Package ‘fishualize’

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Type Package

Title Color Palettes Based on Fish Species

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Description Implementation of color palettes based on fish species.

License GPL-2

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

Suggests testthat, knitr, rmarkdown, rfishbase, naturalearth, pkgdown

URL https://github.com/nschiett/fishualize

BugReports https://github.com/nschiett/fishualize/issues

Imports ggplot2 (>= 1.0.1), gridExtra, grid, png, downloader, utils, htr, magrittr, stringr, dplyr, tidyr, scales, rlang, curl

RoxygenNote 7.1.1

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Description

Adds a fish silhouette to your plot

Usage

```r
add_fishape(
  family = "Pomacanthidae",
  option = "Centropyge_loricula",
  xmin = -Inf,
  xmax = Inf,
  ymin = -Inf,
  ymax = Inf,
  scaled = FALSE,
  xlim = NULL,
  ylim = NULL,
  fill = "#000000",
  alpha = 1
)
```

Arguments

- **family**: character string indicating the fish family.
- **option**: character string indicating the fish species. If NA, the first available option within a family will be selected
- **xmin**: x location giving minimum horizontal location of silhouette
- **xmax**: x location giving maximum horizontal location of silhouette
- **ymin**: y location giving minimum vertical location of silhouette
- **ymax**: y location giving maximum vertical location of silhouette
- **scaled**: logical parameter. If TRUE, location parameters (xmin, xmax, ymin, ymax) should range between 0 and 1. If FALSE, location parameters should be provided according to the values on the plot axes.
- **xlim, ylim**: vectors of length = 2, contains the data limits and must be provided if scaled is TRUE.
- **fill**: color of fish shape
- **alpha**: transparency of fish shape (value between 0 and 1)
Examples

```r
library(ggplot2)

ggplot() + add_fishape(fill = fish(n = 5)[4])

ggplot(diamonds) +
  geom_bar(aes(cut, fill = cut)) +
  scale_fill_fish_d(option = "Naso_lituratus") +
  add_fishape(family = "Acanthuridae",
              option = "Naso_unicornis",
              xmin = 1, xmax = 3, ymin = 15000, ymax = 20000,
              fill = fish(option = "Naso_lituratus", n = 5)[3],
              alpha = 0.8) +
  theme_bw()

## example with relative coordinates

ggplot(diamonds) +
  geom_bar(aes(cut, fill = cut)) +
  scale_fill_fish_d(option = "Naso_lituratus") +
  add_fishape(family = "Acanthuridae",
              option = "Naso_unicornis",
              xmin = 0, xmax = 0.3, ymin = 0.8, ymax = 1,
              scaled = TRUE,
              xlim = c(0.5, 5.5), ylim = c(0, 21000),
              fill = fish(option = "Naso_lituratus", n = 5)[3],
              alpha = 1) +
  theme_bw()
```

fish

**fish Colour Map.**

Description

This function creates a vector of \( n \) equally spaced colors along the 'fish colour map' of your selection

Usage

```r
fish(
  n,
  alpha = 1,
  begin = 0,
  end = 1,
  direction = 1,
  option = "Centropyge_loricula"
)

fish_pal()
```
alpha = 1,
begin = 0,
end = 1,
direction = 1,
option = "Centropyge_loricula"
)

Arguments

n
The number of colors (≥ 1) to be in the palette.

alpha
The alpha transparency, a number in [0,1], see argument alpha in hsv.

begin
The (corrected) hue in [0,1] at which the fish colormap begins.

direction
Sets the order of colors in the scale. If 1, the default, colors are ordered from darkest to lightest. If -1, the order of colors is reversed.

option
A character string indicating the fish species to use.

Value

fish returns a character vector, cv, of color hex codes. This can be used either to create a user-defined color palette for subsequent graphics by palette(cv), a col = specification in graphics functions or in par.

Semi-transparent colors (0 < alpha < 1) are supported only on some devices: see rgb.

