarily intended to restrict the range of brightness values so they contrast with a background color, particularly when the background color may be bright or dark.

Note that output is slightly different when supplying one color, compared to supplying a vector of colors. One color is simply restricted to the Crange and Lrange. However, a vector of colors is scaled within the ranges so that relative C and L values are maintained, for visual comparison.

The C and L values are defined by colorspace::polarLUV(), where C is typically restricted to 0..100 and L is typically 0..100. For some colors, values above 100 are allowed.

Values are restricted to the given numeric range using one of three methods, set via the CLmethod argument.

As an example, consider what should be done when Crange <- c(10,70) and the C values are Cvalues <- c(50, 60, 70, 80).

1. "floor" uses jamba::noiseFloor() to apply fixed cutoffs at the minimum and maximum range. This method has the effect of making all values outside the range into an equal final value.
2. "scale" will apply jamba::normScale() to rescale only values outside the given range. For example, c(Crange, Cvalues) as the initial range, it constrains values to c(Crange). This method has the effect of maintaining the relative difference between values.
3. "expand" will simply apply jamba::normScale() to fit the values to the minimum and maximum range values. This method has the effect of forcing colors to fit the full numeric range, even when the original differences between values were small.

In case (1) above, Cvalues will become `c(50, 60, 70, 70)`. In case (2) above, Cvalues will become `c(44, 53, 61, 70)` In case (3) above, Cvalues will become `c(10, 30, 50, 70)`

Note that colors with C (chroma) values less than `Cgrey` will not have the C value changed, in order to maintain colors at a greyscale, without colorizing them. Particularly for pure `grey`, which has `C=0`, but is still required to have a hue H, it is important not to increase `C`.

Value

vector of colors after applying the chroma (C) and luminance (L) ranges.

See Also

Other jam color functions: `alpha2col()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
cl <- c("red", "blue", "navy", "yellow", "orange");
cl_lite <- applyCLrange(cl, lightMode=TRUE);
cl_dark <- applyCLrange(cl, lightMode=FALSE);

# individual colors
cl_lite_ind <- sapply(cl, applyCLrange, lightMode=TRUE);
cl_dark_ind <- sapply(cl, applyCLrange, lightMode=FALSE);

# display colors
showColors(list(`input colors`=cl,
   `lightMode=TRUE, vector`=cl_lite,
   `lightMode=TRUE, individual`=cl_lite_ind,
   `lightMode=FALSE, vector`=cl_dark,
   `lightMode=FALSE, individual`=cl_dark_ind))
printDebug(cl, lightMode=TRUE);
```

`applyXlsxCategoricalFormat` *Add categorical colors to 'Excel' 'xlsx' worksheets*

Description

Add categorical colors to 'Excel' 'xlsx' worksheets

Usage

```
applyXlsxCategoricalFormat(
  xlsxFile,
  sheet = 1,
  rowRange = NULL,
  colRange = NULL,
  colorSub = NULL,
  colorSubText = setTextContrastColor(colorSub),
  trimCatNames = TRUE,
  overwrite = TRUE,
  wrapText = FALSE,
  stack = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

`xlsxFile`	`character` filename to a file with ".xlsx" extension, or `Workbook` object defined in the `openxlsx` package. When `xlsxFile` is a `Workbook` the output is not saved to a file.
`sheet`	`integer` index of the worksheet or worksheets.
`rowRange, colRange`	`integer` vectors of rows and columns to apply categorical colors in the 'Excel' 'xlsx' worksheet, passed as `openxlsx::readWorkbook(..., rows=rowRange, cols=colRange)`. This step defines which columns are read from each workbook, however when `colorSub` is provided as a `list` whose names are intended to match `colnames()`, only matching colnames are processed.
`colorSub`	one of the following types of input: • Named `character` vector of valid R colors, whose names correspond to values in worksheet cells. • Named `list` whose names correspond to colnames one or more workbooks in `sheet`. Each list element should be a `character` vector named by column values, or color `function` that takes column values and returns a `character` vector of colors for each value.
`colorSubText`	optional `character` vector of colors, whose names correspond to values in the worksheet cells. In absence of a specific text color, `setTextContrastColor()` is used to define a contrasting text color to be visible on the colored background.
`trimCatNames`	`logical` whether to trim whitespace and punctuation from `colorSub` and from 'Excel' cell fields before matching colors to 'Excel' values.
`overwrite`	`logical` indicating whether new cell color styles should be forced overwrite of previous cell styles.
`wrapText`	`logical` indicating whether to wrap text.
`stack`	`logical` indicating whether new color rules should be applied above existing styles, many of whose styles may not affect the specific cell color, for example the font size and font name.

verbose	logical indicating whether to print verbose output.
...	additional arguments are ignored.

Details

This function is a convenient wrapper for applying categorical color formatting to cell background colors, and applies a contrasting color to the text in cells using setTextContrastColor(). It uses a named character vector of colors supplied as colorSub to define cell background colors, and optionally colorSubText to define a specific color for the cell text.

Value

Workbook object as defined by the openxlsx package is returned invisibly with invisible(). This Workbook can be used in argument wb to provide a speed boost when saving multiple sheets to the same file.

See Also

Other jam export functions: applyXlsxConditionalFormat(), readOpenxlsx(), set_xlsx_colwidths(), set_xlsx_rowheights(), writeOpenxlsx()

Examples

```
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
   df <- data.frame(a=LETTERS[1:5], b=1:5);
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test");

   colorSub <- nameVector(
      rainbow2(5, s=c(0.8, 1), v=c(0.8, 1)),
      LETTERS[1:5]);
   applyXlsxCategoricalFormat(out_xlsx,
      sheet="jamba_test",
      colorSub=colorSub
   )
}
```

---

applyXlsxConditionalFormat

Xlsx Conditional formatting

Description

Xlsx Conditional formatting

Usage

```
applyXlsxConditionalFormat(
  xlsxFile,
  sheet = 1,
  fcColumns = NULL,
  fcGrep = NULL,
  fcStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  fcRule = c(-6, 0, 6),
  fcType = "colourScale",
  lfcColumns = NULL,
  lfcGrep = NULL,
  lfcStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  lfcRule = c(-3, 0, 3),
  lfcType = "colourScale",
  hitColumns = NULL,
  hitGrep = NULL,
  hitStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  hitRule = c(-1.5, 0, 1.5),
  hitType = "colourScale",
  intColumns = NULL,
  intGrep = NULL,
  intStyle = c("#EEECE1", "#FDC99B", "#F77F30"),
  intRule = c(0, 100, 10000),
  intType = "colourScale",
  numColumns = NULL,
  numGrep = NULL,
  numStyle = c("#F2F0F7", "#B4B1D4", "#938EC2"),
  numRule = c(1, 10, 20),
  numType = "colourScale",
  pvalueColumns = NULL,
  pvalueGrep = NULL,
  pvalueStyle = c("#F77F30", "#FDC99B", "#EEECE1"),
  pvalueRule = c(0, 0.01, 0.05),
  pvalueType = "colourScale",
  verbose = FALSE,
  startRow = 2,
  overwrite = TRUE,
  ...
)
```

Arguments

xlsxFile	character filename to a file with ".xlsx" extension, or Workbook object defined in the openxlsx package. When xlsxFile is a Workbook the output is not saved to a file.
sheet	integer or character, either the worksheet number, in order or character worksheet name. This vector can contain multiple values, which will cause conditional formatting to be applied to each worksheet in the order given.

`fcColumns`, `lfcColumns`, `hitColumns`, `intColumns`, `numColumns`, `pvalueColumns`
: integer column indices, or character colnames indicating which columns are to be treated as each of the various column types.

`fcGrep`, `lfcGrep`, `hitGrep`, `intGrep`, `numGrep`, `pvalueGrep`
: optional character vector which is used by `provigrep` to colnames(x). This process may be more convenient to apply formatting to known colname character patterns, rather than supplying exact column indices or colnames.

`fcStyle`, `lfcStyle`, `hitStyle`, `intStyle`, `numStyle`, `pvalueStyle`
: color vector of length=3, corresponding to the numeric thresholds defined by the corresponding Rules.

`fcRule`, `lfcRule`, `hitRule`, `intRule`, `numRule`, `pvalueRule`
: numeric vector of length=3, used to define three numeric thresholds for color gradients to be applied.

`fcType`, `lfcType`, `hitType`, `intType`, `numType`, `pvalueType`
: character string indicating the type of conditional rule to apply, which in most cases should be "colourScale" which allows three numeric thresholds, and three corresponding colors. For other allowed values, see `openxlsx::conditionalFormatting()`.

`verbose`
: logical indicating whether to print verbose output.

`startRow`
: integer indicating which row to begin applying conditional formatting. In most cases startRow=2, which allows one row for column headers. However, if there are multiple header rows, startRow should be 1 more than the number of header rows.

`overwrite`
: logical indicating whether the original 'Excel' files will be replaced with the new one, or whether a new file will be created.

`...`
: additional parameters are ignored.

Details

This function is a convenient wrapper for applying conditional formatting to 'Excel' 'xlsx' worksheets, with reasonable settings for commonly used data types.

Note that this function does not apply cell formatting, such as numeric formatting as displayed in 'Excel'.

A description of column types follows:

"fc" Fold change, typically positive and negative values, which are formatted to show one decimal place, and use commas to separate thousands places, e.g. 1,020.1. Colors are applied with a neutral midpoint, coloring values which are above and below zero.

"lfc" log fold change, typically positive and negative values, which are formatted to show one decimal place, and use commas to separate thousands places, e.g. 12.1. Colors are applied with a neutral midpoint, coloring values which are above and below zero. Log fold changes have slightly different color thresholds than fold changes.

"hit" Hit columns, often just values like `c(-1,0,1)`, but which could be fold changes for statistical hits for example. They are formatted to show one decimal place, and use commas to separate thousands places, e.g. 1.5. Colors are applied with a neutral midpoint, coloring values which are above and below zero, typically with a fairly low threshold.

"int" Integer columns, which are formatted to hide decimal place values even if present, which can help clean up visible tabular data. They are formatted to use commas to separate thousands places, e.g. 1,020. Colors are applied with a baseline of zero, intended for highlighting two thresholds of values above zero.

"num" Numeric columns, which are formatted to display 2 decimal places, and to use commas to separate thousands places, e.g. 1,020.1. Colors are applied with a baseline of zero, intended for highlighting two thresholds of values above zero.

"pvalue" P-value columns, which are formatted to display scientific notation always, for consistency, with two decimal places, e.g. 1.02e-02. Colors are applied starting at white for P-value of 1 (non-significant) and becoming more red as the P-value approaches 0.01, then 0.0001.

For each column type, one can describe the column using integer indices, or colnames, or optionally use the Grep parameters. The Grep parameters are intended for pattern matching, and may contain a vector of grep patterns which are used by `provigrep()` to match to colnames. The Grep method is particularly useful when applying conditional formatting for multiple worksheets in the same 'xlsx' file, where the colnames are not identical in each worksheet.

Each column type has an associated 3-threshold rule, and three associated colors. In order to apply different thresholds, one would need to call this function multiple times, specifying different subsets of columns corresponding to each set of thresholds. The same process is required in order to apply different color gradients to different columns. Note that styles are by default "stacked", which maintains font and cell border styles without removing them. However, it this "stacking" means that applying two rules to the same cell will not work, since only the first rule will be applied by 'Microsoft Excel'. Interestingly, if multiple conditional rules are applied to the same cell, they will be visible in order inside the 'Microsoft Excel' application.

Value

`Workbook` object as defined by the `openxlsx` package is returned invisibly with `invisible()`. This `Workbook` can be used in argument `wb` to provide a speed boost when saving multiple sheets to the same file.

See Also

Other jam export functions: `applyXlsxCategoricalFormat()`, `readOpenxlsx()`, `set_xlsx_colwidths()`, `set_xlsx_rowheights()`, `writeOpenxlsx()`

Examples

```
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
   df <- data.frame(a=LETTERS[1:5], b=1:5);
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test");

   applyXlsxConditionalFormat(out_xlsx,
      sheet="jamba_test",
      intColumns=2,
      intRule=c(0,3,5),
```

```
      intStyle=c("#FFFFFF", "#1E90FF", "#9932CC")
    )
}
```

`asDate` *convert date DDmmmYYYY to Date*

Description

convert date DDmmmYYYY to Date

Usage

```
asDate(getDateValues, dateFormat = "%d%b%Y", ...)
```

Arguments

`getDateValues`	`character` date, in format recognized by dateFormat
`dateFormat`	`character` string representing the recognized date format, by default `"DDmmmYYYY"`, which recognizes `"23aug2007"`.
`...`	additional parameters are ignored.

Details

This function converts a text date string to Date object, mainly to allow date-related math operations, for example `difftime`.

Value

Date object

See Also

Other jam date functions: `dateToDaysOld()`, `getDate()`

Examples

```
asDate(getDate());
```

asSize *convert numeric value or R object to human-readable size*

Description

convert numeric value or R object to human-readable size

Usage

```
asSize(
  x,
  digits = 3,
  abbreviateUnits = TRUE,
  unitType = "bytes",
  unitAbbrev = gsub("^(.).*$", "\\1", unitType),
  kiloSize = 1024,
  sep = " ",
  ...
)
```

Arguments

x	numeric vector, class object_size which is converted to numeric, any other R object is converted to a single numeric value using utils::object.size().
digits	integer number of digits used by base::format() when formatting the number to create a character string
abbreviateUnits	logical, default TRUE, whether to print abbreviated units, for example using k, M, G, T, P instead of kilo, mega, Giga, Tera, Peta, respectively.
unitType	character string indicating the base unit of measure, by default "bytes". Note that trailing "s" is removed when the number is singular.
unitAbbrev	character string indicating an abbreviated base unit, by default it uses the first character from unitType.
kiloSize	numeric, default 1024, number of base units when converting from to one "kilo" base unit. For computer-based size such as file size and object size, this value is 1024. For other purposes, such as scientific or monetary numbers, this value should usually be 1000.
sep	delimiter used between the numeric value and the unit, default " ".
...	other parameters passed to base::format().

Details

This function returns human-readable size based upon numeric input. Alternatively, when input is any other R object, it calls utils::object.size() to produce a single numeric value which is then used to produce human-readable size.

The default behavior is to report computer size in bytes, where 1024 is considered "kilo", however argument `kiloSize` can be used to produce values where `kiloSize=1000` which is suitable for monetary and other scientific values.

Value

`character` vector representing human-friendly size, based upon the `kiloSize` argument to determine whether to report byte (1024) or scientific (1000) units.

See Also

Other jam string functions: `breaksByVector()`, `fillBlanks()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
asSize(c(1, 10,2010,22000,52200))
#> "1 byte"   "10 bytes" "2 kb"     "21 kb"    "51 kb"

# demonstration of straight numeric units
asSize(c(1, 100, 1000, 10000), unitType="", kiloSize=100)
```

`breakDensity` *Calculate more detailed density of numeric values*

Description

Calculate more detailed density of numeric values

Usage

```
breakDensity(
  x,
  breaks = length(x)/3,
  bw = NULL,
  width = NULL,
  densityBreaksFactor = 3,
  weightFactor = 1,
  addZeroEnds = TRUE,
  baseline = 0,
  floorBaseline = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric vector
breaks	numeric breaks as described for stats::density() except that single integer value is multiplied by densityBreaksFactor.
bw	character name of a bandwidth function, or NULL.
width	NULL or numeric value indicating the width of breaks to apply.
densityBreaksFactor	numeric factor to adjust the width of density breaks, where higher values result in less detail.
weightFactor	optional vector of weights length(x) to apply to the density calculation.
addZeroEnds	logical indicating whether the start and end value should always be zero, which can be helpful for creating a polygon.
baseline	optional numeric value indicating the expected baseline, which is typically zero, but can be set to a higher value to indicate a "noise floor".
floorBaseline	logical indicating whether to apply a noise floor to the output data.
verbose	logical indicating whether to print verbose output.
...	additional parameters are sent to stats::density().

Details

This function is a drop-in replacement for stats::density(), simply to provide a quick alternative that defaults to a higher level of detail. Detail can be adjusted using densityBreaksFactor, where higher values will use a wider step size, thus lowering the detail in the output.

Note that the density height is scaled by the total number of points, and can be adjusted with weightFactor. See Examples for how to scale the y-axis range similar to stats::density().

Value

list output equivalent to stats::density():

- x: The n coordinates of the points where the density is estimated.
- y: The estimated density values, non-negative, but can be zero.
- bw: The bandidth used.
- n: The sample size after elimination of missing values.
- call: the call which produced the result.
- data.name: the deparsed name of the x argument.
- has.na: logical for compatibility, and always FALSE.

See Also

Other jam practical functions: call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
x <- c(stats::rnorm(15000),
   stats::rnorm(5500)*0.25 + 1,
   stats::rnorm(12500)*0.5 + 2.5)
plot(stats::density(x))

plot(breakDensity(x))

plot(breakDensity(x, densityBreaksFactor=200))

# trim values to show abrupt transitions
x2 <- x[x > 0 & x < 4]
plot(stats::density(x2), lwd=2)
lines(breakDensity(x2, weightFactor=1/length(x2)/10), col="red")
graphics::legend("topright", c("stats::density()", "breakDensity()"),
   col=c("black", "red"), lwd=c(2, 1))
```

---

breaksByVector *break a vector into groups*

Description

breaks a vector into groups

Usage

```
breaksByVector(x, labels = NULL, returnFractions = FALSE, ...)
```

Arguments

x	`character` vector of labels
labels	`character` vector of custom labels to represent the items in x
returnFractions	`logical` whether to return fractional coordinates for labels that should be positioned between two labels
...	additional parameters are ignored.

Details

This function takes a vector of values, determines "chunks" of identical values, from which it defines where breaks occur. It assumes the input vector is ordered in the way it will be displayed, with some labels being duplicated consecutively. This function defines the breakpoints where the labels change, and returns the ideal position to put a single label to represent a duplicated consecutive set of labels.

It can return fractional coordinates, for example when a label represents two consecutive items, the fractional coordinate can be used to place the label between the two items.

This function is useful for things like adding labels to `imageDefault()` color image map of sample groupings, where it may be ideal to label only unique elements in a contiguous set.

Value

`list` with the following named elements:

- `"breakPoints"`: The mid-point coordinate between each break. These midpoints would be good for drawing dividing lines for example.
- `"labelPoints"`: The ideal point to place a label to represent the group.
- `"newLabels"`: A vector of labels the same length as the input data, except using blank values except where a label should be drawn. This output is good for text display.
- `"useLabels"`: The unique set of labels, without blanks, corresponding to the coordinates supplied by labelPoints.
- `"breakLengths"`: The integer size of each set of labels.

See Also

Other jam string functions: `asSize()`, `fillBlanks()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
b <- rep(LETTERS[c(1:5, 1)], c(2,3,5,4,3,4));
bb <- breaksByVector(b);
# Example showing how labels can be minimized inside a data.frame
data.frame(b,
   newLabels=bb$newLabels);

# Example showing how to reposition text labels
# so duplicated labels are displayed in the middle
# of each group
bb2 <- breaksByVector(b, returnFractions=TRUE);
ylabs <- c("minimal labels", "all labels");
withr::with_par(adjustAxisLabelMargins(ylabs, 2), {
   withr::local_par(adjustAxisLabelMargins(bb2$useLabels, 1))
   nullPlot(xlim=range(seq_along(b)), ylim=c(0,3),
      doBoxes=FALSE, doUsrBox=TRUE);
   graphics::axis(2, las=2, at=c(1,2), ylabs);
   graphics::text(y=2, x=seq_along(b), b);
   graphics::text(y=1, x=bb2$labelPoints, bb2$useLabels);

## Print axis labels in the center of each group
graphics::axis(3,
   las=2,
   at=bb2$labelPoints,
   labels=bb2$useLabels);

## indicate each region
for (i in seq_along(bb2$breakPoints)) {
   graphics::axis(1,
      at=c(c(0, bb2$breakPoints)[i]+0.8, bb2$breakPoints[i]+0.2),
      labels=c("", ""));
```

```
}
## place the label centered in each region without adding tick marks
graphics::axis(1,
   las=2,
   tick=FALSE,
   at=bb2$labelPoints,
   labels=bb2$useLabels);
## abline to indicate the boundaries, if needed
graphics::abline(v=c(0, bb2$breakPoints) + 0.5,
   lty="dashed",
   col="blue");

})
# The same process is used by imageByColors()
```

`call_fn_ellipsis` *Safely call a function using ellipsis*

Description

Safely call a function using ellipsis

Usage

```
call_fn_ellipsis(FUN, ...)
```

Arguments

`FUN`	`function` that should be called with arguments in `...`
`...`	arguments are passed to `FUN()` in safe manner.

Details

This function is a wrapper function intended to help pass ellipsis arguments `...` from a parent function to an external function in a safe way. It will only include arguments from `...` that are recognized by the external function.

The logic is described as follows:

- When the external function `FUN` arguments `formals()` include ellipsis `...`, then the ellipsis `...` will be passed as-is without change. In this way, any arguments inside the original ellipsis `...` will either match arguments in `FUN`, or will be ignored in that function ellipsis `....`
- When the external function `FUN` arguments `formals()` do not include ellipsis `...`, then named arguments in `...` are passed to `FUN` only when the arguments names are recognized by `FUN`.

Note that arguments therefore must be named.

Value

output from FUN() when called with relevant named arguments from ellipsis ...

See Also

Other jam practical functions: breakDensity(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
new_mean <- function(x, trim=0, na.rm=FALSE) {
   mean(x, trim=trim, na.rm=na.rm)
}
x <- c(1, 3, 5, NA);
new_mean(x, na.rm=TRUE);
# throws an error as expected (below)
tryCatch({
   new_mean(x, na.rm=TRUE, color="red")
}, error=function(e){
   print("Error is expected, shown below:");
   print(e)
})

call_fn_ellipsis(new_mean, x=x, na.rm=TRUE, color="red")
```

---

cell_fun_label *ComplexHeatmap cell function to label heatmap cells*

Description

ComplexHeatmap cell function to label heatmap cells

Usage

```
cell_fun_label(
  m,
  prefix = "",
  suffix = "",
  cex = 1,
  col_hm = NULL,
  outline = FALSE,
  abbrev = FALSE,
  show = NULL,
  rot = 0,
```

```
  sep = "\n",
  verbose = FALSE,
  ...
)
```

Arguments

m	numeric matrix or list of matrix objects. The first matrix object must be numeric and compatible with the color function col_hm.
prefix, suffix	character vectors that define a prefix and suffix for each value in m for each cell.
cex	numeric adjustment for the fontsize used for each label, which is multiplied by the default fontsize=10 to determine the fontsize.
col_hm	function as returned by circlize::colorRamp2() which should be the same function used to create the heatmap
outline	logical indicating whether to draw an outline around each heatmap cell
abbrev	logical indicating whether numeric values should be abbreviated using jamba::asSize(..., kiloSize=1000) which effectively reduces large numbers to k for thousands, M for millions (M for Mega), G for billions (G for Giga), etc.
show	integer used when m is supplied as a list of matrices, in which case show is used to define which values should be used as cell labels. By default, all matrices are used.
rot	numeric value used to rotate cell label text, default 0 is horizontal.
sep	character string, default "\n" newline, used when there are multiple labels per cell, which also requires m as a list, and show is NULL or has multiple values.
verbose	logical indicating whether to print verbose output, specifically printing label information for position (1, 1). This output will only be seen when rendering or building the Heatmap object.
...	additional arguments are ignored.

Details

This function serves as a convenient method to add text labels to each cell in a heatmap produced by ComplexHeatmap::Heatmap(), via the argument cell_fun.

Note that this function requires re-using the specific color function used for the heatmap in the call to ComplexHeatmap::Heatmap().

This function is slightly unique in that it allows multiple labels, if m is supplied as a list of matrix objects. In fact, some matrix objects may contain character values with custom labels.

Cell labels are colored based upon the heatmap cell color, which is passed to jamba::setTextContrastColor() to determine whether to use light or dark text color for optimum contrast.

TODO: Option to supply a logical matrix to define a subset of cells to label, for example only labels that meet a filter criteria. Alternatively, the matrix data supplied in m can already be filtered.

TODO: Allow some matrix values that contain character data to use gridtext for custom markdown formatting. That process requires a slightly different method.

Value

`function` sufficient to use as input to `ComplexHeatmap::Heatmap()` argument `cell_fun`.

See Also

Other jam heatmap functions: `heatmap_column_order()`, `heatmap_row_order()`

Examples

```
m <- matrix(stats::rnorm(16)*2, ncol=4)
colnames(m) <- LETTERS[1:4]
rownames(m) <- letters[1:4]
col_hm <- circlize::colorRamp2(breaks=(-2:2) * 2,
   colors=c("navy", "dodgerblue", "white", "tomato", "red4"))

# the heatmap can be created in one step
hm <- ComplexHeatmap::Heatmap(m,
   col=col_hm,
   heatmap_legend_param=list(
      color_bar="discrete",
      border=TRUE,
      at=-4:4),
   cell_fun=cell_fun_label(m,
      col_hm=col_hm))
ComplexHeatmap::draw(hm)

# the cell label function can be created first
cell_fun <- cell_fun_label(m,
   outline=TRUE,
   cex=1.5,
   col_hm=col_hm)
hm2 <- ComplexHeatmap::Heatmap(m,
   col=col_hm,
   cell_fun=cell_fun)
ComplexHeatmap::draw(hm2)
```

---

checkLightMode *check lightMode for light background color*

Description

check lightMode for light background color

Usage

```
checkLightMode(lightMode = NULL, ...)
```

Arguments

lightMode	logical or NULL, indicating whether the lightMode parameter has been defined in the function call.
...	Additional arguments are ignored.

Details

Check the lightMode status through function parameter, options, or environment variable. If the function defines lightMode, it is used as-is. If lightMode is NULL, then options("jam.lightMode") is used if defined. Otherwise, it tries to detect whether the R session is running inside Rstudio using the environmental variable "RSTUDIO", and if so it assumes lightMode==TRUE.

To set a default lightMode, add options("jam.lightMode"=TRUE) to .Rprofile, or to the relevant R script.

Value

logical or length=1, indicating whether lightMode is defined

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
checkLightMode(TRUE);
checkLightMode();
```

---

check_pkg_installed *Lightweight method to check if an R package is installed*

Description

Lightweight method to check if an R package is installed

Usage

```
check_pkg_installed(x, ...)
```

Arguments

x	character string of package or packages to test.
...	additional arguments are ignored.

Details

There are many methods to test for an installed package, this function represents possibly the most gentle and rapid approach. It simply calls `system.file(package="")`, which checks in the context of the active R session and uses the relevant `.libPaths()`.

This approach does not use `require()` because that actually loads the package, which can take time and resources.

This approach also does not use `installed.packages()` which can also take substantial time if many packages are installed on a system.

Value

`logical` indicating whether each value in `x` represents an installed R package.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
check_pkg_installed("methods")

check_pkg_installed(c("jamba",
   "multienrichjam",
   "venndir",
   "methods",
   "blah"))
```

---

col2alpha *get R color alpha value*

Description

Return the alpha transparency per R color

Usage

```
col2alpha(x, maxValue = 1, ...)
```

Arguments

`x`	`character` R compatible color, either a color name, hex value, or a mixture of the two. Any value compatible with `grDevices::col2rgb()`.
`maxValue`	`numeric` maximum value to return, useful when the downstream alpha range should be 255. By default maxValue=1 is returned.
`...`	Additional arguments are ignored.

Value

numeric vector of alpha values

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
col2alpha(c("red", "#99004499", "beige", "transparent", "#FFFFFF00"))
```

---

col2hcl *convert R color to HCL color matrix*

Description

convert R color to HCL color matrix

Usage

```
col2hcl(
  x,
  maxColorValue = 255,
  model = getOption("jam.model", c("hcl", "polarLUV", "polarLAB")),
  ...
)
```

Arguments

x	character R compatible color, either a color name, hex value, or a mixture of the two. Any value compatible with grDevices::col2rgb().
maxColorValue	numeric maximum value to return, useful when the downstream alpha range should be 255. By default maxValue=1 is returned.
model	character color model to use • "hcl" to use farver HCL • "polarLUV" for the standard R conventional HCL, • "polarLAB" which uses the LAB-based HCL values.
...	additional arguments are ignored.

Details

This function takes an R color and converts to an HCL matrix, using the colorspace package, and RGB and polarLUV functions. It is also used to maintain alpha transparency, to enable interconversion via other color manipulation functions as well.

When `model="hcl"` this function uses `farver::decode_colour()` and bypasses `colorspace`. In future the `colorspace` dependency will likely be removed in favor of using `farver`. In any event, `model="hcl"` is equivalent to using `model="polarLUV"` and `fixup=TRUE`, except that it should be much faster.

Value

`numeric` matrix with H, C, L values.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
col2hcl("#FF000044")
```

`col2hsl` *convert R color to HSL color matrix*

Description

convert R color to HSL color matrix

Usage

```
col2hsl(x, ...)
```

Arguments

`x`	`character` vector with R compatible colors.
`...`	additional arguments are ignored.

Details

This function takes an R color and converts to an HSL matrix, using the `farver` package `farver::decode_colour()` the colorspace package, and `RGB` and `polarLUV` functions. It is also used to maintain alpha transparency, to enable interconversion via other color manipulation functions as well.

When `model="hsl"` this function uses `farver::decode_colour()` and bypasses `colorspace`. In future the `colorspace` dependency will likely be removed in favor of using `farver`. In any event, `model="hsl"` is equivalent to using `model="polarLUV"` and `fixup=TRUE`, except that it should be much faster.

Value

`numeric` matrix of H, S, L color values.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
x <- c("#FF000044", "#FF0000", "firebrick");
names(x) <- x;
showColors(x)
xhsl <- col2hsl(x)
xhsl

xhex <- hsl2col(xhsl)
showColors(list(x=x,
   xhex=xhex),
   groupCellnotes=FALSE)

withr::with_par(list("mfrow"=c(4, 4), "mar"=c(0.2, 1, 4, 1)), {

for (H in seq(from=0, to=360, length.out=17)[-17]) {
S <- 75;
Lseq <- seq(from=15, to=95, by=10);
hsl_gradient <- hsl2col(
   H=H,
   S=85,
   L=Lseq);
hcl_gradient <- hcl2col(
   H=H,
   C=85,
   L=Lseq);
names(hsl_gradient) <- Lseq;
names(hcl_gradient) <- Lseq;
showColors(xaxt="n",
   list(
      hsl=hsl_gradient,
```

```
      hcl=hcl_gradient),
   main=paste0("Hue: ", round(H),
      "\nSat: ", S,
      "\nLum: (as labeled)"),
   groupCellnotes=FALSE)
}
})
```

---

col2hsv *Convert R color to HSV matrix*

Description

Convert R color to HSV matrix

Usage

```
col2hsv(x, ...)
```

Arguments

x	R color
...	additional parameters are ignored

Details

This function takes a valid R color and converts to a HSV matrix. The output can be effectively returned to R color with hsv2col, usually after manipulating the HSV color matrix.

Value

matrix of HSV colors

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
# start with a color vector
# red and blue with partial transparency
colorV <- c("#FF000055", "#00339999");

# confirm the hsv matrix maintains transparency
col2hsv(colorV);
```

```
# convert back to the original color
hsv2col(col2hsv(colorV));
```

`colNum2excelName` *convert column number to 'Excel' column name*

Description

convert column number to 'Excel' column name

Usage

```
colNum2excelName(x, useLetters = LETTERS, zeroVal = "a", ...)
```

Arguments

`x`	`integer` vector
`useLetters`	`character` vector of single-digit characters to use as digits in the resulting column name. Note that these characters can be of almost any length, with any content.
`zeroVal`	`character` single-digit to be used whenever `x==0`, or as a prefix for negative values. In theory there should be no negative input values, but this basic mechanism is used to handle the possibility.
`...`	Additional arguments are ignored.

Details

The purpose is to convert an `integer` column number into a valid 'Excel' column name, using `LETTERS` starting at A. This function implements an arbitrary number of digits, which may or may not be compatible with each version of 'Excel'. 18,278 columns would be the maximum for three digits, "A" through "ZZZ".

This function is useful when referencing 'Excel' columns via another interface such as via openxlsx. It is also used by `makeNames()` when the `numberStyle="letters"`, in order to provide letter suffix values.

One can somewhat manipulate the allowed column names via the `useLetters` argument, which by default uses the entire 26-letter Western alphabet.

Value

`character` vector with length(x)

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
colNum2excelName(1:30)
```

---

color2gradient *Make a color gradient*

Description

Make a color gradient

Usage

```
color2gradient(
  col,
  n = NULL,
  gradientWtFactor = NULL,
  dex = 1,
  reverseGradient = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

`col`	some type of recognized R color input as: • `character` vector of one or more individual colors, each color is expanded into a gradient of length `n`, where `n` is recycled to the number of unique colors. The value `n` is applied in the order the colors appear in `col`. • `list` of color vectors where each vector contains one repeated color • `character` vector of repeated colors, where `n` is defined by the number of each color present.
`n`	`integer` vector of length one or more, which defines the number of colors to return for each gradient. When `n=0` then only duplicated colors will be expanded into a gradient.
`gradientWtFactor`	`numeric` fraction representing the amount to expand a color toward its maximum brightness and darkness. It is recommended to use `dex` and not this argument.

- When `gradientWtFactor=NULL` this value is calculated based upon the number of colors requested, and the initial luminance in HCL space of the starting color.
- When `gradientWtFactor` is defined, values are recycled to `length(col)`, and can be independently applied to each color.

`dex` `numeric` value to apply dramatic dark expansion, where:

- `dex > 1` will make the gradient more dramatic, values
- `dex < 1` will make the gradient less dramatic, and are considered fractions 1/x.
- `dex < 0` will make the gradient less dramatic, and values are internally converted to fractions using `1/(2 + abs(dex))`

`reverseGradient`
: `logical` whether to return light-to-dark gradient (TRUE) or dark-to-light gradient (FALSE).

`verbose` `logical` whether to print verbose output.

`...` other parameters are ignored.

Details

This function converts a single color into a color gradient by expanding the initial color into lighter and darker colors around the central color. The amount of gradient expansion is controlled by gradientWtFactor, which is a weight factor scaled to the maximum available range of bright to dark colors.

As an extension, the function can take a vector of colors, and expand each into its own color gradient, each with its own number of colors. If a vector with supplied that contains repeated colors, these colors are expanded in-place into a gradient, bypassing the value for `n`.

If a list is supplied, a list is returned of the same length, where each vector inside the list is a color gradient of length specified by `n`. If the input list contains multiple values, only the first color is used to define the color gradient.

Value

`character` vector of R colors.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
# given a list, it returns a list
x <- color2gradient(list(Reds=c("red"), Blues=c("blue")), n=c(4,7));
showColors(x);
```

```
# given a vector, it returns a vector
xv <- color2gradient(c(red="red", blue="blue"), n=c(4,7));
showColors(xv);

# Expand colors in place
# This process is similar to color jittering
colors1 <- c("red","blue")[c(1,1,2,2,1,2,1,1)];
names(colors1) <- colors1;
colors2 <- color2gradient(colors1);
showColors(list(`Input colors`=colors1, `Output colors`=colors2));

# You can do the same using a list intermediate
colors1L <- split(colors1, colors1);
showColors(colors1L);
colors2L <- color2gradient(colors1L);
showColors(colors2L);

# comparison of fixed gradientWtFactor with dynamic gradientWtFactor
showColors(list(
   `dynamic\ngradientWtFactor\ndex=1`=color2gradient(
      c("yellow", "navy", "firebrick", "orange"),
      n=3,
      gradientWtFactor=NULL,
      dex=1),
   `dynamic\ngradientWtFactor\ndex=2`=color2gradient(
      c("yellow", "navy", "firebrick", "orange"),
      n=3,
      gradientWtFactor=NULL,
      dex=2),
   `fixed\ngradientWtFactor=2/3`=color2gradient(
      c("yellow", "navy", "firebrick", "orange"),
      n=3,
      gradientWtFactor=2/3,
      dex=1)
))
```

`color_dither` *Make dithered color pattern light-dark*

Description

Make dithered color pattern light-dark

Usage

```
color_dither(
  x,
  L_diff = 4,
  L_max = 90,
```

```
  L_min = 30,
  min_contrast = 1.25,
  direction = 1,
  returnType = c("vector", "list", "matrix"),
  debug = FALSE,
  ...
)
```

Arguments

x	character vector of R colors
L_diff	numeric value added or subtracted from the L in HSL color space for each color, until contrast is at least min_contrast.
L_max, L_min	numeric values that define the permitted range of L values in HSL color space, which ranges from 0 to 100.
min_contrast	numeric minimum contrast as defined by colorspace::contrast_ratio() for the input and potential output color.
direction	numeric that defines the initial direction, where values >= 0 start by making colors lighter, and values < 0 make colors darker.
returnType	character string that defines the output of this function: • vector: two colors for every input color in x • matrix: two rows, input colors on first row, output colors on second row • list: a list with two colors in each element, with input and output colors together in each vector.
debug	logical indicating whether to plot the color iterations using showColors().
...	additional arguments are ignored.

Details

This function serves a very simple purpose, mainly for printDebug() to use subtle alternating light/dark colors for vector output. It takes a color and returns two colors which are slightly lighter and darker than each other, to a minimum contrast defined by colorspace::contrast_ratio().

Value

format defined by argument returnType:

- vector: two colors for every input color in x
- matrix: two rows, input colors on first row, output colors on second row
- list: a list with two colors in each element, with input and output colors together in each vector.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
x <- "firebrick1";
showColors(color_dither(x))

showColors(color_dither(x, direction=-1))

x <- vigrep("^green[0-9]", grDevices::colors())
showColors(color_dither(x))
showColors(color_dither(x, direction=-1, returnType="list"))

x <- c("green1", "cyan", "blue", "red", "gold", "yellow", "pink")
showColors(color_dither(x))

color_dither(x, debug=TRUE)
```

`coordPresets` *Process coordinate adjustment presets*

Description

Process coordinate adjustment presets

Usage

```
coordPresets(
  preset = "default",
  x = 0,
  y = 0,
  adjPreset = "default",
  adjX = 0.5,
  adjY = 0.5,
  adjOffsetX = 0,
  adjOffsetY = 0,
  preset_type = c("plot"),
  verbose = FALSE,
  ...
)
```

Arguments

`preset`	`character` vector of coordinate positions, or the default "default" to use the `x,y` coordinates. • Recognized terms: center, bottom, top, left, right, topleft, topright, bottomleft, bottomright.
`x, y`	`numeric` vectors indicating the default coordinates `x,y`.

adjPreset — character vector of text label positions, or the default "default" to use preset, or when preset="default" the adjX,adjY values are used.

- Recognized terms: center, bottom, top, left, right, topleft, topright, bottomleft, bottomright.

adjX, adjY — numeric vectors indicating default text adjustment values, as described for adj in graphics::text().

adjOffsetX, adjOffsetY — numeric vector used to apply an offset value to the adjX,adjY values, where positive values would place a label farther away from center. Note these units are relative to the text label size, when used with graphics::text(), larger labels will be adjusted more than smaller labels.

preset_type — character string indicating the reference point for the preset boundaries:

- "plot" uses the plot border.
- "margin" uses the margin border. Note that the margin used is the inner margin around the plot figure, not the outer margin which may be applied around multi-panel plot figures.

verbose — logical indicating whether to print verbose output.

... — additional arguments are ignored.

Details

This function is intended to be a convenient way to define coordinates using preset terms like "topleft", "bottom", "center".

Similarly, it is intended to help define corresponding text adjustments, using adj compatible with graphics::text(), using preset terms like "bottomright", "center".

When preset is "default", the original x,y coordinates are used. Otherwise the x,y coordinates are defined using the plot region coordinates, where "left" uses graphics::par("usr")[1], and "top" uses graphics::par("usr")[4].

When adjPreset is "default" it will use the preset to define a reciprocal text placement. For example when preset="topright" the text placement will be equivalent to adjPreset="bottomleft". The adjPreset terms "top", "bottom", "right", "left", and "center" refer to the text label placement relative to x,y coordinate.

If both preset="default" and adjPreset="default" the original adjX,adjY values are returned.

The function is vectorized, and uses the longest input argument, so one can supply a vector of preset and it will return coordinates and adjustments of length equal to the input preset vector. The preset value takes priority over the supplied x,y coordinates.

Value

data.frame after adjustment, where the number of rows is determined by the longest input argument, with colnames:

- x
- y
- adjX

- adjY
- preset
- adjPreset

See Also

Other jam plot functions: adjustAxisLabelMargins(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
# determine coordinates
presetV <- c("top",
   "bottom",
   "left",
   "right",
   "topleft");
cp1 <- coordPresets(preset=presetV);
cp1;

# make sure to prepare the plot region first
jamba::nullPlot(plotAreaTitle="");
graphics::points(cp1$x, cp1$y, pch=20, cex=2, col="red");

# unfortunately graphics::text() does not have vectorized adj
# so it must iterate each row
graphics::title(main="graphics::text() is not vectorized, text is adjacent to edges")
for (i in seq_along(presetV)) {
   graphics::text(cp1$x[i], cp1$y[i],
      labels=presetV[i],
      adj=c(cp1$adjX[i], cp1$adjY[i]));
}

# drawLabels() will be vectorized for unique adj subsets
# and adds a small buffer around text
jamba::nullPlot(plotAreaTitle="");
graphics::title(main="drawLabels() is vectorized, includes small buffer")
drawLabels(txt=presetV,
   preset=presetV)

jamba::nullPlot(plotAreaTitle="");
graphics::title(main="drawLabels() can place labels outside plot edges")
drawLabels(txt=presetV,
   preset=presetV,
   adjPreset=presetV)

# drawLabels() is vectorized for example
jamba::nullPlot(plotAreaTitle="");
graphics::title(main="Use adjPreset to position labels at a center point")
presetV2 <- c("topleft",
```

```
   "topright",
   "bottomleft",
   "bottomright");
cp2 <- coordPresets(preset="center",
   adjPreset=presetV2,
   adjOffsetX=0.1,
   adjOffsetY=0.4);
graphics::points(cp2$x,
   cp2$y,
   pch=20,
   cex=2,
   col="red");
drawLabels(x=cp2$x,
   y=cp2$y,
   adjX=cp2$adjX,
   adjY=cp2$adjY,
   txt=presetV2,
   boxCexAdjust=c(1.15,1.6),
   labelCex=1.3,
   lx=rep(1.5, 4),
   ly=rep(1.5, 4))

# demonstrate margin coordinates
withr::with_par(list("oma"=c(1, 1, 1, 1)), {
nullPlot(xlim=c(0, 1), ylim=c(1, 5));
cpxy <- coordPresets(rep(c("top", "bottom", "left", "right"), each=2),
   preset_type=rep(c("plot", "figure"), 4));
drawLabels(preset=c("top", "top"),
   txt=c("top label relative to figure",
      "top label relative to plot"),
   preset_type=c("figure", "plot"))
graphics::points(cpxy$x, cpxy$y, cex=2,
   col="red4", bg="red1", xpd=NA,
   pch=rep(c(21, 23), 4))
})
```

---

cPaste *paste a list into a delimited vector*

Description

Paste a list of vectors into a character vector, with values delimited by default with a comma.

