Package ‘gggenes’

Title Draw Gene Arrow Maps in 'ggplot2'
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example_genes

A set of example genes.

Description

Genes for example purposes only.

Usage

example_genes

example_subgenes

Format

A data frame with 72 rows and six variables:

- **molecule** the genome
- **gene** the name of the gene
- **start** the start position of the gene
- **end** the end position of the gene
- **strand** the strand of the gene
- **orientation** the orientation of the gene

example_subgenes (143 rows) also contains:

- **subgene** the name of the subgene
- **from** the start position of the subgene segment
- **to** the end position of the subgene segment

An object of class data.frame with 143 rows and 9 columns.
Description

gene.arrow() draws genes as arrows, allowing gene maps to be drawn.

Usage

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**

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

**Description**

`geom_gene_label()` can be used to add a text label to genes drawn with `geom_gene_arrow()`.

**Usage**

```r
geom_gene_label(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  
```
geom_gene_label

    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. De-
   faults 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 'ggfittext' package to fit text to genes. All text drawing options
available in ggfittext::geom_fit_text() (growing, reflowing, etc.) are also available here. For
full details on how these options work, see the documentation for ggfittext::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
geom_subgene_arrow

See Also
gem_gene_arrow

Examples

```r
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()
```

Description

`geom_subgene_arrow()` draws subgenes segments within gene arrows drawn with `geom_gene_arrow()`.

Usage

```r
geom_subgene_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

The start and end locations of the subgene are given with the xsubmin and xsubmax aesthetics. `geom_subgene_arrow()` requires some information about the 'parent' gene, provided with the same aesthetics used for `geom_gene_arrow()`: start and end locations of the 'parent' gene with the xmin and xmax aesthetics, the molecule with the y aesthetic, and optionally the direction with the forward aesthetic. If the geometry of the parent gene has been changed with arrowhead_width, arrowhead_height or arrow_body_height, identical parameters should be given to `geom_subgene_arrow()`.

Aesthetics

- xmin,xmax (start and end of the gene; will be used to determine gene orientation)
- xsubmin,xsubmax (start and end of subgene segment). Should be consistent with xmin/xmax
- 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

`geom_gene_arrow()`, `geom_subgene_label()`

Examples

```r
ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,
       y = molecule)) +
geom_gene_arrow() +
geom_subgene_arrow(data = example_subgenes,
       ggplot2::aes(xmin = start, xmax = end, xsubmin = from, xsubmax = to,
                   y = molecule, fill = gene)) +
ggplot2::facet_wrap(~ molecule, scales = "free")
```

---

`geom_subgene_label()` can be used to add a text label to subgenes drawn with `geom_subgene_arrow()`.
Usage

```r
geom_subgene_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 subgene 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 subgene will not be drawn. Defaults to 4 pt.
- `grow`
  If TRUE, text will be grown as well as shrunk to fill the subgene.
- `reflow`
  If TRUE, text will be reflowed (wrapped) to better fit the subgene.
- `height`
  `grid::unit()` object giving the maximum height of the text. Defaults to 3 mm, which is the default height of gene arrows (and therefore of subgenes) drawn with `geom_gene_arrow()`.

**Details**

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

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

**Aesthetics**

- `xsubmin, xsubmax` (start and end of the subgene; required)
• y (molecule; required)
• colour
• size
• alpha
• family
• fontface
• angle

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

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 ggplot::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 ggplot2::facet_wrap() or ggplot::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_arrow()

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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