Package ‘fishualize’

March 8, 2022

Type Package
Title Color Palettes Based on Fish Species
Version 0.2.3
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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, markdown, 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, htrr, magrittr, stringr, dplyr, tidyr, scales, rlang, curl
RoxygenNote 7.1.2
VignetteBuilder knitr
NeedsCompilation no
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Repository CRAN
Date/Publication 2022-03-08 13:30:02 UTC

R topics documented:

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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)
fish

**Value**

Adds a fish silhouette grob to a ggplot object.

**Examples**

```r
## Not run:
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()

## End(Not run)
```

---

**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.
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 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))
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)
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.

Usage

fishapes()

Value

fishapes returns a dataframe containing the 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**

```r
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)
```

---

**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.
scale_color_fish

Examples

    fish_palettes()


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,
scale_color_fish

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.

Value

Alias of scale_color_fish or scale_fill_fish
Alias of scale_color_fish or scale_fill_fish
Alias of scale_color_fish or scale_fill_fish
Alias of scale_color_fish or scale_fill_fish
Alias of scale_color_fish or scale_fill_fish
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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