Usage

```
cPaste(
  x,
  sep = ",",
  doSort = FALSE,
```

```
  makeUnique = FALSE,
  na.rm = FALSE,
  keepFactors = FALSE,
  checkClass = TRUE,
  useBioc = TRUE,
  useLegacy = FALSE,
  honorFactor = TRUE,
  verbose = FALSE,
  ...
)

cPasteS(
  x,
  sep = ",",
  doSort = TRUE,
  makeUnique = FALSE,
  na.rm = FALSE,
  keepFactors = FALSE,
  checkClass = TRUE,
  useBioc = TRUE,
  ...
)

cPasteSU(
  x,
  sep = ",",
  doSort = TRUE,
  makeUnique = TRUE,
  na.rm = FALSE,
  keepFactors = FALSE,
  checkClass = TRUE,
  useBioc = TRUE,
  ...
)

cPasteUnique(
  x,
  sep = ",",
  doSort = FALSE,
  makeUnique = TRUE,
  na.rm = FALSE,
  keepFactors = FALSE,
  checkClass = TRUE,
  useBioc = TRUE,
  ...
)

cPasteU(
```

```
  x,
  sep = ",",
  doSort = FALSE,
  makeUnique = TRUE,
  na.rm = FALSE,
  keepFactors = FALSE,
  checkClass = TRUE,
  useBioc = TRUE,
  ...
)
```

Arguments

x	list of vectors
sep	character delimiter used to paste multiple values together
doSort	logical indicating whether to sort each vector using mixedOrder().
makeUnique	logical indicating whether to make each vector in the input list unique before pasting its values together.
na.rm	logical indicating whether to remove NA values from each vector in the input list. When na.rm is TRUE and a list element contains only NA values, the resulting string will be "".
keepFactors	logical only used when useLegacy=TRUE and doSort=TRUE; indicating whether to preserve factors, keeping factor level order. When keepFactors=TRUE, if any list element is a factor, all elements are converted to factors. Note that this step combines overall factor levels, and non-factors will be ordered using base::order() instead of jamba::mixedOrder() (for now.)
checkClass	logical, default TRUE, whether to check the class of each vector in the input list. • When TRUE, it confirms the class of each element in the list before processing, to prevent conversion which may otherwise lose information. • For all cases when a known vector is split into a list, checkClass=FALSE is preferred since there is only one class in the resulting list elements. This approach is faster especially for for large input lists, 10000 or more. • When checkClass=FALSE it assumes all entries can be coerced to character, which is fastest, but does not preserve factor levels due to R coersion methods used by unlist().
useBioc	logical indicating whether this function should try to use S4Vectors::unstrsplit() when the Bioconductor package S4Vectors is installed, otherwise it will use a less efficient mapply() operation.
useLegacy	logical indicating whether to enable to previous legacy process used by cPaste().
honorFactor	logical passed to mixedSorts(), whether any factor vector should be sorted in factor level order. When honorFactor=FALSE then even factor vectors are sorted as if they were character vectors, ignoring the factor levels.
verbose	logical indicating whether to print verbose output.
...	additional arguments are passed to mixedOrder() when doSort=TRUE.

Details

- `cPaste()` concatenates vector values using a delimiter.
- `cPasteS()` sorts each vector using `mixedSort()`.
- `cPasteU()` applies `uniques()` to retain unique values per vector.
- `cPasteSU()` applies `mixedSort()` and `uniques()`.

This function is essentially a wrapper for `S4Vectors::unstrsplit()` except that it also optionally applies uniqueness to each vector in the list, and sorts values in each vector using `mixedOrder()`.

The sorting and uniqueness is applied to the `unlisted` vector of values, which is substantially faster than any `apply` family function equivalent. The uniqueness is performed by `uniques()`, which itself will use `S4Vectors::unique()` if available.

Value

`character` vector with the same names and in the same order as the input list `x`.

See Also

Other jam list functions: `heads()`, `jam_rapply()`, `list2df()`, `mergeAllXY()`, `mixedSorts()`, `rbindList()`, `relist_named()`, `rlengths()`, `sclass()`, `sdim()`, `uniques()`, `unnestList()`

Examples

```
L1 <- list(CA=LETTERS[c(1:4,2,7,4,6)], B=letters[c(7:11,9,3)]);

cPaste(L1);
#               CA                 B
# "A,B,C,D,B,G,D,F"   "g,h,i,j,k,i,c"

cPaste(L1, doSort=TRUE);
#               CA                 B
# "A,B,B,C,D,D,F,G"   "c,g,h,i,i,j,k"

## The sort can be done with convenience function cPasteS()
cPasteS(L1);
#               CA                 B
# "A,B,B,C,D,D,F,G"   "c,g,h,i,i,j,k"

## Similarly, makeUnique=TRUE and cPasteU() are the same
cPaste(L1, makeUnique=TRUE);
cPasteU(L1);
#           CA             B
# "A,B,C,D,G,F" "g,h,i,j,k,c"

## Change the delimiter
cPasteSU(L1, sep="; ")
#                CA                  B
# "A; B; C; D; F; G" "c; g; h; i; j; k"

# test mix of factor and non-factor
```

```
L2 <- c(
   list(D=factor(letters[1:12],
      levels=letters[12:1])),
   L1);
L2;
cPasteSU(L2, keepFactors=TRUE);

# tricky example with mix of character and factor
# and factor levels are inconsistent
# end result: factor levels are defined in order they appear
L <- list(entryA=c("miR-112", "miR-12", "miR-112"),
   entryB=factor(c("A","B","A","B"),
      levels=c("B","A")),
   entryC=factor(c("C","A","B","B","C"),
      levels=c("A","B","C")),
   entryNULL=NULL)
L;
cPaste(L);
cPasteU(L);

# by default keepFactors=FALSE, which means factors are sorted as characters
cPasteS(L);
cPasteSU(L);
# keepFactors=TRUE will keep unique factor levels in the order they appear
# this is the same behavior as unlist(L[c(2,3)]) on a list of factors
cPasteSU(L, keepFactors=TRUE);
levels(unlist(L[c(2,3)]))
```

`dateToDaysOld` *convert date to age in days*

Description

convert date to age in days

Usage

```
dateToDaysOld(testDate, nowDate = Sys.Date(), units = "days", ...)
```

Arguments

`testDate`	`character` date recognized by `asDate()`, representing the test date.
`nowDate`	`character` date recognized by `asDate()`, representing the reference date, by default the current day.
`units`	`character` indicating the units, as used by `difftime()`.
`...`	additional parameters are ignored.

Value

integer value with the number of calendar days before the current date, or the `nowDate` if supplied.

See Also

Other jam date functions: `asDate()`, `getDate()`

Examples

```
dateToDaysOld("23aug2007")
```

`decideMfrow` *Decide plot panel rows, columns for graphics::par(mfrow)*

Description

Decide plot panel rows, columns for graphics::par(mfrow)

Usage

```
decideMfrow(
  n,
  method = c("aspect", "wide", "tall"),
  doTest = FALSE,
  xyratio = 1,
  trimExtra = TRUE,
  ...
)
```

Arguments

`n`	`integer` number of plot panels
`method`	`character` string indicating the type of layout to favor.
	"aspect" uses the device size and aspect ratio of the plot to try to maintain roughly square plot panels.
	"wide" tries to keep the columns and rows similar, erring on the side of more columns than rows.
	"tall" tries to keep the columns and rows similar, erring on the side of more rows than columns.
`doTest`	`logical` whether to provide a visual test. Note that `n` is required as the number of plot panels requested.
`xyratio`	`numeric` default 1, with the desired target x-to-y ratio. For example, to have plots slightly wider (x width) than tall (y height), use `xyratio=1.3`. The observed device aspect ratio is divided by `xyratio` to determine the target aspect ratio of plot panels.

trimExtra	logical default TRUE, whether to trim blank rows or columns in the expected layout when it would be entirely blank. For example, n=4 may produce c(3, 2) output to meet the desired aspect ratio, however with trimExtra=TRUE it would be reduced to c(2, 2) to minimize unused whitespace.
...	additional parameters are ignored.

Details

This function returns the recommended rows and columns of panels to be used in graphics::par("mfrow") with R base plotting. It attempts to use the device size and plot aspect ratio to keep panels roughly square. For example, a short-wide device would have more columns of panels than rows; a tall-thin device would have more rows than columns.

The doTest=TRUE argument will create n number of panels with the recommended layout, as a visual example.

Note this function calls getPlotAspect(), therefore if no plot device is currently open, the call to graphics::par() will open a new graphics device.

Value

numeric vector length=2, with the recommended number of plot rows and columns, respectively. It is intended to be used directly in this form: graphics::par("mfrow"=decideMfrow(n=5))

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
# display a test visualization showing 6 panels
withr::with_par(list("mar"=c(2, 2, 2, 2)), {
decideMfrow(n=6, doTest=TRUE);
})

# use a custom target xyratio of plot panels
withr::with_par(list("mar"=c(2, 2, 2, 2)), {
decideMfrow(n=3, xyratio=3, doTest=TRUE);
})

# a manual demonstration creating 6 panels
n <- 6;
withr::with_par(list(
   "mar"=c(2, 2, 2, 2),
   "mfrow"=decideMfrow(n)), {
for(i in seq_len(n)){
   nullPlot(plotAreaTitle=paste("Plot", i));
}
})
```

deg2rad *Convert degrees to radians*

Description

Convert degrees to radians

Usage

```
deg2rad(x, ...)
```

Arguments

x	numeric vector, expected to be degree values between zero and 360.
...	other parameters are ignored.

Details

This function simply converts degrees which range from 0 to 360, into radians which range from zero to pi*2.

Value

numeric vector after coverting degrees to radians.

See Also

Other jam numeric functions: noiseFloor(), normScale(), rad2deg(), rowGroupMeans(), rowRmMadOutliers(), warpAroundZero()

Examples

```
deg2rad(rad2deg(c(pi*2, pi/2)))/pi;
```

drawLabels *Draw text labels on a base R plot*

Description

Draw text labels on a base R plot

Usage

```
drawLabels(
  txt = NULL,
  newCoords = NULL,
  x = NULL,
  y = NULL,
  lx = NULL,
  ly = NULL,
  segmentLwd = 1,
  segmentCol = "#00000088",
  drawSegments = TRUE,
  boxBorderColor = "#000000AA",
  boxColor = "#FFEECC",
  boxLwd = 1,
  drawBox = TRUE,
  drawLabels = TRUE,
  font = 1,
  labelCex = 0.8,
  boxCexAdjust = 1.9,
  labelCol = alpha2col(alpha = 0.8, setTextContrastColor(boxColor)),
  doPlot = TRUE,
  xpd = NA,
  preset = "default",
  adjPreset = "default",
  preset_type = "plot",
  adjX = 0.5,
  adjY = 0.5,
  panelWidth = "default",
  trimReturns = TRUE,
  text_fn = getOption("jam.text_fn", graphics::text),
  verbose = FALSE,
  ...
)
```

Arguments

txt	`character` vector of labels, length equal to `x` and `y`.

newCoords — data.frame optional, typically as a result of a previous call to drawLabels(). In general, it should contain colnames equivalent to the function parameters of drawLabels().

x, y — numeric vector of x- and y- coordinates.

lx, ly — numeric optional vector of segment endpoint coordinates, used to draw a line from x,y coordinates to the segment lx,ly coordinate.

segmentLwd, segmentCol — numeric vector of segment line widths, and character colors, respectively. Each vector will be recycled to length(txt) as needed.

drawSegments — logical whether to draw segments, where applicable.

boxBorderColor — character vector of colors used for the box border around each label.

boxColor — character vector of colors used for the box background behind each label.

boxLwd — numeric vector of box line widths, sent to graphics::rect(), this vector will be recycled to length(txt).

drawBox — logical whether to draw boxes behind each text label.

drawLabels — logical whether to draw each text label.

font — integer vector of font values as described in graphics::par(), where 1=normal, 2=bold, 3=italics, 4=bold-italics.

labelCex — numeric vector of cex values used for text labels, recycled to length(txt) as needed.

boxCexAdjust — numeric vector length=2, used to expand the x-width and y-height of the box around around text labels.

labelCol — character vector of label colors, by default it calls jamba::setTextContrastColor() to generate a color to contrast the background box color.

doPlot — logical whether to perform any plot operations. Set FALSE to calculate coordinates and return a data.frame of label coordinates, which can then be manipulated before calling drawLabels() again.

xpd — logical value compatible with graphics::par("xpd"), where NA allows labels anywhere in the device region, TRUE retricts labels within the figure region, and FALSE restricts labels within the plot region.

preset — character vector passed to coordPresets() used to position text labels relative to the x,y coordinate, where "topleft" will position the label so the entire label box is top-left of the point, therefore the point will be at the bottom-right corner of the label box. When preset is anything by "none" the adjX and adjY values are ignored.

preset_type, adjPreset — character passed to coordPresets() to define orientation of each label relative to the x,y coordinate.

adjX, adjY — numeric the text adjustment of labels relative to the x,y coordinate. The values are recycled to length(txt).

panelWidth — character string or vector, recycled to the number of labels to be displayed. The argument indicates whether to size each label box relative to the plot panel width, intended when the label preset and adjPreset are set for the label to be

inside the plot panel, e.g. `preset="top", adjPreset="top"`, or `preset="topleft", adjPreset="top`
Either both are centered, or one is "right" and the other is "left". In these cases, the label box is expanded to the full plot panel width, thus filling the full visible x-axis range for the plot panel. Allowed values for `panelWidth`:

- `"default"` size label boxes by text dimensions
- `"force"` size label to full plot panel width
- `"minimum"` size label at least the plot panel width, or larger if necessary to fit the text label
- `"maximum"` size label to the text label width, but no larger than the plot panel width

`trimReturns` `logical` whether to trim leading and trailing return (newline) characters from labels.

`text_fn` `function` used to render text, by default it checks `getOption("jam.text_fn", graphics::text)` which then defaults to `graphics::text`.

- This argument is specifically to enable `jamba::shadowText()`, for example `text_fn=jamba::shadowText`.
- Previous to version 0.0.107.900, one could assign `text <- jamba::shadowText` however that option was removed to make jamba more compliant with recommended R code, and ready for CRAN.

`verbose` `logical` whether to print verbose output.

`...` additional arguments are passed to `graphics::segments()` when segments are drawn, to `graphics::rect()` when label boxes are drawn, and to `graphics::text()` when text labels are drawn.

Details

This function takes a vector of coordinates and text labels, and draws the labels with colored rectangles around each label on the plot. Each label can have unique font, cex, and color, and are drawn using vectorized operations.

To enable shadow text include argument: `text_fn=jamba::shadowText`

TODO: In future allow rotated text labels. Not that useful within a plot panel, but sometimes useful when draw outside a plot, for example axis labels.

Value

invisible data.frame containing label coordinates used to draw labels. This data.frame can be manipulated and provided as input to `drawLabels()` for subsequent customized label positioning.

See Also

Other jam plot functions: `adjustAxisLabelMargins()`, `coordPresets()`, `decideMfrow()`, `getPlotAspect()`, `groupedAxis()`, `imageByColors()`, `imageDefault()`, `minorLogTicksAxis()`, `nullPlot()`, `plotPolygonDensity()`, `plotRidges()`, `plotSmoothScatter()`, `shadowText()`, `shadowText_options()`, `showColors()`, `sqrtAxis()`, `usrBox()`

Examples

```
nullPlot(plotAreaTitle="");
dl_topleft <- drawLabels(x=graphics::par("usr")[1],
   y=graphics::par("usr")[4],
   txt="Top-left\nof plot",
   preset="topleft",
   boxColor="blue4");

drawLabels(x=graphics::par("usr")[2],
   y=graphics::par("usr")[3],
   txt="Bottom-right\nof plot",
   preset="bottomright",
   boxColor="green4");

drawLabels(x=mean(graphics::par("usr")[1:2]),
   y=mean(graphics::par("usr")[3:4]),
   txt="Center\nof plot",
   preset="center",
   boxColor="purple3");

graphics::points(x=c(graphics::par("usr")[1], graphics::par("usr")[2],
      mean(graphics::par("usr")[1:2])),
   y=c(graphics::par("usr")[4], graphics::par("usr")[3],
      mean(graphics::par("usr")[3:4])),
   pch=20,
   col="red",
   xpd=NA);

nullPlot(plotAreaTitle="");
graphics::title(main="place label across the full top plot panel", line=2.5)
dl_top <- drawLabels(
   txt=c("preset='topright', adjPreset='topright', \npanelWidth='force'",
      "preset='topright',\nadjPreset='bottomleft'",
      "preset='bottomleft', adjPreset='topright',\npanelWidth='force'"),
   preset=c("topright", "topright", "bottomleft"),
   adjPreset=c("topleft", "bottomleft", "topright"),
   panelWidth=c("force", "none", "force"),
   boxColor=c("red4",
      "blue4",
      "purple3"));
graphics::box(lwd=2);

withr::with_par(list("mfrow"=c(1, 3), "xpd"=TRUE), {

isub <- c(force="Always full panel width",
   minimum="At least full panel width or larger",
   maximum="No larger than panel width");
for (i in c("force", "minimum", "maximum")) {
nullPlot(plotAreaTitle="", doMargins=FALSE);
graphics::title(main=paste0("panelWidth='", i, "'\n",
   isub[i]));
drawLabels(labelCex=1.2,
```

```
    txt=c("Super-wide title across the top\npanelWidth='force'",
    "bottom label"),
    preset=c("top", "bottom"),
    panelWidth=i,
    boxColor="red4")
}
})
```

`exp2signed` *exponentiate log2 values with directionality*

Description

exponentiate log2 values with directionality

Usage

```
exp2signed(x, offset = 1, base = 2, ...)
```

Arguments

`x`	`numeric` vector
`offset`	`numeric` subtracted from exponentiated values prior to multiplying by the `sign(x)`.
`base`	`numeric` value indicating the logarithmic base used. For example `base=2` indicates values were transformed using `log2()`.
`...`	additional arguments are ignored.

Details

This function is the reciprocal to `log2signed()`.

It #' exponentiates the absolute values of `x`, then subtracts the `offset`, then multiplies results by the `sign(x)`.

The `offset` is typically used to maintain directionality of values during log transformation by requiring all absolute values to be 1 or larger, thus by default `offset=1`.

Value

numeric vector of exponentiated values.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
x <- c(-100:100)/10;
z <- log2signed(x);
#plot(x=x, y=z, xlab="x", ylab="log2signed(x)")
plot(x=x, y=exp2signed(z), xlab="x", ylab="exp2signed(log2signed(x))")
plot(x=z, y=exp2signed(z), xlab="log2signed(x)", ylab="exp2signed(log2signed(x))")
```

`fillBlanks` *Fill blank entries in a vector*

Description

Fill blank entries in a vector

Usage

```
fillBlanks(x, blankGrep = c("[ \t]*"), first = "", ...)
```

Arguments

`x`	character vector
`blankGrep`	vector of grep patterns, or `NA`, indicating the type of entry to be considered blank. Each `blankGrep` pattern is searched using `jamba::proigrep()`, which by default uses case-insensitive regular expression pattern matching.
`first`	options character string intended when the first entry of `x` is blank. By default `""` is used.
`...`	additional parameters are ignored.

Details

This function takes a character vector and fills any blank (missing) entries with the last non-blank entry in the vector. It is intended for situations like imported 'Excel' data, where there may be one header value representing a series of cells.

The method used does not loop through the data, and should scale fairly well with good efficiency even for extremely large vectors.

Value

`character` vector where blank entries are filled with the most recent non-blank value.

See Also

Other jam string functions: `asSize()`, `breaksByVector()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
x <- c("A", "", "", "", "B", "C", "", "", NA,
   "D", "", "", "E", "F", "G", "", "");
data.frame(x, fillBlanks(x));
```

`fixYellow` *Fix yellow color*

Description

Fix yellow color to be less green than default "yellow"

Usage

```
fixYellow(col, Hrange = c(70, 100), Hshift = -20, fixup = TRUE, ...)
```

Arguments

`col`	R color, either in hex color format or using values from `grDevices::colors()`.
`Hrange`	numeric vector whose range defines the region of hues to be adjusted. By default hues between 80 and 90 are adjusted. If NULL, `HCL` is return unchanged.
`Hshift`	numeric value length one, used to adjust the hue of colors within the range `Hrange`. If NULL, `HCL` is return unchanged.
`fixup`	`logical`, default TRUE, whether to apply fixup to the resulting color, passed to `hcl2col()`
`...`	additional arguments are passed to `col2hcl()`, and `hcl2col()`.

Details

This function "fixes" the color yellow, which by default appears green especially when darkened. The effect of this function is to make yellows appear more red, which appears more visibly yellow even when the color is darkened.

This function is intended to be tolerant to missing values. For example if any of the values `col`, `Hrange`, or `Hshift` are length 0, the original `col` is returned unchanged.

Value

returns a vector of R colors the same length as input `col`. In the event `col`, `Hrange`, or `Hshift` have length 0, or if any step in the conversion produces length 0, then the original `col` is returned.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
yellows <- vigrep("yellow", grDevices::colors());
fixedYellows <- fixYellow(yellows);
showColors(list(yellows=yellows,
   fixedYellows=fixedYellows));
```

`fixYellowHue` *Fix yellow color hue*

Description

Fix yellow color hue to be less green than default "yellow"

Usage

```
fixYellowHue(HCL, Hrange = c(80, 90), Hshift = -15, ...)
```

Arguments

`HCL`	numeric matrix with HCL color values, as returned by `col2hcl()`, but requiring only one rowname `"H"` representing the color hue on a scale of 0 to 360. If input data does not contain numeric values with rowname "H", `HCL` is return unchanged.
`Hrange`	numeric vector whose range defines the region of hues to be adjusted. By default hues between 80 and 90 are adjusted. If NULL, `HCL` is return unchanged.
`Hshift`	numeric value length one, used to adjust the hue of colors within the range `Hrange`. If NULL, `HCL` is return unchanged.
`...`	additional arguments are ignored.

Details

This function "fixes" the color yellow, which by default appears green especially when darkened. The effect of this function is to make yellows appear more red, which appears more visibly yellow even when the color is darkened.

This function is intended to be tolerant to missing values. For example if any of the values `HCL`, `Hrange`, or `Hshift` are length 0, the original `HCL` is returned unchanged.

Value

returns the input `HCL` data where rowname `"H"` has hue values adjusted accordingly. In the event `HCL`, `Hrange`, or `Hshift` have length 0, the original `HCL` is returned. If input data does not meet the expected format, the input `HCL` is returned unchanged.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
yellows <- vigrep("yellow", grDevices::colors());
yellowsHCL <- col2hcl(yellows);
fixedYellowsHCL <- fixYellowHue(yellowsHCL);
fixedYellows <- hcl2col(fixedYellowsHCL);
showColors(list(yellows=yellows,
   fixedYellows=fixedYellows));
```

---

formatInt *Format an integer as a string*

Description

Format an integer as a string

Usage

```
formatInt(
  x,
  big.mark = ",",
  trim = TRUE,
  forceInteger = TRUE,
  scientific = FALSE,
  ...
)
```

Arguments

x	numeric vector or matrix
big.mark, trim, scientific	passed to base::format() but configured with defaults intended for integer values: • big.mark="," adds comma between thousands. • trim=TRUE to trim excess whitespace. • scientific=FALSE to prevent exponential notation.
forceInteger	logical, default TRUE, whether to round numeric to integer prior to calling base::format().
...	Additional arguments are ignored.

Details

This function is a quick wrapper function around `base::format()` to display integer values as text strings. It will also return a matrix if the input is a matrix.

Value

`character` vector if `x` is a vector, or if `x` is a matrix a matrix will be returned.

See Also

Other jam string functions: `asSize()`, `breaksByVector()`, `fillBlanks()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
x <- c(1234, 1234.56, 1234567.89);
## By default, commas are used for big.mark, and decimal values are hidden
formatInt(x);

## By default, commas are used for big.mark
formatInt(x, forceInteger=FALSE);
```

`getAxisLabel` *Get axis label for minorLogTicks*

Description

Get axis label for minorLogTicks

Usage

```
getAxisLabel(
  i,
  asValues,
  logAxisType = c("normal", "flip", "pvalue"),
  logBase,
  base_limit = 2,
  offset = 0,
  symmetricZero = (offset > 0),
  ...
)
```

Arguments

i	numeric axis value
asValues	logical indicating whether the value should be evaluated.
logAxisType	character string with the type of axis values: • "normal": axis values as-is. • "flip": inverted axis values, for example where negative values should be displayed as negative log-transformed values. • "pvalue": for values transformed as -log10(pvalue)
logBase	numeric logarithmic base
base_limit	numeric value indicating the minimum value that should be written as an exponential.
offset	numeric value of offset used for log transformation.
symmetricZero	logical indicating whether negative values should be displayed as negative log-transformed values.
...	additional arguments are ignored.

Details

This function is intended to be called internally by jamba::minorLogTicks().

Value

character or expression axis label as appropriate.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
x <- log10(c(1, 2, 5, 10, 20, 50, 100, 200, 500))
getAxisLabel(x, asValues=TRUE, logBase=10)

x1exp <- c(1, 2, 3, 4, 5)
plot(1:6, main="exponential values")
for (i in seq_along(x1exp)) {
   text(x=i, y=i + 0.2,
      getAxisLabel(x1exp[i], asValues=FALSE, logBase=10))
}

x1exp <- c(-3:3)
plot(-3:3, main="log2 fold change values")
for (i in seq_along(x1exp)) {
   text(x=i, y=i + 0.3 - 4,
```

```
      getAxisLabel(x1exp[i],
         logAxisType="flip",
         asValues=TRUE, logBase=2))
}

x1exp <- c(1, 2, 3, 4, 5)
plot(1:6, main="P-value style")
for (i in seq_along(x1exp)) {
   text(x=i, y=i + 0.2,
      getAxisLabel(x1exp[i],
      logAxisType="pvalue", asValues=FALSE, logBase=10))
}
```

`getColorRamp` *get color ramp by name, color, or function*

Description

get color ramp by name, color, or function

Usage

```
getColorRamp(
  col,
  n = 15,
  trimRamp = c(0, 0),
  gradientN = 15,
  defaultBaseColor = "grey99",
  reverseRamp = FALSE,
  alpha = TRUE,
  gradientWtFactor = NULL,
  dex = 1,
  lens = 0,
  divergent = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

`col` one of the following:

- `character` vector of two or more R colors. A color gradient will be defined using these colors in order with `colorRampPalette()`.
- `character` vector length=1 with one R color. A color gradient is defined from `defaultBaseColor` to `col` using `color2gradient()`. To adjust the range of light to dark luminance, use the `dex` argument, where higher values increase the range, and lower values decrease the range.

- character vector length=1, with one recognized color ramp name: any color palette from RColorBrewer, for example rownames(RColorBrewer::brewer.pal.info()); any color palette function name from viridisLite.
- character vector length=1, with one color function name, for example col="rainbow_hcl". Input is equivalent to supplying one color function, see below.
- function whose first argument expects integer number of colors to return, for example col=viridisLite::viridis defines the function itself as input.
- function derived from circlize::colorRamp2(), recognized by having attribute names "breaks" and "colors". Note that only the colors are used for the individual color values, not the break points.

n — integer number of output colors to return, or NULL if the output should be a color function in the form function(n) which returns n colors.

trimRamp — integer vector, expanded to length=2 as needed, which defines the number of colors to trim from the beginning and end of the color vector, respectively. When reverseRamp=TRUE, the colors are reversed before the trimming is applied. If the two trimRamp values are not identical, symmetric divergent color scales will no longer be symmetric.

gradientN — integer number of colors to expand gradient colors prior to trimming colors.

defaultBaseColor — character vector indicating a color from which to begin a color gradient, only used when col is a single color.

reverseRamp — logical indicating whether to reverse the resulting color ramp. This value is ignored when a single value is supplied for col, and where "_r" or "_rev" is detected as a substring at the end of the character value.

alpha — logical indicating whether to honor alpha transparency whenever colorRampPalette is called. If colors contain no alpha transparency, this setting has no effect, otherwise the alpha value is applied by grDevices::colorRampPalette() using a linear gradient between each color.

gradientWtFactor — numeric value used to expand single color input to a gradient, using color2gradient(), prior to making a full gradient to the defaultBaseColor. Note that dex is the preferred method for adjusting the range of light to dark for the given color col.

dex — numeric darkness expansion factor, used only with input col is a single color, which is then split into a color gradient using defaultBaseColor by calling color2gradient(). The dex factor adjusts the range of dark to light colors, where higher values for dex increase the range, making the changes more dramatic.

lens, divergent — arguments sent to warpRamp() to apply a warp effect to the color ramp, to compress or expand the color gradient: lens scales the warp effect, with positive values compressing colors toward baseline and negative values expanding colors near baseline; divergent is a logical indicating whether the middle color is considered the baseline.

verbose — logical whether to print verbose output

... — additional arguments are ignored.

Details

This function accepts a color ramp name, a single color, a vector of colors, or a function names, and returns a simple vector of colors of the appropriate length, suitable as input to a number of plotting functions.

When n is NULL, this function returns a color function, wrapped by grDevices::colorRampPalette(). The colors used are defined by gradientN, so the grDevices::colorRampPalette() function actually uses a starting palette of gradientN number of colors.

When n is an integer greater than 0, this function returns a vector of colors with length n.

When col is a single color value, a color gradient is created by appending defaultColorBase to the output of color2gradient(..., n=3, gradientWtFactor=gradientWtFactor). These 4 colors are used as the internal palette before applying grDevices::colorRampPalette() as appropriate. In this case, gradientWtFactor is used to adjust the strength of the color gradient. The intended use is: getColorRamp("red", n=5). To remove the leading white color, use getColorRamp("red", n=5, trimRamp=c(1,0)).

When col contains multiple color values, they are used to define a color ramp directly.

When col is not a color value, it is compared to known color palettes from RColorBrewer::RColorBrewer and viridisLite, and will use the corresponding color function or color palette.

When col refers to a color palette, the suffix "_r" may be used to reverse the colors. For example, getColorRamp(col="RdBu_r", n=9) will recognize the RColorBrewer color palette "RdBu", and will reverse the colors to return blue to red, more suitable for heatmaps where high values associated with heat are colored red, and low values associated with cold are colored blue.

The argument reverseRamp=TRUE may be used to reverse the returned colors.

Color functions from viridisLite are recognized: "viridis", "cividis", "inferno", "magma", "plasma".

The argument trimRamp is used to trim colors from the beginning and end of a color ramp, respectively. This mechanism is useful to remove the first or last color when those colors may be too extreme. Note that internally, colors are expanded to length gradientN, then trimmed, then the corresponding n colors are returned.

The trimRamp argument is also useful when returning a color function, which occurs when n=NULL. In this case, colors are expanded to length gradientN, then are trimmed using the values from trimRamp, then the returned function can be used to create a color ramp of arbitrary length.

Note that when reverseRamp=TRUE, colors are reversed before trimRamp is applied.

By default, alpha transparency will be maintained if supplied in the input color vector. Most color ramps have no transparency, in which case transparency can be added after the fact using alpha2col().

Value

character vector of R colors, or when N is NULL, function sufficient to create R colors.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), hcl2col(), hsl2col(), hsv2col(),

isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
# get a gradient using red4
red4 <- getColorRamp("red4");
showColors(getColorRamp(red4));

# make a custom gradient
BuOr <- getColorRamp(c("dodgerblue","grey10","orange"));
showColors(BuOr);
colorList <- list(red4=red4, BuOr=BuOr);

# From RColorBrewer use a brewer name
RdBu <- getColorRamp("RdBu");
RdBu_r <- getColorRamp("RdBu_r");
colorList <- c(colorList, list(RdBu=RdBu, RdBu_r=RdBu_r));
showColors(RdBu);

if (requireNamespace("viridisLite", quietly=TRUE)) {
   viridisV <- getColorRamp("viridis");
   colorList <- c(colorList, list(viridis=viridisV));
}

# for fun, put a few color ramps onto one plot
showColors(colorList, cexCellnote=0.7);

showColors(list(`white background\ncolor='red'`=getColorRamp("red"),
   `black background\ncolor='red'`=getColorRamp("red", defaultBaseColor="black"),
   `white background\ncolor='gold'`=getColorRamp("gold"),
   `black background\ncolor='gold'`=getColorRamp("gold", defaultBaseColor="black")))
```

---

getDate *get simple date string*

Description

get simple date string in the format DDmonYYYY such as 17jul2018.

Usage

```
getDate(t = Sys.time(), trim = TRUE, dateFormat = "%d%b%Y", ...)
```

Arguments

t	current time in an appropriate class such as "POSIXct" or "POSIXt". The default is output of Sys.time().

`trim`	`logical` whether to trim the output of `format()` in the event that multiple values are sent for argument `t`.
`dateFormat`	`character` string representing the recognized date format, by default `"DDmmmYYYY"`, which recognizes `"23aug2007"`.
`...`	additional parameters sent to `format()`.

Details

Gets the current date in a simplified text string. Use `asDate()` to convert back to Date object.

Value

`character` vector with simplified date string

See Also

Other jam date functions: `asDate()`, `dateToDaysOld()`

Examples

```
getDate();
```

`getPlotAspect` *Get aspect ratio for coordinates, plot, or device*

Description

Get aspect ratio for coordinates, plot, or device

Usage

```
getPlotAspect(
  type = c("coords", "plot", "device"),
  parUsr = graphics::par("usr"),
  parPin = graphics::par("pin"),
  parDin = graphics::par("din"),
  ...
)
```

Arguments

`type`	`character` type of aspect ratio to calculate.
	"coords" calculates plot coordinate aspect ratio, which is helpful for creating proper circular shapes, for example, where the x-axis and y-axis ranges are very different. Note that this calculation does also correct for margin sizes.

"plot" calculates plot aspect ratio, based upon the actual size of the plot, independent of the numeric coordinate range of the plot. This aspect ratio reflects the relative visual height and width of the plot area, ignoring margins.

"device" calculates plot aspect ratio, based upon the complete graphical device, i.e. the full space including all panels, margins, and plot areas.

`parUsr`, `parPin`, `parDin`
: `numeric` values equivalent to their respective `graphics::par()` output, from `graphics::par("usr")`, `graphics::par("pin")`, and `graphics::par("din")`. Values can be supplied directly, which among other things, prevents opening a graphical device if one is not already opened. Any call to `graphics::par()` will otherwise cause a graphic device to be opened, which may not be desired on a headless R server.

`...`
: additional parameters are ignored.

Value

`numeric` plot aspect ratio for a plot device, of the requested type, see the `type` argument.

See Also

Other jam plot functions: `adjustAxisLabelMargins()`, `coordPresets()`, `decideMfrow()`, `drawLabels()`, `groupedAxis()`, `imageByColors()`, `imageDefault()`, `minorLogTicksAxis()`, `nullPlot()`, `plotPolygonDensity()`, `plotRidges()`, `plotSmoothScatter()`, `shadowText()`, `shadowText_options()`, `showColors()`, `sqrtAxis()`, `usrBox()`

Examples

```
withr::with_par(list("mfrow"=c(2, 4), "mar"=c(1, 1, 1, 1)), {
for (i in 1:8) {
   nullPlot(plotAreaTitle=paste("Plot", i), xlim=c(1,100), ylim=c(1,10),
      doMargins=FALSE);
   graphics::axis(1, las=2);
   graphics::axis(2, las=2);
}
# device aspect inside the 2x4 layout
getPlotAspect("plot");
})
# device aspect outside the 2x4 layout
getPlotAspect("plot");
```

---

grepls *Search for objects in the environment*

Description

Search for objects in the environment

Usage

```
grepls(
  x,
  where = "all",
  ignore.case = TRUE,
  searchNames = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

x	character string used as a grep pattern
where	character string compatible with base::ls() or if installed, AnnotationDbi::ls(). A special value "all" will search all environments on the search path base::search() in order.
ignore.case	logical indicating whether the pattern match is case-insensitive.
searchNames	logical indicating whether names should also be searched, which is only relevant for AnnDb objects, for example org.Mm.egSYMBOL2EG from the org.Mm.eg.db Bioconductor package.
verbose	logical indicating whether to print verbose output.
...	additional parameters are ignored.

Details

This function searches the active R environment for an object name using vigrep() (value, case-insensitive grep). It is helpful when trying to find an object using a substring, for example grepls("statshits").

Value

character vector of matching object names, or if where="all" it returns a named list whose names indicate the search environment name, and whose entries are matching object names within each environment.

See Also

Other jam grep functions: igrep(), igrepHas(), igrepl(), provigrep(), unigrep(), unvigrep(), vgrep(), vigrep()

Examples

```
# Find all objects named "grep", which should find
# base grep() and jamba::vigrep() among other results.
grepls("grep");

# Find objects in the local environment
allStatsHits <- c(1:12);
someStatsHits <- c(1:3);
```

```
grepls("statshits");
# shortcut way to search only the .GlobalEnv, the active local environment
grepls("statshits", 1);

# return objects with "raw" in the name
grepls("raw");

# Require "Raw" to be case-sensitive
grepls("Raw", ignore.case=FALSE)
```

`groupedAxis` *Draw grouped axis labels*

Description

Draw grouped axis labels given a character vector.

Usage

```
groupedAxis(
  side = 1,
  x,
  group_style = c("partial_grouped", "grouped", "centered"),
  las = 2,
  returnFractions = TRUE,
  nudge = 0.2,
  do_abline = FALSE,
  abline_lty = "solid",
  abline_col = "grey40",
  do_plot = TRUE,
  ...
)
```

Arguments

`side`	`integer` indicating the axis side, passed to `graphics::axis()`. 1=bottom, 2=left, 3=top, 4=right.
`x`	`character` vector of axis labels
`group_style`	`character` string indicating the style of label: • `"partial_grouped"` - uses square bracket to bound 2+ repeated entries, and single line tick mark for non-repeated entries. • `"grouped"` - uses square bracket to bound each set of repeated entries including non-repeated entries. • `"centered"` - only labels the center of each group of repeated entries with no bracket bounding the entries.

las	integer indicating whether labels should be perpendicular, see graphics::par("las").
returnFractions	logical passed to breaksByVector() to calculate label positions. Set returnFractions=FALSE and all labels will only appear at integer locations on the axis.
nudge	numeric adjustment for labels away from the plot border.
do_abline	logical indicating whether to draw graphics::abline() lines inside the plot to indicate the exact breakpoints between each group of labels.
abline_lty	line type compatible with graphics::par("lty"), used when do_abline=TRUE.
abline_col	character color used when do_abline=TRUE.
do_plot	logical whether to plot the resulting axis, as an option to suppress the output and do something else with the data.frame of coordinates returned by this function.
...	additional arguments are passed to breaksByVector(), and/or to graphics::axis().

Details

This function extends breaksByVector() specifically for axis labels. It is intended where character labels are spaced at integer steps, and some labels are expected to be repeated.

Value

data.frame invisibly, which contains the relevant axis coordinates, labels, and whether the coordinate should appear with a tick mark.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
withr::with_par(list("mar"=c(4,4,6,6)), {
b <- rep(LETTERS[1:5], c(2,3,5,4,3));
b2 <- c(b[1:2], makeNames(b[3:5]), b[6:16]);
nullPlot(doBoxes=FALSE,
   doUsrBox=TRUE,
   xlim=c(0,18),
   ylim=c(0,18));

groupedAxis(1, b);
groupedAxis(2, b, group_style="grouped");
groupedAxis(2, b, group_style="centered");
groupedAxis(3, b2, do_abline=TRUE);
groupedAxis(4, b2, group_style="grouped");
graphics::mtext(side=1, "group_style='partial_grouped'", line=2, las=0);
graphics::mtext(side=2, "group_style='grouped'", line=2, las=0);
graphics::mtext(side=3, "group_style='partial_grouped'", line=2, las=0);
```

```
graphics::mtext(side=4, "group_style='grouped'", line=2, las=0);
})
```

---

gsubOrdered *Global substitution into ordered factor*

Description

Global substitution into ordered factor

Usage

```
gsubOrdered(
  pattern,
  replacement,
  x,
  ignore.case = FALSE,
  perl = FALSE,
  fixed = FALSE,
  useBytes = FALSE,
  sortFunc = mixedSort,
  ...
)
```

Arguments

pattern, replacement, x, ignore.case, perl, fixed, useBytes	arguments sent to base::gsub()
sortFunc	function used to sort factor levels, which is not performed if the input x is a factor.
...	additional arguments are passed to sortFunc

Details

This function is an extension of base::gsub() that returns an ordered factor output. When input is also a factor, the output factor levels are retained in the same order, after applying the string substitution.

This function is very useful when making changes via base::gsub() to a factor with ordered levels, because it retains the the order of levels after modification.

Tips:

- To convert a character vector to a factor, whose levels are sorted, use sortFunc=sort.
- To convert a character vector to a factor, whose levels are the order they appear in the input x, use sortFunc=c.
- To convert a character vector to a factor, whose levels are sorted alphanumerically, use sortFunc=mixedSort.

Value

factor whose levels are based upon the order of input levels when the input x is a factor; or if the input x is not a factor, it is converted to a factor using the provided sort function sortFunc.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubs(), makeNames(), nameVector(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
x <- c(paste0(
   rep(c("first", "second", "third"), 2),
   rep(c("Section", "Choice"), each=3)),
   "Choice");
f <- factor(x, levels=x);
f;

# default gsub() will return a character vector
gsub("(first|second|third)", "", f)
# converting to factor resets the factor level order
factor(gsub("(first|second|third)", "", f))

## gsubOrdered() maintains the factor level order
gsubOrdered("(first|third)", "", f)
gsubOrdered("(first)", "", f)

# to convert character vector to factor, levels in order they appear
gsubOrdered("", "", x, sortFunc=c)

# to convert character vector to factor, levels alphanumeric sorted
gsubOrdered("", "", x, sortFunc=mixedSort)
```

---

gsubs *Pattern replacement with multiple patterns*

Description

Pattern replacement with multiple patterns

Usage

```
gsubs(
  pattern,
  replacement,
  x,
  ignore.case = TRUE,
```

```
  replaceMultiple = rep(TRUE, length(pattern)),
  ...
)
```

Arguments

pattern	character vector of patterns
replacement	character vector of replacements
x	character vector with input data to be curated
ignore.case	logical indicating whether to perform pattern matching in case-insensitive manner, where ignore.case=TRUE will ignore the uppercase/lowercase distinction.
replaceMultiple	logical vector indicating whether to perform global substitution, where replaceMultiple=FALSE will only replace the first occurrence of the pattern, using base::sub(). Note that this vector can refer to individual entries in pattern.
...	additional arguments are passed to base::gsub() or base::sub().

Details

This function is a simple wrapper around base::gsub() when considering a series of pattern-replacement combinations. It applies each pattern match and replacement in order and is therefore not vectorized.

When x input is a list each vector in the list is processed, somewhat differently than processing one vector.

1. When the list contains another list, or when length(x) < 100, each value in x is iterated calling gsubs(). This process is the slowest option, however not noticeble until x has length over 10,000.
2. When the list does not contain another list and all values are non-factor, or all values are factor, they are unlisted, processed as a vector, then relisted. This process is nearly the same speed as processing one single vector, except the time it takes to confirm the list element classes.
3. When values contain a mix of non-factor and factor values, they are separately unlisted, processed by gsubs(), then relisted and combined afterward. Again, this process is only slightly slower than option 2 above, given that it calls gsubs() twice, with two vectors.
4. Note that factor values at input are replaced with character values at output, consistent with gsub().

Value

character vector when input x is an atomic vector, or list when input x is a list.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), makeNames(), nameVector(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
gsubs(c("one", "two"), c("three", "four"), "one two five six")
gsubs(c("one", "two"), c("three"), "one two five six")
```

`handleArgsText` *Handle function arguments as text*

Description

Handles a list or list of lists, converting to human-readable text format

Usage

```
handleArgsText(
  argTextA,
  name = "",
  col1 = "mediumpurple2",
  col2 = "mediumaquamarine",
  colT = "dodgerblue3",
  colF = "red1",
  colNULL = "grey60",
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  adjustRgb = getOption("jam.adjustRgb"),
  indent = "",
  useCollapseList = ",\n      ",
  useCollapseBase = ", ",
  level = 1,
  debug = 0,
  useColor = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

`argTextA`	object passed by `jargs()` when iteratively parsing function argument values.
`name`	`character` name of the argument.
`col1`, `col2`, `colT`, `colF`, `colNULL`	`character` colors used as defaults for first and second arguments, TRUE, FALSE, NULL, respectively.
`lightMode`	`logical` or `NULL`, indicating whether the text background color is light, thus imposing a maximum brightness for colors displayed. It use lightMode if defined by the function caller, otherwise it will use `getOption("jam.lightMode")`

	if defined, lastly it will attempt to detect whether running inside Rstudio by checking the environment variable "RSTUDIO", and if so it will assume lightMode==TRUE.
Crange	numeric range of chroma values, ranging between 0 and 100. When NULL, default values will be assigned to Crange by setCLranges().
Lrange	numeric range of luminance values, ranging between 0 and 100. When NULL, default values will be assigned to Lrange by setCLranges().
adjustRgb	numeric value adjustment used during the conversion of RGB colors to ANSI colors, which is inherently lossy. If not defined, it uses the default returned by setCLranges() which itself uses getOption("jam.adjustRgb") with default=0. In order to boost color contrast, an alternate value of -0.1 is suggested.
indent	character string used as a prefix in output to help apply text indent.
useCollapseList	character string inserted between multiple values to split list entries across multiple lines.
useCollapseBase	character string used to separate multiple values in a vector which is not split across multiple lines.
level	integer indicating the level of depth in iterative parsing.
debug	integer value, greater than 0 will cause debug-type verbose output, useful because parameters are hard!
useColor	logical whether to display results in color, if the crayon package is available, and terminal console is capable.
verbose	logical whether to print verbose output.
...	Additional arguments are ignored.

