Package ‘ggseqlogo’

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Type Package

Title A 'ggplot2' Extension for Drawing Publication-Ready Sequence Logos

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Description The extensive range of functions provided by this package makes it possible to draw highly versatile sequence logos. Features include, but not limited to, modifying colour schemes and fonts used to draw the logo, generating multiple logo plots, and aiding the visualisation with annotations. Sequence logos can easily be combined with other plots 'ggplot2' plots.

License LGPL

URL https://github.com/omarwagih/ggseqlogo

BugReports https://github.com/omarwagih/ggseqlogo/issues

Encoding latin1

Imports ggplot2

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

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Description

Plots sequence logo as a layer on ggplot

Usage

```r
geom_logo(data = NULL, method = "bits", seq_type = "auto",
namespace = NULL, font = "roboto_medium", stack_width = 0.95,
rev_stack_order = F, col_scheme = "auto", low_col = "black",
high_col = "yellow", na_col = "grey20", plot = T, ...)
```

Arguments

data Character vector of sequences or named list of sequences. All sequences must have same width.
method Height method, can be one of "bits" or "probability" (default: "bits")
seq_type Sequence type, can be one of "auto", "aa", "dna", "rna" or "other" (default: "auto", sequence type is automatically guessed)
namespace Character vector of single letters to be used for custom namespaces. Can be alphanumeric, including Greek characters.
font Name of font. See list_fonts for available fonts.
stack_width Width of letter stack between 0 and 1 (default: 0.95)
rev_stack_order If TRUE, order of letter stack is reversed (default: FALSE)
col_scheme Color scheme applied to the sequence logo. See list_col_schemes for available fonts. (default: "auto", color scheme is automatically picked based on seq_type). One can also pass custom color scheme objects created with the make_col_scheme function
low_col, high_col Colors for low and high ends of the gradient if a quantitative color scheme is used (default: "black" and "yellow").
na_col Color for letters missing in color scheme (default: "grey20")
plot If FALSE, plotting data is returned
... Additional arguments passed to layer params
Examples

```r
# Load sample data
data(ggseqlogo_sample)

# Produce single sequence logo using geom_logo
p1 = ggseqlogo( seqs_dna[[1]] )
```

---

**Description**

`ggseqlogo` is a shortcut for generating sequence logos. It adds the `ggseqlogo` theme `theme_logo` by default, and facets when multiple input data are provided. It serves as a convenient wrapper, so to customise logos beyond the defaults here, please use `geom_logo`.

**Usage**

```r
ggseqlogo(data, facet = "wrap", scales = "free_x", ncol = NULL, nrow = NULL, ...)
```

**Arguments**

- `data` Character vector of sequences or named list of sequences. All sequences must have same width
- `facet` Facet type, can be 'wrap' or 'grid'
- `scales` Facet scales, see `facet_wrap`
- `ncol` Number of columns, works only when `facet='wrap'`, see `facet_wrap`
- `nrow` Number of rows, same as `ncol`
- `...` Additional arguments passed to `geom_logo`

**Examples**

```r
# Load sample data
data(ggseqlogo_sample)

# Plot a single DNA sequence logo
p1 = ggseqlogo( seqs_dna[[1]] )
print(p1)

# Plot multiple sequence logos at once
p2 = ggseqlogo( seqs_dna )
print(p2)
```
list_col_schemes  List color schemes available in ggseqlogo

Description
List color schemes available in ggseqlogo

Usage
list_col_schemes(v = T)

Arguments
v If true, font names are printed to stderr. Otherwise, color scheme names are returned as a character vector

list_fonts  List fonts available in ggseqlogo

Description
List fonts available in ggseqlogo

Usage
list_fonts(v = T)

Arguments
v If true, font names are printed to stderr. Otherwise, font names are returned as a character vector

make_col_scheme  Create new sequence logo color scheme

Description
Create new sequence logo color scheme

Usage
make_col_scheme(chars = NULL, groups = NULL, cols = NULL, values = NULL, name = "")
pfms_dna

List of position frequency matrices for transcription factors

Description

List of position frequency matrices for transcription factors

seqs_aa

List of aligned kinase-substrate binding sequences

Description

List of aligned kinase-substrate binding sequences

seqs_dna

List of aligned transcription factor binding sequences

Description

List of aligned transcription factor binding sequences
theme_logo

ggseqlogo custom theme

Description

ggseqlogo custom theme

Usage

theme_logo(base_size = 12, base_family = "")

Arguments

base_size    font base size
base_family  font base family
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