Package ‘ggdiceplot’

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Title DicePlot Visualization for 'ggplot2'

Version 1.1.0

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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 7.3.3

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

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

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

LazyData true

Depends R (>= 4.1.0)

NeedsCompilation no

Repository CRAN

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Contents

`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 Visualization*

Description

This toy dataset (`sample_dice_data1`) is used to demonstrate the `geom_dice()` function. It simulates log fold-change (LFC) and adjusted p-values (q-values) for a range of oral taxa across disease types and specimen sites.

Usage

```
data(sample_dice_data1)
```

Format

A data frame with 160 rows and 5 columns:

taxon Character. Microbial taxon name (8 taxa).

disease Character. Disease condition (Caries, Periodontitis, Healthy, Gingivitis).

specimen Character. Body site specimen (Saliva, Plaque, Tongue, Buccal, Gingival).

lfc Numeric. Simulated log2 fold change value; may contain NA.

q Numeric. Simulated adjusted p-value (q-value); may contain NA.

Examples

```
data(sample_dice_data1)
head(sample_dice_data1)
```

`sample_dice_data2` *Sample Dice Dataset 2 for Visualization*

Description

`sample_dice_data2` is a toy dataset designed to demonstrate `geom_dice()` with multiple specimen types. It simulates log2 fold-change (LFC) and adjusted p-values (q-values) for oral taxa across disease conditions and specimen sites, with some missing values.

Usage

```
data(sample_dice_data2)
```

Format

A data frame with 160 rows and 5 columns:

taxon Character. Microbial taxon name (8 taxa).

disease Character. Disease condition (Caries, Periodontitis, Healthy, Gingivitis).

specimen Character. Body site specimen (Saliva, Plaque, Tongue, Buccal, Gingival).

lfc Numeric. Simulated log2 fold change; may contain NA.

q Numeric. Simulated adjusted p-value (q-value); may contain NA.

Examples

```
data(sample_dice_data2)
head(sample_dice_data2)
```

`sample_dice_large` *Large Sample Dice Dataset*

Description

`sample_dice_large` is a larger toy dataset with 60 taxa, designed to test `geom_dice()` at higher density. It simulates log2 fold-change and q-values with approximately 50\

Usage

```
data(sample_dice_large)
```

Format

A data frame with 480 rows and 6 columns:

taxon Character. Taxon name (Taxon_1 through Taxon_60).

disease Character. Disease condition (Caries, Periodontitis, Healthy, Gingivitis).

specimen Character. Specimen type (Saliva, Plaque).

replicate Integer. Replicate identifier.

lfc Numeric. Simulated log2 fold change; may contain NA.

q Numeric. Simulated adjusted p-value; may contain NA.

Examples

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

`sample_dice_miRNA` *Sample miRNA Dice Dataset*

Description

`sample_dice_miRNA` is a toy dataset for demonstrating `geom_dice()` with categorical fill mapping. It simulates miRNA dysregulation across compounds and organs, with direction (Up, Down, Unchanged) as the fill variable.

Usage

```
data(sample_dice_miRNA)
```

Format

A data frame with approximately 90 rows and 5 columns:

miRNA Factor. miRNA identifier (miR-1 through miR-5).

Compound Factor. Treatment compound (Control, Compound_1 through Compound_4).

Organ Factor. Target organ (Lung, Liver, Brain, Kidney).

log2FC Numeric. Simulated log2 fold change.

direction Factor. Regulation direction (Down, Unchanged, Up).

Examples

```
data(sample_dice_miRNA)
head(sample_dice_miRNA)
```

`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

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