Package: charisma (via r-universe)

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Type Package

Title Reproducible Color Characterization of Digital Images for Biological Studies

Version 1.0.0

Description Provides a standardized and reproducible framework for characterizing and classifying discrete color classes from digital images of biological organisms. The package automatically determines the presence or absence of 10 human-visible color categories (black, blue, brown, green, grey, orange, purple, red, white, yellow) using a biologically-inspired Color Look-Up Table (CLUT) that partitions HSV color space. Supports both fully automated and semi-automated (interactive) workflows with complete provenance tracking for reproducibility. Pre-processes images using the 'recolorize' package (Weller et al. 2024 <doi:10.1111/ele.14378>) for spatial-color binning, and integrates with 'pavo' (Maia et al. 2019 <doi:10.1111/2041-210X.13174>) for color pattern geometry statistics. Designed for high-throughput analysis and seamless integration with downstream evolutionary analyses.

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URL https://github.com/shawntz/charisma, https://shawnschwartz.com/charisma/

BugReports https://github.com/shawntz/charisma/issues

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LazyData true

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Contents

`charisma` *Characterize color classes in biological images*

Description

The primary function of `charisma` is to characterize the distribution of human-visible color classes present in an image. This function provides a standardized and reproducible framework for classifying colors into discrete categories using a biologically-inspired Color Look-Up Table (CLUT).

Usage

```
charisma(
  img_path,
  threshold = 0,
  auto.drop = TRUE,
  interactive = FALSE,
  plot = FALSE,
  pavo = TRUE,
  logdir = NULL,
```

```
  stack_colors = TRUE,
  bins = 4,
  cutoff = 20,
  k.override = NULL,
  clut = charisma::clut
)
```

Arguments

`img_path`	Character string specifying the path to an image file, or a `recolorize` object (for use with `charisma2`).
`threshold`	Numeric value between 0 and 1 specifying the minimum proportion of pixels required for a color to be retained. Colors with proportions below this threshold are automatically removed. Default is 0.0 (retain all colors).
`auto.drop`	Logical. If `TRUE`, automatically removes the background layer (layer 0) from color counts. Default is `TRUE`.
`interactive`	Logical. If `TRUE`, enables manual intervention for color merging and replacement operations. Saves all states for full reproducibility. Default is `FALSE`.
`plot`	Logical. If `TRUE`, generates diagnostic plots during processing. Default is `FALSE`.
`pavo`	Logical. If `TRUE`, computes color pattern geometry statistics using the **pavo** package. Default is `TRUE`.
`logdir`	Character string specifying the directory path for saving output files. If provided, saves timestamped .RDS (charisma object) and .PDF (diagnostic plots) files. Default is `NULL` (no files saved).
`stack_colors`	Logical. If `TRUE`, stacks color proportions in plots. Default is `TRUE`.
`bins`	Integer specifying the number of bins for each RGB channel in the histogram method. Default is 4 (resulting in 4^3 = 64 cluster centers).
`cutoff`	Numeric value specifying the Euclidean distance threshold for combining similar color clusters. Default is 20.
`k.override`	Integer to force a specific number of color clusters, bypassing automatic detection. Default is `NULL`.
`clut`	Data frame containing the Color Look-Up Table with HSV boundaries for each color class. Default is `charisma::clut` (10 human-visible colors: black, blue, brown, green, grey, orange, purple, red, white, yellow).

Details

The `charisma` pipeline consists of three main stages:

1. **Image preprocessing**: Uses `recolorize::recolorize2()` to perform spatial-color binning, removing noisy pixels and creating a smoothed representation of dominant colors.
2. **Color classification**: Converts RGB cluster centers to HSV color space and matches them against non-overlapping HSV ranges defined in the CLUT using `charisma::color2label()`.
3. **Optional manual curation**: In interactive mode, users can merge color clusters (e.g., c(2,3)) or replace pixels between clusters to refine classifications.

The workflow can be run fully autonomously or with varying degrees of manual intervention. All operations are logged for complete reproducibility.

