Package ‘fishualize’

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Title  Color Palettes Based on Fish Species
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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)
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**

| fishapes | Available fish silhouettes |

**Description**

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

**Usage**

fishapes()

**Value**

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

**Examples**

fishapes()

---

**fishcolors**

| 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 ($\geq 1$) 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()

--

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, 
  discrete = FALSE 
)
scale_color_fish

```r
end = 1,
direction = 1
)
```

```r
scale_fill_fish_d(
  option = "Centropyge_loricula",
  ...,  
  alpha = 1,
  begin = 0,
  end = 1, 
  direction = 1
)
```

```r
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`
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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