Package ‘palettetown’

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Type Package
Title Use Pokemon Inspired Colour Palettes
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Description Use Pokemon(R) inspired palettes with additional 'ggplot2' scales. Palettes are the colours in each Pokemon's sprite, ordered by how common they are in the image. The first 386 Pokemon are currently provided.
Suggests ggplot2, magrittr
Imports grDevices, stats, graphics
License MIT + file LICENSE
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Get a pokemon palette. Alias for pokepal.

Description

Get a pokemon palette by either giving a pokemon number or name. The recommended syntax for this function is 'Magikarp' %>% ichooseyou using the pipe operator %>% from the magrittr package. To specify the spread parameter use 'Snorlax' %>% ichooseyou(5)

Usage

ichooseyou(pokemon = 1, spread = NULL)

Arguments

- pokemon: An integer or character pokemon name
- spread: How many, quite distinct, colours should be returned. See details.

Details

If spread is given an integer, the full palette is clustered into that many groups (ward clustering in HSV space). The most common colour in each cluster is then returned. It is hoped this will give a good balance between reflecting the pokemons colouring while giving relatively distinct colours.

See Also

pokepal

Examples

library(magrittr)
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pal <- 'Hoothoot' %>% ichooseyou
pal2 <- 'Pichu' %>% ichooseyou(6)

Pokemon inspired colour palettes.

Description

Pokemon inspired colour palettes.

Author(s)

Tim CD Lucas
pokedex

Display pokemon palettes.

Description
Display 10 pokemon palettes starting from a name or number. If no name or number is given, 10 of the better palettes are displayed. Pokedex is a Trademark of Nintendo.

Usage
pokedex(pokemon = NULL, spread = NULL, cb = NULL)

Arguments
- **pokemon**: An integer or character pokemon name
- **spread**: How many, quite distinct, colours should be returned. See details.
- **cb**: A number between 1 and 4 to select ten of 40 colourblind friendly (Deuteranomaly) palettes. pokemon is ignored if used, but spread works as normal.

Details
If spread is given an integer, the full palette is clustered into that many groups (ward clustering in HSV space). The most common colour in each cluster is then returned. It is hoped this will give a good balance between reflecting the pokemons colouring while giving relatively distinct colours. Thanks to Luis Verde for the colourblind suitable selection.

Examples
- pokedex()
- pokedex('Metapod')
- pokedex(5, spread = 2)
- pokedex(cb = 3)
- pokedex(cb = 2, spread = 6)

pokepal

Get a pokemon palette.

Description
Get a pokemon (R) palette by either giving a pokemon number or name.

Usage
pokepal(pokemon = 1, spread = NULL)
**scale_colour_poke**

**Arguments**

- **pokemon**: An integer or character pokemon name
- **spread**: How many, quite distinct, colours should be returned. See details.

**Details**

If `spread` is given an integer, the full palette is clustered into that many groups (ward clustering in HSV space, using only hue and downweighted saturation). The most common colour in each cluster is then returned. It is hoped this will give a good balance between reflecting the pokemons’ colouring while giving relatively distinct colours.

A few pokemons have odd names. Argument `pokemon` ignores letter case. Female and Male Nidoran are named NidoranF and NidoranM respectively. Mr. Mime should be either ‘Mr. Mime’ or ‘mr. mime’. The full stop and space are needed.

**See Also**

`ichooseyou`

**Examples**

```r
pal <- pokepal(3)
plot(1:length(pal), col = pal)
```

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**Description**

Get a pokemon palette by either giving a pokemon number or name.

**Usage**

```r
scale_colour_poke(..., pokemon = 1, spread = NULL)
scale_fill_poke(..., pokemon = 1, spread = NULL)
scale_color_poke(..., pokemon = 1, spread = NULL)
```

**Arguments**

- `...`: Other arguments passed on to `discrete_scale` to control name, limits, breaks, labels and so forth.
- **pokemon**: An integer or character pokemon name
- **spread**: How many, quite distinct, colours should be returned. See details.
Details

If `spread` is given an integer, the full palette is clustered into that many groups (ward clustering in HSV space). The most common colour in each cluster is then returned. It is hoped this will give a good balance between reflecting the pokemons colouring while giving relatively distinct colours.

Examples

```r
library(ggplot2)
qplot(Sepal.Length, Sepal.Width, colour = Species, data=iris) +
  scale_colour_poke(pokemon = 'Metapod')
```
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