Value

A `charisma` object (list) containing:

`centers`	RGB cluster centers
`pixel_assignments`	Pixel-to-cluster mapping
`classification`	Discrete color labels from CLUT
`color_mask_LUT`	Mapping of clusters to averaged colors
`color_mask_LUT_filtered`	Color mapping after threshold applied
`merge_history`	Record of all merge operations performed
`replacement_history`	Record of all replacement operations performed
`merge_states`	List of charisma states after each merge
`replacement_states`	List of charisma states after each replacement
`pavo_stats`	Color pattern geometry metrics (if pavo = TRUE)
`prop_threshold`	Threshold value used
`path`	Path to original image
`logdir`	Directory where outputs were saved
`auto_drop`	Value of auto.drop parameter
`bins`	Value of bins parameter
`cutoff`	Value of cutoff parameter
`clut`	CLUT used for classification
`stack_colors`	Value of stack_colors parameter

References

Schwartz, S.T., Tsai, W.L.E., Karan, E.A., Juhn, M.S., Shultz, A.J., McCormack, J.E., Smith, T.B., and Alfaro, M.E. (2025). charisma: An R package to perform reproducible color characterization of digital images for biological studies. (In Review).

Weller, H.I., Hiller, A.E., Lord, N.P., and Van Belleghem, S.M. (2024). **recolorize**: An R package for flexible colour segmentation of biological images. Ecology Letters, 27(2):e14378.

See Also

`charisma2` for re-analyzing saved charisma objects, `color2label` for RGB to color label conversion, `validate` for CLUT validation, `plot.charisma` for visualization

Examples

```
# Basic usage with example image
img <- system.file("extdata", "Tangara_fastuosa_LACM60421.png",
                   package = "charisma")
result <- charisma(img)

# With threshold to remove minor colors
result <- charisma(img, threshold = 0.05)

# Save outputs to directory
out_dir <- file.path(tempdir(), "charisma_outputs")
result <- charisma(img, threshold = 0.05, logdir = out_dir)

# View results
plot(result)


# Interactive mode with manual curation (only runs in interactive sessions)
if (interactive()) {
  img <- system.file("extdata", "Tangara_fastuosa_LACM60421.png",
                     package = "charisma")
  result <- charisma(img, interactive = TRUE, threshold = 0.0)
}
```

`charisma2` *Re-analyze and edit saved charisma objects*

Description

The `charisma2` function allows users to step through and edit previously saved `charisma` objects. This function enables rewinding to specific merge or replacement states, applying different thresholds, or continuing interactive editing from any saved state, ensuring full reproducibility of the analysis.

Usage

```
charisma2(
  charisma.obj,
  interactive = TRUE,
  new.threshold = NULL,
  which.state = c("none", "merge", "replace"),
  state.index = NULL,
  k.override = NULL
)
```

Arguments

charisma.obj	A charisma object to be re-analyzed. Cannot be a charisma2 object (attempting to run charisma2 on a charisma2 object will produce an error).
interactive	Logical. If TRUE, enters interactive mode for manual color adjustments. Default is TRUE.
new.threshold	Numeric value between 0 and 1 to apply a different color proportion threshold than the original analysis. If NULL, uses the original threshold. Default is NULL.
which.state	Character string specifying which state to revert to. Options are "none" (most recent state), "merge" (specific merge state), or "replace" (specific replacement state). Default is "none".
state.index	Integer specifying which state index to revert to when which.state is "merge" or "replace". Must be provided if which.state is not "none". Default is NULL.
k.override	Integer to force a specific number of color clusters. Default is NULL.

Details

The charisma2 function provides powerful state management capabilities:

- **State rewinding**: Jump to any previous merge or replacement state
- **Re-thresholding**: Apply different color proportion thresholds without re-running the entire pipeline
- **Continued editing**: Resume interactive editing from saved states
- **Full provenance**: All operations maintain complete history for reproducibility

Note: Interactive adjustment of merge states is disabled if replacement states exist, as replacement operations depend on post-merge cluster indices.

Value

A charisma2 object (also of class charisma) containing the same structure as a charisma object, with updated states based on the specified reversion point and any new operations performed.

