Package: mycolorsTB (via r-universe)

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Type Package

Title Color Palettes for Mycobacterium Tuberculosis Data Visualization

Version 0.1.1

Description Colour palettes and helper functions for visualising Mycobacterium tuberculosis genomic and epidemiological data with 'ggplot2' and 'ggtree'. The package provides predefined palettes, scale functions, tree/cladogram helpers, and convenient preview tools to ensure consistent branding in pathogen-omics visualisations. The palettes were developed as part of the 'mycolorsTB' project <`https://github.com/PathoGenOmics-Lab/mycolorsTB`>.

License GPL-3

Encoding UTF-8

Imports ggplot2, ape, ggtree

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.1

NeedsCompilation no

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Contents

`classicTB` *ClassicTB Color Palette*

Description

An unnamed vector of 14 colors derived from the `classicTB` theme.

Usage

```
classicTB
```

Format

A character vector of 14 hex color codes.

Source

Color palette designed by the PathoGenOmics Lab.

`mycolors` *Mycolors Color Palette*

Description

A named vector of 14 colors designed for visualizing Mycobacterium tuberculosis lineages.

Usage

```
mycolors
```

Format

A character vector of 14 hex color codes, named with lineage identifiers.

Source

Color palette designed by the PathoGenOmics Lab.

`pathogenomics` *PathoGenOmics Color Palette*

Description

A palette of 8 colors from the PathoGenOmics Lab theme.

Usage

```
pathogenomics
```

Format

A character vector of 8 hex color codes.

Source

Color palette designed by the PathoGenOmics Lab.

`plot_tb_cladogram` *Plot a Phylogenetic Cladogram with TB Lineage Colors*

Description

Visualizes a phylogenetic tree as a cladogram, coloring tips with the `mycolors` palette.

Usage

```
plot_tb_cladogram(newick_text)
```

Arguments

`newick_text`	A character string with the tree in Newick format.

Value

A ggplot object representing the phylogenetic cladogram.

Examples

```
tree_text <- "(L8,((L1,(L7,(L4,(L2,L3)))),(L5,((A2,(A3,A4)),(A1,(L10,(L6,L9)))))));"
plot_tb_cladogram(tree_text)
```

`plot_tb_tree` *Plot a Phylogenetic Tree with TB Lineage Colors*

Description

Reads a tree in Newick format and plots it using ggtree, coloring tips with the `mycolors` palette.

Usage

```
plot_tb_tree(newick_text)
```

Arguments

`newick_text`	A character string with the tree in Newick format.

Value

A ggplot object representing the phylogenetic tree.

Examples

```
tree_text <- "(L8,((L1,(L7,(L4,(L2,L3)))),(L5,((A2,(A3,A4)),(A1,(L10,(L6,L9)))))));"
plot_tb_tree(tree_text)
```

`scale_color_classicTB` *Scale Color for ggplot2 Using classicTB Palette*

Description

Applies the `classicTB` palette to the color aesthetic in a ggplot.

Usage

```
scale_color_classicTB()
```

Value

A ggplot2 scale object.

`scale_color_mycolors` *Scale Color for ggplot2 Using mycolors Palette*

Description

Applies the `mycolors` palette to the color aesthetic in a ggplot.

Usage

```
scale_color_mycolors()
```

Value

A ggplot2 scale object.

`scale_fill_classicTB` *Scale Fill for ggplot2 Using classicTB Palette*

Description

Applies the `classicTB` palette to the fill aesthetic in a ggplot.

Usage

```
scale_fill_classicTB()
```

Value

A ggplot2 scale object.

`scale_fill_mycolors` *Scale Fill for ggplot2 Using mycolors Palette*

Description

Applies the `mycolors` palette to the fill aesthetic in a ggplot.

Usage

```
scale_fill_mycolors()
```

Value

A ggplot2 scale object.

`tb_palette` *Generate n colors from a mycolorsTB palette*

Description

Uses color interpolation to create a custom number of colors from a given palette.

Usage

```
tb_palette(n, palette_name = "classicTB")
```

Arguments

`n`	The number of colors to generate.
`palette_name`	The name of the palette to use ("mycolors", "classicTB", or "pathogenomics").

Value

A character vector of n hex color codes.

Examples

```
# Generate 20 colors from the 'classicTB' palette
my_custom_colors <- tb_palette(20, "classicTB")
plot(1:20, 1:20, col = my_custom_colors, pch = 19, cex = 3)
```

`view_palette` *Display a color palette*

Description

Generates a ggplot visualization of a specified package palette.

Usage

```
view_palette(palette_name = "mycolors")
```

Arguments

`palette_name`	The name of the palette to display ("mycolors", "classicTB", or "pathogenomics").

Value

A ggplot object showing the colors of the chosen palette.

Examples

```
view_palette("mycolors")
view_palette("classicTB")
```

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