Package 'ggdiceplot'

August 21, 2025

Title Dice Plot Visualization for 'ggplot2'

Version 0.1.0

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Description Provides 'ggplot2' extensions for creating dice-based visualizations where each dot position represents a specific categorical variable. The package includes geom_dice() for displaying presence/absence of categorical variables using traditional dice patterns. Each dice position (1-6) represents a different category, with dots shown only when that category is present. This allows intuitive visualization of up to 6 categorical variables simultaneously.

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Encoding UTF-8

RoxygenNote 7.3.2

URL https://github.com/maflot/ggdiceplot

BugReports https://github.com/maflot/ggdiceplot/issues

Imports ggplot2 (>= 3.4.0), grid, legendry, scales

LazyData true

Depends R (>= 4.1.0), dplyr

NeedsCompilation no

Repository CRAN

Date/Publication 2025-08-21 20:02:06 UTC

Contents

GeomDice *A ggplot2 layer for creating dice representations*

Description

`geom_dice()` creates a layer that displays dice-like symbols where each dot represents a specific category. Dots are only shown when that categorical variable is present in the data, allowing compact visual encoding.

Usage

```
geom_dice(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ndots = NULL,
  x_length = NULL,
  y_length = NULL,
  na.rm = FALSE,
  show.legend = TRUE,
  inherit.aes = TRUE,
  ...
)
```

Arguments

`mapping`	Set of aesthetic mappings created by `aes()`. Must include: • `x`, `y`: Position of the dice. • `dots`: The categories present (usually as a string or factor).
`data`	A data frame. If `NULL`, inherits from the plot.
`stat`	The statistical transformation to use.
`position`	Position adjustment.
`ndots`	Integer (1–6): number of positions shown per dice.
`x_length`	x_length Numeric: used for aspect ratio.
`y_length`	y_length Numeric: used for aspect ratio.
`na.rm`	Remove missing values if `TRUE`.
`show.legend`	Whether to include in legend.
`inherit.aes`	If `FALSE`, overrides the default aesthetics.
`...`	Additional arguments passed to `layer()`.

Value

A `ggplot2` layer that draws dice with categorical dot encodings.

Examples

```
library(ggplot2)

df <- data.frame(
  x = 1:3,
  y = 1,
  dots = c("A,B", "A,C,E", "F")
)

ggplot(df, aes(x, y, dots = dots)) +
  geom_dice(ndots = 6, x_length = 3, y_length = 1)
```

`make_offsets` *Calculate Dice Dot Offsets*

Description

Computes the (x, y) offset positions for drawing dots on dice faces.

Usage

```
make_offsets(n, width = 0.5, height = 0.5, pad = 0.1)
```

Arguments

`n`	Integer from 1 to 6, indicating the number of dots on the die face.
`width`	Total width of the die face (default: 0.5).
`height`	Total height of the die face (default: 0.5).
`pad`	Padding to apply around the dot grid (default: 0.1).

Value

A data.frame with `key`, `x`, and `y` columns indicating dot positions.

`sample_dice_data1` *Sample Dice Dataset for Basic Visualization*

Description

A toy dataset for demonstrating the `geom_dice()` function. It simulates log fold-change (LFC) and adjusted p-values (q-values) for oral taxa across disease types and specimen sites.

Usage

```
data("sample_dice_data1")
```

Format

A data frame with 48 rows and 5 variables:

`taxon` character. Microbial taxon name

`disease` character. Disease condition (Caries, Periodontitis, Healthy, Gingivitis)

`specimen` character. Body site specimen (Saliva, Plaque)

`lfc` numeric. Simulated log2 fold change value

`q` numeric. Simulated adjusted p-value (q-value)

Details

This dataset contains simulated microbiome data across different oral health conditions and specimen types. It is designed to demonstrate basic dice plot functionality with categorical mapping of diseases to dice positions.

Source

Simulated data for package demonstration purposes.

Examples

```
data(sample_dice_data1)
head(sample_dice_data1)

# Basic dice plot example
library(ggplot2)
ggplot(sample_dice_data1, aes(x = specimen, y = taxon)) +
  geom_dice(aes(dots = disease, fill = lfc, size = -log10(q)),
            ndots = 4, show.legend = TRUE)
```

`sample_dice_data2` *Extended Sample Dice Dataset*

Description

An extended toy dataset for demonstrating advanced `geom_dice()` functionality with missing data handling and more complex scenarios.

Usage

```
data("sample_dice_data2")
```

Format

A data frame with variables:

`taxon` character. Microbial taxon name

`disease` character. Disease condition

`specimen` character. Body site specimen

`replicate` numeric. Replicate number

`lfc` numeric. Log2 fold change value (may contain NA)

`q` numeric. Adjusted p-value (q-value, may contain NA)

Details

This dataset extends sample_dice_data1 with additional complexity including missing values and edge cases. It is designed to demonstrate how dice plots handle missing data and various data preprocessing scenarios.

Source

Simulated data for package demonstration purposes.

Examples

```
data(sample_dice_data2)
head(sample_dice_data2)

# Example with missing data handling
library(ggplot2)
ggplot(sample_dice_data2, aes(x = specimen, y = taxon)) +
  geom_dice(aes(dots = disease, fill = lfc, size = -log10(q)),
            ndots = 4, na.rm = TRUE, show.legend = TRUE)
```

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sample_dice_large *Large Sample Dataset for Performance Testing*

Description

A larger toy dataset for testing `geom_dice()` performance and demonstrating scalability with bigger datasets.

Usage

```
data("sample_dice_large")
```

Format

A data frame with variables:

`taxon` character. Microbial taxon name

`disease` character. Disease condition

`specimen` character. Body site specimen

`replicate` numeric. Replicate number

`lfc` numeric. Log2 fold change value

`q` numeric. Adjusted p-value (q-value)

Details

This dataset contains a larger number of observations than the basic sample datasets. It is designed to test performance and demonstrate how dice plots scale with larger data, including automatic sizing and boundary validation.

Source

Simulated data for package demonstration purposes.

Examples

```
data(sample_dice_large)
head(sample_dice_large)
dim(sample_dice_large)

# Example with larger dataset
library(ggplot2)
ggplot(sample_dice_large, aes(x = specimen, y = taxon)) +
  geom_dice(aes(dots = disease, fill = lfc, size = -log10(q)),
            ndots = 6, na.rm = TRUE, show.legend = TRUE) +
  theme_minimal() +
  theme(axis.text.y = element_text(size = 8))
```

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scale_dots_discrete *Discrete Scale for Dice Dot Colors*

Description

Creates a ggplot2 discrete scale for dice dot aesthetics.

Usage

```
scale_dots_discrete(..., aesthetics = "dots")
```

Arguments

`...`	Passed to `ggplot2::discrete_scale()`
`aesthetics`	Character string of the target aesthetic (default: "dots")

Value

A ggplot2 scale

`theme_dice` *Dice Theme for ggplot2*

Description

A minimal ggplot2 theme for dice plots.

Usage

```
theme_dice(x_length, y_length, ...)
```

Arguments

`x_length`	Width of the plotting area (kept for compatibility)
`y_length`	Height of the plotting area (kept for compatibility)
`...`	Additional arguments passed to `theme_grey()`

Value

A ggplot2 theme

Index