Package 'gggenes'

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Title Draw Gene Arrow Maps in 'ggplot2'

Version 0.5.1

Description A 'ggplot2' extension for drawing gene arrow maps.

Depends R (>= 3.6)

Imports grid (>= 3.3.0), ggplot2 (>= 2.2.1), ggfittext (>= 0.8.0), rlang (>= 0.2.0)

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Repository CRAN

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Contents

`example_dummies` *A set of example dummy alignment genes.*

Description

Dummy genes, similar to those generated with `make_alignment_dummies()`, for example purposes only.

Usage

```
example_dummies
```

Format

A data frame with eight rows and three variables:

molecule the genome

start the start position of the dummy

end the end position of the dummy

gene the name of the dummy gene

`example_features` *A set of example genetic features.*

Description

Genetic features for example purposes only.

Usage

```
example_features
```

Format

A data frame with 23 rows and five variables:

molecule the genome

name the name of the feature

type the type of the feature

position the position of the feature

forward is the feature oriented, and if so in the forward direction?

`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.

geom_feature *A 'ggplot2' geom to draw point genetic features*

Description

geom_feature() draws lines to indicate the positions of point genetic features, for example restriction sites, origins of replication or transcription start sites.

Usage

```
geom_feature(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = FALSE,
  feature_height = unit(3, "mm"),
  feature_width = unit(3, "mm"),
  arrowhead_width = unit(2, "mm"),
  ...
)
```

Arguments

mapping, data, stat, position, na.rm, show.legend, inherit.aes, ...
: As standard for ggplot2. inherit.aes is set to FALSE by default, as features are not likely to share any plot aesthetics other than y.

feature_height
: grid::unit() object giving the height of a feature above the molecule line. Can be set as a negative value to draw features below the line. Defaults to 3 mm.

feature_width
: grid::unit() object giving the width of a feature (distance from the elbow to the tip of the arrow). Only relevant for oriented features. Defaults to 3 mm.

arrowhead_width
: grid::unit() object giving the width of the arrowhead indicating the direction of an oriented feature. Only relevant for oriented features. Defaults to 2 mm.

Details

Features are drawn as vertical lines extending from the horizontal line representing the molecule. The position of the feature is expressed with the x aesthetic. Optionally, the forward aesthetic can be used to specific an orientation for the feature (e.g. the direction of transcription), in which case an angled arrowhead will be added. The forward aesthetic assumes that the x-axis is oriented in the normal direction, i.e. increasing from left to right; if it is not, the values in forward will need to be inverted manually.

Aesthetics

- x (required; position of the feature)
- y (required; molecule)
- forward (optional; if TRUE, or a value coercible to TRUE, the feature will be drawn with an arrowhead pointing right, if FALSE, pointing left, if NA, the feature will be drawn as a vertical line)
- alpha
- colour
- linetype
- size

See Also

`geom_feature_label()`

Examples

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

---

geom_feature_label *A 'ggplot2' geom to add text labels to point genetic features*

Description

`geom_feature_label()` adds text labels to features drawn with `geom_feature()`.

Usage

```
geom_feature_label(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = FALSE,
  feature_height = unit(4, "mm"),
  label_height = unit(3, "mm"),
  ...
)
```

Arguments

`mapping`, `data`, `stat`, `position`, `na.rm`, `show.legend`, `inherit.aes`, `...`
: As standard for ggplot2. inherit.aes is set to FALSE by default, as features are not likely to share any plot aesthetics other than y.

`feature_height`
: `grid::unit()` object giving the height of the feature being labelled, and hence the distance of the label above or below the molecule line. Can be set as a negative value for features drawn below the line. Defaults to 4 mm, to align labels with the default height of `geom_feature()`.

`label_height`
: `grid::unit()` object giving the height of the label text. Defaults to 3 mm.

Details

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

Aesthetics

- x (required; position of the feature)
- y (required; molecule)
- label (required; the label text)
- forward (optional; will draw text in the appropriate location for features with angled arrowheads)
- colour
- size
- alpha
- family
- fontface
- angle

See Also

`geom_feature()`

Examples

```
ggplot2::ggplot(example_genes, ggplot2::aes(xmin = start, xmax = end,
                                            y = molecule, fill = gene)) +
  geom_gene_arrow() +
  geom_feature(data = example_features, ggplot2::aes(x = position, y = molecule,
                                                     forward = forward)) +
  geom_feature_label(data = example_features,
                     ggplot2::aes(x = position, y = molecule, label = name,
                                  forward = forward)) +
  ggplot2::facet_wrap(~ molecule, scales = "free")
```

geom_gene_arrow *A 'ggplot2' geom to draw genes as arrows*

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 '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)
- label (the label text; 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()
```

---

geom_subgene_arrow *A 'ggplot2' geom to draw subgene segments of gene arrows*

Description

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

Usage

```
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 FALSE, or coercible to FALSE, 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

```
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 *A 'ggplot2' geom to add text labels to subgenes*

Description

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

Usage

```
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

`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'.`theme_genes_flipped()` is like `theme_genes()`, but for flipped coordinates.

Usage

```
theme_genes()

theme_genes_flipped()
```

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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