Package: palettephines (via r-universe)

June 9, 2026

Type Package

Title Analytical Color Palettes for Philippine Phenology

Version 0.1.3

Description Provides specialized color palettes representing phenological transitions and biological lifecycles within Philippine landscapes. Rather than abstract gradients, these scales are anchored to topologically grounded states such as agricultural maturity, seasonal vegetation shifts, and environmental readiness. Palettes are indexed against the Biologische Bundesanstalt, Bundessortenamt und CHemische Industrie (BBCH) scale (Meier, 2023) <`https://www.openagrar.de/servlets/MCRFileNodeServlet/openagrar_derivate_00010428/BBCH-Skala_en.pdf`> for terrestrial vegetation and the Reef Health Index (RHI) framework (McField and Kramer, 2007) <`https://www.healthyreefs.org`> for marine ecosystems. This ensures scientific interoperability across archipelagic spatial models, aligning with global standards for ecological state-transition modeling (Schwartz, 2013) <doi:10.1007/978-94-007-6925-0>.

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URL `https://github.com/pinasr/palettephines`

BugReports `https://github.com/pinasr/palettephines/issues`

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Depends R (>= 4.1.0)

Imports ggplot2, graphics, grDevices

Suggests knitr, rmarkdown, sf, dplyr, sfdep, tidyr, roroph, rnaturalearth, rnaturalearthdata

VignetteBuilder knitr

X-schema.org-keywords data-visualization, philippine-biome, phenology

Repository https://pinasr.r-universe.dev

Date/Publication 2026-06-09 12:36:41 UTC

RemoteUrl https://github.com/pinasr/palettephines

RemoteRef HEAD

RemoteSha b653379a95b840bda0562670f48a3ba961be9bb1

Contents

`cite_phines` *Translate values to Phenological States*

Description

Translate values to Phenological States

Usage

```
cite_phines(palette, value)
```

Arguments

`palette`	Name of the palette.
`value`	A numeric value between 0 and 1.

Value

A `character string` representing the biological stage and scientific code (e.g., "Seedling (BBCH 10)"). This maps a normalized value to its ecological meaning.

Examples

```
cite_phines("palay_harvest", 0.8)
cite_phines("forest_transition", 0.2)
```

`phines` *Generate Phenological Palettes*

Description

Generate Phenological Palettes

Usage

```
phines(name, n = NULL, direction = 1)
```

Arguments

`name`	Palette name (palay_harvest, mangga_pico, coral_bleach, red_tide_watch, forest_transition)
`n`	Number of colors. If NULL, returns the anchor colors.
`direction`	1 for standard, -1 for reversed.

Value

A `character vector` of hex colors. If `n` is NULL, returns the original anchor colors; otherwise, returns an interpolated vector of length `n` for smooth gradients.

Examples

```
phines("palay_harvest", n = 5)
phines("mangga_pico", direction = -1)
```

`phines_metadata` *Philippine Phenological Palette Metadata*

Description

Internal list containing hex codes and scientific stages (BBCH, MSI, and ST-Mod).

Usage

```
phines_metadata
```

Format

An object of class `list` of length 5.

Value

A nested `list` where each element represents a palette containing vectors of colors, biological stages, and scientific codes.

`scale_fill_phines` *ggplot2 Scales for palettephines*

Description

ggplot2 Scales for palettephines

Usage

```
scale_fill_phines(palette = "palay_harvest", discrete = TRUE, ...)

scale_color_phines(palette = "palay_harvest", discrete = TRUE, ...)
```

Arguments

`palette`	Palette name.
`discrete`	Logical, if TRUE returns a discrete scale.
`...`	Passed to ggplot2 scale functions.

Value

A `ggplot2` scale object (class `ScaleDiscrete` or `ScaleContinuous`) to be added to a ggplot object. This maps data values to the phenological colors of the Philippines.

Examples

```
library(ggplot2)
ggplot(mtcars, aes(x = wt, y = mpg, fill = factor(cyl))) +
   geom_point(shape = 21, size = 3) +
   scale_fill_phines("palay_harvest")
```

`show_phines` *Visual Preview of Palettes*

Description

Visual Preview of Palettes

Usage

```
show_phines(name)
```

Arguments

`name`	Palette name.

Value

No return value, called for side effects. This function generates a plot in the active graphics device showing the color blocks of the palette.

Examples

```
# Use oldpar to respect user's graphical settings
oldpar <- par(no.readonly = TRUE)
show_phines("coral_bleach")
par(oldpar)
```

Index