Details

This function is a rare non-exported function intended to be called by jargs(), but separated in order to help isolate the logical steps required.

Value

character vector including ANSI coloring when available.

See Also

Other jam internal functions: jamCalcDensity(), make_html_styles(), make_styles(), smoothScatterJam()

Examples

```
cat(paste0(handleArgsText(formals(graphics::hist.default)), "\n"), sep="")
```

`hcl2col` *convert HCL to R color*

Description

Convert an HCL color matrix to vector of R hex colors

Usage

```
hcl2col(
  x = NULL,
  H = NULL,
  C = NULL,
  L = NULL,
  ceiling = 255,
  maxColorValue = 255,
  alpha = NULL,
  fixup = TRUE,
  model = getOption("jam.model", c("hcl", "polarLUV", "polarLAB")),
  verbose = FALSE,
  ...
)
```

Arguments

`x`	matrix of colors, with rownames `"H"`, `"C"`, `"L"`, or if not supplied it looks for vectors `H`, `C`, and `L` accordingly. It can alternatively be supplied as an object of class `polarLUV`.
`H`, `C`, `L`	numeric vectors supplied as an alternative to `x`, with ranges 0 to 360, 0 to 100, and 0 to 100, respectively.
`ceiling`	numeric value indicating the maximum values allowed for `R`, `G`, and `B` after conversion by `colorspace::as(x, "RGB")`. This ceiling is applied after the `maxColorValue` is used to scale numeric values, and is intended to correct for the occurrence of values above 255, which would be outside the typical color gamut allowed for RGB colors used in R. In general, this value should not be modified.
`maxColorValue`	numeric value indicating the maximum RGB values, typically scaling values to a range of 0 to 255, from the default returned range of 0 to 1. In general, this value should not be modified.
`alpha`	optional vector of alpha values. If not supplied, and if `x` is supplied as a matrix with rowname `"alpha"`, then values will be used from `x["alpha",]`.
`fixup`	boolean indicating whether to use `colorspace::hex(...,fixup=TRUE)` for conversion to R hex colors, **which is not recommended** since this conversion applies some unknown non-linear transformation for colors outside the color gamut. It is here is an option for comparison, and if specifically needed.

model	character string indicating the color model to use: • hcl (default) uses farver • polarLUV uses colorspace polarLUV • polarLAB uses 'colorspace polarLAB
verbose	logical whether to print verbose output.
...	other arguments are ignored.

Details

This function takes an HCL matrix,and converts to an R color using the colorspace package colorspace::polarLUV() and colorspace::hex().

When model="hcl" this function uses farver::encode_colour() and bypasses colorspace. In future the colorspace dependency will likely be removed in favor of using farver. In any event, model="hcl" is equivalent to using model="polarLUV" and fixup=TRUE, except that it should be much faster.

Value

vector of R colors, or where the input was NA, then NA values are returned in the same order.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
# Prepare a basic HCL matrix
hclM <- col2hcl(c(red="red",
   blue="blue",
   yellow="yellow",
   orange="#FFAA0066"));
hclM;

# Now convert back to R hex colors
colorV <- hcl2col(hclM);
colorV;

showColors(colorV);
```

heads *Apply head() across each element in a list of vectors*

Description

Apply head() across each element in a list of vectors

Usage

```
heads(x, n = 6, ...)
```

Arguments

x	`list` of atomic vectors, assumed to be the same atomic type.
n	`integer` maximum number of items to include from each element in the list `x`. When `n` contains multiple values, they are recycled to `length(x)` and applied to each list element in order.
...	additional arguments are passed to `utils::head()`.

Details

Note that this function currently only operates on a list of vectors. This function is notably faster than `lapply(x, head, n)` because it operates on the entire vector in one step.

Also the input `n` can be a vector so that each element in the list has a specific number of items returned.

Value

`list` with at most `n` elements per vector.

See Also

Other jam list functions: `cPaste()`, `jam_rapply()`, `list2df()`, `mergeAllXY()`, `mixedSorts()`, `rbindList()`, `relist_named()`, `rlengths()`, `sclass()`, `sdim()`, `uniques()`, `unnestList()`

Examples

```
l <- list(a=1:10, b=2:5, c=NULL, d=1:100);
heads(l, 1);

heads(l, 2);

heads(l, n=c(2, 1, 3, 5))
```

heatmap_column_order *Return Heatmap column order from ComplexHeatmap heatmap object*

Description

Return Heatmap column order from ComplexHeatmap heatmap object

Usage

```
heatmap_column_order(hm, which_heatmap = NULL)
```

Arguments

hm	Heatmap or HeatmapList object as defined by the Bioconductor package via ComplexHeatmap::Heatmap().
which_heatmap	used to specify a specific heatmap with hm is provided as a HeatmapList. When NULL (default) the first heatmap in hm@ht_list is used. When one value is supplied, only that heatmap is used. When multiple values are supplied, a list is returned. Input can be either: • numeric - indicating the heatmap number in hm@ht_list • character - indicating the heatmap name seen in names(hm@ht_list)

Details

This function is a helpful utility to return the fully qualified list of colnames in a ComplexHeatmap::Heatmap object.

The core intention is for the output to be usable with the original data matrix used in the heatmap. Therefore, the vector values are colnames() when present, or integer column index values when there are no colnames(). If heatmap column_labels are defined, they are returned as names().

Note that names() are assigned inside try() to allow the case where column_labels, or column_title labels cannot be coerced to character values, for example using gridtext for markdown formatting.

Value

output depends upon the heatmap:

- When heatmap columns are grouped using column_split, and when the data matrix contains colnames, returns a character vector of colnames in the order they appear in the heatmap. When there are no colnames, integer column index values are returned. If the heatmap has column labels, they are returned as vector names.
- When columns are grouped using column_split, it returns a list of vectors as described above. The list is named using the column_title labels only when there is an equal number of column labels.

See Also

Other jam heatmap functions: cell_fun_label(), heatmap_row_order()

Examples

```
if (check_pkg_installed("ComplexHeatmap")) {
   set.seed(123);

   mat <- matrix(stats::rnorm(18 * 24),
      ncol=24);
   rownames(mat) <- paste0("row", seq_len(18))
   colnames(mat) <- paste0("column", seq_len(24))

   # obtaining row order first causes a warning message
   hm1 <- ComplexHeatmap::Heatmap(mat);

   # best practice is to draw() and store output in an object
   # to ensure the row orders are absolutely fixed
   hm1_drawn <- ComplexHeatmap::draw(hm1);
   print(heatmap_row_order(hm1_drawn))
   print(heatmap_column_order(hm1_drawn))

   # row and column split
   hm1_split <- ComplexHeatmap::Heatmap(mat,
      column_split=3, row_split=3, border=TRUE);
   hm1_split_drawn <- ComplexHeatmap::draw(hm1_split);
   print(heatmap_row_order(hm1_split_drawn))
   print(heatmap_column_order(hm1_split_drawn))

   # display two heatmaps side-by-side
   mat2 <- mat + stats::rnorm(18*24);
   hm2 <- ComplexHeatmap::Heatmap(mat2, border=TRUE, row_split=4);

   hm1hm2_drawn <- ComplexHeatmap::draw(hm1_split + hm2,
      ht_gap=grid::unit(1, "cm"));
   print(heatmap_row_order(hm1hm2_drawn))
   print(heatmap_row_order(hm1hm2_drawn, which_heatmap=2))
   # by default the order uses the first heatmap
   print(heatmap_column_order(hm1hm2_drawn))
   # the second heatmap can be returned
   print(heatmap_column_order(hm1hm2_drawn, which_heatmap=2))
   # or a list of heatmap orders can be returned
   print(heatmap_column_order(hm1hm2_drawn, which_heatmap=1:2))

   # stacked vertical heatmaps
   hm1hm2_drawn_tall <- ComplexHeatmap::draw(
      ComplexHeatmap::`%v%`(hm1_split, hm2),
      ht_gap=grid::unit(1, "cm"));
   print(heatmap_row_order(hm1hm2_drawn))
   print(heatmap_row_order(hm1hm2_drawn, which_heatmap=2))
   print(heatmap_row_order(hm1hm2_drawn, which_heatmap=1:2))
   print(heatmap_row_order(hm1hm2_drawn,
```

```
      which_heatmap=names(hm1hm2_drawn@ht_list)))

   # annotation heatmap
   ha <- ComplexHeatmap::rowAnnotation(left=rownames(mat))
   ha_drawn <- ComplexHeatmap::draw(ha + hm1)
   print(sdim(ha_drawn@ht_list))
   print(heatmap_row_order(ha_drawn))
   print(heatmap_column_order(ha_drawn))

   # stacked vertical heatmaps with top annotation
   ta <- ComplexHeatmap::HeatmapAnnotation(top=colnames(mat))
   hm1_ha <- ComplexHeatmap::Heatmap(mat,
      left_annotation=ha,
      column_split=3, row_split=3, border=TRUE);
   hm1hm2_drawn_tall <- ComplexHeatmap::draw(
      ComplexHeatmap::`%v%`(ta,
         ComplexHeatmap::`%v%`(hm1_ha, hm2)),
      ht_gap=grid::unit(1, "cm"));
   print(sdim(hm1hm2_drawn_tall@ht_list))
   print(heatmap_row_order(hm1hm2_drawn_tall))
   print(heatmap_row_order(hm1hm2_drawn_tall, 2))
}
```

`heatmap_row_order` *Return Heatmap row order from ComplexHeatmap heatmap object*

Description

Return Heatmap row order from ComplexHeatmap heatmap object

Usage

```
heatmap_row_order(hm, which_heatmap = NULL)
```

Arguments

`hm`	`Heatmap` or `HeatmapList` object as defined by the Bioconductor package via `ComplexHeatmap::Heatmap()`.
`which_heatmap`	`integer`, default NULL, used when the input is a `HeatmapList` with multiple heatmaps.

Details

This function is a helpful utility to return the fully qualified list of rownames in a `ComplexHeatmap::Heatmap` object.

The core intention is for the output to be usable with the original data matrix used in the heatmap. Therefore, the vector values are `rownames()` when present, or `integer` row index values when there are no `rownames()`. If heatmap `row_labels` are defined, they are returned as `names()`.

Note that `names()` are assigned inside `try()` to allow the case where `row_labels`, or `row_title` labels cannot be coerced to `character` values, for example using `gridtext` for markdown formatting.

Final note: It is best practice to draw the heatmap first with `ComplexHeatmap::draw()` then store the output in a new object. This step creates the definitive clustering and therefore the row order is absolutely final, not subject to potential randomness during clustering.

Value

output depends upon the heatmap:

- When heatmap rows are grouped using `row_split`, and when the data matrix contains rownames, returns a `character` vector of rownames in the order they appear in the heatmap. When there are no rownames, `integer` row index values are returned. If the heatmap has row labels, they are returned as vector names.
- When rows are grouped using `row_split`, it returns a `list` of vectors as described above. The `list` is named using the `row_title` labels only when there is an equal number of row labels.

See Also

Other jam heatmap functions: `cell_fun_label()`, `heatmap_column_order()`

Examples

```
# See heatmap_column_order() for examples
```

`hsl2col` *convert HCL to R color*

Description

Convert an HCL color matrix to vector of R hex colors

Usage

```
hsl2col(
  x = NULL,
  H = NULL,
  S = NULL,
  L = NULL,
  alpha = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric matrix of colors, with rownames "H", "S", "L", or if not supplied it looks for vectors H, S, and L accordingly.
H, S, L	numeric vectors supplied as an alternative to x, with ranges 0 to 360, 0 to 100, and 0 to 100, respectively.
alpha	numeric vector of alpha values, default NULL. If not supplied, and if x is supplied as a matrix with rowname "alpha", then values will be used from x["alpha",].
verbose	logical indicating whether to print verbose output.
...	other arguments are ignored.

Details

This function takes an HCL matrix,and converts to an R color using the colorspace package `colorspace::polarLUV()` and `colorspace::hex()`.

When `model="hcl"` this function uses `farver::encode_colour()` and bypasses `colorspace`. In future the `colorspace` dependency will likely be removed in favor of using `farver`. In any event, `model="hcl"` is equivalent to using `model="polarLUV"` and `fixup=TRUE`, except that it should be much faster.

Value

vector of R colors, or where the input was NA, then NA values are returned in the same order.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
# See col2hcl() for more extensive examples

# Prepare a basic HSL matrix
x_colors <- c(red="red",
   blue="blue",
   yellow="yellow",
   orange="#FFAA0066");
hslM <- col2hsl(x_colors);
hslM;

# Now convert back to R hex colors
colorV <- hsl2col(hslM);
colorV;

showColors(list(x_colors=x_colors,
   colorV=nameVector(colorV)));
```

hsv2col *Convert HSV matrix to R color*

Description

Converts a HSV color matrix to R hex color

Usage

```
hsv2col(hsvValue, ...)
```

Arguments

hsvValue	numeric HSV matrix, with rownames c("h","s","v") in any order, and optionally "alpha" rowname for alpha transparency.
...	additional arguments are ignored.

Details

This function augments the grDevices::hsv() function in that it handles output from grDevices::rgb2hsv() or col2hsv(), sufficient to run a series of conversion functions, e.g. hsv2col(col2hsv("red")). This function also maintains alpha transparency, which is not maintained by the grDevices::hsv() function.

Value

character vector of R colors.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
# start with a color vector
# red and blue with partial transparency
colorV <- c("#FF000055", "#00339999");

# confirm the hsv matrix maintains transparency
col2hsv(colorV);

# convert back to the original color
hsv2col(col2hsv(colorV));
```

igrep *case-insensitive grep*

Description

case-insensitive grep

Usage

```
igrep(..., ignore.case = TRUE)
```

Arguments

`...`, `ignore.case`
: parameters sent to `base::grep()`

Details

This function is a simple wrapper around `base::grep()` which runs in case-insensitive mode. It is mainly used to save keystrokes, but is consistently named alongside `vgrep` and `vigrep`.

Value

vector of matching indices

See Also

Other jam grep functions: `grepls()`, `igrepHas()`, `igrepl()`, `provigrep()`, `unigrep()`, `unvigrep()`, `vgrep()`, `vigrep()`

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
igrep("D", V);
igrep("d", V);
vigrep("d", V);
```

igrepHas *vector contains any case-insensitive grep match*

Description

vector contains any case-insensitive grep match

Usage

```
igrepHas(
  pattern,
  x = NULL,
  ignore.case = TRUE,
  minCount = 1,
  naToBlank = FALSE,
  ...
)
```

Arguments

pattern	the grep pattern to use with base::grep()
x	vector to use in the grep
ignore.case	logical default TRUE, meaning the grep will be performed in case-insensitive mode.
minCount	integer minimum number of matches required to return TRUE.
naToBlank	logical whether to convert NA to blank, instead of allowing grep to handle NA values as-is.
...	additional arguments are ignored.

Details

This function checks the input vector for any elements matching the grep pattern. The grep is performed case-insensitive (igrep). This function is particularly useful when checking function arguments or object class, where the class(a) might return multiple values, or where the name of the class might be slightly different than expected, e.g. data.frame, data_frame, DataFrame.

Value

logical indicating whether the grep match criteria were met, TRUE indicates the grep pattern was present in minCount or more number of entries.

See Also

base::grep()

Other jam grep functions: grepls(), igrep(), igrepl(), provigrep(), unigrep(), unvigrep(), vgrep(), vigrep()

Examples

```
a <- c("data.frame","data_frame","tibble","tbl");
igrepHas("Data.*Frame", a);
igrepHas("matrix", a);
```

`igrepl` *case-insensitive logical grepl*

Description

case-insensitive logical grepl

Usage

```
igrepl(..., ignore.case = TRUE)
```

Arguments

`...`, `ignore.case`
: parameters sent to `base::grep()`

Details

This function is a simple wrapper around `base::grepl()` which runs in case-insensitive mode simply by adding default `ignore.case=TRUE`. It is mainly used for convenience.

Value

`logical` vector indicating pattern match

See Also

Other jam grep functions: `grepls()`, `igrep()`, `igrepHas()`, `provigrep()`, `unigrep()`, `unvigrep()`, `vgrep()`, `vigrep()`

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
ig1 <- grepl("D", V);
ig2 <- igrepl("D", V);
ig3 <- grepl("d", V);
ig4 <- igrepl("d", V);
data.frame(V,
   grepl_D=ig1,
   grepl_d=ig3,
   igrepl_D=ig2,
   igrepl_d=ig4);
```

imageByColors *Display color raster image using a matrix of colors*

Description

Display color raster image using a matrix of colors

Usage

```
imageByColors(
  x,
  useRaster = FALSE,
  fixRasterRatio = TRUE,
  maxRatioFix = 100,
  xaxt = "s",
  yaxt = "s",
  doPlot = TRUE,
  cellnote = NULL,
  cexCellnote = 1,
  srtCellnote = 0,
  fontCellnote = 1,
  groupCellnotes = TRUE,
  groupBy = c("column", "row"),
  groupByColors = TRUE,
  adjBy = c("column", "row"),
  adjustMargins = FALSE,
  interpolate = getOption("interpolate", TRUE),
  verbose = FALSE,
  xpd = NULL,
  bty = graphics::par("bty"),
  flip = c("none", "y", "x", "xy"),
  keepTextAlpha = FALSE,
  doTest = FALSE,
  add = FALSE,
  ...
)
```

Arguments

x	matrix or data.frame containing colors
useRaster	logical sent to imageDefault to enable raster rendering, as opposed to polygon rendering. This parameter is highly recommended when the matrix is large (>50 columns or rows).
fixRasterRatio	logical sent to imageDefault.
maxRatioFix	numeric sent to imageDefault.

xaxt, yaxt
: character values compatible with par to determine whether x- and y-axes are plotted. Set both to "n" to suppress display of axes.

doPlot
: logical whether to create a plot, or simply return data which would have been used to create the plot.

cellnote
: matrix or data.frame of labels to be displayed on the image. If groupCellnotes==TRUE labels will be placed in the center of consecutive cells with the same label and identical color. Currently, cell text is colored using setTextContrastColor which uses either white or black depending upon the brightness of the background color.

cexCellnote, srtCellnote, fontCellnote
: numeric vectors, with values applied to cellnote text to be compatible with graphics::par("cex"), graphics::par("srt"), and graphics::par("font"), respectively. If supplied a matrix or data.frame with it is used as-is or expanded to equivalent dimensions of x. If the vector is named by colnames(x) then it is applied by column in order, otherwise it is applied by row, with values recycled to the number of columns or rows, respectively. Note cexCellnote can also be a list, with the list elements being applied to individual cells in order. If the list is named by colnames(x), each list element is applied to values in each column, in order. In future this parameter may also accept a matrix of cex values as input. Final note: values are applied to each cell, but when cell labels are combined with groupCellnotes==TRUE, the value for the first matching cell is used. Remember that values are placed by coordinate, bottom-to-top on the y-axis, and left-to-right on the x-axis.

groupCellnotes
: logical whether to group labels where consecutive cells contain the same label and identical cell colors, thus only displaying one label in the center of these groups.

groupBy
: character value indicating the direction to group cellnotes, when groupCellnotes=TRUE: "row" will group cellnote values by row; "column" will group cellnote values by column. By default, it will first group cellnotes by "row" then by "column".

groupByColors
: logical indicating whether the cellnote grouping should also include the cell color. When groupByColors=FALSE, cellnote values will be grouped together regardless whether the underlying colors change, which may be preferred when applying text label to topographical data.

adjBy
: character value indicating how to apply adjustments for cexCellnote, srtCellnote, and fontCellnote, as described above.

adjustMargins
: logical indicating whether to adjust the axis label margins to ensure enough room to draw the text rownames and colnames.

interpolate
: logical whether to implement image interpolation, by default TRUE when useRaster=TRUE.

verbose
: logical whether to print verbose output.

xpd
: NULL or logical used for graphics::par("xpd") whether to crop displayed output to the plot area.

  - If xpd=NULL then graphics::par("xpd") will not be modified, otherwise graphics::par("xpd"=xpd) will be defined while adding any cell notes, then reverted to its previous value afterward. This parameter is

mainly useful when cellnote labels may overhang the plot space, and would be cropped and not visible if `graphics::par("xpd"=TRUE)`.

`bty` `character` used to control box type, default `graphics::par("bty")`

`flip` `character` string, default "none", with optional axis flip:

- none: perform no axis flip
- x: flip x-axis orientation
- y: flip y-axis orientation
- xy: flip both x- and y-axis orientation

`keepTextAlpha` `logical` defaulit FALSE, passed to `setTextContrastColor()`, whether the text label color should inherit the alpha transparency from the background color. If TRUE then fully transparent background colors will not have a visible label.

`doTest` `logical` whether to run a test showing basic features.

`add` `logical`, default FALSE, whether to add to an existing device, otherwise it creates a new plot.

`...` Additional arguments are ignored.

Details

This function is similar to `image` except that it takes a matrix which already has colors defined for each cell. This function calls `imageDefault` which enables updated use of the `useRaster` functionality.

Additionally, if `cellnote` is supplied, which contains a matrix of labels for the image cells, those labels will also be displayed. By default, labels are grouped, so that only one label is displayed whenever two or more labels appear in consecutive cells. This behavior can be disabled with groupCellnotes=FALSE.

The `groupCellnotes` behavior uses `breaksByVector()` to determine where to place consecutive labels, and it applies this logic starting with rows, then columns. Note that labels are only grouped when both the cell color and the cell label are identical for consecutive cells.

In general, if a large rectangular set of cells contains the same label, and cell colors, the resulting label will be positioned in the center. However, when the square is not symmetric, the label will be grouped only where consecutive columns contain the same groups of consecutive rows for a given label.

It is helpful to rotate labels partially to prevent overlaps, e.g. srtCellnote=10 or srtCellnote=80.

To do:

- Detect the size of the area being labeled and determine whether to rotate the label sideways.
- Detect the size of the label, compared to its bounding box, and resize the label to fit the available space.
- Optionally draw border around contiguous colored and labeled polygons. Whether to draw border based only upon color, or color and label, or just label... it may get confusing.
- Label proper contiguous polygons based upon color and label, especially when color and label are present on multiple rows and columns, but not always the same columns per row.

Value

`list` invisibly, with elements sufficient to create an image plot. This function is called for the byproduct of creating an image visualization.

See Also

Other jam plot functions: `adjustAxisLabelMargins()`, `coordPresets()`, `decideMfrow()`, `drawLabels()`, `getPlotAspect()`, `groupedAxis()`, `imageDefault()`, `minorLogTicksAxis()`, `nullPlot()`, `plotPolygonDensity()`, `plotRidges()`, `plotSmoothScatter()`, `shadowText()`, `shadowText_options()`, `showColors()`, `sqrtAxis()`, `usrBox()`

Examples

```
a1 <- c("red4","blue")[c(1,1,2)];
b1 <- c("yellow","orange")[c(1,2,2)];
c1 <- c("purple","orange")[c(1,2,2)];
d1 <- c("purple","green4")[c(1,2,2)];
df1 <- data.frame(a=a1, b=b1, c=c1, d=d1);

# default using polygons
imageByColors(df1, cellnote=df1);

# using useRaster, edges are slightly blurred with small tables
imageByColors(df1, cellnote=df1, useRaster=TRUE);

# some text features, rotation, font size, etc
imageByColors(df1, cellnote=df1, useRaster=TRUE, adjBy="column",
   cexCellnote=list(c(1.5,1.5,1), c(1,1.5), c(1.6,1.2), c(1.6,1.5)),
   srtCellnote=list(c(90,0,0), c(0,45), c(0,0,0), c(0,90,0)));
```

`imageDefault` *Display a color raster image*

Description

Display a color raster image

Usage

```
imageDefault(
  x = seq_len(nrow(z) + 1) - 0.5,
  y = seq_len(ncol(z) + 1) - 0.5,
  z,
  zlim = range(z[is.finite(z)]),
  xlim = range(x),
  ylim = range(y),
  col = grDevices::hcl.colors(12, "YlOrRd", rev = TRUE),
  add = FALSE,
```

```
  xaxs = "i",
  yaxs = "i",
  xaxt = "n",
  yaxt = "n",
  xlab,
  ylab,
  breaks,
  flip = c("none", "x", "y", "xy"),
  oldstyle = TRUE,
  useRaster = NULL,
  fixRasterRatio = TRUE,
  maxRatioFix = 10,
  minRasterMultiple = NULL,
  rasterTarget = 200,
  interpolate = getOption("interpolate", TRUE),
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric location of grid lines at which the intervals in z are measured.
y	numeric location of grid lines at which the intervals in z are measured.
z	numeric or logical matrix containing the values to be plotted, where NA values are allowed.
zlim	numeric range allowed for values in z.
xlim	numeric range to plot on the x-axis, by default the x range.
ylim	numeric range to plot on the y-axis, by default the y range.
col	character vector of colors to be mapped to values in z.
add	logical whether to add to an existing active R plot, or create a new plot window.
xaxs	character value compatible with graphics::par(xaxs), mainly useful for suppressing the x-axis, in order to produce a custom x-axis range, most useful to restrict the axis range expansion done by R by default.
yaxs	character value compatible with graphics::par(yaxs), mainly useful for suppressing the y-axis, in order to produce a custom y-axis range, most useful to restrict the axis range expansion done by R by default.
xaxt	character value compatible with graphics::par(xaxt), mainly useful for suppressing the x-axis, in order to produce a custom x-axis by other mechanisms, e.g. log-scaled x-axis tick marks.
yaxt	character value compatible with graphics::par(yaxt), mainly useful for suppressing the y-axis, in order to produce a custom y-axis by other mechanisms, e.g. log-scaled y-axis tick marks.
xlab	character label for the x-axis
ylab	character label for the y-axis
breaks	numeric vector of breakpoints for colors.

`flip` character string, default "none", with optional axis flip:

- none: perform no axis flip
- x: flip x-axis orientation
- y: flip y-axis orientation
- xy: flip both x- and y-axis orientation

`oldstyle` logical whether to delineate axis coordinates with an integer spacing for each column and row. Note: the only allowed parameter is TRUE, since useRaster=TRUE requires it. Therefore, this function for consistency will only output this format.

`useRaster` logical whether to force raster image scaling, which is especially useful for large data matrices. In this case a bitmap raster image is created instead of polygons, then the bitmap is scaled to fit the plot space. Otherwise, individual polygons can be obscured on monitor screens, or may result in an extremely large file size when writing to vector image format such as 'PDF' or 'SVG'.

`fixRasterRatio` logical whether to implement a simple workaround to the requirement for square pixels, in the event the x- and y-axis dimensions are not roughly equal.

`maxRatioFix` integer maximum number of times any axis may be replicated to create a matrix of roughly equal x- and y-axis dimensions.

`minRasterMultiple` integer minimum number of times the x- and y-axis will be duplicated, which is mostly useful when creating useRaster=TRUE for small matrix sizes, otherwise the result will be quite blurry. For example, minRasterMultiple=10 will duplicate each axis 10 times. Values are aplied to rows then columns. These values are automatically defined if minRasterMultiple is NULL and rasterTarget is not NULL.

`rasterTarget` integer number of cells below which cells are duplicated in order to maintain detail. The default 200 defines minRasterMultiple=c(1,1) if there are 200 rows and 200 columns, or minRasterMultiple=c(1,100) if there are 200 rows but 2 columns.

`interpolate` logical whether to implement image interpolation, by default TRUE when useRaster=TRUE.

`verbose` logical whether to enable verbose output, useful for debugging.

`...` Additional arguments are ignored.

Details

This function augments the `image` function, in that it handles the useRaster parameter for non-symmetric data matrices, in order to minimize the distortion from image-smoothing when pixels are not square.

The function also by default creates the image map using coordinates where each integer represents the center point of one column or row of data, known in the default `image` function as `oldstyle=TRUE`. For consistency, `imageDefault` will only accept `oldstyle=TRUE`.

Value

`list` composed of elements suitable to call `graphics::image.default()`.

See Also

image

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
ps <- plotSmoothScatter(doTest=TRUE)
```

---

isColor *detect valid R color*

Description

detect valid R color

Usage

```
isColor(x, makeNamesFunc = c, ...)
```

Arguments

x	character vector of potential R colors
makeNamesFunc	function used to make names for the resulting vector
...	additional parameters are ignored

Details

This function determines whether each element in a vector is a valid R color, based upon the R color names, valid hex color format, and the word "transparent" which is valid as an R color.

Value

logical vector with length(x).

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
isColor(c("red", "blue", "beige", "#99000099", "#aa00ff", "#AAE", "bleh"))
```

isFALSEV *Vectorized isFALSE*

Description

Vectorized isFALSE

Usage

```
isFALSEV(x, ...)
```

Arguments

x	vector
...	additional arguments are ignored

Details

This function applies three criteria to an input vector, to determine if each entry in the vector is FALSE:

1. It must be class `logical`.
2. It must not be `NA`.
3. It must evaluate as `FALSE`.

Value

`logical` vector with length matching `x`.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
isFALSEV(c(TRUE, FALSE, NA, TRUE))
```

isTRUEV *Vectorized isTRUE*

Description

Vectorized isTRUE

Usage

```
isTRUEV(x, ...)
```

Arguments

x	vector
...	additional arguments are ignored

Details

This function applies three criteria to an input vector, to determine if each entry in the vector is TRUE:

1. It must be class `logical`.
2. It must not be `NA`.
3. It must evaluate as `TRUE`.

Value

`logical` vector with length matching `x`.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
isTRUEV(c(TRUE, FALSE, NA, TRUE))
```

jamCalcDensity *Calculate scatter plot point density*

Description

Calculate scatter plot point density

Usage

```
jamCalcDensity(x, nbin, bandwidth = NULL, range.x)
```

Arguments

x	numeric matrix with two columns representing x,y coordinates.
nbin	integer number of bins to subdivide the scatterplot, expanded to length 2 to accommodate x and y axis bins.
bandwidth	numeric or NULL representing the bandwidth used for point density determination.
range.x	numeric vector length 2 representing the range of values to consider for point density.

Details

This function is called internally by plotSmoothScatter(), and is an equivalent replacement for grDevices non-exported function .smoothScatterCalcDensity(), understandably a requirement by CRAN. A package should not rely on another package hidden function.

Value

list with elements used internally by plotSmoothScatter(), with: x1, x2, fhat, bandwidth.

See Also

Other jam internal functions: handleArgsText(), make_html_styles(), make_styles(), smoothScatterJam()

Examples

```
sdim(jamCalcDensity(cbind(x=rnorm(1000) + 4, y=rnorm(1000) + 4), nbin=30))
```

jam_rapply *Jam-specific recursive apply*

Description

Jam-specific recursive apply

Usage

```
jam_rapply(x, FUN, how = c("unlist", "list"), ...)
```

Arguments

x	list
FUN	function to be called on non-list elements in x.
how	character string indicating whether to return the list or whether to call unlist() on the result.
...	additional arguments are passed to FUN.

Details

This function is a very lightweight customization to base::rapply(), specifically that it does not remove NULL entries.

Value

vector or list based upon argument how.

See Also

Other jam list functions: cPaste(), heads(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), relist_named(), rlengths(), sclass(), sdim(), uniques(), unnestList()

Examples

```
L <- list(entryA=c("miR-112", "miR-12", "miR-112"),
   entryB=factor(c("A","B","A","B"),
      levels=c("B","A")),
   entryC=factor(c("C","A","B","B","C"),
      levels=c("A","B","C")),
   entryNULL=NULL)
rapply(L, length)
jam_rapply(L, length)

L0 <- list(A=1:3, B=list(C=1:3, D=4:5, E=NULL));
rapply(L0, length)
jam_rapply(L0, length)
```

jargs *Show R function arguments jam-style*

Description

Show R function arguments jam-style

Usage

```
jargs(
  x,
  grepString = NULL,
  sortVars = FALSE,
  useMessage = TRUE,
  asList = TRUE,
  useColor = TRUE,
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  adjustRgb = getOption("jam.adjustRgb"),
  useCollapseBase = ", ",
  verbose = FALSE,
  debug = 0,
  ...
)
```

Arguments

x	function or character name of a function.
grepString	NULL, logical, or character grep regular expression pattern used to filter function arguments by name. Very useful to search a function for arguments with a substring "row". • If logical, it is assumed to be sortVars, and indicates whether to sort the parameter names. • if character it will subset the function arguments by name matching this regular expression pattern.
sortVars	logical whether to sort the function parameter names. • sortVars=FALSE returns arguments in the order they appear in the function definition. • sortVars=TRUE returns arguments sorted alphabetically.
useMessage	logical default TRUE, whether to print output using message(), otherwise text is returned invisibly to be displayed separately.
asList	logical default TRUE, display one entry per line or display results as a data.frame.
useColor	logical whether to display results in color, if the crayon package is available, and terminal console is capable.

lightMode	logical or NULL, indicating whether the text background color is light, thus imposing a maximum brightness for colors displayed. It use lightMode if defined by the function caller, otherwise it will use getOption("jam.lightMode") if defined, lastly it will attempt to detect whether running inside Rstudio by checking the environment variable "RSTUDIO", and if so it will assume lightMode==TRUE.
Crange	numeric range of chroma values, ranging between 0 and 100. When NULL, default values will be assigned to Crange by setCLranges().
Lrange	numeric range of luminance values, ranging between 0 and 100. When NULL, default values will be assigned to Lrange by setCLranges().
adjustRgb	numeric value adjustment used during the conversion of RGB colors to ANSI colors, which is inherently lossy. If not defined, it uses the default returned by setCLranges() which itself uses getOption("jam.adjustRgb") with default=0. In order to boost color contrast, an alternate value of -0.1 is suggested.
useCollapseBase	character string used to combine multiple parameter values.
verbose	logical whether to print verbose output.
debug	integer value, greater than 0 will cause debug-type verbose output, useful because parameters are hard!
...	Additional arguments are installed.

Details

This function displays R function arguments, organized with one argument per line, and colorized using the crayon package if installed.

Output is nicely spaced to help visual alignment of argument names and argument values.

Output can be filtered by character pattern. For example the function ComplexHeatmap::Heatmap() is amazing, and offers numerous arguments. To find arguments relevant to dendrograms, use "dend":

```
jargs(ComplexHeatmap::Heatmap, "dend")
```

NOTE: This function has edge case issues displaying complex function argument values such as nested lists and custom functions. In that case the argument name is printed as usual, and the argument value is displayed as a partial snippet of the default argument value.

Generic functions very often contain no useful parameters, making it difficult to discover required parameters without reading the function documentation from the proper dispatched function and calling package. In that case, try using jargs(functionname.default) for example compare:

```
jargs(barplot)
```

to:

```
jargs(barplot.default)
```

Value

NULL this function called for the byproduct of printing its output.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
args(jargs)
jargs(jargs)

# retrieve parameters involving notes from imageByColors
jargs(imageByColors, "note")
```

---

kable_coloring *Extend kableExtra colorization of 'Rmarkdown' tables*

Description

Extend kableExtra colorization of 'Rmarkdown' tables

Usage

```
kable_coloring(
  df,
  colorSub = NULL,
  background_as_tile = TRUE,
  color_cells = TRUE,
  row_color_by = NULL,
  sep = "_",
  border_left = "1px solid #DDDDDD",
  border_right = FALSE,
  extra_css = "white-space: nowrap;",
  format = "html",
  format.args = list(trim = TRUE, big.mark = ","),
  row.names = NA,
  align = NULL,
  return_type = c("kable", "data.frame"),
  verbose = FALSE,
  ...
)
```

Arguments

df	data.frame input. Note that kable input is not supported.
colorSub	one of the following inputs:

- character vector of R colors, whose names match entries in the data.frame which are given these assigned colors
- function that takes column values as input, and returns a character vector with one color per value, using NA or NULL to indicate "transparent"
- list whose names match colnames(df), where each entry contains either character or function option as described above. A character vector should be named by values expected in each column. A function should take column values as input, and return a character vector with same length of R colors.

background_as_tile
: logical default TRUE, whether the cell background color will appear as a rounded tile (TRUE) or a rectangle (FALSE). Either way, the color does not fill the entire whitespace of the table cell, but only around the text itself.

color_cells
: logical indicating whether to color individual cells, default TRUE. This may be FALSE when also applying row_color_by, so the entire row will be colorized.

row_color_by
: character vector with one or more colnames, indicating how to colorize entire rows of a table. When one column is defined, colors in colorSub are used as normal. When multiple columns are defined, values from each column are concatenated using sep delimiter. Then resulting values are compared with colorSub.

sep
: character delimiter used to combine values in multiple columns when row_color_by is supplied and contains multiple colnames. The delimited character strings are compared to colorSub to assign colors.

border_left, border_right, extra_css
: character values optionally passed to kableExtra::column_spec() as a convenient way to apply borders for each column (border_left, border_right) or enable or disable word-wrapping by column. Some helpful examples:

  - border_left=FALSE: disables left border
  - border_left="1px solid #DDDDDD": light gray 1 pixel left border
  - border_right=FALSE: disables right border
  - border_right="1px solid #DDDDDD": light gray 1 pixel right border
  - extra_css=NULL: disables word-wrap
  - extra_css="whitespace: nowrap;": enables text word-wrap
  - when all options above contain only FALSE or NULL, then kableExtra::column_spec() is not applied.

format
: character passed to knitr::kable(), default "html" which is the intended format for most scenarios. It can be set to NULL to enable auto-detection of the format.

format.args
: list of arguments passed to base::format() intended mainly for numeric columns.

row.names
: logical indicating whether to include rownames(df). When row.names=NA the default is to display rownames if they are not NULL and not equal to 1:nrow(df).

align
: character passed to kableExtra::kable() to define alignment of each column.

return_type	character string indicating the type of data to return. • return_type="kable": (default) returns object with class "kableExtra", "knitr_kable" suitable for downstream processing. • return_type="data.frame": returns a data.frame whose cells contain HTML markup with corresponding colors defined.
verbose	boolean indicating whether to print verbose output.
...	additional arguments are passed to kableExtra::kable() which allows the usual customizations on the initial call.

Details

This function extends the kableExtra package, and is only available for use if the kableExtra package is installed. It is intended to allow specific color assignment of elements in a data.frame, but otherwise uses the kableExtra functions to apply those colors.

The use case is to provide colorized HTML output for 'Rmarkdown', it has not been tested with other format output.

The argument colorSub accepts:

- character vector input where names should match column values
- function that accepts column values and returns a character vector of colors of equal length
- list input where names should match colnames(df), and where each list element should contain either a character vector, or function as described above.

Value

object with class c("kableExtra", "knitr_kable") by default when return_type="kable", suitable to render inside an 'Rmarkdown' or HTML context. Or returns data.frame when return_type="data.frame".

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
expt_df <- data.frame(
   Sample_ID="",
   Treatment=rep(c("Vehicle", "Dex"), each=6),
   Genotype=rep(c("Wildtype", "Knockout"), each=3),
   Rep=paste0("rep", c(1:3)))
expt_df$Sample_ID <- pasteByRow(expt_df[, 2:4])
```

```
# define colors
colorSub <- c(Vehicle="palegoldenrod",
   Dex="navy",
   Wildtype="gold",
   Knockout="firebrick",
   nameVector(
      color2gradient("grey48", n=3, dex=10),
      rep("rep", 3),
      suffix=""),
   nameVector(
      color2gradient(n=3,
         c("goldenrod1", "indianred3", "royalblue3", "darkorchid4")),
      expt_df$Sample_ID))
kbl <- kable_coloring(
   expt_df,
   caption="Experiment design table showing categorical color assignment.",
   colorSub)
# Note that the HTML table is rendered in 'Rmarkdown', not pkgdown
kbl

# return_type="data.frame" is a data.frame with HTML contents
kdf3 <- kable_coloring(
   return_type="data.frame",
   df=expt_df,
   colorSub=colorSub)
kdf3;
```

`list2df` *Convert list of vectors to data.frame with item, value, name*

Description

Convert list of vectors to data.frame with item, value, name

Usage

```
list2df(x, makeUnique = TRUE, useVectorNames = TRUE, ...)
```

Arguments

`x`	list of vectors
`makeUnique`	logical indicating whether the data.frame should contain unique rows.
`useVectorNames`	logical indicating whether vector names should be included in the data.frame, if they exist.
`...`	additional arguments are ignored.

Details

This function converts a list of vectors to a tall data.frame with colnames `item` to indicate the list name, `value` to indicate the vector value, and `name` to indicate the vector name if `useVectorNames=TRUE` and if names exist.

Value

`data.frame` with two columns, or three columns when `useVectorNames=TRUE` and the input `x` contains names.

See Also

Other jam list functions: `cPaste()`, `heads()`, `jam_rapply()`, `mergeAllXY()`, `mixedSorts()`, `rbindList()`, `relist_named()`, `rlengths()`, `sclass()`, `sdim()`, `uniques()`, `unnestList()`

Examples

```
list2df(list(lower=head(letters, 5), UPPER=head(LETTERS, 10)))

list2df(list(lower=nameVector(head(letters, 5)),
   UPPER=nameVector(head(LETTERS, 10))))

list2df(list(lower=nameVector(head(letters, 5)),
   UPPER=nameVector(head(LETTERS, 10))),
   useVectorNames=FALSE)
```

---

lldf *Long listing of R session objects*

Description

Long listing of R session objects

Usage

```
lldf(
  n = Inf,
  envir = -1L,
  items = NULL,
  use_utils_objectsize = TRUE,
  all.names = TRUE,
  ...
)
```

Arguments

n	integer or Inf indicating how many objects to include in the output data.frame.
envir	environment where the list of objects is obtained, default -1L searches the environment of the caller, usually the user workspace. Other recognized options: • character string suitable for as.environment() which recognizes the search path returned by search() • integer or numeric equivalent to environment relative position as used in ls() argument pos.
items	character of items to include, default NULL.
use_utils_objectsize	logical, default TRUE, whether to prefer utils::object.size(), otherwise it will attempt to use pryr::object_size() if the package is installed.
all.names	logical passed to base::ls() indicating whether to include all names, where all.names=TRUE will include hidden objects whose name begin with "." such as ".First".
...	additional arguments are passed to ls(), notably pattern can be passed to subset objects by regular expression.

Details

This function expands base::ls() by also determining the object size, and sorting to display the top n objects by size, largest first.

This package will call pryr::object_size if available, otherwise falls back to utils::object.size().

Value

data.frame with summary of objects and object sizes, sorted by decreasing object size.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
lldf(10);

# custom environment
newenv <- new.env();
newenv$A <- 1:10;
newenv$df <- data.frame(A=1:10, B=11:20);
lldf(envir=newenv);
rm(newenv);
```

`log2signed` *log2 transformation with directionality*

Description

log2 transformation with directionality

Usage

```
log2signed(x, offset = 1, base = 2, ...)
```

Arguments

`x`	`numeric` vector
`offset`	`numeric` value added to the absolute values of `x` prior to applying the log transformation.
`base`	`numeric` value indicating the logarithmic base, by default `2` in order to apply `base::log2()`.
`...`	additional arguments are ignored.

Details

This function applies a log2 transformation but maintains the sign of the input data, allowing for log2 transformation of negative values.

The method applies an offset to the absolute value `abs(x)`, in order to handle values between zero and 1, then applies log2 transformation, then multiplies by the original sign from `sign(x)`.

The argument `offset` is used to adjust values, for example `offset=1` will apply log2 transformation `log2(1 + x)`, except using the absolute value of `x`. This method allows for positive and negative input data to contain values between 0 and 1, and between -1 and 0.

This function could be described as applying a log2 transformation of the "magnitude" of values in `x`, while maintaining the positive or negative directionality.

If any `abs(x)` are less than `offset` this function will raise an error.

