

Package: fishualize (via r-universe)

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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, rmarkdown, rfishbase, rnaturalearth, pkgdown

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

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

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

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VignetteBuilder knitr

Repository <https://nschiett.r-universe.dev>

RemoteUrl <https://github.com/nschiett/fishualize>

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add_fishape	<i>fish silhouette in ggplot2</i>
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Description

Adds a fish silhouette to your plot

Usage

```
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)

Value

Adds a fish silhouette grob to a ggplot object.

Examples

```
## Not run:
library(ggplot2)

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

ggplot(diamonds)+
  geom_bar(aes(cut, fill = cut)) +
  scale_fill_fish_d(option = "Naso_lituratus") +
  add_fishshape(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_fishshape(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

```
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	<i>Visualization of fish color palette</i>
------------	--

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

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

fish_palettes	<i>Available Palettes.</i>
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Description

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

Usage

```
fish_palettes()
```

Value

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

Examples

```
fish_palettes()
```

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_colour_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 <code>discrete_scale</code> or <code>scale_fill_gradientn</code>
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 <code>fish_pal</code> . 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

```
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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