

# Package ‘gggenes’

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**Title** Draw Gene Arrow Maps in 'ggplot2'

**Version** 0.3.1

**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** 6.0.1

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

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

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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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

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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")
```

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geom\_gene\_label      A 'ggplot2' geom to add text labels to gene arrows

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### 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 'ggfittest' package to fit text to tiles. All text drawing options available in 'ggfittest::geom\_fit\_text' (growing, reflowing, etc.) are also available here. For full details on how these options work, see the documentation for 'ggfittest::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()
```

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gggenes

*'gggenes': provides a 'ggplot2' geom and helper functions for drawing gene arrow maps.*

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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'.

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make\_alignment\_dummies

*Prepare dummy data to visually align a single gene across faceted molecules*

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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)
```

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theme\_genes

*A 'ggplot2' theme for drawing gene maps*

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## 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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