Value

numeric vector of log-transformed magnitudes.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
x <- c(-100:100)/10;
log2signed(x);
plot(x=x, y=log2signed(x), xlab="x", ylab="log2signed(x)")
```

`makeColorDarker` *make R colors darker (or lighter)*

Description

Makes R colors darker or lighter based upon darkFactor

Usage

```
makeColorDarker(
  hexColor,
  darkFactor = 2,
  sFactor = 1,
  fixAlpha = NULL,
  verbose = FALSE,
  keepNA = FALSE,
  useMethod = 1,
  ...
)
```

Arguments

`hexColor`	`character` vector of colors to adjust
`darkFactor`	`numeric` value to adjust darkness, values above 1 make the color darker, values below 1 (or below 0) make the color brighter.
`sFactor`	`numeric` value to adjust saturation, values above 1 become more saturated.
`fixAlpha`	`numeric`, default NULL, to assign a fixed alpha transparency value, where 0 is transparent and 1 is opaque.
`verbose`	`logical` indicating whether to print verbose output.
`keepNA`	`logical`, default FALSE, whether to keep NA values as NA values in the output, otherwise NA values are considered grey input.
`useMethod`	`integer` with two alternate methods, 1 is default.
`...`	Additional arguments are ignored.

Details

This function was originally intended to create border colors, or to create slightly darker colors used for labels. It is also useful for for making colors lighter, in adjusting color saturation up or down, or applying alpha transparency during the same step.

Note when colors are brightened beyond value=1, the saturation is gradually reduced in order to produce a visibly lighter color. The saturation minimu is set to 0.2, to maintain at least some amount of color.

Value

`character` vector of R colors.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
colorV <- c("red","orange","purple","blue");
colorVdark2 <- makeColorDarker(colorV, darkFactor=2);
colorVlite2 <- makeColorDarker(colorV, darkFactor=-2);
showColors(cexCellnote=0.7,
   list(
   `darkFactor=2`=colorVdark2,
   `original colors`=colorV,
   `darkFactor=-2`=colorVlite2
   ));

# these adjustments work really well inside a network diagram
# when coloring nodes, and providing an outline of comparable
# color.
plot(x=c(1,2,1,2), y=c(1,2,2,1), pch=21,
   xaxt="n", yaxt="n", xlab="", ylab="",
   xlim=c(0.5,2.5), ylim=c(0.5,2.5),
   bg=colorV, col=colorVdark2, cex=4, lwd=2);
graphics::points(x=c(1,2,1,2), y=c(1,2,2,1), pch=20, cex=4,
   col=colorVlite2);

# Making a color lighter can make it easier to add labels
# The setTextContrastColor() function also helps.
graphics::text(x=c(1,2,1,2), y=c(1,2,2,1), 1:4,
   col=setTextContrastColor(colorVlite2));
```

makeNames *make unique vector names*

Description

make unique vector names

Usage

```
makeNames(
  x,
  unique = TRUE,
  suffix = "_v",
  renameOnes = FALSE,
  doPadInteger = FALSE,
  startN = 1,
  numberStyle = c("number", "letters", "LETTERS"),
  useNchar = NULL,
  renameFirst = TRUE,
  keepNA = TRUE,
  ...
)
```

Arguments

x	character vector to be used when defining names. All other vector types will be coerced to character prior to use.
unique	argument which is ignored, included only for compatibility with base::make.names. All results from makeNames() are unique.
suffix	character separator between the original entry and the version, if necessary.
renameOnes	logical whether to rename single, unduplicated, entries.
doPadInteger	logical whether to pad integer values to a consistent number of digits, based upon all suffix values needed. This output allows for more consistent sorting of names. To define a fixed number of digits, use the useNchar parameter.
startN	integer number used when numberStyle is "number", this integer is used for the first entry to be renamed. You can use this value to make zero-based suffix values, for example.
numberStyle	character style for version numbering
	"number" Use integer numbers to represent each duplicated entry.
	"letters" Use lowercase letters to represent each duplicated entry. The 27th entry uses the pattern "aa" to represent two 26-base digits. When doPadInteger=TRUE, a zero is still used to pad the resulting version numbers, again to allow easy sorting of text values, but also because there is no letter equivalent for the number zero. It is usually best to change the suffix to "_" or "" when using "letters".

"LETTERS" Use uppercase letters to represent each duplicated entry, with the same rules as applied to "letters".

`useNchar` integer or NULL, number of digits to use when padding integer values with leading zero, only relevant when usePadInteger=TRUE.

`renameFirst` logical whether to rename the first entry in a set of duplicated entries. If FALSE then the first entry in a set will not be versioned, even when renameOnes=TRUE.

`keepNA` logical whether to retain NA values using the string "NA". If keepNA is FALSE, then NA values will remain NA, thus causing some names to become `<NA>`, which can cause problems with some downstream functions which assume all names are either NULL or non-NA.

`...` Additional arguments are ignored.

Details

This function extends the basic goal from `make.names` which is intended to make syntactically valid names from a character vector. This makeNames function makes names unique, and offers configurable methods to handle duplicate names. By default, any duplicated entries receive a suffix _v# where # is s running count of entries observed, starting at 1. The `make.names` function, by contrast, renames the second observed entry starting at .1, leaving the original entry unchanged. Optionally, makeNames can rename all entries with a numeric suffix, for consistency.

For example: `A, A, A, B, B, C` becomes: `A_v1, A_v2, A_v3, B_v1, B_v2, C`

Also, makeNames always allows "_".

This makeNames function is similar to `make.unique` which also converts a vector into a unique vector by adding suffix values, however the `make.unique` function intends to allow repeated operations which recognize duplicated entries and continually increment the suffix number. This makeNames function currently does not handle repeat operations. The recommended approach to workaround having pre-existing versioned names would be to remove suffix values prior to running this function. One small distinction from `make.unique` is that makeNames does version the first entry in a set.

Value

character vector of unique names

See Also

Other jam string functions: `asSize()`, `breaksByVector()`, `fillBlanks()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
V <- rep(LETTERS[1:3], c(2,3,1));
makeNames(V);
makeNames(V, renameOnes=TRUE);
makeNames(V, renameFirst=FALSE);
exons <- makeNames(rep("exon", 3), suffix="");
makeNames(rep(exons, c(2,3,1)), numberStyle="letters", suffix="");
```

`make_html_styles` *vectorized make_styles for html span output*

Description

vectorized make_styles for html span output

Usage

```
make_html_styles(
  style = NULL,
  text,
  bg = FALSE,
  bg_style = NULL,
  grey = FALSE,
  Cgrey = getOption("jam.Cgrey"),
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  adjustRgb = getOption("jam.adjustRgb"),
  adjustPower = 1.5,
  fixYellow = TRUE,
  alphaPower = 2,
  setOptions = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

`style`	`character` vector of one or more styles. When `NULL` or `NA`, no style is applied, except when `bg_style` is supplied and is neither `NA` nor `NULL`, in which case entries with a `bg_style` and no `style` will use `setTextContrastColor()` to define a contrasting `style`.
`text`	`character` vector (or coerced to `character`) of one or more values,.
`bg`	`logical` indicating whether the `style` should be applied to the background instead of foreground. This argument is ignored when `bg_style` is supplied.
`bg_style`	`NULL` or a `character` vector of one or more background styles. When this argument is not NULL, it applies both the foreground `style` and background `bg_style` together, and therefore ignores `Crange` and `Lrange` settings.
`grey`	`logical`, default FALSE, whether to use greyscale.
`Cgrey`	`numeric` chroma (C) value, which defines grey colors at or below this chroma. Any colors at or below the grey cutoff will have use ANSI greyscale coloring. To disable, set `Cgrey=-1`.

lightMode	logical indicating whether the background color is light (TRUE is bright), or dark (FALSE is dark.) By default it calls checkLightMode() which queries getOption("lightMode").
Crange	numeric range of chroma values, ranging between 0 and 100. When NULL, default values will be assigned to Crange. When supplied, range(Crange) is used.
Lrange	numeric range of luminance values, ranging between 0 and 100. When NULL, default values will be assigned to Lrange. When supplied, range(Lrange) is used.
adjustRgb	numeric value adjustment used during the conversion of RGB colors to ANSI colors, which is inherently lossy. If not defined, it uses the default returned by setCLranges() which itself uses getOption("jam.adjustRgb") with default=0. In order to boost color contrast, an alternate value of -0.1 is suggested.
adjustPower	numeric adjustment power factor
fixYellow	logical indicating whether to "fix" the darkening of yellow, which otherwise turns to green. Instead, since JAM can, JAM will make the yellow slightly more golden before darkening. This change only affects color hues between 80 and 90. This argument is passed to applyCLrange().
alphaPower	numeric value, used to adjust the RGB values for alpha values less than 255, by raising the ratio to 1/alphaPower, which takes the ratio of square roots. alphaPower=100 for minimal adjustment.
setOptions	character or logical whether to update Crange and Lrange options during the subsequent call to setCLranges(). By default, • "ifnull" will update only options which were previously NULL; • "FALSE" prevents modifying the global options; • "TRUE" will update these options with the current values.
verbose	logical indicating whether to print verbose output
...	additional parameters are ignored

Details

Note this function is experimental.

Value

character vector with the same length as text input vector, where entries are surrounded by the relevant HTML consistent with the style defined at input. In short, a character vector as input, colorized HTML character vector as output.

See Also

Other jam internal functions: handleArgsText(), jamCalcDensity(), make_styles(), smoothScatterJam()

Examples

```
make_html_styles(style=c("red", "orange"), text=c("one ", "two"))
```

make_styles *vectorized make_styles for crayon output*

Description

vectorized make_styles for crayon output

Usage

```
make_styles(
  style = NULL,
  text,
  bg = FALSE,
  bg_style = NULL,
  grey = FALSE,
  colors = NULL,
  Cgrey = getOption("jam.Cgrey", 5),
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  adjustRgb = getOption("jam.adjustRgb"),
  adjustPower = 1.5,
  fixYellow = TRUE,
  colorTransparent = "grey45",
  alphaPower = 2,
  setOptions = c("ifnull", "FALSE", "TRUE"),
  verbose = FALSE,
  ...
)
```

Arguments

style	character vector of one or more styles. When NULL or NA, no style is applied, except when bg_style is supplied and is neither NA nor NULL, in which case entries with a bg_style and no style will use setTextContrastColor() to define a contrasting style.
text	character vector (or coerced to character) of one or more values,.
bg	logical indicating whether the style should be applied to the background instead of foreground. This argument is ignored when bg_style is supplied.
bg_style	NULL or a character vector of one or more background styles. When this argument is not NULL, it applies both the foreground style and background bg_style together, and therefore ignores Crange and Lrange settings.
grey	logical, default FALSE, whether to use greyscale.
colors	integer, default NULL, number of colors for console output, when NULL it calls crayon::num_colors() to detect console capabilities.

Cgrey	numeric chroma (C) value, which defines grey colors at or below this chroma. Any colors at or below the grey cutoff will have use ANSI greyscale coloring. To disable, set Cgrey=-1.
lightMode	logical indicating whether the background color is light (TRUE is bright), or dark (FALSE is dark.) By default it calls checkLightMode() which queries getOption("lightMode").
Crange	numeric range of chroma values, ranging between 0 and 100. When NULL, default values will be assigned to Crange. When supplied, range(Crange) is used.
Lrange	numeric range of luminance values, ranging between 0 and 100. When NULL, default values will be assigned to Lrange. When supplied, range(Lrange) is used.
adjustRgb	numeric value adjustment used during the conversion of RGB colors to ANSI colors, which is inherently lossy. If not defined, it uses the default returned by setCLranges() which itself uses getOption("jam.adjustRgb") with default=0. In order to boost color contrast, an alternate value of -0.1 is suggested.
adjustPower	numeric adjustment power factor
fixYellow	logical indicating whether to "fix" the darkening of yellow, which otherwise turns to green. Instead, since JAM can, JAM will make the yellow slightly more golden before darkening. This change only affects color hues between 80 and 90. This argument is passed to applyCLrange().
colorTransparent	character color used to substitute for "transparent" which a valid R color, but not a valid color for the crayon package.
alphaPower	numeric value, used to adjust the RGB values for alpha values less than 255, by raising the ratio to 1/alphaPower, which takes the ratio of square roots. alphaPower=100 for minimal adjustment.
setOptions	character or logical whether to update Crange and Lrange options during the subsequent call to setCLranges(). By default, • "ifnull" will update only options which were previously NULL; • "FALSE" prevents modifying the global options; • "TRUE" will update these options with the current values.
verbose	logical indicating whether to print verbose output
...	additional parameters are ignored

Details

This function is essentially a vectorized version of crayon::make_style() in order to style a vector of character strings with a vector of foreground and background styles.

Value

character vector with the same length as text input vector, where entries are surrounded by the relevant encoding consistent with the style defined at input. In short, a character vector as input, a colorized character vector as output.

See Also

Other jam internal functions: handleArgsText(), jamCalcDensity(), make_html_styles(), smoothScatterJam()

Examples

```
cat(make_styles(style=c("red", "yellow"), text=c("one ", "two")), "\n")
```

---

mergeAllXY *Merge list of data.frames retaining all rows*

Description

Merge list of data.frames retaining all rows

Usage

```
mergeAllXY(...)
```

Arguments

...	arguments are handled as described: • named arguments are passed through to base::merge.data.frame(), with the exception of all.x and all.y which are both defined all.x=TRUE and all.y=TRUE. and all other arguments are assumed to be data.frame or equivalent, and are merged in order they appear as arguments. The order of these data.frame objects should not affect the output content, but will affect the row and column order of the resulting data.frame.

Details

This function is a wrapper around base::merge.data.frame() except that it allows more than two data.frame objects, and applies default arguments all.x=TRUE and all.y=TRUE for each merge operation to ensure that all rows are kept.

Value

data.frame after iterative calls to base::merge.data.frame().

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mixedSorts(), rbindList(), relist_named(), rlengths(), sclass(), sdim(), uniques(), unnestList()

Examples

```
df1 <- data.frame(City=c("New York", "Los Angeles", "San Francisco"),
   State=c("New York", "California", "California"))
df2 <- data.frame(Team=c("Yankees", "Mets", "Giants", "Dodgers"),
   City=c("New York", "New York", "San Francisco", "Los Angeles"))
df3 <- data.frame(State=c("New York", "California"),
   `State Population`=c(39.24e9, 8.468e9),
   check.names=FALSE)
mergeAllXY(df1, df3, df2)

df4 <- data.frame(check.names=FALSE,
   CellLine=rep(c("ul3", "dH1A", "dH1B"), each=2),
   Treatment=c("Vehicle", "Dex"))
df4$CellLine <- factor(df4$CellLine,
   levels=c("ul3", "dH1A", "dH1B"))
df4$Treatment <- factor(df4$Treatment,
   levels=c("Vehicle", "Dex"))
df5 <- data.frame(
   Treatment=rep(c("Vehicle", "Dex"), each=3),
   Time=c("0h", "12h", "24h"))
df6 <- data.frame(check.names=FALSE,
   CellLine=c("ul3", "dH1A", "dH1B"),
   Type=c("Control", "KO", "KO"))
mergeAllXY(df4, df5, df6)

# note the factor order is maintained
mergeAllXY(df4, df5, df6)$CellLine
mergeAllXY(df4, df5)$Treatment

# merge "all" can append rows to a data.frame
df4b <- data.frame(check.names=FALSE,
   CellLine=rep("dH1C", 2),
   Treatment=c("Vehicle", "Dex"))
mergeAllXY(df4, df4b)

# factor order is maintained, new levels are appended
mergeAllXY(df4, df4b)$CellLine

# merge proceeds except shows missing data
mergeAllXY(df4, df4b, df5, df6)

# note that appending rows is tricky, the following is incorrect
df6b <- data.frame(check.names=FALSE,
   CellLine="dH1C",
   Type="KO")
mergeAllXY(df4, df4b, df5, df6, df6b)

# but it can be resolved by merging df6 and df6b
mergeAllXY(df4, df4b, df5, mergeAllXY(df6, df6b))

# it may be easier to recognize by sorting with mixedSortDF()
mixedSortDF(honorFactor=TRUE,
```

```
   mergeAllXY(df4, df4b, df5, mergeAllXY(df6, df6b)))

# again, factor order is maintained
mergeAllXY(df4, df4b, df5, sort=FALSE, mergeAllXY(df6, df6b))$CellLine

# the result can be sorted properly
mixedSortDF(honorFactor=TRUE,
   mergeAllXY(df4, df4b, df5, mergeAllXY(df6, df6b)))
```

`middle` *Return the middle portion of data similar to head and tail*

Description

Return the middle portion of data similar to head and tail

Usage

```
middle(x, n = 10, evenly = TRUE, ...)
```

Arguments

`x`	input data that can be subset
`n`	`numeric` number of entries to return
`evenly`	`logical` indicating whether to return evenly spaced entries along the full length of `x`. When `evenly=FALSE` only the middle `n` entries are returned.
`...`	additional arguments are ignored.

Details

This function is very simple, and is intended to mimic `head()` and `tail()` to inspect data without looking at every value

Value

an object of class equivalent to `x`.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
x <- 1:101;
middle(x);
middle(x, evenly=TRUE)

xdf <- data.frame(n=1:101,
   excel_colname=jamba::colNum2excelName(1:101));
middle(xdf)
middle(xdf, evenly=TRUE)
```

`minorLogTicks` *Calculate major and minor tick marks for log-scale axis*

Description

Calculate major and minor tick marks for log-scale axis

Usage

```
minorLogTicks(
  side = NULL,
  lims = NULL,
  logBase = 2,
  displayBase = 10,
  logStep = 1,
  minorWhich = c(2, 5),
  asValues = TRUE,
  offset = 0,
  symmetricZero = (offset > 0),
  col = "black",
  col.ticks = col,
  combine = FALSE,
  logAxisType = c("normal", "flip", "pvalue"),
  verbose = FALSE,
  ...
)
```

Arguments

`side`	`integer` value indicating which axis to produce tick marks, 1=bottom, 2=left, 3=top, 4=right.
`lims`	`numeric` vector length=2, indicating specific numeric range to use for tick marks.
`logBase`	`numeric` value indicating the logarithmic base, assumed to be applied to the numeric `lims` limits, or the axis range, previously.
`displayBase`	`numeric` value indicating the base used to position axis labels, typically `displayBase=10` is used to draw labels at typical positions.

logStep	integer value indicating the number of log steps between major axis label positions. Typically logStep=1 will draw a label every log position based upon displayBase, for example displayBase=10 and logStep=1 will use c(1,10,100,1000); and displayBase=10 and logStep=2 would use c(1,100,10000).
minorWhich	integer vector of values to label, where those integer values are between 1 and displayBase, for example displayBase=10 may label only c(2,5), which implies minor tick labels at c(2, 5, 20, 50, 200, 500). Any minor labels which would otherwise equal a major tick position are removed. By default, when displayBase=2, minorWhich=c(1.5) which has the effect of drawing one minor label between each two-fold major tick label.
asValues	logical indicating whether to create exponentiated numeric labels. When asValues=FALSE, it creates expression objects which include the exponential value. Use asValues=FALSE and logAxisType="pvalue" to draw P-value labels.
offset	numeric value added during log transformation, typically of the form log(1 + x) where offset=1. The offset is used to determine the accurate numeric label such that values of 0 are properly labeled by the original numeric value.
symmetricZero	logical indicating whether numeric values are symmetric around zero. For example, log fold changes should use symmetricZero=TRUE which ensures a log2 value of -2 is labeled -4 to indicate a negative four fold change. If symmetricZero=FALSE a log2 value of -2 would be labeled 0.0625.
col, col.ticks	character color used for the axis label, and axis tick marks, respectively, default "black".
combine	logical, default FALSE, whether to combine major and minor ticks into one continuous set of major tick marks.
logAxisType	character string indicating the type of log axis: • normal: typical axis style and orientation • flipped: used for reverse orientation • pvalue: used for -log10(pvalue) orientation.
verbose	logical indicating whether to print verbose output.
...	additional parameters are ignored.

Details

This function is called by minorLogTicksAxis(), and it may be better to use that function, or logFoldAxis() or pvalueAxis() which has better preset options.

This function calculates log units for the axis of an existing base R plot. It calculates appropriate tick and label positions for:

- major steps, which are typically in log steps; and
- minor steps, which are typically a subset of steps at one lower log order.

For example, log 10 steps would be: c(1, 10, 100, 1000), and minor steps would be c(2, 5, 20, 50, 200, 500, 2000, 5000).

Motivation:

This function is motivated to fill a few difficult cases:

1. Label axis ticks properly when used together with `offset`. For example `log2(1 + x)` uses `offset=1`. Other offsets can be used as relevant.
2. Create axis labels which indicate negative fold change values, for example `-2` in log2 fold change units would be labeled with fold change `-4`, and not `0.0625`.
3. Use symmetric tick marks around x=0 when applied to log fold changes.
4. Display actual P-values when plotting `log10(Pvalue)`, which is common for volcano plots.

Value

`list` of axis tick positions, and corresponding labels, for major and minor ticks. Note that labels may be `numeric`, `character`, or `expression`. Specifically when `expression` the `graphics::axis()` must be called once per label.

- majorTicks: `numeric` position of each major tick mark
- minorTicks: `numeric` position of each minor tick mark
- allTicks: `numeric` position of each major tick mark
- majorLabels: label to show for each tick mark
- minorLabels: label to show for each tick mark
- minorSet: the `numeric` steps requested for minor ticks
- minorWhich: the `numeric` steps requested for minor labels
- allLabelsDF: `data.frame` with all tick marks and labels, with colname `"use"` indicating whether the label is displayed beside each tick mark.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
## This example shows how to draw axis labels manually,
## but the function minorLogTicksAxis() is easier to use.
xlim <- c(0,4);
nullPlot(xlim=xlim, doMargins=FALSE);
mlt <- minorLogTicks(1,
   logBase=10,
   offset=1,
   minTick=0);
maj <- subset(mlt$allLabelsDF, type %in% "major");
graphics::axis(1, las=2,
   at=maj$tick, label=maj$text);
min <- subset(mlt$allLabelsDF, type %in% "minor");
graphics::axis(1, las=2, cex.axis=0.7,
   at=min$tick, label=min$text,
   col="blue");
graphics::text(x=log10(1+c(0,5,50,1000)), y=rep(1.7, 4),
```

```
   label=c(0,5,50,1000), srt=90);

nullPlot(xlim=c(-4,10), doMargins=FALSE);
abline(v=0, lty=2)
graphics::axis(3, las=2);
minorLogTicksAxis(1, logBase=2, displayBase=10, symmetricZero=TRUE);

nullPlot(xlim=c(-4,10), doMargins=FALSE);
graphics::axis(3, las=2);
minorLogTicksAxis(1, logBase=2, displayBase=10, offset=1);
x2 <- stats::rnorm(1000) * 40;
d2 <- stats::density(log2(1+abs(x2)) * ifelse(x2<0, -1, 1));
lines(x=d2$x, y=normScale(d2$y)+1, col="green4");

nullPlot(xlim=c(0,10), doMargins=FALSE);
graphics::axis(3, las=2);
minorLogTicksAxis(1, logBase=2, displayBase=10, offset=1);
x1 <- c(0, 5, 15, 200);
graphics::text(y=rep(1.0, 4), x=log2(1+x1), label=x1, srt=90, adj=c(0,0.5));
graphics::points(y=rep(0.95, 4), x=log2(1+x1), pch=20, cex=2, col="blue");
```

`minorLogTicksAxis` *Display major and minor tick marks for log-scale axis*

Description

Display major and minor tick marks for log-scale axis, with optional offset for proper labeling of `log2(1+x)` with numeric offset.

Log fold axis

Usage

```
minorLogTicksAxis(
  side = NULL,
  lims = NULL,
  logBase = 2,
  displayBase = 10,
  offset = 0,
  symmetricZero = (offset > 0),
  majorCex = 1,
  minorCex = 0.65,
  doMajor = TRUE,
  doMinor = TRUE,
  doLabels = TRUE,
  doMinorLabels = TRUE,
  asValues = TRUE,
  logAxisType = c("normal", "flip", "pvalue"),
```

```
  padj = NULL,
  doFormat = TRUE,
  big.mark = ",",
  scipen = 10,
  minorWhich = c(2, 5),
  logStep = 1,
  cex = 1,
  las = 2,
  col = "black",
  col.ticks = col,
  minorLogTicksData = NULL,
  verbose = FALSE,
  ...
)

logFoldAxis(
  side = NULL,
  lims = NULL,
  logBase = 2,
  displayBase = 2,
  offset = 0,
  symmetricZero = TRUE,
  asValues = TRUE,
  minorWhich = NULL,
  doMinor = TRUE,
  doMinorLabels = NULL,
  scipen = 1,
  ...
)

pvalueAxis(
  side = 2,
  lims = NULL,
  displayBase = 10,
  logBase = 10,
  logAxisType = "pvalue",
  asValues = FALSE,
  doMinor = FALSE,
  doMinorLabels = FALSE,
  scipen = 1,
  ...
)
```

Arguments

side	integer indicating the axis side, 1=bottom, 2=left, 3=top, 4=right.
lims	NULL or numeric range for which the axis tick marks will be determined. If NULL then the corresponding graphics::par("usr") will be used.

logBase
: numeric value indicating the log base units, which will be used similar to how base is used in log(x, base).

displayBase
: numeric value indicating the log base units to use when determining the numeric label position. For example, data may be log2 scaled, and yet it is visually intuitive to show log transformed axis units in base 10 units. See examples.

offset
: numeric offset used in transforming the numeric data displayed on this axis. For example, a common technique is to transform data using log2(1+x) which adds 1 to values prior to the log2 transformation. In this case, offset=1, which ensures the axis labels exactly match the initial numeric value prior to the log2 transform.

symmetricZero
: logical indicating whether numeric values are symmetric around zero. For example, log fold changes should use symmetricZero=TRUE which ensures a log2 value of -2 is labeled -4 to indicate a negative four fold change. If symmetricZero=FALSE a log2 value of -2 would be labeled 0.0625.

majorCex, minorCex
: numeric base text size factors, relative to cex=1 for default text size. These factors are applied in addition to existing graphics::par("cex") values, preserving any global text size defined there.

doMajor, doMinor, doLabels, doMinorLabels
: logical, default TRUE, whether to display each type of tick and label.

- doMajor display major ticks, at displayBase positions
- doMinor display minor ticks at intermediate positions
- doLabels display any labels
- doMinorLabels display minor labels

asValues
: logical, default TRUE, whether to print the exponentiated value, otherwise FALSE will print the log value.

logAxisType
: character string with the type of axis values:

- "normal": axis values as-is.
- "flip": inverted axis values, for example where negative values should be displayed as negative log-transformed values.
- "pvalue": for values transformed as -log10(pvalue)

padj
: numeric vector length 2, which is used to position axis labels for the minor and major labels, respectively. For example, padj=c(0,1) will position minor labels just to the left of the tick marks, and major labels just to the right of tick marks. This example is helpful when minor labels bunch up on the right side of each section.

doFormat
: logical indicating whether to apply base::format() to format numeric labels.

big.mark, scipen
: arguments passed to base::format() when doFormat=TRUE.

minorWhich
: integer vector indicating which of the minor tick marks should be labeled. Labels are generally numbered from 2 to displayBase-1. So by default, log 10 units would add minor tick marks and labels to the c(2,5) position. For log2 units only, the second label is defined at 1.5, which shows minor labels at c(3, 6, 12), which are 1.5 * c(2, 4, 8).

logStep integer the number of log units per "step", typically 1.

cex, col, col.ticks, las
parameters used for axis label size, axis label colors, axis tick mark colors, and label text orientation, respectively.

minorLogTicksData
list object created by running jamba::minorLogTicks(), which allows inspecting and modifying the content for custom control.

verbose logical indicating whether to print verbose output.

... Additional arguments are ignored.

Details

This function displays log units on the axis of an existing base R plot. It calls jamba::minorLogTicks() which calculates appropriate tick and label positions.

Note: This function assumes the axis values have already been log-transformed. Make sure to adjust the offset to reflect the method of log-transformation, for example:

- log2(1+x) would require logBase=2 and offset=1 in order to represent values properly at or near zero.
- log(0.5+x) would require logBase=exp(1) and offset=0.5.
- log10(x) would require logBase=10 and offset=0.

The defaults logBase=2 and displayBase=10 assume data has been log2-transformed, and displays tick marks using the common base of 10. To display tick marks at two-fold intervals, use displayBase=2.

This function was motivated in order to label log-transformed data properly in some special cases, like using log2(1+x) where the resulting values are shifted "off by one" using standard log-scaled axis tick marks and labels.

For log fold changes, set symmetricZero=TRUE, which will create negative log scaled fold change values as needed for negative values. For example, this option would label a logBase=2 value of -2 as -4 and not as 0.25.

Note that by default, whenever offset > 0 the argument symmetricZero=TRUE is also defined, since a negative value in that scenario has little meaning. This behavior can be turned off by setting symmetricZero=FALSE.

Value

list with vectors:

- majorLabels: character vector of major axis labels
- majorTicks: numeric vector of major axis tick positions
- minorLabels: character vector of minor axis labels
- minorTicks: numeric vector of minor axis tick positions
- allLabelsDF: data.frame containing all axis tick positions and corresponding labels.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
plotPolygonDensity(0:100, breaks=100);

plotPolygonDensity(0:100, breaks=50, log="x",
   main="plotPolygonDensity() uses minorLogTicksAxis()",
   xlab="x (log-scaled)");

plotPolygonDensity(log2(1+0:100), breaks=50,
   main="manually called minorLogTicksAxis(logBase=2)",
   xaxt="n",
   xlab="x (log-scaled)");
minorLogTicksAxis(1, offset=1, logBase=2);

plotPolygonDensity(log10(1+0:100), breaks=50,
   main="manually called minorLogTicksAxis(logBase=10)",
   xaxt="n",
   xlab="x (log-scaled)");
minorLogTicksAxis(1, offset=1, logBase=10);

# example with log fold axes
k <- c(-5:5)
plot(x=k, y=k, xaxt="n", yaxt="n",
   xlab="log2 base, displaying tick marks with log10 intervals",
   ylab="log2 base, displaying tick marks with log2 intervals")
axis(3, las=2)
axis(4, las=2)
lfax <- logFoldAxis(side=1, logBase=2, displayBase=2)
lfay <- logFoldAxis(side=2, logBase=2, displayBase=10)
# optionally add x-axis ablines
abline(v=lfax$allTicks, lty="dotted", col="grey88")
abline(v=lfax$majorTicks, lty="dashed", col="grey82")
# optionally add y-axis ablines
abline(h=lfay$allTicks, lty="dotted", col="grey88")
abline(h=lfay$majorTicks, lty="dashed", col="grey82")

# example showing volcano plot features
set.seed(123);
n <- 1000;
vdf <- data.frame(lfc=rnorm(n) * 2)
vdf$`-log10 (padj)` <- abs(vdf$lfc) * abs(rnorm(n))
plotSmoothScatter(vdf, xaxt="n", yaxt="n", xlab="Fold change",
   main="Volcano plot\ndisplayBase=2")
logFoldAxis(1)
pvalueAxis(2)
```

```
plotSmoothScatter(vdf, xaxt="n", yaxt="n", xlab="Fold change",
   main="Volcano plot\ndisplayBase=10")
logFoldAxis(1, displayBase=10)
pvalueAxis(2)
```

`mixedOrder` *order alphanumeric values keeping numeric values in proper order*

Description

order alphanumeric values keeping numeric values in proper order

Usage

```
mixedOrder(
  x,
  ...,
  blanksFirst = TRUE,
  na.last = NAlast,
  keepNegative = FALSE,
  keepInfinite = FALSE,
  keepDecimal = FALSE,
  ignore.case = TRUE,
  useCaseTiebreak = TRUE,
  honorFactor = FALSE,
  returnDebug = FALSE,
  returnType = c("order", "rank"),
  NAlast = TRUE,
  verbose = FALSE,
  debug = FALSE
)
```

Arguments

`x`	input vector
`...`	additional parameters are sent to `mixedOrder()`.
`blanksFirst`	`logical` whether to order blank entries before entries containing a value.
`na.last`	`logical` whether to move NA entries to the end of the sort. When `na.last=TRUE` then `NA` values will always be last, even following blanks and infinite values. When `na.last=FALSE` then `NA` values will always be first, even before blanks and negative infinite values.
`keepNegative`	`logical` whether to keep '-' associated with adjacent numeric values, in order to sort them as negative values. Note that `keepNegative=TRUE` also forces `keepDecimal=TRUE`, and enables matching of scientific notation such as `-1.23e-10` as a numeric value. When `keepNegative=FALSE` the dash `"-"` is treated as a common delimiter.

keepInfinite `logical` whether to allow "Inf" in the input `x` to be considered a numeric infinite value. Note that `"-Inf"` is only treated as a negative infinite value when `keepNegative=TRUE`. Also note that `"Inf"` is only recognized as infinite when it appears between non-character delimiters, and not part of a larger character string like `"Information"`. Be careful with `keepInfinite=TRUE` when sorting gene symbols, there are gene symbols like `"Inf3"` which should not be sorted as infinite. Lastly, infinite values are sorted at the end, notably after all character values which differs from some mixed sorting algorithms.

keepDecimal `logical` whether to keep the decimal in numbers, sorting as a true number and not as a version number. By default keepDecimal=FALSE``, which means "v1.200" will be ordered Decimal=TRUE, the numeric sort orders "v1.200"before"v1.30"‘.

ignore.case `logical` whether to ignore uppercase and lowercase characters when defining the sort order.

useCaseTiebreak `logical` indicating whether to break ties when `ignore.case=TRUE`, using mixed case as a tiebreaker.

honorFactor `logical` indicating whether to honor the order of `levels` if the input `x` is a `factor`. The default `honorFactor=FALSE` is to maintain consistent legacy behavior. The purpose of this function is to enable alphanumeric sorting, which is not the purpose of sorting by factor levels.

returnDebug `logical` indicating whether to include additional debug info as attributes.

returnType `character` string to define the return type:

- "order": returns `integer` order, equivalent to `order()`
- "rank": returns `integer` rank, equivalent to `rank()`

NAlast `logical` DEPRECATED in favor of `na.last` for consistency with other base R functions.

verbose `logical` whether to print verbose output.

debug `logical` indicating whether to return intermediate data useful only for debugging purposes.

Details

This function is a refactor of `gtools` mixedorder() which was the source of inspiration for this function, thanks to Gregory R. Warnes! This function was designed to improve the efficiency for large vectors, and to handle special cases slightly differently. It was driven by some need to sort gene symbols, and miRNA symbols in numeric order, for example:

test set: miR-12,miR-1,miR-122,miR-1b,miR-1a,miR-2

`sort`**:** miR-1,miR-12,miR-122,miR-1a,miR-1b,miR-2

`gtools::mixedsort`**:** miR-122,miR-12,miR-2,miR-1,miR-1a,miR-1b

`mixedSort`**:** miR-1,miR-1a,miR-1b,miR-2,miR-12,miR-122

This function does not by default consider negative numbers as negative, instead it treats ’-’ as a delimiter, unless keepNegative=TRUE.

When keepNegative=TRUE this function also recognizes scientific notation, for example "1.23e-2" will be treated as numeric 0.0123. Note that keepNegative=TRUE also forces keepDecimal=TRUE.

When keepDecimal=TRUE this function maintains numeric values that include one ".".

This function is the core of a family of mixedSort functions:

mixedSort() Applies mixedOrder() to an input vector.

mixedSorts() Applies mixedOrder() to a list of vectors, returning the list where each vector is independently sorted.

mixedSortDF() Applies mixedOrder() to each column of a data.frame or comparable object, optionally specifying the order of columns used during the sort.

Extra thanks to Gregory R. Warnes for the gtools mixedorder() that proved to be so useful it ultimately inspired this function.

Value

integer vector of orders derived from x, or when returnType="rank" an integer vector of ranks allowing ties. The rank is therefore valid for use in chains, such as multiple columns of a data.frame.

See Also

gtools::mixedorder(), gtools::mixedsort()

Other jam sort functions: mixedSort(), mixedSortDF(), mixedSorts(), mmixedOrder()

Examples

```
x <- c("miR-12","miR-1","miR-122","miR-1b", "miR-1a","miR-2");
mixedOrder(x);
x[mixedOrder(x)];
mixedSort(x);
order(x);
x[order(x)];
sort(x);

## Complex example including NA, blanks, and infinite "Inf"
x <- c("Inf",
   "+Inf12",
   NA,
   "-Inf14",
   "-",
   "---",
   "Jnf12",
   "Hnf12",
   "--",
   "Information");
## By default, strings are sorted as-is, "Hnf" before "Inf" before "Jnf"
## blanks are first, NA values are last
x[mixedOrder(x)];

## blanks are last, but before NA values which are also last
```

```
x[mixedOrder(x, blanksFirst=FALSE)];

## Recognize infinite, but not the negative sign
## Now infinite values are at the end, ordered by the number that follows.
x[mixedOrder(x, blanksFirst=FALSE, keepInfinite=TRUE)]

## Now also recognize negative infinite values,
## which puts "-Inf14" at the very beginning.
x[mixedOrder(x, blanksFirst=FALSE, keepInfinite=TRUE, keepNegative=TRUE)]

# test factor level order
factor1 <- factor(c("Cnot9", "Cnot8", "Cnot10"))
sort(factor1)
mixedSort(factor1)
factor1[mixedOrder(factor1)]
factor1[mixedOrder(factor1, honorFactor=TRUE)]
```

`mixedSort` *sort alphanumeric values keeping numeric values in proper order*

Description

sort alphanumeric values keeping numeric values in proper order

Usage

```
mixedSort(
  x,
  blanksFirst = TRUE,
  na.last = NAlast,
  keepNegative = FALSE,
  keepInfinite = FALSE,
  keepDecimal = FALSE,
  ignore.case = TRUE,
  useCaseTiebreak = TRUE,
  honorFactor = FALSE,
  sortByName = FALSE,
  verbose = FALSE,
  NAlast = TRUE,
  ...
)
```

Arguments

`x`	`vector`
`blanksFirst`	`logical` whether to order blank entries before entries containing a value.
`na.last`	`logical` indicating whether to move NA entries at the end of the sort.

keepNegative	logical whether to keep '-' associated with adjacent numeric values, in order to sort them as negative values.
keepInfinite	logical whether to allow "Inf" to be considered a numeric infinite value.
keepDecimal	logical whether to keep the decimal in numbers, sorting as a true number and not as a version number. By default keepDecimal=FALSE, which means "v1.200" should be ordered before "v1.30". When keepDecimal=TRUE, the numeric sort considers only "1.2" and "1.3" and sorts in that order.
ignore.case	logical whether to ignore uppercase and lowercase characters when defining the sort order. Note that when x is factor the factor levels are converted using unique(toupper(levels(x))), therefore the values in x will be sorted by factor level.
useCaseTiebreak	logical indicating whether to break ties when ignore.case=TRUE, using mixed case as a tiebreaker.
honorFactor	logical, default TRUE, indicating whether to honor factor level order in the output, otherwise when FALSE it sorts as character.
sortByName	logical whether to sort the vector x by names(x) instead of sorting by x itself.
verbose	logical whether to print verbose output.
NAlast	logical deprecated in favor of argument na.last for consistency with base::sort().
...	additional parameters are sent to mixedOrder.

Details

This function is a refactor of gtools mixedsort(), a clever bit of R coding from the gtools package. It was extended to make it slightly faster, and to handle special cases slightly differently. It was driven by the need to sort gene symbols, miRNA symbols, chromosome names, all with proper numeric order, for example:

test set: miR-12,miR-1,miR-122,miR-1b,mir-1a

gtools::mixedsort: miR-122,miR-12,miR-1,miR-1a,mir-1b

mixedSort: miR-1,miR-1a,miR-1b,miR-12,miR-122

The function does not by default recognize negative numbers as negative, instead it treats '-' as a delimiter, unless keepNegative=TRUE.

This function also attempts to maintain '.' as part of a decimal number, which can be problematic when sorting IP addresses, for example.

This function is really just a wrapper function for mixedOrder(), which does the work of defining the appropriate order.

The sort logic is roughly as follows:

- Split each term into alternating chunks containing character or numeric substrings, split across columns in a matrix.
- Apply appropriate ignore.case logic to the character substrings, effectively applying toupper() on substrings

- Define rank order of character substrings in each matrix column, maintaining ties to be resolved in subsequent columns.
- Convert `character` to `numeric` ranks via `factor` intermediate, defined higher than the highest `numeric` substring value.
- When `ignore.case=TRUE` and `useCaseTiebreak=TRUE`, an additional tiebreaker column is defined using the `character` substring values without applying `toupper()`.
- A final tiebreaker column is the input string itself, with `toupper()` applied when `ignore.case=TRUE`.
- Apply order across all substring columns.

Therefore, some expected behaviors:

- When `ignore.case=TRUE` and `useCaseTiebreak=TRUE` (default for both) the input data is ordered without regard to case, then the tiebreaker applies case-specific sort criteria to the final product. This logic is very close to default `sort()` except for the handling of internal `numeric` values inside each string.

Value

`vector` of values from argument `x`, ordered by `mixedOrder()`. The output class should match `class(x)`.

See Also

Other jam sort functions: `mixedOrder()`, `mixedSortDF()`, `mixedSorts()`, `mmixedOrder()`

Examples

```
x <- c("miR-12","miR-1","miR-122","miR-1b", "miR-1a", "miR-2");
sort(x);
mixedSort(x);

# test honorFactor
mixedSort(factor(c("Cnot9", "Cnot8", "Cnot10")))
mixedSort(factor(c("Cnot9", "Cnot8", "Cnot10")), honorFactor=TRUE)

# test ignore.case
mixedSort(factor(c("Cnot9", "Cnot8", "CNOT9", "Cnot10")))
mixedSort(factor(c("CNOT9", "Cnot8", "Cnot9", "Cnot10")))
mixedSort(factor(c("Cnot9", "Cnot8", "CNOT9", "Cnot10")), ignore.case=FALSE)
mixedSort(factor(c("Cnot9", "Cnot8", "CNOT9", "Cnot10")), ignore.case=TRUE)

mixedSort(factor(c("Cnot9", "Cnot8", "CNOT9", "Cnot10")), useCaseTiebreak=TRUE)
mixedSort(factor(c("CNOT9", "Cnot8", "Cnot9", "Cnot10")), useCaseTiebreak=FALSE)
```

mixedSortDF *sort data.frame keeping numeric values in proper order*

Description

sort data.frame keeping numeric values in proper order

Usage

```
mixedSortDF(
  df,
  byCols = seq_len(ncol(df)),
  na.last = TRUE,
  decreasing = NULL,
  useRownames = FALSE,
  verbose = FALSE,
  blanksFirst = TRUE,
  keepNegative = FALSE,
  keepInfinite = FALSE,
  keepDecimal = FALSE,
  ignore.case = TRUE,
  useCaseTiebreak = TRUE,
  sortByName = FALSE,
  honorFactor = TRUE,
  ...
)
```

Arguments

df	data.frame input
byCols	one of two types of input: 1. integer vector referring to the order of columns to be used by mmixedOrder() to order the data.frame. Note that negative values will reverse the sort order for the corresponding column number. To sort rownames(df) use zero 0, and to reverse sorting rownames(x) use -0.1 where the negative sign will reverse the sort, and -0.1 will be rounded to 0. 2. character vector of values in colnames(df), optionally including prefix "-" to reverse the sort. Note that the argument decreasing can also be used to specify columns to have reverse sort, either as a single value or vector to be applied to each column in byCols. To sort rownames(df) use "rownames" or "row.names". To reverse sorting rownames(df) use "-rownames" or "-row.names".
na.last	logical whether to move NA entries to the end of the sort. When na.last=TRUE then NA values will always be last, even following blanks and infinite values. When na.last=FALSE then NA values will always be first, even before blanks and negative infinite values.

decreasing — NULL or logical vector indicating which columns in byCols should be sorted in decreasing order. By default, the sign(byCols) is used to define the sort order of each column, but it can be explicitly overridden with this decreasing parameter.

useRownames — logical whether to use rownames(df) as a last tiebreaker in the overall rank ordering. This parameter has the primary effect of assuring a reproducible result, provided the rownames are consistently defined, or if rownames are actually row numbers. When useRownames=FALSE then rows that would otherwise be ties will be returned in the same order they were provided in df.

verbose — logical whether to print verbose output. When verbose=2 there is slightly more verbose output.

blanksFirst, keepNegative, keepInfinite, keepDecimal, ignore.case, useCaseTiebreak, sortByName — arguments passed to mmixedOrder(), except sortByName which is not passed along.

honorFactor — logical, default TRUE, indicating whether to honor factor level order in the output, otherwise when FALSE it sorts as character.

... — additional arguments passed to mmixedOrder() for custom sort options as described in mixedSort().

Details

This function is a wrapper around mmixedOrder() so it operates on data.frame columns in the proper order, using logic similar that used by base::order() when operating on a data.frame. The sort order logic is fully described in mixedSort() and mixedOrder().

Note that byCols can either be given as integer column index values, or character vector of colnames(x). In either case, using negative prefix - will reverse the sort order of the corresponding column.

For example byCols=c(2, -1) will sort column 2 increasing, then column 1 decreasing.

Similarly, one can supply colnames(df), such as byCols=c("colname2", "-colname1"). Values are matched as-is to colnames(df) first, then any values not matched are compared again after removing prefix - from the start of each character string. Therefore, if colnames(df) contains "-colname1" it will be matched as-is, but "--colname1" will only be matched after removing the first -, after which the sort order will be reversed for that column.

For direct control over the sort order of each column defined in byCols, you can supply logical vector to argument decreasing, and this vector is recycled to length(byCols).

Finally, for slight efficiency, only unique columns defined in byCols are used to determine the row order, so even if a column is defined twice in byCols, only the first instance is passed to mmixedOrder() to determine row order.

Value

data.frame whose rows are ordered using mmixedOrder().

See Also

Other jam sort functions: mixedOrder(), mixedSort(), mixedSorts(), mmixedOrder()

Examples

