

Package ‘gggenes’

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Title Draw Gene Arrow Maps in 'ggplot2'

Version 0.3.2

Description Provides a 'ggplot2' geom and helper functions for drawing gene arrow maps.

Depends R (>= 3.3.0)

Imports grid (>= 3.3.0), ggplot2 (>= 2.2.1), ggfittext (>= 0.4.3), rlang (>= 0.2.0)

License GPL-2

LazyData true

RoxygenNote 6.1.0

URL <https://github.com/wilkox/gggenes>

BugReports <https://github.com/wilkox/gggenes/issues>

Suggests testthat, knitr, rmarkdown, vdiff

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example_genes	<i>A set of example genes.</i>
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Description

Genes for example purposes only.

Usage

```
example_genes
```

Format

A data frame with 118 rows and four variables:

molecule the genome
start the start position of the gene
end the end position of the gene
gene the name of the gene
strand the strand of the gene

geom_gene_arrow	<i>A 'ggplot2' geom to draw genes as arrows</i>
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Description

'geom_gene_arrow' draws genes as arrows, allowing gene maps to be drawn.

Usage

```
geom_gene_arrow(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, arrowhead_width = grid::unit(4, "mm"),
  arrowhead_height = grid::unit(4, "mm"),
  arrow_body_height = grid::unit(3, "mm"), ...)
```

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...

As standard for ggplot2.

arrowhead_width

grid::unit object giving the width of the arrowhead. Defaults to 4 mm. If the gene is drawn smaller than this width, only the arrowhead will be drawn, compressed to the length of the gene.

arrowhead_height

grid::unit object giving the height of the arrowhead. Defaults to 4 mm.

arrow_body_height

grid::unit object giving the height of the body of the arrow. Defaults to 3 mm.

Details

This geom draws genes as arrows along a horizontal line representing the molecule. The start and end locations of the gene are expressed with the 'xmin' and 'xmax' aesthetics, while the molecule can be specified with the 'y' aesthetic. Optionally, an additional 'forward' aesthetic can be used to reverse the orientation of some or all genes from that implied by 'xmin' and 'xmax'.

Unless the plot is faceted with a free x scale, all the molecules will share a common x axis. This means that if the locations are very different across different molecules, the genes might appear very small and squished together with a lot of unnecessary empty space. To get around this, either facet the plot with 'scales = "free_x"', or normalise the gene locations if their exact locations are not important.

See 'make_alignment_dummies' for a method to align genes between molecules.

Aesthetics

- xmin,xmax (start and end of the gene; will be used to determine gene orientation)
- y (molecule)
- forward (if any value that is not TRUE, or coercible to TRUE, the gene arrow will be drawn in the opposite direction to that determined by 'xmin' and 'xmax')
- alpha
- colour
- fill
- linetype
- size

See Also

theme_genes, make_alignment_dummies, geom_gene_label

Examples

```
ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,  
                                             y = molecule, fill = gene)) +  
  geom_gene_arrow() +  
  ggplot2::facet_wrap(~ molecule, scales = "free")
```

geom_gene_label A 'ggplot2' geom to add text labels to gene arrows

Description

'geom_gene_label' can be used to add a text label to genes drawn with 'geom_gene_arrow'.

Usage

```
geom_gene_label(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", na.rm = FALSE, show.legend = FALSE,
  inherit.aes = TRUE, padding.x = grid::unit(1, "mm"),
  padding.y = grid::unit(0.1, "lines"), align = "centre",
  min.size = 4, grow = F, reflow = F, height = grid::unit(3, "mm"),
  ...)
```

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...	Standard geom arguments as for 'ggplot2::geom_text'.
padding.x, padding.y	'grid::unit' object, giving horizontal or vertical padding around the text. Defaults to 1 mm and 0.1 lines respectively.
align	Where inside the gene to place the text label. Default is 'centre'; other options are 'left' and 'right'.
min.size	Minimum font size, in points. If provided, text that would need to be shrunk below this size to fit inside the gene arrow will not be drawn. Defaults to 4 pt.
grow	If 'TRUE', text will be grown as well as shrunk to fill the arrow.
reflow	If 'TRUE', text will be reflowed (wrapped) to better fit the arrow.
height	grid::unit object giving the maximum height of the text. Defaults to 3 mm, which is the default height of gene arrows drawn with 'geom_gene_arrow'.

Details

'geom_gene_label' uses the 'ggfittxt' package to fit text to tiles. All text drawing options available in 'ggfittxt::geom_fit_text' (growing, reflowing, etc.) are also available here. For full details on how these options work, see the documentation for 'ggfittxt::geom_fit_text'.

Standard 'ggplot2' aesthetics for text are supported (see Aesthetics).

Aesthetics

- xmin,xmax (start and end of the gene; required)
- y (molecule; required)
- colour

- size
- alpha
- family
- fontface
- angle

See Also

geom_gene_arrow

Examples

```
ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,  
y = molecule, fill = gene, label = gene)) +  
  geom_gene_arrow() +  
  geom_gene_label() +  
  ggplot2::facet_wrap(~ molecule, ncol = 1, scales = "free") +  
  theme_genes()
```

gggenes	<i>'gggenes': provides a 'ggplot2' geom and helper functions for drawing gene arrow maps.</i>
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Description

This package provides a 'ggplot2' geom, 'geom_gene_arrow' a theme, 'theme_genes', and a helper function for visually aligning genes, 'make_alignment_dummies'.

make_alignment_dummies	<i>Prepare dummy data to visually align a single gene across faceted molecules</i>
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Description

'make_alignment_dummies' helps you to visually align genes across molecules that have been faceted with a free x scale. The output of this function is a data frame of dummy genes. If these dummy genes are added to a 'ggplot2' plot with 'geom_blank', they will extend the x axis range in such a way that the start or end of a selected gene is visually aligned across the facets.

Usage

```
make_alignment_dummies(data, mapping, on, side = "left")
```

Arguments

data	Data frame of genes. This is almost certainly the same data frame that will later be passed to 'ggplot2::ggplot'.
mapping	Aesthetic mapping, created with 'ggplot2::aes'. Must contain the following aesthetics: 'xmin', 'xmax', 'y', and 'id' (a unique identifier for each gene).
on	Name of gene to be visually aligned across facets. This gene must be present in 'data', in the column mapped to the 'id' aesthetic.
side	Should the visual alignment be of the 'left' (default) or 'right' side of the gene?

Examples

```
dummies <- make_alignment_dummies(example_genes, ggplot2::aes(xmin = start,
  xmax = end, y = molecule, id = gene), on = "genE")

ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,
  y = molecule, fill = gene)) +
  geom_gene_arrow() +
  ggplot2::geom_blank(data = dummies) +
  ggplot2::facet_wrap(~ molecule, scales = "free", ncol = 1)
```

 theme_genes

A 'ggplot2' theme for drawing gene maps

Description

This theme removes extraneous plot elements for drawing an 'arrows-on-a-string' style gene map in 'ggplot2'.

Usage

```
theme_genes()
```

Details

This theme removes strip text (the text that labels facets when you use 'facet_wrap' or 'facet_grid'). This makes it easier to draw molecules on different x scales by setting the y aesthetic to the molecule, then faceting with 'facet_grid(~ molecule, scales = "free")'.

See Also

```
geom_gene_arrows
```

Examples

```
ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,  
                                             y = molecule, fill = gene)) +  
geom_gene_arrow() +  
ggplot2::facet_wrap(~ molecule, scales = "free") +  
theme_genes()
```

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