Examples

library(ggplot2)
library(fishualize)

dat <- data.frame(x = rnorm(1e4), y = rnorm(1e4))
print(ggplot(dat, aes(x = x, y = y)) +
  stat_density_2d(geom = "raster",
  aes(fill = after_stat(density)), contour = FALSE) +
  scale_fill_gradientn(colors = fish(128, option = "Ostracion_cubicus")))

pal <- fish(256, option = "Thalassoma_hardwicke", direction = -1)
print(image(volcano, col = pal))

fishapes

Available fish silhouettes

Description

This function returns a dataframe containing the all the available fish silhouettes accessible through the 'fishualize' package.
**fishcolors**

**Usage**

fishapes()

**Value**

fishapes returns a dataframe containing all the available fish silhouettes available to use.

**Examples**

fishapes()

---

**fishcolors**

*Original fish color database*

**Description**

A dataset containing some colour palettes inspired by fish species

**Usage**

fishcolors

**Format**

A data frame containing all the colours used in the palette:

- option: It is intended to be a general option for choosing the specific colour palette.
- hex: hex color code

**fishualize**

*Visualization of fish color palette*

**Description**

This function creates an image of the specified fish color palette.

**Usage**

fishualize(option = "Centropyge_loricula", n = 5, ...)

**Arguments**

- **option**
  - A character string indicating the fish species to use.
- **n**
  - The number of colors (≥ 1) to be in the palette.
- **...**
  - Other arguments as can be specified in the function fish. See ?fishualize::fish for details.
Value

`fishualize` returns a visualisation of the specified color palette.

Examples

```r
fishualize::fishualize()
fishualize::fishualize(option = "Zanclus_cornutus", n = 8)
```

---

```r
table
  fish_palettes  Available Palettes.
```

### Description

This function returns a vector containing the names of all the available palettes in the `fishualize` package.

### Usage

```r
fish_palettes()
```

### Value

`fish_palettes` returns a character vector with the names of the fish palettes available to use.

### Examples

```r
fish_palettes()
```

---

```r
table
  scale_color_fish  fish colour scales
```

### Description

Uses the fish color scale.
Usage

scale_color_fish(
  option = "Centropyge_loricula",
  ..., alpha = 1,
  begin = 0,
  end = 1,
  direction = 1,
  discrete = FALSE
)

scale_colour_fish(
  option = "Centropyge_loricula",
  ..., alpha = 1,
  begin = 0,
  end = 1,
  direction = 1,
  discrete = FALSE
)

scale_color_fish_d(
  option = "Centropyge_loricula",
  ..., alpha = 1,
  begin = 0,
  end = 1,
  direction = 1
)

scale_color_fish_d(
  option = "Centropyge_loricula",
  ..., alpha = 1,
  begin = 0,
  end = 1,
  direction = 1
)

scale_fill_fish_d(
  option = "Centropyge_loricula",
  ..., alpha = 1,
  begin = 0,
  end = 1,
  direction = 1
)
scale_fill_fish(
  option = "Centropyge_loricula",
  ..., 
  alpha = 1, 
  begin = 0, 
  end = 1, 
  direction = 1, 
  discrete = FALSE
)

Arguments

- **option**: A character string indicating the fish species to use.
- **...** parameters to `discrete_scale` or `scale_fill_gradientn`
- **alpha**: pass through parameter to `fish`
- **begin**: The (corrected) hue in [0,1] at which the fish colormap begins.
- **end**: The (corrected) hue in [0,1] at which the fish colormap ends.
- **direction**: Sets the order of colors in the scale. If 1, the default, colors are as output by `fish_pal`. If -1, the order of colors is reversed.
- **discrete**: generate a discrete palette? (default: FALSE - generate continuous palette)

Details

For `discrete == FALSE` (the default) all other arguments are as to `scale_fill_gradientn` or `scale_color_gradientn`. Otherwise the function will return a `discrete_scale` with the plot-computed number of colors.

Examples

```r
library(ggplot2)
library(fishualize)

ggplot(diamonds, aes(factor(cut), fill=factor(cut))) +
  geom_bar() +
  scale_fill_fish(discrete = TRUE, option = "Centropyge_loricula")

ggplot(mtcars, aes(factor(gear), fill=factor(carb))) +
  geom_bar() +
  scale_fill_fish(discrete = TRUE, option = "Trimma_lantana")

ggplot(mtcars, aes(x = mpg, y = disp, colour = drat)) +
  geom_point(size = 4) +
  scale_colour_fish(option = "Ostracion_cubicus", direction = -1)
```
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