```
# start with a vector of miRNA names
x <- c("miR-12","miR-1","miR-122","miR-1b", "miR-1a","miR-2");
# add some arbitrary group information
g <- rep(c("Air", "Treatment", "Control"), 2);
# create a data.frame
df <- data.frame(group=g,
   miRNA=x,
   stringsAsFactors=FALSE);

# input data
df;

# output when using order()
df[do.call(order, df), , drop=FALSE];

# output with mixedSortDF()
mixedSortDF(df);

# mixedSort respects factor order
# reorder factor levels to demonstrate.
# "Control" should come first
gf <- factor(g, levels=c("Control", "Air", "Treatment"));
df2 <- data.frame(groupfactor=gf,
   miRNA=x,
   stringsAsFactors=FALSE);

# now the sort properly keeps the group factor levels in order,
# which also sorting the miRNA names in their proper order.
mixedSortDF(df2);


x <- data.frame(l1=letters[1:10],
   l2=rep(letters[1:2+10], 5),
   L1=LETTERS[1:10],
   L2=rep(LETTERS[1:2+20], each=5));
set.seed(123);
rownames(x) <- sample(seq_len(10));
x;

# sort by including rownames
mixedSortDF(x, byCols=c("rownames"));
mixedSortDF(x, byCols=c("L2", "-rownames"));

# demonstrate sorting a matrix with no rownames
m <- matrix(c(2, 1, 3, 4), ncol=2);
mixedSortDF(m, byCols=-2)

# add rownames
rownames(m) <- c("c", "a");
mixedSortDF(m, byCols=0)
mixedSortDF(m, byCols="-rownames")
```

```
mixedSortDF(m, byCols="rownames")

mixedSortDF(data.frame(factor1=factor(c("Cnot9", "Cnot8", "Cnot10"))), honorFactor=FALSE)

# test date columns
testfiles <- system.file(package="jamba", c("TODO.md", "README.md", "NEWS.md"))
testinfo <- file.info(testfiles)
testinfo
mixedSortDF(testinfo, byCols="mtime")
```

`mixedSorts` *sort alphanumeric values within a list format*

Description

sort alphanumeric values within a list format

Usage

```
mixedSorts(
  x,
  blanksFirst = TRUE,
  na.last = NAlast,
  keepNegative = FALSE,
  keepInfinite = TRUE,
  keepDecimal = FALSE,
  ignore.case = TRUE,
  useCaseTiebreak = TRUE,
  sortByName = FALSE,
  na.rm = FALSE,
  verbose = FALSE,
  NAlast = TRUE,
  honorFactor = TRUE,
  xclass = NULL,
  indent = 0,
  debug = FALSE,
  ...
)
```

Arguments

x	vector
blanksFirst	logical whether to order blank entries before entries containing a value.
na.last	logical indicating whether to move NA entries at the end of the sort.
keepNegative	logical whether to keep '-' associated with adjacent numeric values, in order to sort them as negative values.

keepInfinite	logical whether to allow "Inf" to be considered a numeric infinite value.
keepDecimal	logical whether to keep the decimal in numbers, sorting as a true number and not as a version number. By default keepDecimal=FALSE, which means "v1.200" should be ordered before "v1.30". When keepDecimal=TRUE, the numeric sort considers only "1.2" and "1.3" and sorts in that order.
ignore.case	logical whether to ignore uppercase and lowercase characters when defining the sort order. Note that when x is factor the factor levels are converted using unique(toupper(levels(x))), therefore the values in x will be sorted by factor level.
useCaseTiebreak	logical indicating whether to break ties when ignore.case=TRUE, using mixed case as a tiebreaker.
sortByName	logical whether to sort the vector x by names(x) instead of sorting by x itself.
na.rm	logical, default FALSE, indicating whether to remove NA values.
verbose	logical whether to print verbose output.
NAlast	logical deprecated in favor of argument na.last for consistency with base::sort().
honorFactor	logical, default TRUE, used to enforce factor level sort order, when FALSE it sorts as character.
xclass	character vector of classes in x, used for slight optimization to re-use this vector if it has already been defined for x. When NULL it is created within this function.
indent	numeric used only when verbose=TRUE to determine the number of spaces indented for verbose output, passed to printDebug().
debug	logical, default FALSE, whether to print detailed debug output.
...	additional parameters are sent to mixedOrder.

Details

This function is an extension to mixedSort() to sort each vector in a list. It applies the sort to the whole unlisted vector then splits back into list form.

In the event the input is a nested list of lists, only the first level of list structure is maintained in the output data. For more information, see rlengths() which calculates the recursive nested list sizes. An exception is when the data contained in x represents multiple classes, see below.

When data in x represents multiple classes, for example character and factor, the mechanism is slightly different and not as well- optimized for large length x. The method uses rapply(x, how="replace", mixedSort) which recursively, and iteratively, calls mixedSort() on each vector, and therefore returns data in the same nested list structure as provided in x.

When data in x represents only one class, data is unlist() to one large vector, which is sorted with mixedSort(), then split back into list structure representing x input.

Value

list after applying mixedSort() to its elements.

See Also

Other jam sort functions: mixedOrder(), mixedSort(), mixedSortDF(), mmixedOrder()

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), rbindList(), relist_named(), rlengths(), sclass(), sdim(), uniques(), unnestList()

Examples

```
# set up an example list of mixed alpha-numeric strings
set.seed(12);
x <- paste0(sample(letters, replace=TRUE, 52), rep(1:30, length.out=52));
x;
# split into a list as an example
xL <- split(x, rep(letters[1:5], c(6,7,5,4,4)));
xL;

# now run mixedSorts(xL)
# Notice "e6" is sorted before "e30"
mixedSorts(xL)

# for fun, compare to lapply(xL, sort)
# Notice "e6" is sorted after "e30"
lapply(xL, sort)

# test super-long list
xL10k <- rep(xL, length.out=10000);
names(xL10k) <- as.character(seq_along(xL10k));
print(head(mixedSorts(xL10k), 10))

# Now make some list vectors into factors
xF <- xL;
xF$c <- factor(xL$c)
# for fun, reverse the levels
xF$c <- factor(xF$c,
   levels=rev(levels(xF$c)))
xF
mixedSorts(xF)

# test super-long list
xF10k <- rep(xF, length.out=10000);
names(xF10k) <- as.character(seq_along(xF10k));
print(head(mixedSorts(xF10k), 10))

# Make a nested list
set.seed(1);
l1 <- list(
   A=sample(nameVector(11:13, rev(letters[11:13]))),
   B=list(
      C=sample(nameVector(4:8, rev(LETTERS[4:8]))),
      D=sample(nameVector(LETTERS[2:5], rev(LETTERS[2:5])))
   )
)
l1;
```

```
# The output is a nested list with the same structure
mixedSorts(l1);
mixedSorts(l1, sortByName=TRUE);

# Make a nested list with two sub-lists
set.seed(1);
l2 <- list(
   A=list(
      E=sample(nameVector(11:13, rev(letters[11:13])))
   ),
   B=list(
      C=sample(nameVector(4:8, rev(LETTERS[4:8]))),
      D=sample(nameVector(LETTERS[2:5], rev(LETTERS[2:5])))
   )
)
l2;
# The output is a nested list with the same structure
mixedSorts(l2);
mixedSorts(l2, sortByName=TRUE);

# when one entry is missing
L0 <- list(A=3:1,
   B=list(C=c(1:3,NA,0),
   D=LETTERS[c(4,5,2)],
   E=NULL));
L0
mixedSorts(L0)
mixedSorts(L0, na.rm=TRUE)
```

`mmixedOrder` *order alphanumeric values from a list*

Description

order alphanumeric values from a list

Usage

```
mmixedOrder(
  ...,
  decreasing = FALSE,
  blanksFirst = TRUE,
  na.last = NAlast,
  keepNegative = FALSE,
  keepInfinite = FALSE,
  keepDecimal = FALSE,
  ignore.case = TRUE,
  useCaseTiebreak = TRUE,
```

```
  sortByName = FALSE,
  NAlast = TRUE,
  honorFactor = TRUE,
  verbose = FALSE,
  matrixAsDF = TRUE
)
```

Arguments

`...`	arguments treated as a `list` of vectors to be ordered in proper order, based upon the mechanism by `base::order()`, and as such `data.frame` is equivalent to a `list`.
`decreasing`	`logical`, default FALSE, used to reverse the sort order.
`blanksFirst, na.last, keepNegative, keepInfinite, keepDecimal, ignore.case, useCaseTiebreak, sortByName`	arguments passed to `mixedOrder()`, except `sortByName` which is not passed along.
`NAlast`	`logical` deprecated in favor of argument `na.last` for consistency with `base::sort()`.
`honorFactor`	`logical`, default TRUE, used to enforce factor level sort order, when FALSE it sorts as `character`.
`verbose`	`logical` indicating whether to print verbose output, passed as `verbose - 1` to `mixedOrder()`.
`matrixAsDF`	`logical` if `...` supplies only one matrix object, then `matrixAsDF=TRUE` will cause it to be converted to a `data.frame`, then coerce to a `list` before processing. By default, in the event only one matrix object is supplied, this conversion is performed, in order to define a sort order based upon each column in order, consistent with behavior of `data.frame` input.

Details

This function is a minor extension to `mixedOrder()`, "multiple `mixedOrder()`", which accepts `list` input, similar to how `base::order()` operates. This function is mainly useful when sorting something like a `data.frame`, where ties in column 1 should be maintained then broken by non-equal values in column 2, and so on.

This function essentially converts any non-numeric column to a factor, whose levels are sorted using `mixedOrder()`. That factor is converted to numeric value, multiplied by `-1` when `decreasing=TRUE`. Finally the list of numeric vectors is passed to `base::order()`.

In fact, `mixedSortDF()` calls this `mmixedOrder()` function, in order to sort a `data.frame` properly by column.

See `mixedOrder()` and `mixedSort()` for a better description of how the sort order logic operates.

Value

`integer` vector of row orders

See Also

Other jam sort functions: `mixedOrder()`, `mixedSort()`, `mixedSortDF()`, `mixedSorts()`

Examples

```
# test factor level order
factor1 <- factor(c("Cnot9", "Cnot8", "Cnot10"))
sort(factor1)
mixedSort(factor1)
factor1[mixedOrder(factor1)]
factor1[mixedOrder(factor1, honorFactor=FALSE)]
factor1[mixedOrder(factor1, honorFactor=TRUE)]

factor1[mmixedOrder(list(factor1))]
factor1[mmixedOrder(list(factor1), honorFactor=FALSE)]
factor1[mmixedOrder(list(factor1), honorFactor=TRUE)]
```

---

nameVector *assign unique names for a vector*

Description

assign unique names for a vector

Usage

```
nameVector(x, y = NULL, makeNamesFunc = makeNames, ...)
```

Arguments

x	`character` vector, or `data.frame` or equivalent (matrix, or tibble) with two columns, the second column is used to name values in the first column.
y	`character` or NULL, with names. If NULL then x is used. Note that y is recycled to the length of x, prior to being sent to the makeNamesFunc. In fringe cases, y can be a matrix, data.frame, or tibble, in which case `pasteByRow()` will be used to create a character string to be used for vector names. Note this case is activated only when x is not a two column matrix, data.frame, or tibble.
makeNamesFunc	`function` to make names unique, by default `makeNames()` which ensures names are unique.
...	passed to `makeNamesFunc`, or to `pasteByRow()` if y is a two column data.frame, matrix, or tibble. Thus, `sep` can be defined here as a delimiter between column values.

Details

This function assigns unique names to a vector, if necessary it runs `makeNames` to create unique names. It differs from `setNames` in that it ensures names are unique, and when no names are supplied, it uses the vector itself to define names. It is helpful to run this function inside an `lapply` function call, which by default maintains names, but does not assign names if the input data did not already have them.

When used with a data.frame, it is particularly convenient to pull out a named vector of values. For example, log2 fold changes by gene, where the gene symbols are the name of the vector.

```
nameVector(genedata[,c("Gene","log2FC")])
```

Value

vector with names defined

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
# it generally just creates names from the vector values
nameVector(LETTERS[1:5]);

# if values are replicated, the makeNames() function makes them unique
V <- rep(LETTERS[1:5], each=3);
nameVector(V);

# for a two-column data.frame, it creates a named vector using
# the values in the first column, and names in the second column.
df <- data.frame(seq_along(V), V);
df;
nameVector(df);

# Lastly, admittedly a fringe case, it can take a multi-column data.frame
# to generate labels:
nameVector(V, df);
```

---

nameVectorN *define a named vector using vector names*

Description

define a named vector using vector names

Usage

```
nameVectorN(x, makeNamesFunc = makeNames, ...)
```

Arguments

x	character vector or any object which has names available names(x).
makeNamesFunc	function used to create unique names, in the event that the names(x) are not unique.
...	Additional arguments are ignored.

Details

This function creates a vector from the names of the input vector, then assigns the same as names. The utility is mainly for lapply functions which maintain the name of a vector in its output. The reason to run lapply using names is so the lapply function is operating only on the name and not the data it references, which can be convenient when the name of the element is useful to known inside the function body. The reason to name the names, is so the list object returned by lapply is also named with these same consistent names.

Consider a list of data.frames, each of which represents stats results from a contrast and fold change. The data.frame may not indicate the name of the contrast, while the list itself may be named by the contrast. One would lapply(nameVectorN(listDF), function(iName)iName) which allows the internal function access to the name of each list element. This could for example be added to the data.frame.

Value

vector of names, whose names are uniquely assigned using makeNames using the values of the vector.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
# a simple integer vector with character names
L <- nameVector(1:5, LETTERS[1:5]);
L;

# we can make a vector of names, retaining the names
nameVectorN(L);

# Now consider a named list, where the name is important
# to keep for downstream work.
K <- list(A=(1:3)^3, B=7:10, C=(1:4)^2);
K;
# Typical lapply-style work does not operate on the name,
# making it difficult to use the name inside the function.
# Here, we just add the name to the colnames, but anything
# could be useful.
lapply(K, function(i){
```

```
    data.frame(mean=mean(i), median=stats::median(i));
 });

# So the next step is to run lapply() on the names
lapply(names(K), function(i){
   iDF <- data.frame(mean=mean(K[[i]]), median=stats::median(K[[i]]));
   colnames(iDF) <- paste(c("mean", "median"), i);
   iDF;
})
# The result is good, but the list is no longer named.
# The nameVectorN() function is helpful for maintaining the names.

# So we run lapply() on the named-names, which keeps the names in
# the resulting list, and sends it into the function.
lapply(nameVectorN(K), function(i){
   iDF <- data.frame(mean=mean(K[[i]]), median=stats::median(K[[i]]));
   colnames(iDF) <- paste(c("mean", "median"), i);
   iDF;
});
```

`newestFile` *Return the newest file from a vector of files*

Description

Return the newest file from a vector of files

Usage

```
newestFile(x, timecol = "mtime", n = 1, ...)
```

Arguments

`x`	`character` vector of files, specifying file path where required.
`timecol`	`character` value from the output of `base::file.info()` indicating the time column used to order files. By default `"mtime"` refers to the time the file was last modified.
`n`	`integer` number of files to return, in order of the most recent to the least recent. By default `n=1` returns only the one newest file.
`...`	additional parameters are ignored.

Details

This function returns the newest file, defined by the most recently modified time obtained from `base::file.info()`.

Value

`character` vector `length=1` of the most recently modified file from the input vector `x`. Note that any files not found are removed, using `base::file.exists()`, which means invalid symlinks will be ignored.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`, `setPrompt()`

Examples

```
newestFile(list.files());
```

---

noiseFloor *Apply noise floor and ceiling to numeric vector*

Description

Apply noise floor and ceiling to numeric vector

Usage

```
noiseFloor(
  x,
  minimum = 0,
  newValue = minimum,
  adjustNA = FALSE,
  ceiling = NULL,
  newCeiling = ceiling,
  ...
)
```

Arguments

`x`	`numeric` vector or matrix
`minimum`	`numeric` floor value
`newValue`	`numeric`, by default the same as the floor value. Sometimes it can be useful to define a different value, one example is to define values as `NA`, or another distinct number away from the floor.
`adjustNA`	`logical` whether to change `NA` values to the `newValue`.
`ceiling`	`numeric` value, optionally a ceiling. If defined, then values above the ceiling value are set to `newCeiling`.

newCeiling	numeric value when ceiling is defined, values above the ceiling are set to this numeric value.
...	additional parameters are ignored.

Details

A noise floor is useful when detected numeric values are sometimes below a clear noise threshold, and where some downstream ratio may be calculated using these values. Applying a noise floor ensures the ratios and not artificially higher, especially in cases where the values involved are least reliable. This procedure is expected to produce more conservative and appropriate ratios in that scenario.

A ceiling is similar, values above the ceiling are set to the ceiling, which is practical when values above a certain threshold are conceptually similar to those at the threshold. One clear example is plotting `-log10(Pvalue)` when the range of P-values might approach 1e-1000. In this case, setting a ceiling of 50 conceptually equates P-values below 1e-50, while also restricting the axis range of a plot.

The ability to set values at the floor to a different value, using `newValue` different from `minimum`, is intended to allow separation of numeric values from the floor for illustrative purposes.

Value

`numeric` vector or `matrix`, matching the input type `x` where numeric values are fixed to the `minimum` and `ceiling` values as defined by `newValue` and `newCeiling`, respectively.

See Also

Other jam numeric functions: `deg2rad()`, `normScale()`, `rad2deg()`, `rowGroupMeans()`, `rowRmMadOutliers()`, `warpAroundZero()`

Examples

```
# start with some random data
n <- 2000;
x1 <- stats::rnorm(n);
y1 <- stats::rnorm(n);

# apply noise floor and ceiling
x2 <- noiseFloor(x1, minimum=-2, ceiling=2);
y2 <- noiseFloor(y1, minimum=-2, ceiling=2);

# apply noise floor and ceiling with custom replacement values
xm <- cbind(x=x1, y=y1);
xm3 <- noiseFloor(xm,
   minimum=-2, newValue=-3,
   ceiling=2, newCeiling=3);

withr::with_par(list("mfrow"=c(2,2)), {
plotSmoothScatter(x1, y1);
plotSmoothScatter(x2, y2);
plotSmoothScatter(xm3);
```

```
})
```

`normScale` *Scale a numeric vector from 0 to 1*

Description

Scale a numeric vector from 0 to 1

Usage

```
normScale(
  x,
  from = 0,
  to = 1,
  low = min(x, na.rm = TRUE),
  high = max(x, na.rm = TRUE),
  naValue = NA,
  singletMethod = c("mean", "min", "max"),
  ...
)
```

Arguments

`x`	`numeric` vector.
`from`	the minimum `numeric` value to re-scale the input numeric vector.
`to`	the maximum `numeric` value to re-scale the input numeric vector.
`low`	`numeric` value defining the low end of the input numeric range, intended when input values might not contain the entire numeric range to be re-scaled.
`high`	`numeric` value defining the high end of the input numeric range, intended when input values might not contain the entire numeric range to be re-scaled.
`naValue`	optional `numeric` value used to replace `NA`, usually by replacing `NA` with zero.
`singletMethod`	`character` value describing how to handle singlet input values, for example how to scale the number 5 by itself. • "mean" then it uses the average of `from` and `to`, • "min" uses the `from` value, and • "max" uses the `to` value.
`...`	additional parameters are ignored.

Details

This function is intended as a quick way to scale numeric values between 0 and 1, however other ranges can be defined as needed.

NA values are ignored and will remain NA in the output. To handle NA values, use the `rmNA()` function, which can optionally replace NA with a fixed numeric value.

The parameters `low` and `high` are used optionally to provide a fixed range of values expected for `x`, which is useful for consistent scaling of `x`. Specifically, if `x` may be a vector of numeric values ranging from 0 and 100, you would define `low=0` and `high=100` so that `x` will be consistently scaled regardless what actual range is represented by `x`.

Note that when `x` contains only one value, and `low` and `high` are not defined, then `x` will be scaled based upon the argument `singletMethod`. For example, if you provide `x=2` and want to scale `x` values to between 0 and 10... `x` can either be the `mean` value `5`; the `minimum` value `0`; or the `maximum` value `10`.

However, if `low` or `high` are defined, then x will be scaled relative to that range.

Value

`numeric` vector after applying the transformations.

See Also

Other jam numeric functions: `deg2rad()`, `noiseFloor()`, `rad2deg()`, `rowGroupMeans()`, `rowRmMadOutliers()`, `warpAroundZero()`

Examples

```
# Notice the first value 1 is re-scaled to 0
normScale(1:11);

# Scale values from 0 to 10
normScale(1:11, from=0, to=10);

# Here the low value is defined as 0
normScale(1:10, low=0);

normScale(c(10,20,40,30), from=50, to=65);
```

`nullPlot` *Create a blank plot with optional labels*

Description

Create a blank plot with optional labels for margins

Usage

```
nullPlot(
  xaxt = "n",
  yaxt = "n",
  xlab = "",
  ylab = "",
  col = "transparent",
  xlim = c(1, 2),
  ylim = c(1, 2),
  las = graphics::par("las"),
  doBoxes = TRUE,
  doUsrBox = doBoxes,
  fill = "#FFFF9966",
  doAxes = FALSE,
  doMargins = TRUE,
  marginUnit = c("lines", "inches"),
  plotAreaTitle = "Plot Area",
  plotSrt = 0,
  plotNumPrefix = "",
  bty = "n",
  showMarginsOnly = FALSE,
  add = FALSE,
  ...
)
```

Arguments

xaxt	character value compatible withoptions("xaxt")
yaxt	character value compatible with options("xaxt")
xlab	character x-axis label
ylab	character y-axis label
col	character colors passed to plot()
xlim	numeric x-axis range
ylim	numeric y-axis range
las	integer value indicating whether axis labels should be parallel (1) or perpendicular (2) to the axis line.
doBoxes	logical whether to draw annotated boxes around the plot and inner and outer margins.
doUsrBox	logical whether to draw a colored bow indicating the exact plot space, using the function usrBox().
fill	character R color used to fill the background of the plot as used by usrBox().
doAxes	logical whether to draw default x- and y-axes.
doMargins	logical whether to label margins, only active when doBoxes=TRUE.
marginUnit	character indicating the units used for margin labels.

plotAreaTitle	character label printed in the center of the plot area.
plotSrt	numeric angle for the plotAreaTitle, which is good for labeling this plot with vertical text when displaying a plot panel inside a grid layout, where the plot is taller than it is wide.
plotNumPrefix	character or integer label appended as suffix to margin labels, which is useful when annotating multiple plots in a grid layout, where labels are sometimes quite close together. This label is but a simple attempt to sidestep the real problem of fitting labels inside each visual component.
bty	character passed plot(), default "n" suppresses the default box, which can then be optionally drawn based upon the doBoxes parameter.
showMarginsOnly	logical whether to create a new plot or to annotate an existing active plot.
add	logical whether to add to an existing active R plot, or create a new plot window.
...	additional arguments are ignored.

Details

This function creates an empty plot space, using the current graphics::par() settings for margins, text size, etc. By default it displays a box around the plot window, and labels the margins and plot area for review. It can be useful as a visual display of various base graphics settings, or to create an empty plot window with pre-defined axis ranges. Lastly, one can use this function to create a "blank" plot which uses a defined background color, which can be a useful precursor to drawing an image density which may not cover the whole plot space.

Value

no output, this function is called for the byproduct of creating a blank plot, optionally annotating the margins.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
nullPlot()

nullPlot(doBoxes=FALSE)
```

padInteger *prefix integers with leading zeros*

Description

prefix integers with leading zeros

Usage

```
padInteger(x, padCharacter = "0", useNchar = NULL, ...)
```

Arguments

x	integer, numeric, or character vector. In reality, only nchar(x) is required to determine padding.
padCharacter	character with nchar(padCharacter)==1, used to pad each digit as a prefix.
useNchar	NULL or integer number of digits used, or if the maximum nchar(x) is higher, that number of digits is used. Note useNchar is mostly useful when all numbers are less than 10, but the desired output is to have a fixed number of digits 2 or higher.
...	additional parameters are ignored.

Details

The purpose of this function is to pad integer numbers so they contain a consistent number of digits, which is helpful when sorting values as character strings.

Value

character vector of length(x).

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), nameVectorN(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
padInteger(c(1, 10, 20, 300, 5000))
```

padString *pad a character string to a fixed length*

Description

pad a character string to a fixed length

Usage

```
padString(
  x,
  stringLength = max(nchar(x)),
  padCharacter = " ",
  justify = "left",
  ...
)
```

Arguments

x	character vector
stringLength	integer length for the resulting character strings in x. By default, all strings are padded to the length of the longest entry, however stringLength can be defined to impose strict number of characters for all entries.
padCharacter	character string with nchar=1 used for padding.
justify	character string with "left", "right", "center" to indicate alignment of the resulting text string.
...	additional parameters are ignored.

Value

character vector of length(x)

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), nameVectorN(), padInteger(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount(), ucfirst()

Examples

```
padString(c("one","two","three"));
padString(c("one","two","three","four"), padCharacter="_", justify="center");
```

pasteByRow *Paste data.frame rows into character vector*

Description

Paste data.frame rows into a character vector, optionally removing empty fields in order to avoid delimiters being duplicated.

Usage

```
pasteByRow(
  x,
  sep = "_",
  na.rm = TRUE,
  condenseBlanks = TRUE,
  includeNames = FALSE,
  sepName = ":",
  blankGrep = "^[ ]*$",
  verbose = FALSE,
  ...
)
```

Arguments

x	data.frame or comparable object such as matrix or tibble.
sep	character string separator to use between columns.
na.rm	logical whether to remove NA values, or include them as "NA" strings.
condenseBlanks	logical whether to condense blank or empty values without including an extra delimiter between columns.
includeNames	logical whether to include the colname delimited prior to the value, using sepName as the delimiter.
sepName	character string relevant when includeNames=TRUE, this value becomes the delimiter between name:value.
blankGrep	character string used as regular expression pattern in grep() to recognize blank entries; by default any field containing no text, or only whitespace, is considered a blank entry.
verbose	logical whether to print verbose output.
...	additional arguments are ignored.

Details

This function is intended to paste data.frame (or matrix, or tibble) values for each row of data. It differs from using apply(x, 2, paste):

- it handles factors without converting to integer factor level numbers.

- it also by default removes blank or empty fields, preventing the delimiter from being included multiple times, per the `condenseBlanks` argument.
- it is notably faster than apply, by means of running `paste()` on each column of data, making the output vectorized, and scaling rather well for large `data.frame` objects.

The output can also include name:value pairs, which can make the output data more self-describing in some circumstances. That said, the most basic usefulness of this function is to create row labels.

Value

`character` vector of length `nrow(x)`.

See Also

Other jam string functions: `asSize()`, `breaksByVector()`, `fillBlanks()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRowOrdered()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
# create an example data.frame
a1 <- c("red","blue")[c(1,1,2)];
b1 <- c("yellow","orange")[c(1,2,2)];
d1 <- c("purple","green")[c(1,2,2)];
df2 <- data.frame(a=a1, b=b1, d=d1);
df2;

# the basic output
pasteByRow(df2);

# Now remove an entry to show the empty field is skipped
df2[3,3] <- "";
pasteByRow(df2);

# the output tends to make good rownames
rownames(df2) <- pasteByRow(df2);

# since the data.frame contains colors, we display using
# imageByColors()
withr::with_par(list("mar"=c(5,10,4,2)), {
imageByColors(df2, cellnote=df2);
})
```

---

pasteByRowOrdered *Paste data.frame rows into an ordered factor*

Description

Paste data.frame rows into an ordered factor

Usage

```
pasteByRowOrdered(
  x,
  sep = "_",
  na.rm = TRUE,
  condenseBlanks = TRUE,
  includeNames = FALSE,
  keepOrder = FALSE,
  byCols = seq_len(ncol(x)),
  na.last = TRUE,
  ...
)
```

Arguments

x	data.frame
sep	character separator to use between columns
na.rm	logical whether to remove NA values, or include them as "NA"
condenseBlanks	logical whether to condense blank or empty values without including an extra delimiter between columns.
includeNames	logical whether to include the colname delimited prior to the value, using sepName as the delimiter.
keepOrder	logical indicating whether non-factor columns should order factor levels based upon the existing order of unique items. This option is intended for data.frame whose columns are already sorted in proper order, but where columns are not factor with appropriate factor levels. Note that even when keepOrder=TRUE all existing factor columns will honor the order of factor levels already present in those columns.
byCols	integer or character passed to mixedSortDF(). This argument defines the order of columns sorted by mixedSortDF(), and does not affect the order of columns pasted. Columns are always pasted in the same order they appear in x. This argument byCols was previously passed via ... but is added here to make this connection more direct.
na.last	logical passed to base::factor() to determine whether NA values are first or last in factor level order.
...	additional arguments are passed to jamba::pasteByRow(), and to jamba::mixedSortDF().

Details

This function is an extension to jamba::pasteByRow() which pastes rows from a data.frame into a character vector. This function defines factor levels by running jamba::mixedSortDF(unique(x)) and calling jamba::pasteByRow() on the result. Therefore the original order of the input x is maintained while the factor levels are based upon the appropriate column-based sort.

Note that the ... additional arguments are passed to jamba::mixedSortDF() to customize the column-based sort order, used to define factor levels. A good way to test the order of factors is

to run `jamba::mixedSortDF(unique(x))` with appropriate arguments, and confirm the rows are ordered as expected.

Note also that `jamba::mixedSortDF()` uses `jamba::mixedSort()` which itself performs alphanumeric sort in order to keep values in proper numeric order where possible.

Value

`factor` vector whose levels are defined by existing factor levels, then by sorted values.

See Also

Other jam string functions: `asSize()`, `breaksByVector()`, `fillBlanks()`, `formatInt()`, `gsubOrdered()`, `gsubs()`, `makeNames()`, `nameVector()`, `nameVectorN()`, `padInteger()`, `padString()`, `pasteByRow()`, `sizeAsNum()`, `tcount()`, `ucfirst()`

Examples

```
f <- LETTERS;
df <- data.frame(A=f[rep(1:3, each=2)],
   B=c(NA, f[3]),
   C=c(NA, NA, f[2]))
df

# note that output is consistent with mixedSortDF()
jamba::mixedSortDF(df)
jamba::pasteByRowOrdered(df)

jamba::mixedSortDF(df, na.last=FALSE)
jamba::pasteByRowOrdered(df, na.last=FALSE)

jamba::mixedSortDF(df, byCols=c(3, 2, 1))
jamba::pasteByRowOrdered(df, byCols=c(3, 2, 1))

df1 <- data.frame(group=rep(c("Control", "ABC1"), each=6),
   time=rep(c("Hour2", "Hour10"), each=3),
   rep=paste0("Rep", 1:3))
# default will sort each column alphanumerically
pasteByRowOrdered(df1)

# keepOrder=TRUE will honor existing order of character columns
pasteByRowOrdered(df1, keepOrder=TRUE)
```

---

plotPolygonDensity *Plot distribution and histogram overlay*

Description

Plot distribution and histogram overlay

Usage

```
plotPolygonDensity(
  x,
  doHistogram = TRUE,
  doPolygon = TRUE,
  col = NULL,
  barCol = "#00337799",
  polyCol = "#00449977",
  polyBorder = makeColorDarker(polyCol),
  histBorder = makeColorDarker(barCol, darkFactor = 1.5),
  colAlphas = c(0.8, 0.6, 0.9),
  darkFactors = c(-1.3, 1, 3),
  lwd = 2,
  las = 2,
  u5.bias = 0,
  pretty.n = 10,
  bw = NULL,
  breaks = 100,
  width = NULL,
  densityBreaksFactor = 3,
  axisFunc = graphics::axis,
  bty = "l",
  cex.axis = 1.5,
  doPar = TRUE,
  heightFactor = 0.95,
  weightFactor = NULL,
  main = "Histogram distribution",
  xaxs = "i",
  yaxs = "i",
  xaxt = "s",
  yaxt = "s",
  xlab = "",
  ylab = "",
  log = NULL,
  xScale = c("default", "log10", "sqrt"),
  usePanels = TRUE,
  useOnePanel = FALSE,
  ablineV = NULL,
  ablineH = NULL,
  ablineVcol = "#44444499",
  ablineHcol = "#44444499",
  ablineVlty = "solid",
  ablineHlty = "solid",
  removeNA = TRUE,
  add = FALSE,
  ylimQuantile = 0.99,
  ylim = NULL,
  xlim = NULL,
```

```
  highlightPoints = NULL,
  highlightCol = "gold",
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric vector, or numeric matrix. When a matrix is provided, each column in the matrix is used as its own data source.
doHistogram	logical indicating whether to plot histogram bars.
doPolygon	logical indicating whether to plot the density polygon.
col	character color, or when x is supplied as a matrix, a vector of colors is applied to across plot panels. Note that col will override all colors defined for barCol, polyCol, histBorder, polyBorder.
barCol, polyCol, polyBorder, histBorder	character colors used when col is not supplied. They define colors for the histogram bars, polygon fill, polygon border, and histogram bar border, respectively.
colAlphas	numeric vector with length 3, indicating the alpha transparency to use for histogram bar fill, polygon density fill, and border color, respectively. Alpha transparency should be scaled between 0 (fully transparent) and 1 (fully opaque). These alpha transparency values are applied to each color in col when col is defined.
darkFactors	numeric used to adjust colors when col is defined. Values are applied to histogram bar fill, polygon density fill, and border color, respectively, by calling makeColorDarker().
lwd	numeric line width.
las	integer used to define axis label orientation.
u5.bias, pretty.n	numeric arguments passed to to base::pretty() to define pretty axis label positions.
bw	character string of the bandwidth name to use in the density calculation, passed to jamba::breakDensity(). By default stats::density() calls a very smooth density kernel, which obscures finer details, so the default in jamba::breakDensity() uses a more detailed kernel.
breaks	numeric breaks sent to hist to define the number of histogram bars. It can be in the form of a single integer number of equidistant breaks, or a numeric vector with specific break positions, but remember to include a starting value lower the the lowest value in x, and an ending value higher than the highest value in x. Passed to breakDensity().
width	numeric passed to breakDensity().
densityBreaksFactor	numeric scaling factor to control the level of detail in the density, passed to breakDensity().

axisFunc — function optionally used in place of graphics::axis() to define axis labels.

bty — character string used to define the plot box shape, see graphics::box().

cex.axis — numeric scalar to adjust axis label font size.

doPar — logical indicating whether to apply graphics::par(), specifically when x is supplied as a multi-column matrix. When doPar=FALSE, no panels nor margin adjustments are made at all.

heightFactor — numeric value indicating the height of the y-axis plot scale to use when scaling the histogram and polygon density within each plot panel.

weightFactor — numeric passed to breakDensity().

main — character title to display above the plot, used only when x is supplied as a single numeric vector. Otherwise each plot title uses the relevant colnames(x) value.

xaxs, yaxs, xaxt, yaxt — character string indicating the type of x-axis and y-axis to render, see graphics::par().

xlab, ylab — character labels for x-axis and y-axis, respectively.

log — character vector, optionally containing "x" and/or "y" to to indicate which axes are log-transformed. If "x" %in% log then it sets xScale="log10", both methods are equivalent in defining the log-transformation of the x-axis.

xScale — character string to define the x-axis transformation:

- "default" applies no transform;
- "log10" applies a log10 transform, specifically log10(x + 1)
- "sqrt" applies a sqrt transform.

usePanels — logical indicating whether to separate the density plots into panels when x contains multiple columns. When useOnePanel=FALSE the panels will be defined so that all columns will fit on one page.

useOnePanel — logical indicating whether to define multiple panels on one page. Therefore useOnePanel=TRUE will create multiple pages with one panel on each page, which may work well for output in multi-page 'PDF' files.

ablineV, ablineH — numeric vector representing abline vertical and horizontal positions, respectively. These values are mostly helpful in multi-panel plots, to draw consistent reference lines on each panel.

ablineVcol, ablineHcol — default"#44444499", with the abline color, used when ablineV or ablineH are supplied, respectively.

ablineVlty, ablineHlty — numeric or character indicating the line type to use for ablineV and ablineH, respectively.

removeNA — logical indicating whether to remove NA values prior to running histogram and density calculations. Presence of NA values generally causes both functions to fail.

add — logical indicating whether to add the plot to an existing visualization.

ylimQuantile — numeric value between 0 and 1, indicating the quantile value of the density y values to use for the ylim. This threshold is only applied when ylim is NULL.

ylim, xlim	numeric y-axis and x-axis ranges, respectively. When either is NULL, the axis range is determined independently for each plot panel. Either value can be supplied as a list to control the numeric range for each individual plot, relevant only when x is supplied as a multi-column matrix.
highlightPoints	character vector of optional rownames, or integer values with row indices, for rows to be highlighted. When x is supplied as a matrix, highlightPoints can be supplied as a list of vectors, referring to each column in x. When rows are highlighted, the plot is drawn with all points, then the highlighted points are drawn again over the histogram bars, and polygon density, as relevant.
highlightCol	character vector of colors to use to fill the histogram when highlightPoints is supplied. Multiple values are recycled one per column in x, if x is supplied as a multi-column matrix.
verbose	logical indicating whether to print verbose output.
...	additional arguments are passed to relevant internal functions.

Details

This function is a wrapper around graphics::hist() and stats::density(), with enough customization to cover most of the situations that need customization.

For example log="x" will automatically log-transform the x-axis, keeping the histogram bars uniformly sized. Alternatively, xScale="sqrt" will square root transform the data, and transform the x-axis while keeping the numeric values constant.

It also scales the density profile height to be similar to the histogram bar height, using the 99th quantile of the y-axis value, which helps prevent outlier peaks from dominating the y-axis range, thus obscuring interesting smaller features.

If supplied with a data matrix, this function will create a layout with ncol(x) panels, and plot the distribution of each column in its own panel, using categorical colors from rainbow2().

For a similar style using ggplot2, see plotRidges(), which displays only the density profile for each sample, but in a much more scalable format for larger numbers of columns.

By default NA values are ignored, and the distributions represent non-NA values.

Colors can be controlled using the parameter col, but can be specifically defined for bars with barCol and the polygon with polyCol.

Value

invisible list with density and histogram data output, however this function is called for the by-product of its plot output.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
# basic density plot
set.seed(123);
x <- stats::rnorm(2000);
plotPolygonDensity(x, main="basic polygon density plot");

# fewer breaks
plotPolygonDensity(x,
   breaks=20,
   main="breaks=20");

# log-scaled x-axis
plotPolygonDensity(10^(3+stats::rnorm(2000)), log="x",
   breaks=50,
   main="log-scaled x-axis");

# highlighted points
set.seed(123);
plotPolygonDensity(x,
   highlightPoints=sample(which(abs(x) > 1), size=200),
   breaks=40,
   main="breaks=40");

# hide axis labels
set.seed(123);
plotPolygonDensity(x,
   highlightPoints=sample(which(abs(x) > 1), size=200),
   breaks=40,
   xaxt="n",
   yaxt="n",
   main="breaks=40");

# multiple columns
set.seed(123);
xm <- do.call(cbind, lapply(1:4, function(i){stats::rnorm(2000)}))
plotPolygonDensity(xm, breaks=20)
```

`plotRidges` *Plot ridges density plots for numeric matrix input*

Description

Plot ridges density plots for numeric matrix input

Usage

```
plotRidges(
  x,
```

```
  xScale = c("none", "-log10", "log10"),
  xlab = NULL,
  ylab = NULL,
  title = ggplot2::waiver(),
  subtitle = ggplot2::waiver(),
  caption = ggplot2::waiver(),
  xlim = NULL,
  color_sub = NULL,
  rel_min_height = 0,
  bandwidth = NULL,
  adjust = 1,
  scale = 1,
  share_bandwidth = TRUE,
  ...
)
```

Arguments

x	matrix with numeric values, or a list of numeric vectors. In either case the data is converted to long-tall format before plotting.
xScale	character string indicating whether to transform the x-axis values: • "none": no transformation • "-log10": values are transformed with log10(x) and x-axis labels are adjusted accordingly. • "log10": values are transformed with log10(1 + x) except that negative values are transformed with -log10(1 - x). The x-axis labels are plotted to account for the log10(1 + x) offset.
xlab, ylab	character strings optionally used as x-axis and y-axis labels.
title, subtitle, caption	character string values optionally passed to the relevant downstream ggplot2 functions.
xlim	passed to ggplot2::xlim() to define the x-axis range.
color_sub	character vector named by colnames(x), or when x is a list, names(color_sub) should contain names(x), used to define specific colors for each ridge plot.
rel_min_height	numeric values passed to ggridges::geom_density_ridges2()
bandwidth	numeric value used to define the bandwidth density when share_bandwidth=TRUE which is default. The bandwidth affects the level of detail presented in each ridgeline, and when shared across ridgelines share_bandwidth=TRUE then each ridgeline will use the same consistent level of detail. In this case, it is passed to ggridges::geom_density_ridges2(). Note when bandwidth=NULL a default value is derived from the range of data to be plotted.
adjust	numeric used to adjust the default bandwidth only when bandwidth=NULL. It is intended as a convenient method to adjust the level of detail.
scale	numeric passed directly to ggridges::geom_density_ridges2().

share_bandwidth
: logical indicating whether to supply ggridges::geom_density_ridges2() a specific bandwidth to use for all ridgelines. When share_bandwidth=FALSE then each ridgeline is presented using the default bandwidth in ggridges::geom_density_ridges2().

...
: additional arguments are ignored.

Details

This function is a convenient wrapper for ggridges::geom_density_ridges2(), intended to be analogous to plotPolygonDensity() which differs by plotting each item in a separate plot panel using base graphics. This function plots each item as a ridgeline plot in the same plot window using ggplot2::ggplot().

Value

object with class "gg", "ggplot" with density plot in the form of ridges.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
# multiple columns
set.seed(123);
xm <- do.call(cbind, lapply(1:4, function(i){stats::rnorm(2000)}))
plotRidges(xm)

set.seed(123);
x <- stats::rnorm(2000)
plotRidges(x)
```

---

plotSmoothScatter *Smooth scatter plot with enhancements*

Description

Produce scatter plot using point density instead of displaying individual data points.

Usage

```
plotSmoothScatter(
  x,
  y = NULL,
  bwpi = 50,
  binpi = 50,
  bandwidthN = NULL,
  nbin = NULL,
  expand = c(0.04, 0.04),
  transFactor = 0.25,
  transformation = function(x) x^transFactor,
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL,
  nrpoints = 0,
  colramp = c("white", "lightblue", "blue", "orange", "orangered2"),
  col = "black",
  doTest = FALSE,
  fillBackground = TRUE,
  naAction = c("remove", "floor0", "floor1"),
  xaxt = "s",
  yaxt = "s",
  add = FALSE,
  asp = NULL,
  applyRangeCeiling = TRUE,
  useRaster = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric vector, or data matrix with two or more columns.
y	numeric vector, or if data is supplied via x as a matrix, y is NULL.
bwpi	`numeric` value indicating the bandwidth "per inch" to scale the bandwidth based upon visual space available. This argument is used to define `bandwidthN`, however `bwpi` is only used when `bandwidthN=NULL`. The bandwidth is used to define the 2-dimensional point density.
binpi	`numeric` value indicating the number of bins "per inch", to scale based upon visual space available. This argument is used to define `nbin`, however `binpi` is only used when `nbin=NULL`.
bandwidthN	`integer` number of bandwidth steps to use across the visible plot window. Note that this bandwidth differs from default `graphics::smoothScatter()` in that it uses the visible plot window instead of the data range, so if the plot window is not sufficiently similar to the data range, the resulting smoothed density will

not be visibly distorted. This parameter also permits display of higher (or lower) level of detail.

`nbin` `integer` number of bins to use when converting the kernel density result (which uses bandwidthN above) into a usable image. This setting is effectively the resolution of rendering the bandwidth density in terms of visible pixels. For example `nbin=256` will create 256 visible pixels wide and tall in each plot panel; and `nbin=32` will create 32 visible pixels, with lower detail which may be suitable for multi-panel plots. To use a variable number of bins, try `binpi`.

`expand` `numeric` value indicating the fraction of the x-axis and y-axis ranges to add to create an expanded range, used when `add=FALSE`. The default `expand=c(0.04, 0.04)` mimics the R base plot default which adds 4 percent total, therefore 2 percent to each side of the visible range.

`transFactor` `numeric` value used by the default `transformation` function, which effectively scales the density of points to a reasonable visible distribution. This argument is a convenience method to avoid having to type out the full `transformation` function.

`transformation` `function` which converts point density to a number, typically related to square root or cube root transformation. Note that the default uses `transFactor` but if a custom function is supplied, it will not use `transFactor` unless specified.

`xlim` `numeric` x-axis range, or `NULL` to use the data range.

`ylim` `numeric` y-axis range, or `NULL` to use the data range.

`xlab`, `ylab` `character` labels for x- and y-axis, respectively.

`nrpoints` `integer` number of outlier datapoints to display, as defined by `graphics::smoothScatter()`, however the default here is `nrpoints=0` to avoid additional clutter in the output, and because the default arguments `bwpi`, `binpi` usually indicate all individual points.

`colramp` any input recognized by `getColorRamp()`:

- `character` vector with multiple colors
- `character` string length 1, with valid R color used to create a linear color gradient
- `character` name of a known color gradient from `RColorBrewer` or `viridis`
- `function` that itself produces vector of colors, in the form `function(n)` where `n` defines the number of colors.

`col` `character` string with R color used when `nrpoints` is non-zero, this color defines the color of those points.

`doTest` `logical` indicating whether to create a visual set of test plots to demonstrate the utility of this function.

`fillBackground` `logical` indicating whether to fill the background of the plot panel with the first color in `colramp`. The default `fillBackground=TRUE` is useful since the plot panel may be slightly wider than the range of data being displayed, and when the first color in `colramp` is not the same as the plot device background color. Run a test using: `plotSmoothScatter(doTest=TRUE, fillBackground=FALSE, colramp="viridis")` and compare with: `plotSmoothScatter(doTest=TRUE, colramp="viridis")`

naAction
: character string indicating how to handle NA values, typically when x is NA and y is not NA, or vice versa. valid values:

  "remove" ignore any points where either x or y are NA

  "floor0" change any NA values to zero 0 for either x or y

  "floor1" change any NA values to one 1 for either x or y

  The latter two options are useful when the desired plot should indicate the presence of an NA value in either x or y, while also indicating the the corresponding non-NA value in the opposing axis. The driving use was plotting gene fold changes from two experiments, where the two experiments may not have measured the same genes.

xaxt
: character value compatible with graphics::par(xaxt), used to control the x-axis range, similar to its use in plot() generic functions.

yaxt
: character value compatible with graphics::par(yaxt), used to control the y-axis range, similar to its use in plot() generic functions.

add
: logical whether to add to an existing active R plot, or create a new plot window.

asp
: numeric with optional aspect ratio, as described in graphics::plot.window(), where asp=1 defines x- and y-axis coordinate ranges such that distances between points are rendered accurately. One data unit on the y-axis is equal in length to asp multiplied by one data unit on the x-axis. Notes:

  - When add=TRUE, the value asp is ignored, because the existing plot device is re-used.
  - When add=FALSE and asp is defined with numeric value, a new plot device is opened using plot.window(), and the xlim and ylim values are passed to that function. As a result the graphics::par("usr") values are used to define xlim and ylim for the purpose of determining visible points, relevant to applyRangeCeiling.

applyRangeCeiling
: logical indicating how to handle points outside the visible plot range. Valid values:

  TRUE Points outside the viewing area are fixed to the plot boundaries, in order to represent that there are additional points outside the boundary. This setting is recommended when the reasonable viewing area is smaller than the actual data, for example to be consistent across plot panels, but where you want to indicate that points may be outside the range.

  FALSE Points outside the viewing area is not displayed, with no special visual indication. This setting is useful when data may contain a large number of points at c(0, 0) and the density overwhelms the detail in the rest of the plot. In that case setting xlim=c(1e-10, 10) and applyRangeCeiling=FALSE would obscure these points.

useRaster
: logical indicating whether to produce plots using the graphics::rasterImage() function which produces a plot raster image offline then scales this image to visible plot space. This technique has two benefits:

  1. It produces substantially faster plot output.
  2. Output contains substantially fewer plot objects, which results in much smaller file sizes when saving in 'PDF' or 'SVG' format.

verbose	logical indicating whether to print verbose output.
...	additional arguments are passed to called functions, including getColorRamp(), nullPlot(), smoothScatterJam().

Details

This function intends to make several potentially customizable features of graphics::smoothScatter() plots much easier to customize. For example bandwidthN allows defining the number of bandwidth steps used by the kernel density function, and importantly bases the number of steps on the visible plot window, and not the range of data, which can differ substantially. The nbin argument is related, but is used to define the level of detail used in the image function, which when plotting numerous smaller panels, can be useful to reduce unnecessary visual details.

This function also by default produces a raster image plot with useRaster=TRUE, which adjusts the x- and y-bandwidth to produce visually round density even when the x- and y-ranges are very different.

Comments:

- asp=1 will define an aspect ratio 1, meaning the x-axis and y-axis units will be the same physical size in the output device. When this is true, and fillBackground=TRUE the xlim and ylim values follow logic for plot.default() and plot.window() such that each axis will include at least the xlim and ylim ranges, with additional range included in order to maintain the plot aspect ratio.
- When asp, and any of xlim or ylim, are defined, the data will be "cropped" to respective xlim and ylim values as relevant, after which the plot is drawn with the appropriate plot aspect ratio. When applyRangeCeiling=TRUE, points outside the fixed xlim and ylim range are fixed to the edge of the range, after which the plot is drawn with the requested plot aspect ratio. It is recommended not to define xlim and ylim when also defining asp.
- When add=TRUE the xlim and ylim values are already defined by the plot device. It is recommended not to define xlim and ylim when add=TRUE.

Value

list invisibly, sufficient to reproduce most of the graphical parameters used to create the smooth scatter plot.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), shadowText(), shadowText_options(), showColors(), sqrtAxis(), usrBox()

Examples

```
# doTest=TRUE invisibly returns the test data
x <- plotSmoothScatter(doTest=TRUE);

# so it can be plotted again with different settings
colnames(x) <- c("column_1", "column_2")
```

```
plotSmoothScatter(x, colramp="RdBu_r");
```

---

printDebug *print colorized output to R console*

Description

print colorized output to R console

print colorized output to R console, inverted

print colorized output to HTML

Usage

```
printDebug(
  ...,
  fgText = NULL,
  fgDefault = getOption("jam.fgDefault", c("darkorange1", "dodgerblue")),
  bgText = NULL,
  fgTime = getOption("jam.fgTime", "cyan2"),
  timeStamp = getOption("jam.timeStamp", TRUE),
  comment = getOption("jam.comment", !htmlOut),
  formatNumbers = getOption("jam.formatNumbers", TRUE),
  trim = getOption("jam.trim", TRUE),
  digits = getOption("jam.digits"),
  nsmall = getOption("jam.nsmall", 0L),
  justify = "left",
  big.mark = getOption("jam.big.mark", ","),
  small.mark = getOption("jam.small.mark", "."),
  zero.print = NULL,
  width = NULL,
  doColor = getOption("jam.doColor"),
  splitComments = FALSE,
  collapse = getOption("jam.collapse", ""),
  sep = getOption("jam.sep", ","),
  doReset = NULL,
  detectColors = TRUE,
  dex = 2,
  darkFactor = c(1, 1.5),
  sFactor = c(1, 1.5),
  lightMode = checkLightMode(),
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  removeNA = FALSE,
  replaceNULL = NULL,
  adjustRgb = getOption("jam.adjustRgb"),
```

```
  byLine = FALSE,
  verbose = FALSE,
  indent = "",
  keepNA = TRUE,
  file = getOption("jam.file", ""),
  append = getOption("jam.append", TRUE),
  invert = getOption("jam.invert", FALSE),
  htmlOut = getOption("jam.htmlOut", FALSE)
)

printDebugI(..., invert = TRUE)

printDebugHtml(..., htmlOut = TRUE, comment = FALSE)
```

Arguments

`...`	`character`, `factor`, `numeric` or compatible atomic vectors to be printed to the R console. These arguments are recognized as any un-named argument, or any argument whose name does not match the named arguments below.
`fgText`	one of two formats to define the foreground color for elements in `...` being printed. Each element is colored in order, and when multiple vector values are contained in one `...` element, the color defined in `fgText` is extended. The input types recognized: • `NULL` when no color is defined, one of two outputs: 1. When all values in `...` represent colors, these colors are used to colorize the output text. When `names()` are present they are used as the text labels in place of the vector value. 2. When not all values in `...` represent colors, the default color set is used: `c("darkorange1", "dodgerblue")`. 3. To disable option 1 above, define a specific value for `fgText`, such as `fgText=c("darkorange1", "dodgerblue")`. • `vector` of R compatible colors, recycled to the length of `....` When any element of `...` is a vector with multiple values, the corresponding color in `fgText` is shaded slightly lighter and darker, then recycled to the vector length, so that adjacent values have slightly different color. This behavior is controlled by default argument `splitComments=TRUE`. • `list` of vectors of R compatible colors, recycled to the length of `...`, then applied to each element in `...` in order. When only one color is defined, and multiple values are present in the corresponding `list` element, the color is shaded slightly lighter and darker, then recycled to the vector length, as described above. This behavior is controlled by default argument `splitComments=TRUE`. When multiple colors are defined for the `list` element, these values are recycled to the vector length. • **Note**: When `invert=TRUE` the values for `fgText` and `bgText` are reversed, and if the resulting `fgText` is `NULL` then its color is defined by `setTextContrastColor()` in order to define a contrasting text color.
`fgDefault`	`character` defaults to `getOption("jam.fgDefault", c("darkorange1", "dodgerblue"))`, and is used when colors are not defined by `fgText` or by the input `...` values.

bgText — vector of R colors, or list of vectors, used to define the background color, using the same approach described for fgText. Note that NULL or NA defines the absence of any background color, which is default. When invert=TRUE, which is default for printDebugI(), the values for fgText and bgText are reversed.

fgTime — character R color to colorize the time

timeStamp — logical whether to include a time stamp in output

comment — logical whether to prefix output with '## ' as a comment, or character string used as a prefix.

formatNumbers — logical whether to format numbers using format() which controls the number of digits displayed, and is default. When formatNumbers=FALSE sometimes numeric values that contain integers may be represented as 14.0000000001.

trim, digits, nsmall, justify, big.mark, small.mark, zero.print, width — arguments passed to format().

doColor — logical or NULL indicating whether to colorize output. When doColor is NULL, if the "crayon" package is available, and if crayon detects color is permitted, color is enabled.

splitComments — logical whether to color each element independently without light-dark alternating pattern. The intensity of the adjustment is controlled by dex passed to color2gradient().

collapse — character collapse string used to separate list items, by default "" so text separation is expected in the input data.

sep — character separator used to separate vector elements, when a list items contains a vector.

doReset — logical or NULL, indicating whether to apply crayon::reset() to the delimiter sep. When doReset=TRUE the style on the delimiter is forced to reset, using crayon::reset(), or to remove pre-existing style with crayon::strip_style(). When doReset=NULL and sep contains ANSI escape characters, they are left as-is; when doReset=NULL and sep does not contain ANSI escape characters, sep becomes crayon::reset(sep) which forces the style to be reset between printed values.

detectColors — logical whether to detect and potentially try to correct console color capabilities.

dex — numeric passed to color2gradient() to split a color into a lighter,darker alternating pattern. Until version 0.0.83.900, this process used gradientWtFactor=1 and was not adjustable. Note that when splitComments=TRUE the input values in ... are flattened to a single vector, and colors in fgText are applied directly without adjustment.

darkFactor, sFactor — numeric arguments deprecated.

lightMode — logical or NULL, indicating whether the text background color is light, where lightMode=TRUE indicates the background is white or light enough to require darker text, imposing a maximum brightness for colors displayed. When NULL it calls checkLightMode(), which uses:

- getOption("jam.lightMode") if defined

- otherwise attempts to detect whether the session is running inside RStudio, by checking for environmental variable "RSTUDIO", under the assumption that default RStudio uses a light background, therefore lightMode=TRUE.
- if steps above fail, it uses lightMode=FALSE.
- to force a specific lightMode for all uses, use options: options(jam.lightMode=TRUE) or options(jam.lightMode=FALSE).

Crange, Lrange — numeric range of chroma and luminance values between 0 and 100. When NULL, default values are assigned by setCLranges(). The intent is to restrict the range relative to the console background color, also controlled by lightMode.

removeNA — logical whether to remove NA values and not print to the console.

replaceNULL — character or NULL, optionally replace NULL elements with non-NULL character value, otherwise NULL elements are ignored.

adjustRgb — numeric value adjustment used during the conversion of RGB colors to ANSI colors, which is inherently lossy. If not defined, it uses the default returned by setCLranges() which itself uses getOption("jam.adjustRgb") with default=0. In order to boost color contrast, an alternate value of -0.1 is suggested.

byLine — logical whether to delimit lists by line instead of using collapse to combine them onto one line.

verbose — logical whether to print verbose output

indent — character optional characters used as a prefix to indent output. When numeric it is rounded to integer, then this many character spaces " " are concatenated together to define the indent width. Note that the indent text is not colorized.

keepNA — logical, default TRUE, whether to keep and print NA values.

file — argument passed to cat() to send output to a file or compatible output of cat().

append — logical whether to append output, passed to cat() when file is defined.

invert — logical indicating whether foreground and background colors should be switched, as is default for printDebugI(). Note when the resulting fgText is NULL, its color is defined by setTextContrastColor() to define a contrasting text color relative to the background color in bgText.

htmlOut — logical indicating whether to print HTML span output, using format <span style="color:fg;backgro This argument is not yet implemented, more testing is required to determine the best mechanism to use for things like 'Rmarkdown' rendering, and R-shiny app rendering.

Details

This function prints colorized output to the R console, with some rules for colorizing the output to help visually distinguish items.

The main intent is to use this function to print pretty debug messages, because color helps identify.

By default, output has the following configurable properties:

- each line begins with a comment, controlled by default comment=getOption("jam.comment", TRUE) which by default uses "##", but which can be defined to use a different prefix, or FALSE for no prefix at all.

- each line includes time and date stamp controlled by `timeStamp=getOption("jam.timeStamp", TRUE)` which by default includes the current time and date.
- each line formats `numeric` values, controlled by `formatNumbers=getOption("jam.formatNumbers", TRUE)`, which determines whether to apply arguments `big.mark` and `small.mark` to make numeric values more readable.
- each entry in `...` is printed with its own foreground color `fgText`, background color `bgText`, with a slight lighter/darker dithering effect to add minor visual distinction for multiple values.
- Values in each `vector` are concatenated by `sep=","` by default.
- Each `list` is concatenated by `collapse=""` by default.

Additional convenience rules:

- For convenience, when the last `...` argument is a `character` vector of colors, it is assumed to be `fgText`.
- When the only entry in `...` is a `character` vector of R colors, the names are printed using the color vector for `fgText`, or if no names exist the colors are printed using the color vector for `fgText`.
- For `printDebugI()` or `invert=TRUE`, colors typically assigned to `fgText` are instead assigned to `bgText`.
- For very specific color assignments, `fgText` and/or `bgText` can be defined as a `list` of `character` vectors of R colors, in which case the `list` overall is recycled to the length `...` to be printed, and within each vector of `...` printed the corresponding color vector is recycled to the length of that vector.

For use inside 'Rmarkdown' `.Rmd` documents, current recommendation is to define the R output with `results='asis'` like this:

```
\`\`\`{r block_name, results='asis'}
# some R code here
\`\`\`
```

Then define a global option to turn off the comment prefix in `printDebug()`: `options("jam.comment"=FALSE)`

For colorized text, it may require `"html_output"` rendering of the `.Rmd` 'Rmarkdown' file, as well as this option to enable HTML formatting by `printDebug()`: `options("jam.htmlOut"=TRUE)`.

This function prints colorized output to the R console, using the same logic as `printDebug` except by default the color is inverted so the default `fgText` colors are applied to the background.

This function prints colorized output in HTML form, using the same logic as `printDebug()` except by default the output is HTML. The intended use is for 'Rmarkdown' with chunk option `results='asis'`, which causes the HTML code to be interpreted directly as HTML.

This function internally calls `printDebug()` which then calls `make_html_styles()`. The text is surrounded by `<span color='#FFFFFF'>` HTML formatting.

Value

`NULL` invisibly, this function is called for the side effect of printing output using `cat()`.

`NULL` invisibly, this function is called for the side effect of printing output using `cat()`.

`NULL` invisibly, this function is called for the side effect of printing output using `cat()`.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

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Examples

```
printDebug("Testing ", "default ", "printDebug().");
printDebug("List of vectors:", c("one", "two", "three"));

# By default, there is no space between separate elements in `...`
printDebug("List of vectors:", c("one", "two", "three"),
   c("four", "five", "six"));
# To add a space " " between elements, use collapse
printDebug("List of vectors:", c("one", "two", "three"),
   c("four", "five", "six"), collapse=" ");

# slightly different style, one entry per line, indented:
printDebug("List of vectors:", c("one", "two", "three"),
   c("four", "five", "six"), collapse="\n   ");

# when a vector entirely contains recognized colors,
# the colors are used in the output
printDebug(c("red", "blue", "yellow"));

# When the vector contains colors, the names are used as the label
color_vector <- jamba::nameVector(c("red", "blue", "green","orange"),
   c("group_A", "group_B", "group_C", "group_D"));
printDebug(color_vector);

# Remember the sister function that inverses the colors
printDebugI(color_vector);

printDebug(1:10, fgText="blue", dex=2);
printDebug(1:10, bgText="blue", dex=2);
printDebug(1:10, fgText="orange", dex=2);
```

provigrep *provigrep: progressive case-insensitive value-grep*

Description

case-insensitive value-grep for a vector of patterns

case-insensitive grep for a vector of patterns

Usage

```
provigrep(
  patterns,
  x,
  maxValues = NULL,
  sortFunc = c,
  rev = FALSE,
  returnType = c("vector", "list"),
  ignore.case = TRUE,
  value = TRUE,
  ...
)

proigrep(..., value = FALSE)
```

Arguments

patterns	character vector of regular expression patterns, ultimately passed to base::grep().
x	character vector that is the subject of base::grep().
maxValues	integer or NULL, the maximum matching entries to return per grep pattern. Note that each grep pattern may match multiple values, and values are only returned at most once each, so restricting items returned by one grep pattern may allow an item to be matched by subsequent patterns, see examples. This argument is most commonly used with maxValues=1 which returns only the first matching entry per pattern.
sortFunc	function or NULL, used to sort entries within each set of matching entries. Use NULL to avoid sorting entries.
rev	logical whether to reverse the order of matching entries. Use TRUE if you would like entries matching the patterns to be placed last, and entries not matching the grep patterns to be placed first. This technique is effective at placing "noise names" at the end of a long vector, for example.
returnType	character indicating whether to return a vector or list. A list will be in order of the grep patterns, using empty elements to indicate when no entries matched each pattern. This output is useful when you would like to know which patterns matched specific entries.

ignore.case	logical parameter sent to base::grep(), TRUE runs in case-insensitive mode, as by default.
value	logical indicating whether to return the matched value, or when value=FALSE the index position is returned.
...	additional arguments are passed to vigrep().

Details

Purpose is to provide "progressive vigrep()",which is value-returning, case-insensitive grep, starting with an ordered vector of grep patterns. For example, it returns entries in the order they are matched, by the progressive use of grep patterns.

It is particularly good when using multiple grep patterns, since grep() does not accept multiple patterns as input. This function also only returns the unique matches in the order they were matched, which alleviates the need to run a series of grep() functions and collating their results.

It is mainly to allow for prioritized ordering of matching entries, where one would like certain matching entries first, followed by another set of matching entries, without duplication. For example, one might grep for a few patterns, but want certain pattern hits to be listed first.

Value

character vector with entries in x reordered to match the order of patterns provided, or list when returnType="list" named by patterns in the order provided. When value=FALSE then it returns integer index values of x.

See Also

Other jam grep functions: grepls(), igrep(), igrepHas(), igrepl(), unigrep(), unvigrep(), vgrep(), vigrep()

Examples

```
# a rather comical example
# set up a test set with labels containing several substrings
set.seed(1);
testTerms <- c("robot","tree","dog","mailbox","pizza","noob");
testWords <- pasteByRow(t(combn(testTerms,3)));

# now pull out entries matching substrings in order
provigrep(c("pizza", "dog", "noob", "."), testWords);
# more detail about the sort order is shown with returnType="list"
provigrep(c("pizza", "dog", "noob", "."), testWords, returnType="list");
# rev=TRUE will reverse the order of the list
provigrep(c("pizza", "dog", "noob", "."), testWords, returnType="list", rev=TRUE);
provigrep(c("pizza", "dog", "noob", "."), testWords, rev=TRUE);

# another example showing ordering of duplicated entries
set.seed(1);
x <- paste0(
   sample(letters[c(1,2,2,3,3,3,4,4,4,4)]),
   sample(1:5));
```

```
x;
# sort by letter
provigrep(letters[1:4], x)

# show more detail about how the sort is performed
provigrep(letters[1:4], x, returnType="list")

# rev=TRUE will reverse the order of pattern matching
# which is most useful when "." is the last pattern:
provigrep(c(letters[1:3], "."), x, returnType="list")
provigrep(c(letters[1:3], "."), x, returnType="list", rev=TRUE)

# example demonstrating maxValues
# return in list format
provigrep(c("[ABCD]", "[CDEF]", "[FGHI]"), LETTERS, returnType="list")

# maxValues=1
provigrep(c("[ABCD]", "[CDEF]", "[FGHI]"), LETTERS, returnType="list", maxValues=1)
provigrep(c("[ABCD]", "[CDEF]", "[FGHI]"), LETTERS, returnType="list", maxValues=1, value=FALSE)
proigrep(c("[ABCD]", "[CDEF]", "[FGHI]"), LETTERS, maxValues=1)
```

`rad2deg` *Convert radians to degrees*

Description

Convert radians to degrees

Usage

```
rad2deg(x, ...)
```

Arguments

`x`	`numeric` vector, expected to be radian values between zero and pi*2.
`...`	other parameters are ignored.

Details

This function simply converts radians which range from zero to pi*2, into degrees which range from 0 to 360.

Value

`numeric` vector after coverting radians to degrees.

See Also

Other jam numeric functions: deg2rad(), noiseFloor(), normScale(), rowGroupMeans(), rowRmMadOutliers(), warpAroundZero()

Examples

```
rad2deg(c(pi*2, pi/2))
```

`rainbow2` *Simple rainbow palette replacement*

Description

Simple rainbow palette replacement using variable saturation and vibrance

Usage

```
rainbow2(n, s = c(0.9, 0.7, 0.88, 0.55), v = c(0.92, 1, 0.85, 0.94), ...)
```

Arguments

n	integer number of colors requested
s, v	numeric vector of values to recycle as saturation and vibrance, respectively. The purpose is to improve visual distinction between adjacent and nearby colors in the color wheel.
...	additional arguments are passed to grDevices::rainbow(): • start,end to control the starting and ending hue [0,1], • alpha for alpha opacity, default NULL adds no alpha, • rev to reverse the color order.

Value

character vector of R colors.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
showColors(list(
   `rainbow(24)`=grDevices::rainbow(24),
   `rainbow2(24)`=rainbow2(24),
   `rainbow2(24, rev=TRUE)`=rainbow2(24, rev=TRUE),
   `rainbow2(24, start=0.5, end=0.499)`=rainbow2(24,
      start=0.5, end=0.5-1e-5),
   `rainbow2(24, rev=TRUE,\nstart=0.5, end=0.499)`=rainbow2(24,
      rev=TRUE, start=0.5, end=0.5-1e-5)))
```

---

rbindList *rbind a list of vectors into matrix or data.frame*

Description

rbind a list of vectors into matrix or data.frame

Usage

```
rbindList(
  x,
  emptyValue = "",
  nullValue = NULL,
  keepListNames = TRUE,
  newColnames = NULL,
  newRownames = NULL,
  fixBlanks = TRUE,
  returnDF = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	list of atomic vector, matrix, or data.frame objects.
emptyValue	character value to use to represent missing values, whenever a blank cell is introduced into the resulting matrix
nullValue	optional value used to replace NULL entries in the input list, useful especially when the data was produced by strsplit() with "". Use nullValue="" to replace NULL with "" and preserve the original list length. Otherwise when nullValue=NULL any empty entries will be silently dropped.
keepListNames	logical whether to use list names as rownames in the resulting matrix or data.frame.
newColnames	NULL or character vector of colnames to use for the resulting matrix or data.frame.

newRownames	NULL or character vector of rownames to use for the resulting matrix or data.frame. If supplied, this value overrides the keepListNames=TRUE use of list names as rownames.
fixBlanks	logical whether to use blank values instead of repeating each vector to the length of the maximum vector length when filling each row of the matrix or data.frame.
returnDF	logical whether to return a data.frame, by default FALSE, a matrix is returned.
verbose	logical whether to print verbose output during processing.
...	Additional arguments are ignored.

Details

The purpose of this function is to emulate do.call(rbind, x) on a list of vectors, while specifically handling when there are different numbers of entries per vector. The output matrix number of columns will be the longest vector (or largest number of columns) in the input list x.

Instead of recycling values in each row to fill the target number of columns, this function fills cells with blank fields, with default argument fixBlanks=TRUE.

In extensive timings tests at the time this function was created, this technique was notably faster than alternatives. It runs do.call(rbind, x) then subsequently replaces recycled values with blank entries, in a manner that is notably faster than alternative approaches such as pre-processing the input data.

Value

matrix unless returnDF=TRUE in which the output is coerced to a data.frame. The rownames by default are derived from the list names, but the colnames are not derived from the vector names. If input x contains data.frame or matrix objects, the output will retain those values.

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), relist_named(), rlengths(), sclass(), sdim(), uniques(), unnestList()

Examples

```
L <- list(a=LETTERS[1:4], b=letters[1:3]);
rbindList(L);
rbindList(L, returnDF=TRUE);
```

readOpenxlsx *Import one or more data.frame from 'Excel' 'xlsx' format*

Description

Import one or more data.frame from 'Excel' 'xlsx' format

Usage

```
readOpenxlsx(
  xlsx,
  sheet = NULL,
  startRow = 1,
  startCol = 1,
  rows = NULL,
  cols = NULL,
  check.names = FALSE,
  check_header = FALSE,
  check_header_n = 10,
  verbose = FALSE,
  ...
)
```

Arguments

xlsx	character path to an 'Excel' file in xlsx format, compatible with openxlsx::read.xlsx().
sheet	one of NULL, character, or integer vector, where: sheet=NULL will import every sheet; character is a vector of sheet names; and integer is a vector of sheet index values. The sheet names are determined with openxlsx::getSheetNames().
startRow	integer indicating the row number to start importing each sheet. • Note startRow can be a vector with length length(sheet), to specify the startRow for each sheet. • Note startRow is ignored when rows is defined for the same sheet, to minimize confusion about using both togetheer.
startCol	integer indicating the first column number to retain after importing each sheet. • Note startCol can be a vector with length length(sheet), to specify the startCol for each sheet. • Note startCol is ignored when cols is defined for the same sheet, to minimize confusion about using both togetheer.
rows	integer vector indicating specific rows to import for each sheet. • To specify different rows for each sheet, supply rows as a list of integer vectors. • Note that when rows is defined for a sheet, it will be used and startRow will be ignored for that same sheet.

cols	integer vector indicating specific column numbers to import for each sheet. • To specify different cols for each sheet, supply cols as a list of integer vectors. • Note that when cols is defined for a sheet, it will be used and startCol will be ignored for that same sheet.
check.names	logical indicating whether to call make.names() on the colnames of each data.frame. • Note that openxlsx::read.xlsx() does not honor check.names=FALSE, so a workaround is applied which loads a single line without column headers, in order to obtain the same data without mangling column headers. If this process fails, another workaround is to use startRow=2 (one higher than previous) and colNames=FALSE.
check_header	logical indicating whether to test for presence of header rows, which may be multi-line column headers. When check_header=TRUE, this method simply tests for the presence of rows that have ncol different than the remaining rows of data in the given sheet. When header rows are detected, the values are assigned to column dimnames of the data.frame.
check_header_n	integer number of rows to test for header rows, only used when check_header=TRUE. This step is intended when the top row(s) contain fewer columns with headers, above actual column headers, for example the first row c("Sample", "", "", "Lane", ""), and the second row c("Name", "Type", "Label", "Name", "Type"). In this case the desired output is "Sample_Name","Sample_Type","Sample_Label","Lane_Na This option default is FALSE due to the number of exceptions seen in real data.
verbose	logical indicating whether to print verbose output.
...	additional arguments are passed to openxlsx::read.xlsx().

Details

This function is equivalent to openxlsx::read.xlsx() with a few minor additions:

1. It returns a list of data.frame objects, one per sheet.
2. It properly reads the colnames with check.names=FALSE.

By default this function returns every sheet for a given xlsx file.

Some useful details:

- Empty columns are not skipped during loading, which means a worksheet whose data starts at column 3 will be returned with two empty columns, followed by data from that worksheet. Similarly, any empty columns in the middle of the data in that worksheet will be included in the output.
- When both startRow and rows are applied, rows takes priority and will be used instead of startRows. In fact startRows will be defined startRows <- min(rows) for each relevant worksheet. However, for each worksheet either argument can be NULL.

Value

list of data.frame objects, one per sheet in xlsx.

See Also

Other jam export functions: applyXlsxCategoricalFormat(), applyXlsxConditionalFormat(), set_xlsx_colwidths(), set_xlsx_rowheights(), writeOpenxlsx()

Examples

```
# set up a test data.frame
set.seed(123);
lfc <- -3:3 + stats::rnorm(7)/3;
colorSub <- nameVector(
   rainbow2(7),
   LETTERS[1:7])
df <- data.frame(name=LETTERS[1:7],
   int=round(4^(1:7)),
   num=(1:7)*4-2 + stats::rnorm(7),
   fold=2^abs(lfc)*sign(lfc),
   lfc=lfc,
   pvalue=10^(-1:-7 + stats::rnorm(7)),
   hit=sample(c(-1,0,0,1,1), replace=TRUE, size=7));
df;
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test",
      append=FALSE);
   # now read it back
   df_list <- readOpenxlsx(xlsx=out_xlsx);
   df_list[[1]]
}
```

---

relist_named *relist a vector which allows re-ordered names*

Description

relist a vector which imposes the model object list structure while allowing vector elements and names to be re-ordered

Usage

```
relist_named(x, skeleton, ...)
```

Arguments

x	vector to be applied to the skeleton list structure in order.

skeleton	list object representing the desired final list structure, or vector when the input data x should be returned as-is, without change. Specifically, when skeleton is a vector, the names(x) are maintained without change.
...	additional arguments are ignored.

Details

This function is a simple update to utils::relist() that allows the order of vectors to change, alongside the correct names for each element.

More specifically, this function does not replace the updated names with the corresponding names from the list skeleton, as is the case in default implementation of utils::relist().

This function is called by mixedSorts() which iteratively calls mixedOrder() on each vector component of the input list, and permits nested lists. The result is a single sorted vector which is split into the list components, then relist-ed to the original structure. During the process, it is important to retain vector names in the order defined by mixedOrder().

Value

list object with the same structure as the skeleton.

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), rlengths(), sclass(), sdim(), uniques(), unnestList()

Examples

```
# generate nested list
x <- list(A=nameVector(LETTERS[3:1]),
   B=list(
      E=nameVector(LETTERS[10:7]),
      D=nameVector(LETTERS[5:4])),
   C=list(
      G=nameVector(LETTERS[19:16]),
      F=nameVector(LETTERS[15:11]),
      H=list(
         I=nameVector(LETTERS[22:20]))
      ))
x

# unlisted vector of items
xu <- unlist(unname(x))
# unlisted vector of names
xun <- unname(jam_rapply(x, names));
names(xu) <- xun;

# recursive list element lengths
xrn <- jam_rapply(x, length);
# define factor in order of list structure
xn <- factor(
```

```
   rep(names(xrn),
      xrn),
   levels=names(xrn));

# re-create the original list
xu_new <- unlist(unname(split(xu, xn)))
xnew <- relist_named(xu_new, x);
xnew

# re-order elements
k <- mixedOrder(xu_new);
xuk <- unlist(unname(split(xu[k], xn[k])))
xk <- relist_named(xuk, x);
xk

# the default relist() function does not support this use case
xdefault <- relist(xuk, x);
xdefault
```

`reload_rmarkdown_cache` *Reload 'Rmarkdown' cache*

Description

Reload 'Rmarkdown' cache in the order files were created, into an R environment

Usage

```
reload_rmarkdown_cache(
  dir = ".",
  maxnum = 1000,
  max_cache_name = NULL,
  envir = new.env(),
  file_sort = c("globals", "objects", "ctime", "mtime"),
  preferred_load_types = c("lazyLoad", "load"),
  dryrun = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

`dir`	`character` path to the directory that contains 'Rmarkdown' cache files. Each file is recognized by the file extension `".rdx"`.
`maxnum`	`integer` indicating the maximum number of cache files to re-load, in order.

`max_cache_name` `character` optional string indicating the name of an 'Rmarkdown' cache chunk where this function will stop loading cache data. All cache files after this point will not be loaded. This option is intended to help recreate the data available to a particular 'Rmarkdown' chunk during processing.

`envir` `environment` in which data is populated, default `new.env()` creates a new `environment` which is returned invisibly.

`file_sort` `character` string indicating how to sort cache files, default uses best available, in order: "globals" (global index file), "objects" (object index file), "ctime" (creation time), "mtime" (modification time). The global index is preferred, and other options are intended for rare scenarios when the global index is not available. The methods using `"mtime"` or `"ctime"` **is less accurate**, yet may be sufficient for simple output.

- `"globals"` uses the `"__globals"` file in the cache directory.
- `"objects"` uses the `"__objects"` file in the cache directory.
- `ctime` sorts by file creation time
- `mtime` sorts by file modification time

`preferred_load_types` `character` string indicating the preferred load mechanism, default uses `"lazyLoad"` if '.rdx'/'.rdb' files are available, otherwise `"load"` to load '.RData'/'.rda' files. The 'lazyLoad' '.rdx'/.'rdb' files are created when 'Rmarkdown' options include `cache=TRUE, cache.lazy=TRUE`. The load option is used when `cache=TRUE, cache.lazy=FALSE` which is preferred for some analyses involving large data objects.

`dryrun` `logical` default FALSE, whether to perform a dry-run, which prints messages and does not load the data.

`verbose` `logical` default TRUE, whether to print verbose output. This argument is not passed to other functions.

`...` additional arguments are passed to `lazyLoad()` or `load()` as relevant to the method used to re-load the cache object data.

Details

This function is intended to help re-load 'Rmarkdown' cache files created during the processing/rendering of an 'Rmarkdown' file.

By default, all cached R objects are loaded into the environment defined by `envir`, However, **it is recommended that** `envir` **is used to define a new environment** into which the cached session is loaded.

```
cache_env <- new.env()
reload_rmarkdown_cache(cachedir, envir=cache_env)
```

From then on, the cached data objects can be seen with `ls(cache_env)` and retrieved with `get("objectname", envir=cache_env)`.

If supplied with `maxnum` or `max_cache_name` then the cache will be loaded only up to this point, and not beyond. The recommended method to determine the cache is to use `dryrun=TRUE` to view all sections, then to choose the `integer` number, or `character` name to define the maximum chunk to load.

Value

envir is returned invisibly, with data objects populated into that environment.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), renameColumn(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

---

renameColumn *Rename columns in a data.frame, matrix, tibble, or GRanges object*

Description

Rename columns in a data.frame, matrix, tibble, or GRanges object

Usage

```
renameColumn(x, from, to, verbose = FALSE, ...)
```

Arguments

x	data.frame, matrix, tbl, or GRanges equivalent object. It will work on any object for which colnames() is defined.
from	character vector of colnames expected to be in x. Any values that do not match colnames(x) are ignored.
to	character vector with length(to) == length(from) corresponding to the target name for any colnames that match from.
verbose	logical indicating whether to print verbose output.
...	Additional arguments are ignored.

Details

This function is intended to rename one or more columns in a data.frame, matrix, tibble, or GRanges related object. It will gracefully ignore columns which do not match, in order to make it possible to call the function again without problem.

This function will also recognize input objects GRanges, ucscData, and IRanges, which store annotation in DataFrame accessible via S4Vectors::values(). Note the IRanges package is required, for its generic function values().

The values supplied in to and from are converted from factor to character to avoid coersion by R to integer, which was noted in output prior to jamba version 0.0.72.900.

Value

data.frame or object equivalent to the input x, with columns from renamed to values in to. For genomic ranges objects such as GRanges and IRanges, the colnames are updated in S4Vectors::values(x).

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), rmInfinite(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
df <- data.frame(A=1:5, B=6:10, C=11:15);
df;
df2 <- renameColumn(df,
   from=c("A","C"),
   to=c("a_new", "c_new"));
df2;
df3 <- renameColumn(df2,
   from=c("A","C","B"),
   to=c("a_new", "c_new","b_new"));
df3;
```

---

rgb2col *Convert RGB color matrix to R color*

Description

Convert RGB color matrix to R color

Usage

```
rgb2col(
  red,
  green = NULL,
  blue = NULL,
  alpha = NULL,
  names = NULL,
  maxColorValue = NULL,
  keepNA = TRUE,
  verbose = FALSE,
  ...
)
```

Arguments

red	numeric vector of red values; or RGB numeric matrix with rownames c("red","green","blue") in any order, with optional rowname "alpha"; or character strings with comma-separated rgb values, in format "100,20,10". The latter input is designed to handle web rgb values.
green	numeric vector, or when red is a matrix or comma-delimited character string, this parameter is ignored.
blue	numeric vector, or when red is a matrix or comma-delimited character string, this parameter is ignored.
alpha	numeric vector, or when red is a matrix or comma-delimited character string, this parameter is ignored. Alpha values are always expected in range [0,1], even when maxColorValue is higher than 1. When alpha is FALSE, the alpha transparency is removed. When alpha is TRUE the original alpha transparency is retained without change. If supplying alpha as a numeric vector, use Inf to represent TRUE for alpha values to be kept without change, and use -1 or any negative number to indicate alpha values to remove from the output.
names	character, default NULL, with optional names to apply to output colors.
maxColorValue	numeric maximum value for colors. If NULL then it defaults to 1 unless there are values above 1, in which case it defaults to 255.
keepNA	logical whether to keep NA values, returning NA for any input where red, green, and/or blue are NA. If keepNA==FALSE then it substitutes 0 for any NA values.
verbose	logical indicating whether to print verbose output
...	Additional arguments are ignored.

Details

This function intends to augment the rgb function, which does not handle output from col2rgb. The goal is to handle multiple color conversions, e.g. rgb2col(grDevices::col2rgb("red")). This function also maintains alpha transparency when supplied.

The output is named either by names(red), rownames(red), or if supplied, the value of the parameter names.

Note that alpha is used to define alpha transparency, but has additional control over the output.

- When alpha is FALSE then output colors will not have the alpha transparency, in hex form that means colors are in format "#RRGGBB" and not "#RRGGBBAA".
- When alpha is TRUE the previous alpha transparency values are used without change.
- When alpha is a numeric vector, numeric values are always expected to be in range [0,1], where 0 is completely transparent, and 1 is completely not transparent. Supplied alpha values will override those present in red when red is a matrix like that produced from grDevices::col2rgb(..., alpha=TRUE).
- When alpha is a numeric vector, use -1 or any negative number to indicate the alpha value should be removed.
- When alpha is a numeric vector, use Inf to indicate the alpha transparency should be retained without change.

Therefore, `alpha = c(-1, 0, 1, Inf)` will apply the following, in order: remove alpha; set alpha to 0; set alpha to 1; set alpha to the same as the input color.

Value

`character` vector of R colors.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `unalpha()`, `warpRamp()`

Examples

```
# start with a color vector
# red and blue with partial transparency
colorV <- c("#FF000055", "#00339999");

# Show the output of rgb2col
# make sure to include alpha=TRUE to maintain alpha transparency
grDevices::col2rgb(colorV, alpha=TRUE);

# confirm we can convert from RGB back to the same colors
rgb2col(grDevices::col2rgb(colorV, alpha=TRUE));
```

---

rlengths *lengths for recursive lists*

Description

lengths for recursive lists

Usage

```
rlengths(x, doSum = NULL, ...)
```

Arguments

x	`list` or vector
doSum	`logical` indicating whether to return the overall sum of lengths. When `NULL` it will return the aggregate length of each list element in `x`. When `FALSE` it will return the same list structure of x, with the length of each. When `TRUE` it will return the total length of all elements in `x` as one value.
...	additional parameters are ignored

Details

This function takes a list as input, and returns the length of each list element after running `base::unlist()`.

Value

`integer` value, vector, or list:

- When `doSum is NULL` (default) it returns an `integer` vector with length `length(x)` and names `names(x)`, whose values are the total number of elements in each item in `x` after running `base::unlist()`.
- When `doSum=="TRUE"`, it returns the single `integer` length of all elements in `x`.
- When `doSum=="FALSE"`, it returns the full structure of `x` with the `integer` length of each element.

The parameter `doSum` is intended for internal use, during recursive calls of `rlengths()` to itself. When `doSum is NULL` or `TRUE`, recursive calls to `rlengths()` set `doSum=TRUE`.

See Also

Other jam list functions: `cPaste()`, `heads()`, `jam_rapply()`, `list2df()`, `mergeAllXY()`, `mixedSorts()`, `rbindList()`, `relist_named()`, `sclass()`, `sdim()`, `uniques()`, `unnestList()`

Examples

```
x <- list(
   A=list(
      A1=nameVector(1:3, letters[1:3]),
      A2=list(
         A1a=nameVector(4:7, letters[4:7]),
         A1b=nameVector(11:14, letters[11:14]))),
   B=list(B1=nameVector(1:9, letters[1:9]),
      B2=nameVector(20:25, letters[20:25])));
# default lengths(x) shows length=2 for A and B
lengths(x)
# rlengths(x) shows the total length of A and B
rlengths(x)
```

---

rmInfinite *remove Infinite values*

Description

remove Infinite values

Usage

```
rmInfinite(x, infiniteValue = NULL, ...)
```

Arguments

x	vector input
infiniteValue	NULL to remove Infinite values, or a replacement value
...	additional parameters are ignored

Details

This function removes any positive or negative infinite numerical values, optionally replacing them with a given value or NA.

Value

numeric vector with infinite values either removed, or replaced with the supplied value.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmNA(), rmNAs(), rmNULL(), setPrompt()

Examples

```
rmInfinite(c(1, 5, 4, 10, Inf, 1, -Inf))

rmInfinite(c(1, 5, 4, 10, Inf, 1, -Inf), infiniteValue=1000)
```

---

rmNA *remove NA values*

Description

remove NA values

Usage

```
rmNA(
  x,
  naValue = NULL,
  rmNULL = FALSE,
  nullValue = naValue,
  rmInfinite = TRUE,
  infiniteValue = NULL,
  rmNAnames = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	vector input
naValue	NULL or single replacement value for NA entries. If NULL, then NA entries are removed from the result.
rmNULL	logical whether to replace NULL entries with nullValue
nullValue	NULL or single replacement value for NULL entries. If NULL, then NULL entries are removed from the result.
rmInfinite	logical whether to replace Infinite values with infiniteValue
infiniteValue	value to use when rmInfinite==TRUE to replace entries which are Inf or -Inf.
rmNAnames	logical whether to remove entries which have NA as the name, regardless whether the entry itself is NA.
verbose	logical whether to print verbose output
...	additional arguments are ignored.

Details

This function removes NA values, by default shortening a vector as a result, but optionally replacing NA and Infinite values with fixed values.

Value

vector with NA entries either removed, or replaced with naValue, and NULL entries either removed or replaced by nullValue.

See Also

Other jam practical functions: breakDensity(), call_fn_ellipsis(), checkLightMode(), check_pkg_installed(), colNum2excelName(), color_dither(), exp2signed(), getAxisLabel(), isFALSEV(), isTRUEV(), jargs(), kable_coloring(), lldf(), log2signed(), middle(), minorLogTicks(), newestFile(), printDebug(), reload_rmarkdown_cache(), renameColumn(), rmInfinite(), rmNAs(), rmNULL(), setPrompt()

Examples

```
# by default it removes NA, shortening the vector
rmNA(c(1, 5, 4, NA, 10, NA))

# convenient to replace NA with a fixed value
rmNA(c(1, 5, 4, NA, 10, NA), naValue=0)

m <- matrix(ncol=3, 1:9)
m[1, 2] <- NA;
rmNA(m, naValue=-1)

# by default NA and Inf is removed
rmNA(c(1, 5, 4, NA, 10, NA, Inf, -Inf))
```

```
# NA and Inf can be replaced, note Inf retains the sign
rmNA(c(1, 5, 4, NA, 10, NA, Inf, -Inf), naValue=0, infiniteValue=100)
```

---

rmNAs *remove NA values from list elements*

Description

remove NA values from list elements

Usage

```
rmNAs(
  x,
  naValue = NULL,
  rmNULL = FALSE,
  nullValue = naValue,
  rmInfinite = TRUE,
  infiniteValue = NULL,
  rmNAnames = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	list of vectors
naValue	NULL or single replacement value for NA entries. If NULL, then NA entries are removed from the result.
rmNULL	logical whether to replace NULL entries with nullValue
nullValue	NULL or single replacement value for NULL entries. If NULL, then NULL entries are removed from the result.
rmInfinite	logical whether to replace Infinite values with infiniteValue
infiniteValue	value to use when rmInfinite==TRUE to replace entries which are Inf or -Inf.
rmNAnames	logical whether to remove entries which have NA as the name, regardless whether the entry itself is NA.
verbose	logical whether to print verbose output
...	additional arguments are ignored.

Details

This function removes NA values from vectors in a list, applying the same logic used in rmNA() to each vector. It is somewhat optimized, in that it checks for list elements that have NA values before applying rmNA(). However, it calls rmNA() iteratively on each vector that contains NA in order to preserve the class (factor, character, numeric, etc.) of each vector.

It also optionally applies convenience functions rmNULL() and rmInfinite() as relevant.

Value

`list` where NA entries were removed or replaced with `naValue` in each vector. Empty `list` elements are optionally removed when `rmNULL=TRUE`, or replaced with `nullValue` when defined. When `rmInfinite=TRUE` then infinite values are either removed, or replaced with `infiniteValue` when defined.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNULL()`, `setPrompt()`

Examples

```
testlist <- list(
   A=c(1, 4, 5, NA, 11),
   B=c("B", NA, "C", "Test"))
rmNAs(testlist)

testlist2 <- list(
   A=c(1, 4, 5, NA, 11, Inf),
   B=c(11, NA, 19, -Inf))
rmNAs(testlist2, naValue=-100, infiniteValue=1000)
```

`rmNULL` *remove NULL entries from list*

Description

remove NULL entries from list

Usage

```
rmNULL(x, nullValue = NULL, ...)
```

Arguments

`x`	`list` or other object which may contain NULL.
`nullValue`	`character` optional replacement value, default NULL, which causes the entry to be removed.
`...`	additional arguments are ignored.

Details

This function is a simple helper function to remove NULL from a list, optionally replacing it with another value

Value

list with NULL entries either removed, or replaced with nullValue. This function is typically called so it removed list elements which are NULL, resulting in a list that contains non-NULL entries. This function can also be useful when NULL values should be changed to something else, perhaps a character value "NULL" to be used as a label.

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `setPrompt()`

Examples

```
x <- list(A=1:6, B=NULL, C=letters[11:16]);
rmNULL(x)
rmNULL(x, nullValue=NA)
```

---

rowGroupMeans *Calculate row group means, or other statistics*

Description

Calculate row group means, or other statistics, where: `rowGroupMeans()` calculates row summary stats; and `rowGroupRmOutliers()` is a convenience function to call `rowGroupMeans(..., rmOutliers=TRUE, returnType="input")`.

Usage

```
rowGroupMeans(
  x,
  groups,
  na.rm = TRUE,
  useMedian = TRUE,
  rmOutliers = FALSE,
  crossGroupMad = TRUE,
  madFactor = 5,
  returnType = c("output", "input"),
  rowStatsFunc = NULL,
```

```
  groupOrder = c("same", "sort"),
  keepNULLlevels = FALSE,
  includeAttributes = FALSE,
  verbose = FALSE,
  ...
)

rowGroupRmOutliers(
  x,
  groups,
  na.rm = TRUE,
  rmOutliers = TRUE,
  crossGroupMad = TRUE,
  madFactor = 5,
  returnType = c("input"),
  groupOrder = c("same", "sort"),
  keepNULLlevels = FALSE,
  includeAttributes = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric data matrix
groups	character or factor vector of group labels, either as a character vector, or a factor. See the parameter groupOrder for ordering of group labels in the output data matrix.
na.rm	logical, default TRUE, passed to the stats func to ignore NA values.
useMedian	logical, default TRUE, indicating whether the default stat should be "mean" or "median".
rmOutliers	logical, default FALSE, indicating whether to apply outlier detection and removal.
crossGroupMad	logical indicating whether to calculate row MAD values using the median across groups for each row. The median is calculated using non-NA and non-zero row group MAD values. When crossGroupMad=TRUE it also calculates the non-NA, non-zero median row MAD across all rows, which defines the minimum difference from median applied across all values to be considered an outlier.
madFactor	numeric value indicating the multiple of the MAD value to define outliers. For example madFactor=5 will take the MAD value for a group multiplied by 5, 5*MAD, as a threshold for outliers. So any points more than 5*MAD distance from the median per group are outliers.
returnType	character, default "output", the return data type: • "output" returns one summary stat value per group, per row;

- "input" is useful when rmOutliers=TRUE in that it returns a matrix with the same dimensions as the input, except with outlier points replaced with NA.

rowStatsFunc function, default NULL, which takes a numeric matrix as input, and returns a numeric vector equal to the number of rows of the input data matrix. When supplied, useMedian is ignored. Examples: base::rowMeans(), matrixStats::rowMedians(), matrixStats::rowMads.

groupOrder character string indicating how character group labels are ordered in the final data matrix, when returnType="output". Note that when groups is a factor, the factor levels are kept in that order. Otherwise, "same" keeps groups in the same order they appear in the input matrix; "sort" applies jamba::mixedSort() to the labels.

keepNULLlevels logical, default FALSE, whether to keep factor levels even when there are no corresponding columns in x. When TRUE and returnType="output" the output matrix will contain one colname for each factor level, with NA values used to fill empty factor levels. This mechanism can be helpful to ensure that output matrices have consistent colnames.

includeAttributes
logical, default FALSE, whether to include attributes with "n" number of replicates per group, and "nLabel" with replicate label in n=# form.

verbose logical indicating whether to print verbose output.

... additional parameters are passed to rowStatsFunc, and if rmOutliers=TRUE to jamba::rowRmMadOutliers().

Details

This function by default calculates group mean values per row in a numeric matrix. However, the stat function can be changed to calculate row medians, row MADs, etc.

An added purpose of this function is optional outlier filtering, via calculation of MAD values and applying a MAD threshold cutoff. The intention is to identify technical outliers that otherwise adversely affect the calculated group mean or median values. To inspect the data after outlier removal, use the parameter returnType="input" which will return the input data matrix with NA substituted for outlier points. Outlier detection and removal is performed by jamba::rowRmMadOutliers().

Value

numeric matrix based upon returnType:

- When returnType="output" the output is a numeric matrix with the same number of columns as the number of unique groups labels. When groups is a factor and keepNULLlevels=TRUE, the number of columns will be the number of factor levels, otherwise it will be the number of factor levels used in groups.
- When returnType="input" the output is a numeric matrix with the same dimensions as the input data. This output is intended for use with rmOutliers=TRUE which will replace outlier points with NA values. Therefore, this matrix can be used to see the location of outliers.

The function also returns attributes when includeAttributes=TRUE, although the default is FALSE. The attributes describe the number of samples per group overall:

attr(out, "n") The attribute "n" is used to describe the number of replicates per group.

attr(out, "nLabel") The attribute "nLabel" is a simple text label in the form "n=3".

Note that when rmOutliers=TRUE the number of replicates per group will vary depending upon the outliers removed. In that case, remember that the reported "n" is always the total possible columns available prior to outlier removal.

See Also

Other jam numeric functions: deg2rad(), noiseFloor(), normScale(), rad2deg(), rowRmMadOutliers(), warpAroundZero()

Examples

```
x <- matrix(ncol=9, stats::rnorm(90));
colnames(x) <- LETTERS[1:9];
use_groups <- rep(letters[1:3], each=3)
rowGroupMeans(x, groups=use_groups)

# rowGroupRmOutliers returns the input data after outlier removal
rowGroupRmOutliers(x, groups=use_groups, returnType="input")

# rowGroupMeans(..., returnType="input") also returns the input data
rowGroupMeans(x, groups=use_groups, rmOutliers=TRUE, returnType="input")

# rowGroupMeans with outlier removal
rowGroupMeans(x, groups=use_groups, rmOutliers=TRUE)
```

---

rowRmMadOutliers *Remove outlier points per row by MAD factor threshold*

Description

Remove outlier points per row by MAD factor threshold

Usage

```
rowRmMadOutliers(
  x,
  madFactor = 5,
  na.rm = TRUE,
  minDiff = 0,
  minReps = 3,
  includeAttributes = FALSE,
  rowMadValues = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

x	numeric matrix
madFactor	numeric value to multiply by each row MAD to define the threshold for outlier detection.
na.rm	logical indicating whether to ignore NA values when calculating the MAD value. It should probably always be TRUE, however setting to FALSE will prevent any calculations in rows that contain NA values, which could be useful.
minDiff	numeric value indicating the minimum difference from median to qualify as an outlier. This value protects against removing outliers which are already extremely similar. Consider this example: • Three numeric values: c(10.0001, 10.0002, 10.001). • The third value differs from median by only 0.0008. • The third value 10.001 is 5x MAD factor away from median. • minDiff = 0.01 would require the minimum difference from median to be at least 0.01 to be eligible to be an outlier point.
minReps	numeric minimum number of non-NA values per row for outliers to be filtered on the row. This argument is typically only relevant for rows with n=2 non-NA values, and when rowMadValues is supplied and may define a threshold less than half the difference in the two points on the given row. Otherwise, n=2 defines each point at exactly 1x MAD from median, and would therefore never be considered an outlier.
includeAttributes	logical indicating whether to return attributes that describe the threshold and type of threshold used per row, in addition to the madFactor and minDiff values defined.
rowMadValues	numeric optional set of row MAD values to use, which is mostly helpful when combining MAD values across multiple samples groups on each row of data, where the combined MAD values may be more reliable than individual group MAD values.
verbose	logical indicating whether to print verbose output.
...	additional parameters are ignored.

Details

This function applies outlier detection and removal per row of the input numeric matrix.

- It first calculates MAD per row.
- The MAD threshold cutoff is a multiple of the MAD value, defined by madFactor, multiplying the per-row MAD by the madFactor.
- The absolute difference from median is calculated for each point.
- Outlier points are defined:
  1. Points with MAD above the MAD threshold, and
  2. Points with difference from median at or above minDiff

The minDiff parameter affects cases such as 3 replicates, where all replicates are well within a known threshold indicating low variance, but where two replicates might be nearly identical. Consider:

- Three numeric values: c(10.0001, 10.0002, 10.001).
- The third value differs from median by only 0.0008.
- The third value 10.001 is 5x MAD factor away from median.
- minDiff = 0.01 would require the minimum difference from median to be at least 0.01 to be eligible to be an outlier point.

One option to define minDiff from the data is to use: minDiff <- stats::median(rowMads(x))

In this case, the threshold is defined by the median difference from median across all rows. This type of threshold will only be reasonable if the variance across all rows is expected to be fairly similar.

This function is substantially faster when the matrixStats package is installed, but will use the apply(x, 1, mad) format as a last option.

Assumptions:

1. This function assumes the input data is appropriate for the use of MAD as a summary statistic.
2. Specifically, numeric values per row are expected to be roughly normally distributed.
3. Outlier points are assumed to be present in less than half overall non-NA data.
4. Outlier points are assumed to be technical outliers, and therefore not the direct result of the experimental measurements being studied. Technical outliers are often caused by some instrument measurement, methodological failure, or other upstream protocol failure.

The default threshold of 5x MAD factor is a fairly lenient criteria, above which the data may even be assumed not to conform to most downstream statistical techniques.

For measurements considered to be more robust, or required to be more robust, the threshold 2x MAD is applied. This criteria is usually a reasonable expectation of housekeeper gene expression across replicates within each sample group.

Value

numeric matrix with the same dimensions as the input x matrix. Outliers are replaced with NA.

If includeAttributes=TRUE then attributes will be included:

- outlierDF which is a data.frame with colnames
  - rowMedians: numeric median on each row
  - rowMadValues: numeric MAD for each row
  - rowThresholds: numeric threshold after applying madFactor and minDiff
  - rowReps: integer number of non-NA values in the input data
  - rowTypes: factor indicating the type of threshold: "madFactor" means the row applied the normal MAD * madFactor threshold; "minDiff" means the row applied the minDiff threshold which was the larger threshold.
- minDiff with the numeric value supplied
- madFactor with the numeric MAD factor threshold supplied
- outliersRemoved with the integer total number of new NA values produced by the outlier removal process.

See Also

Other jam numeric functions: deg2rad(), noiseFloor(), normScale(), rad2deg(), rowGroupMeans(), warpAroundZero()

Examples

```
set.seed(123);
x <- matrix(ncol=5, stats::rnorm(25))*5 + 10;
## Define some outlier points
x[1:2,3] <- x[1:2,3]*5 + 50;
x[2:3,2] <- x[2:3,2]*5 - 100;
rownames(x) <- head(letters, nrow(x));

rowRmMadOutliers(x, madFactor=5);

x2 <- rowRmMadOutliers(x, madFactor=2,
   includeAttributes=TRUE);
x2

x3 <- rowRmMadOutliers(x2,
   madFactor=2,
   rowMadValues=attr(x2, "outlierDF")$rowMadValues,
   includeAttributes=TRUE);
x3
```

---

sclass *return the classes of a list of objects*

Description

return the classes of a list of objects

Usage

```
sclass(x, ...)
```

Arguments

x	an S3 object inheriting from class `list`, or an S4 object.
...	additional parameters are ignored.

Details

This function takes a `list` and returns the classes for each object in the list. In the event an object class has multiple values, the returned object is a list, otherwise is a vector. If x is an S4 object, then `methods::slotNames(x)` is used, and the class is returned for each S4 slot.

When x is a data.frame, data.table, tibble, or similar DataFrame table-like object, the class of each column is returned.

For the special case where x is an S4 object with one slotName ".Data", the values in x@.Data are coerced to a list. One example of this case is with limma::MArrayLM-class.

When x is a matrix, the class of each column is returned for consistency, even though the class of each column should be identical.

For more more information about a list-like object, including the lengths/dimensions of the elements, see sdim() or ssdim().

Value

character vector with the class of each list element, or column name, depending upon the input class(x).

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), relist_named(), rlengths(), sdim(), uniques(), unnestList()

Examples

```
sclass(list(LETTERS=LETTERS, letters=letters));

sclass(data.frame(B=letters[1:10], C=2:11))
```

---

sdim *print dimensions of list object elements*

Description

sdim() prints the name and dimensions of list object elements, such as a list of data.frame

ssdim() prints the name and dimensions of nested elements of list objects, for example a list of list objects that each contain other objects.

sdima() prints the name and dimensions of object attributes(x). It is useful for summarizing the attributes() of an object.

ssdima() prints the name and dimensions of nested elements of list object attributes(), for example a list of list objects that each contain other objects. It is useful for comparing attributes across list elements.

This function prints the dimensions of a list of objects, usually a list of data.frame objects, but extended to handle more complicated lists, including even S4 object methods::slotNames().

Over time, more object types will be made compatible with this function. Currently, igraph objects will print the number of nodes and edges, but requires the igraph package to be installed.

Usage

```
sdim(
  x,
  includeClass = TRUE,
  doFormat = FALSE,
  big.mark = ",",
  verbose = FALSE,
  ...
)

sdima(
  x,
  includeClass = TRUE,
  doFormat = FALSE,
  big.mark = ",",
  verbose = FALSE,
  ...
)

ssdima(
  x,
  includeClass = TRUE,
  doFormat = FALSE,
  big.mark = ",",
  verbose = FALSE,
  ...
)

ssdim(
  x,
  includeClass = TRUE,
  doFormat = FALSE,
  big.mark = ",",
  verbose = FALSE,
  ...
)
```

Arguments

x	one of several recognized object classes: • an S3 object inheriting from class "list", including a nested list of lists or simple list • an S3 atomic object, which returns only the length • a single multi-dimensional object such as data.frame, matrix, array, tibble, or similar, which returns only its dimensions. • an S4 object in which case it used methods::slotNames(x) to traverse the object structure

- an "environment" object, in which case ls(envir=x) is used to traverse the object structure.
- When the object is S4 that inherits "List" from the S4Vectors package, it will attempt to use the proper subset functions from S4Vectors via names(x), but that process only works properly if the S4Vectors package is previously loaded, otherwise it reverts to using methods::slotNames(x).

includeClass	logical indicating whether to print the class of each element in the input x object. Note that for S4 objects, each element will be the object returned for each of methods::slotNames(x).
doFormat	logical indicating whether to format the dimensions using format(...,big.mark=","), which is mainly useful for extremely large dimensions. This parameter should probably become more broadly useful and respectful for different locales.
big.mark	character value used when doFormat=TRUE, used in the call to format(...,big.mark).
verbose	logical whether to print verbose output
...	additional parameters are ignored.

Value

data.frame where each row indicates the dimensions of each element in the input list. When includeClass is TRUE it will include a column class which indicates the class of each list element. When the input list contains arrays with more than two dimensions, the first two dimensions are named "rows" and "columns" with additional dimensions named "dim3" and so on. Any list element with fewer than that many dimensions will only have values populated to the relevant dimensions, for example a character vector will only populate the length.

data.frame which describes the dimensions of the objects in attributes(x).

list of data.frame each of which describes the dimensions of the objects in attributes(x).

list of data.frame, each row indicates the dimensions of each element in the input list. When includeClass is TRUE it will include a column class which indicates the class of each list element. When the input list contains arrays with more than two dimensions, the first two dimensions are named "rows" and "columns" with additional dimensions named "dim3" and so on. Any list element with fewer than that many dimensions will only have values populated to the relevant dimensions, for example a character vector will only populate the length.

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), relist_named(), rlengths(), sclass(), uniques(), unnestList()

Examples

```
L <- list(LETTERS=LETTERS,
   letters=letters,
   lettersDF=data.frame(LETTERS, letters));
sdim(L)

LL <- list(L=L, A=list(1:10))
sdim(LL)
```

```
ssdim(LL)

m <- matrix(1:9,
   ncol=3,
   dimnames=list(
      Rows=letters[1:3],
      Columns=LETTERS[1:3]));
sdima(m);
ssdima(m);
```

`setCLranges` *Get Chroma and Luminance ranges for the given lightMode*

Description

Return Crange, Lrange, Cgrey, adjustRgb values for the given lightMode, intended to provide ranges suitable for contrasting text displayed on a light or dark background.

Usage

```
setCLranges(
  lightMode = NULL,
  Crange = getOption("jam.Crange"),
  Lrange = getOption("jam.Lrange"),
  Cgrey = getOption("jam.Cgrey", 5),
  adjustRgb = getOption("jam.adjustRgb", 0),
  setOptions = c("FALSE", "ifnull", "TRUE"),
  verbose = FALSE,
  ...
)
```

Arguments

`lightMode`	boolean indicating whether the background color is light (TRUE is bright), or dark (FALSE is dark.) By default it calls `checkLightMode()` which queries `getOption("lightMode")`.
`Crange`	numeric range of chroma values, ranging between 0 and 100. By default, `getOptions("Crange")` is used, otherwise defaults will be assigned based upon `lightMode`.
`Lrange`	numeric range of luminance values, ranging between 0 and 100. By default, `getOptions("Crange")` is used, otherwise defaults will be assigned based upon `lightMode`.
`Cgrey`	numeric chroma (C) value, which defines grey colors at or below this chroma. Any colors at or below the grey cutoff will have their C values unchanged. This mechanism prevents converting black to red, for example. To disable the effect, set `Cgrey=-1`.

adjustRgb	numeric color adjustment factor, used during the conversion of RGB colors to the ANSI-compatible colors used by the crayon pacakge. The ANSI color range does not include a full RGB palette, and the conversion is somewhat lossy. By default, getOptions("jam.adjustRgb") is used to store a globally re-usable value.
setOptions	character or logical whether to update options() "jam.Crange" and "jam.Lrange", with the following behavior: • "ifnull" will update only options() which were previously NULL • FALSE or "FALSE" does not update options() • TRUE or "TRUE" will update options() with values determined by this function.
verbose	logical indicating whether to print verbose output.
...	additional arguments are ignored.

Details

This function is intended mainly for internal use by jamba such as printDebug(), and make_styles(), which is also mainly intended for console text or other printed text output. The utility of this function is to store the logic of determining sensible default ranges.

Companion functions:

- applyCLranges() is used to apply the ranges to a vector of R colors.
- checkLightMode() is used to detect whether console output is expected to have a light or dark background.

Value

list with elements:

Crange Numeric vector of length 2, defining the HCL chroma (C) range.

Lrange Numeric vector of length 2, defining the HCL luminance (L) range.

adjustRgb Numeric vector of length 1, defining the adjustment to apply during RGB-to-ANSI color conversion.

Cgrey Numeric vector of length 1, defining the HCL chroma (C) value below which colors are considered greyscale, and are converted to ANSI greyscale colors. HCL chroma ranges from 0 to 100. Set value Cgrey=-1 or Cgrey=FALSE to disable this logic, causing colors to be matched using all available ANSI color values.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setTextContrastColor(), showColors(), unalpha(), warpRamp()

Examples

```
setCLranges(lightMode=FALSE)
```

setPrompt *set R prompt with project name and R version*

Description

set R prompt with project name and R version

Usage

```
setPrompt(
  projectName = "unnamed",
  useColor = TRUE,
  projectColor = "yellow",
  bracketColor = "white",
  Rcolors = c("white", "white", "white"),
  PIDcolor = NA,
  promptColor = "white",
  usePid = TRUE,
  resetPrompt = FALSE,
  addEscape = NULL,
  updateOptions = TRUE,
  debug = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

projectName	character string, default "unnamed", used as a label to represent the project work.
useColor	logical whether to define a color prompt if the crayon package is installed.
projectColor, bracketColor, Rcolors, PIDcolor, promptColor	character colors used when useColor==TRUE and the crayon package is installed: • projectColor colors the project name; • bracketColor colors the curly brackets around the project; • Rcolors can be a vector of 3 colors, colorizing "R", the "-" divider, and the R version; • PIDcolor colors the PID when usePid=TRUE; and • promptColor colors the ">" at the end of the prompt.
usePid	logical whether to include the process ID in the prompt. Including the PID is helpful for the rare occasion when a process is hung and needs to be stopped directly.
resetPrompt	logical whether to revert all changes to the prompt back to the default R prompt, that is, no color and no projectName.

addEscape	logical or NULL indicating whether to wrap color encoding ANSI inside additional escape sequences. This change is helpful for linux-based (readline-based) R consoles, by telling the console not to count ANSI color control characters as visible characters when determining word wrapping on the console. Note that RStudio does not work well with this setting. If you find that the word-wrap is incorrect in the R console, try addEscape=TRUE. Apparently most versions of RStudio will already adjust (and prevent) colorizing the prompt during editing, presumably to sidestep the problem of calculating the correct character length. By default when addEscape is NULL, it checks whether environmental variable RSTUDIO equals "1" (running inside RStudio) then sets addEscape=FALSE; otherwise it defines addEscape=TRUE. In most cases for commandline prompts, addEscape=TRUE is helpful and not problematic.
updateOptions	logical whether to update the user options() with options(prompt="..."), default TRUE.
debug	logical indicating whether to print the ANSI control character output for the full prompt, for visual review.
verbose	logical whether to print verbose output.
...	additional parameters are passed to make_styles() which is only relevant with the argument useColor=TRUE.

Details

This function sets a simple, colorized R prompt with useful information:

- projectName
- R version, major and minor included
- Process ID (PID)

The prompt is defined in options("prompt").

Where Am I?:
It is useful for the question: "What version of R?" In rare cases, multiple R versions can be active at once (!), see the rig package for this exciting capability.

What Am I Doing?:
The core question addressed is : "What am I working on?" The project name is especially useful when working with multiple active R sessions.

How Do I Stop This Thing?:
It may also be useful for the question "How do I stop this thing", by returning the Process ID to be used to kill a long-running process without fear of killing the **wrong** long-running process.

Can It Have Color?:
Then of course, meeting the above requirements, at least make it pretty.

Word-Wrap Gone Awry:
A color-encoded prompt may sometimes interfere with word-wrapping on the R console. A long line may wrap prematurely before reaching the right edge of the screen. There are two frequent causes of this issue:

1. `options("width")` is sometimes defined too narrow for the screen. When resizing the console, this option should be updated, and sometimes this update fails. To fix, either resize the window briefly again, or define `options("width")` manually. (Or debug the reason that this option is not being updated.)
2. The terminal `locale` is sometimes mismatched with the terminal, usually caused by a layer of terminal emulation which is not compatible with ANSI color codes, or ANSI escape codes.
   - Some examples: 'PuTTY' on 'Windows', GNU 'screen', 'tmux'.
   - Check `Sys.env("LC_ALL")`. The most common results are `"C"` for generic C-type output, or a Unicode/UTF-8 locale such as `"en_US.UTF-8"` ('enUS' is English-USA in this context). In general, Unicode/UTF-8 is recommended, with benefit that it more readily displays other Unicode characters. However, sometimes the terminal environment (PuTTY or iTerm) is expecting one locale, but is receiving another. Either switching the terminal expected locale, or the R console locale, may resolve the mismatch.

R uses 'readline' for unix-like systems by default, and issues related to using color prompt are handled at that level.

The 'readline' library allows escaping ANSI color characters so they do not contribute to the estimated line width, and these codes are used in `setPrompt()`.

The final workaround is `useColor=FALSE`, but that would be a sad outcome.

Value

`list` named `"prompt"`, suitable to use in `options()` with the recommended prompt. When `updateOptions=FALSE` use: `options(setPrompt("projectName"))`

See Also

Other jam practical functions: `breakDensity()`, `call_fn_ellipsis()`, `checkLightMode()`, `check_pkg_installed()`, `colNum2excelName()`, `color_dither()`, `exp2signed()`, `getAxisLabel()`, `isFALSEV()`, `isTRUEV()`, `jargs()`, `kable_coloring()`, `lldf()`, `log2signed()`, `middle()`, `minorLogTicks()`, `newestFile()`, `printDebug()`, `reload_rmarkdown_cache()`, `renameColumn()`, `rmInfinite()`, `rmNA()`, `rmNAs()`, `rmNULL()`

Examples

```
setPrompt("jamba")

setPrompt("jamba", projectColor="purple");

setPrompt("jamba", usePid=FALSE);

setPrompt(resetPrompt=TRUE);
```

`setTextContrastColor` *Define visible text color*

Description

Given a vector or colors, define a contrasting color for text, typically using either white or black. The `useGrey` argument defines the offset from pure white and pure black, to use a contrasting grey shade.

Usage

```
setTextContrastColor(
  color,
  hclCutoff = 60,
  rgbCutoff = 127,
  colorModel = c("hcl", "rgb"),
  useGrey = 0,
  keepAlpha = FALSE,
  alphaLens = 0,
  bg = NULL,
  ...
)
```

Arguments

`color`	character vector with one or more R-compatible colors.
`hclCutoff`	numeric threshold above which a color is judged to be bright, therefore requiring a dark text color. This comparison uses the L value from the `col2hcl()` function, which scales colors from 1 to 100.
`rgbCutoff`	numeric threshold above which a color is judged to be bright, therefore requiring a dark text color. The mean r,g,b value is used.
`colorModel`	Either 'hcl' or 'rgb' to indicate how the colors will be judged for overall brightness. The 'hcl' method uses the L value, which more reliably represents overall visible lightness.
`useGrey`	numeric threshold used to define dark and bright text colors, using the R greyscale gradient from 0 to 100: `useGrey=10` implies `"grey10"` and `"grey90"` for the contrasting text colors; `useGrey=15` is useful if labels may also overlap white or black space, since the text will never be fully white or black.
`keepAlpha`	logical indicates whether the input color alpha transparency should be maintained in the text color. By default, text alpha is not maintained, and instead is set to alpha=1, fully opaque.
`alphaLens`	numeric value used to adjust the effect of alpha transparency, where positive values emphasize the background color, and negative values emphasize the foreground (transparent) color.

bg — vector of R colors, used as a background when determining the brightness of a semi-transparent color. The corresponding brightness value from the bg is applied via weighted mean to the input color brightness, the result is compared the the relevant cutoff. By default graphics::par("bg") is used to determine the default plot background color, only when there is an open graphics device, otherwise calling graphics::par("bg") would open a graphics device, which is not desireable. When no graphics device is open, and when bg=NULL, the default is bg="white".

... — additional arguments are ignored.

Details

The color is expected to represent a background color, the output is intended to be a color with enough contrast to read text legibly.

The brightness of the color is detected dependent upon the colorModel: when "hcl" the luminance L is compared to hclCutoff; when "rgb" the brightness is the sum of the RGB channels which is compared to rgbCutoff. In most cases the "hcl" and L will be more accurate.

When color contains transparency, an optional argument bg represents the figure background color, as if the color is used to draw a color-filled rectangle. In this case, the bg and color are combined to determine the resulting actual color. This scenario is mostly useful when plotting text labels on a dark background, such as black background with colored text boxes.

Value

character vector of R colors.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), showColors(), unalpha(), warpRamp()

Examples

```
color <- c("red","yellow","lightblue","darkorchid1","blue4");
setTextContrastColor(color);

# showColors() uses setTextContrastColor() for labels
showColors(color)
# printDebugI() uses setTextContrastColor() for foreground text
printDebugI(color)

# demonstrate the effect of alpha transparency
colorL <- lapply(nameVector(c(1, 0.9, 0.8, 0.6, 0.3)), function(i){
   nameVector(alpha2col(color, alpha=i), color);
})
jamba::showColors(colorL,
   groupCellnotes=FALSE,
   srtCellnote=seq(from=15, to=-15, length.out=5));
```

```
graphics::title(ylab="alpha", line=1.5);

# change background to dark blue
withr::with_par(list("bg"="navy", "col"="white", "col.axis"="white"), {
jamba::showColors(colorL,
   groupCellnotes=FALSE,
   srtCellnote=seq(from=15, to=-15, length.out=5))
graphics::title(ylab="alpha", line=1.5);
})

# Example using transparency and drawLabels()
bg <- "blue4";
col <- fixYellow("palegoldenrod");
nullPlot(fill=bg, plotAreaTitle="", doMargins=FALSE);
for (alpha in c(0.1, 0.3, 0.5, 0.7, 0.9)) {
   labelCol <- setTextContrastColor(
      alpha2col("yellow", alpha),
      bg=bg);
   drawLabels(x=1 + alpha,
      y=2 - alpha,
      labelCex=1.5,
      txt="Plot Title",
      boxColor=alpha2col(col, alpha),
      boxBorderColor=labelCol,
      labelCol=labelCol);
}
```

`set_xlsx_colwidths` *Set column widths in Xlsx files*

Description

Set column widths in Xlsx files

Usage

```
set_xlsx_colwidths(
  xlsxFile,
  sheet = 1,
  cols = seq_along(widths),
  widths = 11,
  ...
)
```

Arguments

`xlsxFile`	`character` filename to a file with ".xlsx" extension, or `Workbook` object defined in the `openxlsx` package. When `xlsxFile` is a `Workbook` the output is not saved to a file.

sheet	integer sheet number or character sheet name, passed to openxlsx::setColWidths() indicating the worksheet to affect.
cols	integer vector indicating the column numbers to affect.
widths	numeric vector indicating the width of each column defined by cols.
...	additional arguments are passed to openxlsx::setColWidths().

Details

This function is a light wrapper to perform these steps from the very useful openxlsx R package:

- openxlsx::loadWorkbook()
- openxlsx::setColWidths()
- openxlsx::saveWorkbook()

Value

Workbook object as defined by the openxlsx package is returned invisibly with invisible(). This Workbook can be used in argument wb to provide a speed boost when saving multiple sheets to the same file.

See Also

Other jam export functions: applyXlsxCategoricalFormat(), applyXlsxConditionalFormat(), readOpenxlsx(), set_xlsx_rowheights(), writeOpenxlsx()

Examples

```
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
   df <- data.frame(a=LETTERS[1:5], b=1:5);
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test");

   ## By default, cols starts at column 1 and continues to length(widths)
   set_xlsx_colwidths(out_xlsx,
      sheet="jamba_test",
      widths=rep(20, ncol(df))
   )
}
```

`set_xlsx_rowheights` *Set row heights in Xlsx files*

Description

This function is a light wrapper to perform these steps from the very useful `openxlsx` R package:

Usage

```
set_xlsx_rowheights(
  xlsxFile,
  sheet = 1,
  rows = seq_along(heights) + 1,
  heights = 17,
  ...
)
```

Arguments

`xlsxFile`	`character` filename to a file with ".xlsx" extension, or `Workbook` object defined in the `openxlsx` package. When `xlsxFile` is a `Workbook` the output is not saved to a file.
`sheet`	`integer` sheet number or `character` sheet name, passed to `openxlsx::setRowHeights()` indicating the worksheet to affect.
`rows`	`integer vector` indicating the row numbers to affect.
`heights`	`numeric vector` indicating the height of each column defined by `rows`.
`...`	additional arguments are passed to `openxlsx::setRowHeights()`.

Details

- `openxlsx::loadWorkbook()`
- `openxlsx::setRowHeights()`
- `openxlsx::saveWorkbook()`

Note that when only the argument `heights` is defined, the argument `rows` will point to row 2 and lower, thus skipping the first (header) row. Define `rows` specifically in order to affect the header row as well.

Value

`Workbook` object as defined by the `openxlsx` package is returned invisibly with `invisible()`. This `Workbook` can be used in argument `wb` to provide a speed boost when saving multiple sheets to the same file.

See Also

Other jam export functions: `applyXlsxCategoricalFormat()`, `applyXlsxConditionalFormat()`, `readOpenxlsx()`, `set_xlsx_colwidths()`, `writeOpenxlsx()`

Examples

```
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
   df <- data.frame(a=LETTERS[1:5], b=1:5);
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test");

   ## by default, rows will start at row 2, skipping the header
   set_xlsx_rowheights(out_xlsx,
      sheet="jamba_test",
      heights=rep(17, nrow(df))
   )

   ## to include the header row
   set_xlsx_rowheights(out_xlsx,
      sheet="jamba_test",
      rows=seq_len(nrow(df)+1),
      heights=rep(17, nrow(df)+1)
   )
}
```

---

shadowText *Draw text with shadow border*

Description

Draw text with shadow border

Usage

```
shadowText(
  x,
  y = NULL,
  labels = NULL,
  col = "white",
  bg = setTextContrastColor(col),
  r = getOption("jam.shadow.r", 0.15),
  offset = c(0.15, -0.15),
  n = getOption("jam.shadow.n", 8),
  outline = getOption("jam.outline", TRUE),
  alphaOutline = getOption("jam.alphaOutline", 0.4),
  shadow = getOption("jam.shadow", FALSE),
  shadowColor = getOption("jam.shadowColor", "black"),
  alphaShadow = getOption("jam.alphaShadow", 0.2),
  shadowOrder = c("each", "all"),
```

```
  cex = graphics::par("cex"),
  font = graphics::par("font"),
  doTest = FALSE,
  ...
)
```

Arguments

x, y	numeric coordinates, either as vectors x and y, or x as a two-color matrix recognized by `grDevices::xy.coords()`.
labels	vector of labels to display at the corresponding xy coordinates.
col, bg, shadowColor	the label color, and background (outline) color, and shadow color (if `shadow=TRUE`), for each element in `labels`. Colors are applied in order, and recycled to `length(labels)` as needed. By default bg will choose a contrasting color, based upon `setTextContrastColor()`. Also by default, the shadow is "black" true to its name, since it is expected to darken the area around it.
r	the outline radius, expressed as a fraction of the width of the character "A" as returned by `graphics::strwidth()`.
offset	the outline offset position in xy coordinates, expressed as a fraction of the width of the character "A" as returned by `graphics::strwidth()`, and `graphics::strheight()`, respectively. The offset is only applied when `shadow=TRUE` to enable the shadow effect.
n	`numeric` steps around the label used to create the outline. A higher number may be useful for very large font sizes, otherwise 8 is a reasonably good balance between detail and the number of labels added.
outline	`logical` whether to enable outline drawing.
alphaOutline, alphaShadow	`numeric` alpha transparency to use for the outline and shadow colors, respectively.
shadow	`logical` whether to enable shadow drawing.
shadowOrder	`character` value indicating when shadows are drawn relative to drawing labels: `"each"` draws each shadow with each label, so that shadows will overlap previous labels; `"all"` draws all shadows first then all labels, so labels will always appear above all shadows. See examples.
cex	`numeric` scalar applied to font size, default `graphics::par("cex")`.
font	`character` applied to font family, default `graphics::par("font")`.
doTest	`logical` whether to create a visual example of output. Note that it calls `usrBox` to color the plot area, and the background can be overridden with something like `fill="navy"`.
...	other parameters are passed to `text`. Note that certain parameters are not vectorized in that function, such as `srt` which requires only a fixed value. To rotate each label independently, multiple calls to `text` or `shadowText` must be made. Other parameters like `adj` only accept up to two values, and those two values affect all label positioning.

Details

Draws text with the same syntax as `graphics::text()` except that this function adds a contrasting color border around the text, which helps visibility when the background color is either not known, or is not expected to be a fixed contrasting color.

The function draws the label n times with the chosed background color, then the label itself atop the background text. It does not typically have a noticeable effect on rendering time, but it may impact downstream uses in vector file formats like 'SVG' and 'PDF', where text is stored as proper text and font objects. Take care when editing text that the underlying shadow text is also edited in sync.

The parameter `doTest=TRUE` will display a visual example. The background color can be modified with `fill="navy"` for example.

Value

invisible `list` of components used to call `graphics::text()`, including: x, y, allColors, allLabels, cex, font.

See Also

Other jam plot functions: `adjustAxisLabelMargins()`, `coordPresets()`, `decideMfrow()`, `drawLabels()`, `getPlotAspect()`, `groupedAxis()`, `imageByColors()`, `imageDefault()`, `minorLogTicksAxis()`, `nullPlot()`, `plotPolygonDensity()`, `plotRidges()`, `plotSmoothScatter()`, `shadowText_options()`, `showColors()`, `sqrtAxis()`, `usrBox()`

Examples

```
shadowText(doTest=TRUE);
shadowText(doTest=TRUE, fill="navy");
shadowText(doTest=TRUE, fill="red4");

# example showing labels with overlapping shadows
withr::with_par(list("mfrow"=c(1, 2)), {
nullPlot(doBoxes=FALSE);
graphics::title(main="shadowOrder='each'");
shadowText(x=c(1.5, 1.65), y=c(1.5, 1.55),
   labels=c("one", "two"), cex=c(2, 4), shadowOrder="each")
nullPlot(doBoxes=FALSE);
graphics::title(main="shadowOrder='all'");
shadowText(x=c(1.5, 1.65), y=c(1.5, 1.55),
   labels=c("one", "two"), cex=c(2, 4), shadowOrder="all")
})
```

---

shadowText_options *Get and set options for shadowText*

Description

Get and set options for shadowText

Usage

```
shadowText_options(
  r = getOption("jam.shadow.r", 0.15),
  n = getOption("jam.shadow.n", 8),
  outline = getOption("jam.outline", TRUE),
  alphaOutline = getOption("jam.alphaOutline", 0.4),
  shadow = getOption("jam.shadow", FALSE),
  shadowColor = getOption("jam.shadowColor", "black"),
  alphaShadow = getOption("jam.alphaShadow", 0.2),
  r_ex = 1,
  alpha_ex = 1,
 preset = c("none", "default", "bold", "bold white", "bold black", "both", "shadow",
    "bold shadow", "bold white shadow", "bold black shadow", "bold both"),
  verbose = FALSE,
  ...
)
```

Arguments

r	numeric radius used for outline or shadow
n	numeric number of shadow steps to render around each text label
outline	logical indicating whether to render shadowText as an outline (default), or when outline=FALSE it renders a drop shadow offset using offset which by default is slightly down and to the right of the text labels.
alphaOutline	numeric value for alpha transparency used for label outlines when outline=TRUE, with values expected between 0 (fully transparent) and 1 (not transparent).
shadow	logical indicating whether to render shadowText as a shadow, or not (default).
shadowColor	character R color which defines the color used for the outline or shadow for each text label.
alphaShadow	numeric value for alpha transparency used for label shadows when shadow=TRUE, with values expected between 0 (fully transparent) and 1 (not transparent).
r_ex	numeric expansion factor used to adjust the radius r. The value for r is defined based upon the arguments provided, then is multiplied by the r_ex expansion factor. The result is stored in option "jam.shadow.r".
alpha_ex	numeric expansion factor used to adjust the alpha transparency of both alphaOutline and alphaShadow. Values will be maintained no lower than 0 and no higher than 1. The values for alphaOutline and alphaShadow are defined based upon the arguments provided, then are multiplied by the alpha_ex expansion factor. The result is clipped to range 0,1 using jamba::noiseFloor(). The resulting values are stored in options "jam.alphaOutline" and "jam.alphaShadow", respectively.
preset	character string which defines a preset with associated settings. Any value other than "none" will cause all other options to use the preset settings. • "none": no preset settings are applied • "default": reverts all options to the original default values, which produces an outline, and not a drop shadow. The color will use shadowColor

which allows using all other settings from this preset, except with custom color.

- "bold": makes output produce visibly more distinct outline, with no drop shadow. The color will use shadowColor which allows using all other settings from this preset, except with custom color.
- "bold white": same as "bold" except default text color is white
- "bold black": same as "bold" except default text color is black
- "both": applies "default" and enables drop shadow
- "shadow": uses suggested default values to produce a drop shadow, and not an outline. The color will use shadowColor which allows using all other settings from this preset, except with custom color.
- "bold shadow": same as "shadow" except the shadow is more distinct. The color will use shadowColor which allows using all other settings from this preset, except with custom color.
- "bold white shadow": same as "bold shadow" with white shadow
- "bold black shadow": same as "bold shadow" with black shadow
- "bold both": same as "bold" except also enables bold shadow

verbose — logical indicating whether to print verbose output

... — additional arguments are ignored.

Details

This function is intended to be a convenient method to get and set options to be used with jamba::shadowText(). This function stores the resulting values in options() for use by shadowText().

Value

list with the following options for shadowText():

- jam.shadow.r
- jam.shadow.n
- jam.outline
- jam.alphaOutline
- jam.shadow
- jam.shadowColor
- jam.alphaShadow

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), showColors(), sqrtAxis(), usrBox()

Examples

```
nullPlot(doBoxes=FALSE, xlim=c(-1, 4), ylim=c(-1, 4), asp=1);
usrBox(fill="grey")
cex <- 1.2
graphics::axis(1);graphics::axis(2, las=2)
shadowText_options(preset="default")
shadowText(x=0, y=3, "default", cex=cex)
shadowText_options(preset="bold")
shadowText(x=0, y=2, "bold", cex=cex)
shadowText_options(preset="bold white")
shadowText(x=0, y=1, col="black", "bold white", cex=cex)
shadowText_options(preset="bold black")
shadowText(x=0, y=0, col="white", "bold black", cex=cex)
shadowText_options(preset="shadow")
shadowText(x=3, y=3, "shadow", cex=cex)
shadowText_options(preset="bold shadow")
shadowText(x=3, y=2, "bold shadow", cex=cex)
shadowText_options(preset="bold white shadow")
shadowText(x=3, y=1, col="black", "bold white shadow", cex=cex)
shadowText_options(preset="bold black shadow")
shadowText(x=3, y=0, col="white", "bold black shadow", cex=cex)
shadowText_options(preset="both")
shadowText(x=1.5, y=3, col="white", "both", cex=cex)
shadowText(x=1.5, y=2.5, col="black", "both", cex=cex)
shadowText_options(preset="bold both")
shadowText(x=1.5, y=2, col="white", "bold both", cex=cex)
shadowText(x=1.5, y=1, col="black", "bold both", cex=cex)
shadowText(x=1.5, y=0.5, col="blue3", "bold both", cex=cex, font=2)
shadowText(x=1.5, y=0, col="indianred1", "bold both", cex=cex, font=2)
shadowText_options(preset="default")
```

`showColors` *Show colors from a vector or list*

Description

Show colors from a vector or list

Usage

```
showColors(
  x,
  labelCells = NULL,
  transpose = FALSE,
  srtCellnote = NULL,
  adjustMargins = TRUE,
  makeUnique = FALSE,
  doPlot = TRUE,
```

```
  ...
)
```

Arguments

x	one of these input types: • character vector of colors • function to produce colors, for example circlize::colorRamp2() • list with any combination of character or function
labelCells	logical whether to label colors atop the color itself. If NULL (default) it will only display labels with 40 or fewer items on either axis.
transpose	logical whether to transpose the colors to display top-to-bottom, instead of left-to-right.
srtCellnote	numeric angle to rotate text when labelCells=TRUE. When set to NULL, labels are vertical srtCellnote=90 when transpose=FALSE and horizontal srtCellnote=0 when transpose=TRUE.
adjustMargins	logical indicating whether to call adjustAxisLabelMargins() to adjust the x- and y-axis label margins to accomodate the label size. • Note when an axis is hidden by using xaxt="n" or xaxt="n", the respective margin will not be adjusted. • The arguments in ... take precedence over graphics::par(), when deciding whether to adjust margins. However if xaxt="s" and graphics::par("xaxt"="n") the margin will be adjusted but not displayed. In this way the axes can be adjusted without displaying the labels, so the labels can be rendered later if needed.
makeUnique	logical indicating whether to display only the first unique color. When x is supplied as a list this operation will display the first unique color for each list element. Also, when x is a list, just to be fancy, makeUnique is recycled to length(x) so certain list elements can display unique values, while others display all values.
doPlot	logical indicating whether to produce a visual plot. Note this function returns the color matrix invisibly.
...	additional parameters are passed to imageByColors().

Details

This function simply displays colors for review, using imageByColors() to display colors and labels across the plot space.

When supplied a list, each row in imageByColors() represents an entry in the list. Nothing fancy.

Value

invisible color matrix used by imageByColors(). When the input x is empty, or cannot be converted to colors when x contains a function, the output returns NULL.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), sqrtAxis(), usrBox()

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), unalpha(), warpRamp()

Examples

```
x <- color2gradient(list(Reds=c("red"), Blues=c("blue")), n=c(4,7));
showColors(x);

showColors(getColorRamp("firebrick3"))

if (requireNamespace("RColorBrewer", quietly=TRUE)) {
   RColorBrewer_namelist <- rownames(RColorBrewer::brewer.pal.info);
   y <- lapply(nameVector(RColorBrewer_namelist), function(i){
      n <- RColorBrewer::brewer.pal.info[i, "maxcolors"]
      j <- RColorBrewer::brewer.pal(n, i);
      nameVector(j, seq_along(j));
   });
   showColors(y, cexCellnote=0.6, cex.axis=0.7, main="Brewer Colors");
}
if (requireNamespace("viridisLite", quietly=TRUE)) {
   # given one function name it will display discrete colors
   showColors(viridisLite::viridis)
   # a list of functions will show each function output
   showColors(list(viridis=viridisLite::viridis,
      inferno=viridisLite::inferno))

   # grab the full viridis color map
   z <- rgb2col(viridisLite::viridis.map[,c("R","G","B")]);
   # split the colors into a list
   viridis_names <- c(A="magma",
      B="inferno",
      C="plasma",
      D="viridis",
      E="cividis",
      F="rocket",
      G="mako",
      H="turbo")
   y <- split(z,
      paste0(viridisLite::viridis.map$opt, ": ",
      viridis_names[viridisLite::viridis.map$opt]));
   showColors(y, labelCells=TRUE, xaxt="n", main="viridis.map colors");
}

# demonstrate makeUnique=TRUE
```

```
j1 <- getColorRamp("rainbow", n=7);
names(j1) <- seq_along(j1);
j2 <- rep(j1, each=3);
names(j2) <- makeNames(names(j2), suffix="_rep");
j2
showColors(list(
   j1=j1,
   j2=j2,
   j3=j2),
   makeUnique=c(FALSE, FALSE, TRUE))
```

`sizeAsNum` *convert size to numeric value*

Description

convert size to numeric value

Usage

```
sizeAsNum(x, kiloSize = 1024, verbose = FALSE, ...)
```

Arguments

`x`	`character` vector. When `x` is numeric, it is returned as-is; otherwise `x` is coerced to `character` with `as.character()` and will throw an error if it fails.
`kiloSize`	`numeric` number of base units when converting from one base unit, to one "kilo" base unit. For file sizes, this value is 1024, but for other purposes this value may be 1000, like one thousand units is `"1k units"`.
`verbose`	`logical` indicating whether to print verbose output. The output includes a `data.frame` summarizing the input, and the unit matched, and the final value. If `verbose==2` it will return this `data.frame` for review.
`...`	additional arguments are ignored.

Details

This function is intended to provide the inverse of `asSize()` by converting an abbreviated size into a full numeric value.

It makes one simplifying assumption, that the first character in the unit is enough to determine the unit. This assumption also means the units are currently case-sensitive, for example `Mega` requires upper-case `"M"`, because `"milli"` which is not supported, requires `"m"`.

Unit abbreviations recognized:

- `k` - kilo - size is defined by `kiloSize`
- `M` - Mega - size is defined by `kiloSize ^ 2`

- G - Giga - size is defined by kiloSize ^ 3
- T - Tera - size is defined by kiloSize ^ 4
- P - Peta - size is defined by kiloSize ^ 5

Everything else is considered to have no abbreviated units, thus the numeric value is returned as-is.

Note that the round trip asSize() followed by sizeAsNum() will not produce identical values, because the intermediate value is rounded by digits in asSize().

Value

numeric vector representing the numeric value represented by an abbreviated size.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), tcount(), ucfirst()

Examples

```
x <- asSize(c(1, 10,2010,22000,52200), unitType="")
x
#> "1"   "10" "2k"     "21k"    "51k"
sizeAsNum(x)

sizeAsNum(x, kiloSize=1000)
```

---

smoothScatterJam *Smooth scatter plot, Jam style*

Description

Produce smooth scatter plot, a helper function called by plotSmoothScatter().

Usage

```
smoothScatterJam(
  x,
  y = NULL,
  nbin = 256,
  bandwidth,
  colramp = grDevices::colorRampPalette(c("white", "lightblue", "blue", "orange",
    "orangered2")),
  nrpoints = 100,
  pch = ".",
  cex = 1,
  col = "black",
```

```
  transformation = function(x) x^0.25,
  postPlotHook = graphics::box,
  xlab = NULL,
  ylab = NULL,
  xlim,
  ylim,
  add = FALSE,
  xaxs = graphics::par("xaxs"),
  yaxs = graphics::par("yaxs"),
  xaxt = graphics::par("xaxt"),
  yaxt = graphics::par("yaxt"),
  useRaster = NULL,
  ...
)
```

Arguments

x	numeric vector, or data matrix with two or more columns.
y	numeric vector, or if data is supplied via x as a matrix, y is NULL.
nbin	integer number of bins to use when converting the kernel density result (which uses bandwidthN above) into a usable image. For example, nbin=123 is the default used by graphics::smoothScatter(), however the plotSmoothScatter() function default is higher (256).
bandwidth	numeric vector used to define the y- and x-axis bandwidths, respectively, passed to KernSmooth::bkde2D(), which calculates the underlying 2-dimensional kernel density. The plotSmoothScatter() function was motivated by never wanting to define this number directly, instead auto-calculation suitable values.
colramp	function that takes one numeric argument and returns that integer number of colors, by default 256.
nrpoints	integer number of outlier datapoints to display, as defined by graphics::smoothScatter(), however the default here is nrpoints=0 to avoid additional clutter in the output, and because the default argument bandwidthN usually indicates all individual points.
pch	integer point shape used when nrpoints>0.
cex	numeric point size expansion factor used when nrpoints>0.
col	character R color used when nrpoints>0.
transformation	function which converts point density to a number, typically related to square root or cube root transformation.
postPlotHook	function or NULL, NULL default. When function is supplied, it is called after producing the image. By default it is simply used to draw a box around the image, but could be used to layer additional information atop the image plot, for example contours, labels, etc.
xlab	character x-axis label
ylab	character y-axis label
xlim	numeric x-axis range for the plot

ylim	numeric y-axis range for the plot
add	logical whether to add to an existing active R plot, or create a new plot window.
xaxs	character value compatible with graphics::par("xaxs"), mainly useful for suppressing the x-axis, in order to produce a custom x-axis range, most useful to restrict the axis range expansion done by R by default.
yaxs	character value compatible with graphics::par("yaxs"), mainly useful for suppressing the y-axis, in order to produce a custom y-axis range, most useful to restrict the axis range expansion done by R by default.
xaxt	character value compatible with graphics::par("xaxt"), mainly useful for suppressing the x-axis, in order to produce a custom x-axis by other mechanisms, e.g. log-scaled x-axis tick marks.
yaxt	character value compatible with graphics::par("yaxt"), mainly useful for suppressing the y-axis, in order to produce a custom y-axis by other mechanisms, e.g. log-scaled y-axis tick marks.
useRaster	NULL or logical indicating whether to invoke graphics::rasterImage() to produce a raster image. If NULL, it determines whether to produce a raster image within the imageDefault() function, which checks the options using getOption("preferRaster", FALSE) to determine among other things, whether the user prefers raster images, and if the grDevices::dev.capabilities() supports raster.
...	additional arguments are passed to imageDefault() and optionally to plotPlotHook() when supplied.

Details

For general purposes, use plotSmoothScatter() as a replacement for graphics::smoothScatter(), which produces better default settings for pixel size and density bandwidth.

This function is only necessary in order to override the graphics::smoothScatter() function which calls graphics::image.default(). Instead, this function calls imageDefault() which is required in order to utilize custom raster image scaling, particularly important when the x- and y-axis ranges are not similar, e.g. where the x-axis spans 10 units, but the y-axis spans 10,000 units.

Value

list of elements sufficient to call graphics::image(), also by default this function is called for the byproduct of creating a figure.

See Also

graphics::smoothScatter()

Other jam internal functions: handleArgsText(), jamCalcDensity(), make_html_styles(), make_styles()

Examples

```
x1 <- rnorm(1000);
y1 <- (x1 + 5)* 4  + rnorm(1000);
smoothScatterJam(x=x1, y=y1, bandwidth=c(0.05, 0.3))
```

`sqrtAxis` *Determine square root axis tick mark positions*

Description

Determine square root axis tick mark positions, including positive and negative range values.

Usage

```
sqrtAxis(
  side = 1,
  x = NULL,
  pretty.n = 10,
  u5.bias = 1,
  big.mark = ",",
  plot = TRUE,
  las = 2,
  cex.axis = 0.6,
  ...
)
```

Arguments

`side`	`integer` value indicating the axis position, as used by `graphics::axis()`, 1=bottom, 2=left, 3=top, 4=right. Note that when `x` is supplied, the numeric range is defined using values in `x` and not the axis side.
`x`	optional `numeric` vector representing the numeric range to be labeled. When supplied, the numeric range of `x` is used and not the axis side.
`pretty.n`	`numeric` value indicating the number of desired tick marks, passed to `pretty()`.
`u5.bias`	`numeric` value passed to `pretty()` to influence the frequency of intermediate tick marks.
`big.mark`	`character` value passed to `format()` which helps visually distinguish numbers larger than 1000.
`plot`	`logical` indicating whether to plot the axis tick marks and labels.
`las, cex.axis`	`numeric` values passed to `graphics::axis()` when drawing the axis. The custom default `las=2` plots labels rotated perpendicular to the axis.
`...`	additional parameters are passed to `pretty()`, and to `graphics::axis()` when `plot=TRUE`.

Details

This function calculates positions for tick marks for data that has been transformed with `sqrt()`, specifically a directional transformation like `sqrt(abs(x)) * sign(x)`.

If `x` is supplied, it is used to define the numeric range, otherwise the observed range is taken based upon `side`. If neither `x` nor `side` is supplied, or if the numeric range is empty or zero width, it returns `NULL`.

The main goal of this function is to provide reasonably placed tick marks using integer values.

Value

invisible `numeric` vector with axis positions, named by normal space numeric labels. The primary use is to add numeric axis tick marks and labels.

See Also

Other jam plot functions: `adjustAxisLabelMargins()`, `coordPresets()`, `decideMfrow()`, `drawLabels()`, `getPlotAspect()`, `groupedAxis()`, `imageByColors()`, `imageDefault()`, `minorLogTicksAxis()`, `nullPlot()`, `plotPolygonDensity()`, `plotRidges()`, `plotSmoothScatter()`, `shadowText()`, `shadowText_options()`, `showColors()`, `usrBox()`

Examples

```
plot(-3:3*10, -3:3*10, xaxt="n")
x <- sqrtAxis(1)
abline(v=x, col="grey", lty="dotted")
abline(h=pretty(par("usr")[3:4]), col="grey", lty="dotted")

# slightly different label placement with u5.bias=0
plot(-3:3*10, -3:3*10, xaxt="n")
x <- sqrtAxis(1, u5.bias=0)
abline(v=x, col="grey", lty="dotted")
abline(h=pretty(par("usr")[3:4]), col="grey", lty="dotted")
```

---

tcount *frequency of entries, ordered by frequency*

Description

frequency of entries, ordered by frequency

Usage

```
tcount(
  x,
  minCount = NULL,
  doSort = TRUE,
```

```
  maxCount = NULL,
  nameSortFunc = sort,
  ...
)
```

Arguments

x	character, numeric, factor vector input to use when calculating frequencies.
minCount	optional integer minimum frequency, any results with fewer counts observed will be omitted from results.
doSort	logical whether to sort results decreasing by frequency.
maxCount	optional integer maximum frequency for returned results.
nameSortFunc	function used to sort results after sorting by frequency. For example, one might use mixedSort(). If nameSortFunc=NULL then no name sort will be applied.
...	additional parameters are ignored.

Details

This function mimics output from table() with two key differences. It sorts the results by decreasing frequency, and optionally filters results for a minimum frequency. It is effective when checking for duplicate values, and ordering them by the number of occurrences.

This function is useful when working with large vectors of gene identifiers, where it is not always obvious whether genes are replicated in a particular technological assay. Transcript microarrays for example, can contain many replicated genes, but often only a handful of genes are highly replicated, while the rest are present only once or twice on the array.

Value

integer vector of counts, named by the unique input values in x.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), ucfirst()

Examples

```
testVector <- rep(c("one", "two", "three", "four"), c(1:4));
tcount(testVector);
tcount(testVector, minCount=2);
```

ucfirst *Uppercase the first letter in each word*

Description

Uppercase the first letter in each word

Usage

```
ucfirst(x, lowercaseAll = FALSE, firstWordOnly = FALSE, ...)
```

Arguments

x	character vector.
lowercaseAll	logical indicating whether to force all letters to lowercase before applying uppercase to the first letter.
firstWordOnly	logical indicating whether to apply the uppercase only to the first word in each string. Note that it still applies the logic to every entry in the input vector x.
...	additional arguments are ignored.

Details

This function is a simple mimic of the Perl function ucfirst which converts the first letter in each word to uppercase. When lowercaseAll=TRUE it also forces all other letters to lowercase, otherwise mixedCase words will retain capital letters in the middle of words.

Value

character vector where letters are converted to uppercase.

See Also

Other jam string functions: asSize(), breaksByVector(), fillBlanks(), formatInt(), gsubOrdered(), gsubs(), makeNames(), nameVector(), nameVectorN(), padInteger(), padString(), pasteByRow(), pasteByRowOrdered(), sizeAsNum(), tcount()

Examples

```
ucfirst("TESTING_ALL_UPPERCASE_INPUT")
ucfirst("TESTING_ALL_UPPERCASE_INPUT", TRUE)
ucfirst("TESTING_ALL_UPPERCASE_INPUT", TRUE, TRUE)

ucfirst("testing mixedCase upperAndLower case input")
ucfirst("testing mixedCase upperAndLower case input", TRUE)
ucfirst("testing mixedCase upperAndLower case input", TRUE, TRUE)
```

unalpha *Remove alpha transparency from colors*

Description

Remove alpha transparency from colors

Usage

```
unalpha(x, keepNA = FALSE, ...)
```

Arguments

x	`character` vector of R colors
keepNA	`logical` indicating whether `NA` values should be kept and therefore returned as `NA`. When `keepNA=FALSE` (default for backward compatibility) `NA` values are converted to `"#FFFFFF"` as done by `grDevices::col2rgb()`.
...	additional arguments are ignored.

Details

This function simply removes the alpha transparency from R colors, returned in hex format, for example `"#FF0000FF"` becomes `"#FF0000"`, or `"blue"` becomes `"#0000FF"`.

It also silently converts R color names to hex format, where applicable.

Value

character vector of R colors in hex format.

See Also

Other jam color functions: `alpha2col()`, `applyCLrange()`, `col2alpha()`, `col2hcl()`, `col2hsl()`, `col2hsv()`, `color2gradient()`, `fixYellow()`, `fixYellowHue()`, `getColorRamp()`, `hcl2col()`, `hsl2col()`, `hsv2col()`, `isColor()`, `kable_coloring()`, `makeColorDarker()`, `rainbow2()`, `rgb2col()`, `setCLranges()`, `setTextContrastColor()`, `showColors()`, `warpRamp()`

Examples

```
unalpha(c("#FFFF00DD", "red", NA, "#0000FF", "transparent"))

unalpha(c("#FFFF00DD", "red", NA, "#0000FF", "transparent"), keepNA=TRUE)
```

unigrep *case-insensitive grep, returning unmatched indices*

Description

case-insensitive grep, returning unmatched indices

Usage

```
unigrep(..., ignore.case = TRUE, invert = TRUE)
```

Arguments

`...`, `ignore.case`, `invert`
: parameters sent to `base::grep()`

Details

This function is a simple wrapper around `base::grep()` which runs in case-insensitive mode, and returns unmatched entries. It is mainly used to save keystrokes, but is consistently named alongside `vgrep` and `vigrep`, and quite helpful for writing concise code.

Value

vector of non-matching indices

See Also

Other jam grep functions: `grepls()`, `igrep()`, `igrepHas()`, `igrepl()`, `provigrep()`, `unvigrep()`, `vgrep()`, `vigrep()`

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
unigrep("D", V);
igrep("D", V);
```

uniques *apply unique to each element of a list*

Description

Apply unique to each element of a list, usually a list of vectors

Usage

```
uniques(
  x,
  keepNames = TRUE,
  incomparables = FALSE,
  useBioc = TRUE,
  useSimpleBioc = FALSE,
  xclass = NULL,
  ...
)
```

Arguments

x	input list of vectors
keepNames	boolean indicating whether to keep the list element names in the returned results.
incomparables	see unique() for details, this value is only sent to S4Vectors::unique() when the Bioconductor package S4Vectors is installed, and is ignored otherwise for efficiency.
useBioc	logical, default TRUE, indicating whether this function should try to use S4Vectors::unique() when the Bioconductor package S4Vectors is installed, otherwise it will use a somewhat less efficient bulk operation.
useSimpleBioc	logical, default FALSE, whether to use a legacy mechanism with S4Vectors and is maintained for edge cases where it might be faster.
xclass	character optional vector of classes, used to invoke optimized logic when the class is known upfront.
...	additional arguments are ignored.

Details

This function will attempt to use S4Vectors::unique() which is substantially faster than any apply family function, especially for very long lists. However, when S4Vectors is not installed, it applies uniqueness to the unlisted vector of values, which is also substantially faster than the apply family functions for long lists, but which may still be less efficient than the C implementation provided by S4Vectors.

Value

list with unique values in each list element.

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), relist_named(), rlengths(), sclass(), sdim(), unnestList()

Examples

```
L1 <- list(CA=nameVector(LETTERS[c(1:4,2,7,4,6)]),
   B=letters[c(7:11,9,3)],
   C2=NULL,
   D=nameVector(LETTERS[4]));
L1;
uniques(L1);

uniques(L1, useBioc=FALSE);
```

`unnestList` *Un-nest a nested list into a simple list*

Description

Un-nest a nested list into a simple list

Usage

```
unnestList(
  x,
  addNames = FALSE,
  unnamedBase = "x",
  parentName = NULL,
  sep = ".",
  makeNamesFunc = makeNames,
  stopClasses = c("dendrogram", "data.frame", "matrix", "package_version", "tbl",
    "data.table"),
  extraStopClasses = getOption("jam.stopClasses"),
  ...
)
```

Arguments

x	`list` potentially containing nested lists.
addNames	`logical` indicating whether to add names to the list elements when names are not already present. When `addNames=TRUE` and no names are present `unnamedBase` is used to define names.
unnamedBase	`character` value used as a base for naming any un-named lists, using the format `makeNamesFunc(rep(unnamedBase, n))`.
parentName	`character` with optional prefix, used as parent name, default is NULL.

sep — character delimiter used between nested list names.

makeNamesFunc — function that takes a character vector and returns non-duplicated character vector of equal length. By default it uses jamba::makeNames().

stopClasses — vector of classes that should not be un-nested, useful in case some classes inherit list properties.

extraStopClasses — vector of additional values for stopClasses, created mostly to show that options("jam.stopClasses" can be used to define stopClasses, for example when this function is called but where arguments cannot be conveniently passed through the calling function.

... — additional arguments are ignored.

Details

This function inspects a list, and unlists each entry resulting in a simple list of non-list entries as a result. Sometimes when concatenating lists together, one list gets added as a list-of-lists. This function resolves that problem by providing one flat list.

Value

list that has been flattened so that it contains no list elements. Note that it may contain some list-like objects such as data.frame, defined by stopClasses.

See Also

Other jam list functions: cPaste(), heads(), jam_rapply(), list2df(), mergeAllXY(), mixedSorts(), rbindList(), relist_named(), rlengths(), sclass(), sdim(), uniques()

Examples

```
L <- list(A=letters[1:10],
   B=list(C=LETTERS[3:9], D=letters[4:11]),
   E=list(F=list(G=LETTERS[3:9], D=letters[4:11])));
L;

# inspect the data using str()
str(L);

unnestList(L);

# optionally change the delimiter
unnestList(L, sep="|");

# example with nested lists of data.frame objects
df1 <- data.frame(a=1:2, b=letters[3:4]);
DFL <- list(A=df1,
   B=list(C=df1, D=df1),
   E=list(F=list(G=df1, D=df1)));
str(DFL);
unnestList(DFL);
str(unnestList(DFL));
```

```
# packageVersion() returns class "package_version"
# where is.list(packageVersion("base")) is TRUE,
# but it cannot ever be subsetted as a list with x[[1]],
# and thus it breaks this function
identical(is.list(packageVersion("base")), is.list(packageVersion("base"))[[1]])
unnestList(lapply(nameVector(c("base","graphics")), packageVersion))
```

`unvigrep` *case-insensitive grep, returning unmatched values*

Description

case-insensitive grep, returning unmatched values

Usage

```
unvigrep(..., ignore.case = TRUE, value = TRUE, invert = TRUE)
```

Arguments

`...`, `ignore.case`, `value`, `invert`
: parameters sent to `base::grep()`

Details

This function is a simple wrapper around `base::grep()` which runs in case-insensitive mode, and returns unmatched values. It is mainly used to save keystrokes, but is consistently named alongside `vgrep` and `vigrep`, and quite helpful for writing concise code. It is particularly useful for removing unwanted entries from a long vector, for example removing accession numbers from a long vector of gene symbols in order to review gene annotations.

Value

vector of non-matching indices

See Also

Other jam grep functions: `grepls()`, `igrep()`, `igrepHas()`, `igrepl()`, `provigrep()`, `unigrep()`, `vgrep()`, `vigrep()`

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
unigrep("D", V);
igrep("D", V);
```

usrBox *Draw colored box indicating R plot space*

Description

Draw colored box indicating the active R plot space

Usage

```
usrBox(
  fill = "#FFFF9966",
  label = NULL,
  parUsr = graphics::par("usr"),
  debug = FALSE,
  ...
)
```

Arguments

fill	character R color used to fill the background of the plot
label	character text optionally used to label the center of the plot space, default NULL
parUsr	numeric vector length 4, indicating the R plot space, consistent with graphics::par("usr"). It can thus be used to define a different area, though using the rect function directly seems more appropriate.
debug	logical whether to print the parUsr value being used.
...	additional arguments are ignored.

Details

This function simply draws a box indicating the active plot space, and by default it shades the box light yellow with transparency. It can be useful to indicate the active plot area while allowing pre-drawn plot elements to be shown, or can be useful precursor to provide a colored background for the plot.

The plot space is defined using graphics::par("usr") and therefore requires an active R device is already opened.

Value

no output, this function is called for the byproduct of adding a box in the usr plot space of an R graphics device.

See Also

Other jam plot functions: adjustAxisLabelMargins(), coordPresets(), decideMfrow(), drawLabels(), getPlotAspect(), groupedAxis(), imageByColors(), imageDefault(), minorLogTicksAxis(), nullPlot(), plotPolygonDensity(), plotRidges(), plotSmoothScatter(), shadowText(), shadowText_options(), showColors(), sqrtAxis()

Examples

```
# usrBox() requires that a plot device is already open
nullPlot(doBoxes=FALSE);
usrBox();
```

---

vgrep *grep, returning values*

Description

grep, returning values

Usage

```
vgrep(..., value = TRUE, ignore.case = FALSE)
```

Arguments

`...`, `value`, `ignore.case`
: parameters sent to `base::grep()`

Details

This function is a simple wrapper around `base::grep()` which returns matching values. It is particularly helpful when grabbing values from a vector, but where the case (uppercase or lowercase) is known.

Value

vector of matching values

See Also

Other jam grep functions: `grepls()`, `igrep()`, `igrepHas()`, `igrepl()`, `provigrep()`, `unigrep()`, `unvigrep()`, `vigrep()`

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
vgrep("D", V);
vgrep("d", V);
vigrep("d", V);
```

vigrep *case-insensitive grep, returning values*

Description

case-insensitive grep, returning values

Usage

```
vigrep(..., value = TRUE, ignore.case = TRUE)
```

Arguments

..., value, ignore.case	parameters sent to base::grep()

Details

This function is a simple wrapper around base::grep() which runs in case-insensitive mode, and returns matching values. It is particularly helpful when grabbing values from a vector.

Value

vector of matching values

See Also

Other jam grep functions: grepls(), igrep(), igrepHas(), igrepl(), provigrep(), unigrep(), unvigrep(), vgrep()

Examples

```
V <- paste0(LETTERS[1:5], LETTERS[4:8]);
vigrep("d", V);
```

warpAroundZero *Warp a vector of numeric values relative to zero*

Description

Warp a vector of numeric values relative to zero

Usage

```
warpAroundZero(x, lens = 5, baseline = 0, xCeiling = NULL, ...)
```

Arguments

x	numeric vector
lens	numeric value which defines the lens factor, where lens > 0 will compress values near zero, and lens < 0 will expand values near zero and compress values near the maximum value. If lens == 0 the numeric values are not changed.
baseline	numeric value describing the baseline, for example when the central value is non-zero. The baseline is subtracted from x, the warp is applied, then the baseline is added to the result.
xCeiling	numeric maximum value used for the color warp range, useful for consistency. When xCeiling is not supplied, the maximum difference from baseline is used. When xCeiling is defined, and baseline is non-zero, the effective value used is (xCeiling - baseline).
...	additional arguments are ignored.

Details

This function warps numeric values using a log curve transformation, such that values are either more compressed near zero, or more compressed near the maximum values. For example, a vector of integers from -10 to 10 would be warped so the intervals near zero were smaller than 1, and intervals farthest from zero are greater than 1.

The main driver for this function was the desire to compress divergent color scales used in heatmaps, in order to enhance smaller magnitude numeric values. Existing color ramps map the color gradient in a linear manner relative to the numeric range, which can cause extreme values to dominate the color scale. Further, a linear application of colors is not always appropriate.

Value

numeric vector after applying the warp function.

See Also

Other jam numeric functions: deg2rad(), noiseFloor(), normScale(), rad2deg(), rowGroupMeans(), rowRmMadOutliers()

Examples

```
x <- c(-10:10);
xPlus10 <- warpAroundZero(x, lens=10);
xMinus10 <- warpAroundZero(x, lens=-10);

plot(x=x, y=xPlus10, type="b", pch=20, col="dodgerblue",
   main="Comparison of lens=+10 to lens=-10");
graphics::points(x=x, y=xMinus10, type="b", pch=18, col="orangered");
graphics::abline(h=0, v=0, col="grey", lty="dashed", a=0, b=1);
graphics::legend("topleft",
   legend=c("lens=+10", "lens=-10"),
   col=c("dodgerblue","orangered"),
   pch=c(20,18),
```

```
   lty="solid",
   bg="white");

# example showing the effect of a baseline=5
xPlus10b5 <- warpAroundZero(x, lens=10, baseline=5);
xMinus10b5 <- warpAroundZero(x, lens=-10, baseline=5);
plot(x=x, y=xPlus10b5, type="b", pch=20, col="dodgerblue",
   main="Comparison of lens=+10 to lens=-10",
   ylim=c(-10,15),
   sub="baseline=+5");
graphics::points(x=x, y=xMinus10b5, type="b", pch=18, col="orangered");
graphics::abline(h=5, v=5, col="grey", lty="dashed", a=0, b=1);
graphics::legend("topleft",
   legend=c("lens=+10", "lens=-10"),
   col=c("dodgerblue","orangered"),
   pch=c(20,18),
   lty="solid",
   bg="white");
```

---

warpRamp *Warp colors in a color ramp*

Description

Warp colors in a color ramp

Usage

```
warpRamp(
  ramp,
  lens = 5,
  divergent = TRUE,
  expandFactor = 10,
  plot = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

ramp	character vector of R colors
lens	numeric lens factor, centered at zero, where positive values cause colors to change more rapidly near zero, and negative values cause colors to change less rapidly near zero and more rapidly near the extreme.
divergent	logical indicating whether the ramp represents divergent colors, which are assumed to be symmetric above and below zero. Otherwise, colors are assumed to begin at zero.

expandFactor	numeric factor used to expand the color ramp prior to selecting the nearest warped numeric value as the result of warpAroundZero(). This value should not need to be changed unless the lens is extremely high (>100).
plot	logical indicating whether to plot the input and output color ramps using showColors().
verbose	logical indicating whether to print verbose output.
...	additional parameters are passed to showColors().

Details

This function takes a vector of colors in a color ramp (color gradient) and warps the gradient using a lens factor. The effect causes the color gradient to change faster or slower, dependent upon the lens factor.

The main intent is for heatmap color ramps, where the color gradient changes are not consistent with meaningful numeric differences being shown in the heatmap. In short, this function enhances colors.

Value

character vector of R colors, with the same length as the input vector ramp.

See Also

Other jam color functions: alpha2col(), applyCLrange(), col2alpha(), col2hcl(), col2hsl(), col2hsv(), color2gradient(), fixYellow(), fixYellowHue(), getColorRamp(), hcl2col(), hsl2col(), hsv2col(), isColor(), kable_coloring(), makeColorDarker(), rainbow2(), rgb2col(), setCLranges(), setTextContrastColor(), showColors(), unalpha()

Examples

```
BuRd <- rev(RColorBrewer::brewer.pal(11, "RdBu"));
BuRdPlus5 <- warpRamp(BuRd, lens=2, plot=TRUE);
BuRdMinus5 <- warpRamp(BuRd, lens=-2, plot=TRUE);

Reds <- RColorBrewer::brewer.pal(9, "Reds");
RedsL <- lapply(nameVector(c(-10,-5,-2,0,2,5,10)), function(lens){
   warpRamp(Reds, lens=lens, divergent=FALSE)
});
showColors(RedsL);
```

---

writeOpenxlsx *Export a data.frame to 'Excel' 'xlsx' format*

Description

Export a data.frame to 'Excel' 'xlsx' format

Usage

```
writeOpenxlsx(
  x,
  file = NULL,
  wb = NULL,
  sheetName = "Sheet1",
  startRow = 1,
  startCol = 1,
  append = FALSE,
  headerColors = c("lightskyblue1", "lightskyblue2"),
  columnColors = c("aliceblue", "azure2"),
  highlightHeaderColors = c("tan1", "tan2"),
  highlightColors = c("moccasin", "navajowhite"),
  borderColor = "gray75",
  borderPosition = "BottomRight",
  highlightColumns = NULL,
  numColumns = NULL,
  fcColumns = NULL,
  lfcColumns = NULL,
  hitColumns = NULL,
  intColumns = NULL,
  pvalueColumns = NULL,
  numFormat = "#,##0.00",
  fcFormat = "#,##0.0",
  lfcFormat = "#,##0.0",
  hitFormat = "#,##0.0",
  intFormat = "#,##0",
  pvalueFormat = "[>0.01]0.00#;0.00E+00",
  numRule = c(1, 10, 20),
  fcRule = c(-6, 0, 6),
  lfcRule = c(-3, 0, 3),
  hitRule = c(-1.5, 0, 1.5),
  intRule = c(0, 100, 10000),
  pvalueRule = c(0, 0.01, 0.05),
  numStyle = c("#F2F0F7", "#B4B1D4", "#938EC2"),
  fcStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  lfcStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  hitStyle = c("#4F81BD", "#EEECE1", "#C0504D"),
  intStyle = c("#EEECE1", "#FDA560", "#F77F30"),
  pvalueStyle = c("#F77F30", "#FDC99B", "#EEECE1"),
  doConditional = TRUE,
  doCategorical = TRUE,
  colorSub = NULL,
  freezePaneColumn = 0,
  freezePaneRow = 2,
  doFilter = TRUE,
  fontName = "Arial",
  fontSize = 12,
```

```
  minWidth = getOption("openxlsx.minWidth", 8),
  maxWidth = getOption("openxlsx.maxWidth", 40),
  autoWidth = TRUE,
  colWidths = NULL,
  wrapCells = FALSE,
  wrapHeaders = TRUE,
  headerRowMultiplier = 5,
  keepRownames = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	data.frame to be saved to an 'Excel' 'xlsx' file.
file	character valid path to save an 'Excel' 'xlsx' file. If the file exists, and append=TRUE the new data will be added to the existing file withthe defined sheetName. • Note when file=NULL the output is not saved to a file, instead the Workbook object is returned by this function. The Workbook object can be passed as argument wb in order to add multiple sheets to the same Workbook prior to saving them together. This operation is intended to provide a substantial improvement in speed.
wb	Workbook object as defined in R package openxlsx. When this argument is defined, data is not imported from file, and instead the workbook data is used from wb. This option is intended to improve speed of writing several sheets to the same output file, by preventing the slow read/write steps each time a new sheet is added.
sheetName	character value less with a valid 'Excel' 'xlsx' worksheet name. At this time (version 0.0.29.900) the sheetName is restricted to 31 characters, with no puntuation except "-" and "_".
startRow, startCol	integer indicating the row and column number to start with the top,left cell written to the worksheet, default are 1.
append	logical default FALSE, whether to append to file (TRUE), or to write over an existing file. The append=TRUE is useful when adding a worksheet to an existing file.
headerColors, columnColors, highlightHeaderColors, highlightColors, borderColor, borderPosition	default values for the 'Excel' worksheet background and border colors. As of version 0.0.29.900, colors must use valid 'Excel' color names.
highlightColumns, numColumns, fcColumns, lfcColumns, hitColumns, intColumns, pvalueColumns	integer vector referring the column number in the input data.frame x to define as each column type, as relevant.
numFormat, fcFormat, lfcFormat, hitFormat, intFormat, pvalueFormat	character string with valid 'Excel' cell formatting, for example "#,##0.00" defines a column to use comma-delimited numbers above one thousand, and display two decimal places in all numeric cells. See [https://support.microsoft.com]

topic "Excel Create and apply a custom number format." or "Excel Number format codes" for more details. Some examples below:

- "#,##0" : display only integer values, using comma as delimiter for every thousands place. The number 2142.12 would be represented: "2,142"
- "###0.0" : display numeric values rounded to the 0.1 place, using no comma delimiter for values above one thousand. The number 2142.12 would be represented: "2142.1"
- "[>0.01]0.00#;0.00E+00" : this rule is a conditional format, values above 0.01 are represented as numbers rounded to the thousandths position 0.001; values below 0.01 are represented with scientific notation with three digits. The number 0.1256 would be represented: "0.126" The number 0.001256 would be represented: "1.26E-03"
- "[Red]#,###.00_);[Blue](#,###.00);[Black]0.00_)" : this format applies to positive values, negative values, and zero, in order delimited by semicolons. Positive values are colored red. The string "_)" adds whitespace (defined by "_") equale to the width of the character ")" to the end of positive values. Negative values are surrounded by parentheses "()" and are colored blue. Values equal to zero are represented with two trailing digits, and whitespace ("_") equal to width ")". The whitespace at the end of positive values and zero are used to align all values at the same decimal position.

numRule, fcRule, lfcRule, hitRule, intRule, pvalueRule
: numeric vector length=3 indicating the breakpoints for 'Excel' to apply conditional color formatting, using the corresponding style. Note that all conditional formatting applied by this function uses the "3-Color Scale", therefore there should be three values, and three corresponding colors in the corresponding Style arguments.

numStyle, fcStyle, lfcStyle, intStyle, hitStyle, pvalueStyle
: character vector length=3 containing three valid R colors. Note that alpha transparency will be removed prior to use in 'Excel', as required. Note that all conditional formatting applied by this function uses the "3-Color Scale", therefore there should be three colors, which match three values in the corresponding Rule arguments.

doConditional
: logical indicating whether to apply conditional formatting of cells, with this function only the background cell color (and contrasting text color) is affected.

doCategorical
: logical indicating whether to apply categorical color formatting, of only the background cell colors and contrasting text color. This argument requires colorSub be defined.

colorSub
: character vector of R colors, whose names refer to cell values in the input x data.frame.

freezePaneColumn, freezePaneRow
: integer value of the row or column before which the 'Excel' "freeze panes" is applied. Note that these values are adjusted relative by startRow and startCol in the 'Excel' worksheet, so that the values are applied relative to the data.frame argument x.

doFilter
: logical indicating whether to enable column filtering by default.

fontName	character default font configuration, containing a valid 'Excel' font name.
fontSize	numeric default font size in 'Excel' point units.
minWidth, maxWidth, autoWidth	numeric minimum, maximum size for each 'Excel' cell, in character units as defined by 'Excel', used when autoWidth=TRUE to restrict cell widths to this range. Note that the argument colWidths is generally preferred, if the numeric widths can be reasonable calculated or anticipated upfront. When autoWidth=FALSE 'Excel' typically auto-sizes cells to the width of the largest value in each column, which may not be ideal when values are extremely large.
colWidths	numeric width of each column in x, recycled to the total number of columns required. Note that when keepRownames=TRUE, the first column will contain rownames(x), therefore the length of colWidths in that case will be ncol(x) + 1.
wrapCells	logical default FALSE, indicating whether to enable word-wrap within cells.
wrapHeaders	logical indicating whether to enable word wrap for column headers, which is helpful when autoWidth=TRUE since it fixed the cell width while allowing the column header to be seen.
headerRowMultiplier	numeric value to define the row height of the first header row in 'Excel'. This value is defined as a multiple of subsequent rows, and should usually represent the maximum number of lines after word-wrapping, as relevant. This argument is helpful when wrapHeaders=TRUE and autoWidth=TRUE.
keepRownames	logical indicating whether to include rownames(x) in its own column in 'Excel'.
verbose	logical indicating whether to print verbose output.
...	additional arguments are passed to applyXlsxConditionalFormat() and applyXlsxCategoricalForma as relevant.

Details

This function is a minor but useful customization of the openxlsx::saveWorkbook() and associated functions, intended to provide some pre-configured formatting of known column types, typically relevant to statistical values, and in some cases, gene or transcript expression values.

There are numerous configurable options when saving an 'Excel' worksheet, most of the defaults in this function are intended not to require changes, but are listed as formal function arguments to make each option visibly obvious.

If colorSub is supplied as a named vector of colors, then by default text values will be colorized accordingly, which can be especially helpful when including data with categorical text values.

This function pre-configures formatting options for the following column data types, each of which has conditional color-formatting, defined numeric ranges, and color scales.

int integer values, where numeric values are formatted without visible decimal places, and the big.mark="," standard is used to help visually distinguish large integers. The color scale is by default c(0, 100, 10000).

num numeric values, with fixed number of visible decimal places, which helps visibly align values along each row.

hit numeric type, a subset of "int" intended when data is flagged with something like a "+1" or "-1" to indicate a statistical increase or decrease.

pvalue P-value, where numeric values range from 1 down near zero, and values are formatted consistently with scientific notation.

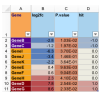
fc numeric fold change, whose values are expected to range from 1 and higher, and -1 and lower. Decimal places are by default configured to show one decimal place, to simplify the 'Excel' visual summary.

lfc numeric log fold change, whose values are expected to be centered at zero. Decimal places are by default configured to show one decimal place, to simplify the 'Excel' visual summary.

highlight character and undefined columns to be highlighted with a brighter background color, and bold text.

For each column data type, a color scale and default numeric range is defined, which allows conditional formatting of cells based upon expected ranges of values.

A screenshot of the file produced by the example is shown below.



Value

`Workbook` object as defined by the `openxlsx` package is returned invisibly with `invisible()`. This `Workbook` can be used in argument `wb` to provide a speed boost when saving multiple sheets to the same file.

See Also

Other jam export functions: `applyXlsxCategoricalFormat()`, `applyXlsxConditionalFormat()`, `readOpenxlsx()`, `set_xlsx_colwidths()`, `set_xlsx_rowheights()`

Examples

```
# set up a test data.frame
set.seed(123);
lfc <- -3:3 + stats::rnorm(7)/3;
colorSub <- nameVector(
   rainbow2(7),
   LETTERS[1:7])
df <- data.frame(name=LETTERS[1:7],
   int=round(4^(1:7)),
   num=(1:7)*4-2 + stats::rnorm(7),
   fold=2^abs(lfc)*sign(lfc),
   lfc=lfc,
   pvalue=10^(-1:-7 + stats::rnorm(7)),
   hit=sample(c(-1,0,0,1,1), replace=TRUE, size=7));
df;
# write to tempfile for examples
if (check_pkg_installed("openxlsx")) {
   out_xlsx <- tempfile(pattern="writeOpenxlsx_", fileext=".xlsx")
```

```
   writeOpenxlsx(x=df,
      file=out_xlsx,
      sheetName="jamba_test",
      colorSub=colorSub,
      intColumns=2,
      numColumns=3,
      fcColumns=4,
      lfcColumns=5,
      pvalueColumns=6,
      hitColumn=7,
      freezePaneRow=2,
      freezePaneColumn=2,
      append=FALSE);
   # now read it back
   df_list <- readOpenxlsx(xlsx=out_xlsx);
   sdim(df_list)
}
```

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