References

Schwartz, S.T., Tsai, W.L.E., Karan, E.A., Juhn, M.S., Shultz, A.J., McCormack, J.E., Smith, T.B., and Alfaro, M.E. (2025). charisma: An R package to perform reproducible color characterization of digital images for biological studies. (In Review).

See Also

charisma for initial color classification, plot.charisma for visualization

Examples

```
# Load a previously saved charisma object
obj <- system.file("extdata", "Tangara_fastuosa.RDS", package = "charisma")
obj <- readRDS(obj)

## Not run:
# Examples that require objects with merge/replacement states
# (These examples show the syntax but won't run with the provided test data)

# Revert to a specific merge state (if merge states exist)
if (length(obj$merge_states) >= 2) {
  result <- charisma2(obj, which.state = "merge", state.index = 2)
}

# Revert to a specific replacement state (if replacement states exist)
if (length(obj$replacement_states) >= 1) {
  result <- charisma2(obj, which.state = "replace", state.index = 1)
}

# Re-enter interactive mode with original threshold
obj <- system.file("extdata", "Tangara_fastuosa.RDS", package = "charisma")
obj <- readRDS(obj)
result <- charisma2(obj, interactive = TRUE)

## End(Not run)
```

---

clut *Default Color (Labels) Look Up Table (CLUT)*

Description

This LUT contains all color boundaries which cut up the continuous HSV color space into 10 discrete color labels (i.e., black, white, grey, brown, red, orange, yellow, green, blue, and purple).

Usage

```
clut
```

Format

A data frame with color boundary definitions for HSV color space. Each row defines the HSV ranges for a specific discrete color category.

Details

These color boundaries were determined by forming consensus across three experts in the biology of color. Color boundaries were intentionally tuned to reflect accurate color label classifications for images of various bird and fish museum specimens.

Although we attempted to determine color boundaries in an object fashion, there are of course perceptual biases and variability across computer models/ displays that can influence whether any given color at the boundary of the continuous color space is ultimately called one color over another.

Accordingly, we gladly welcome further optimization of the default color LUT and/or submissions of color LUTS specifically tuned to any given organism or stimulus. Leveraging contributions from the community will only help `charisma` be more useful for everybody who would like to use it!

See Also

`charisma` for the main classification pipeline, `validate` for CLUT validation

Examples

```
# View the default CLUT
head(clut)
```

`color2label` *Convert RGB color triplets to discrete color labels*

Description

This function classifies an RGB color triplet into one of the discrete color categories defined in the Color Look-Up Table (CLUT) by testing for membership within non-overlapping HSV ranges.

Usage

```
color2label(color_triplet, verbose = FALSE, clut = charisma::clut)
```

Arguments

`color_triplet`	Numeric vector of length 3 containing RGB values (0-255 scale). The vector should be c(red, green, blue).
`verbose`	Logical. If `TRUE`, prints the color triplet and classification results for debugging. Default is `FALSE`.
`clut`	Data frame containing the Color Look-Up Table with HSV boundaries for each color class. Default is `charisma::clut`.

Details

The classification process involves:

1. Converting RGB to HSV (using `rgb2hsv`)
2. Scaling HSV to match CLUT ranges (H: 0-360, S: 0-100, V: 0-100)
3. Testing the HSV coordinate against all color definitions in the CLUT
4. Returning the single matching color label

Each color in the CLUT has non-overlapping HSV ranges that partition the entire HSV color space. If multiple matches occur, a warning is issued as this indicates overlapping color boundaries in the CLUT.

Value

Character string indicating the matched color label from the CLUT. Returns "NA" if the input contains NA values.

References

Schwartz, S.T., Tsai, W.L.E., Karan, E.A., Juhn, M.S., Shultz, A.J., McCormack, J.E., Smith, T.B., and Alfaro, M.E. (2025). charisma: An R package to perform reproducible color characterization of digital images for biological studies. (In Review).

See Also

charisma for the main classification pipeline, validate for CLUT validation

Examples

```
# Classify a blue RGB color
color2label(c(0, 0, 255))

# Classify a red RGB color
color2label(c(255, 0, 0))

# Verbose output for debugging
color2label(c(128, 128, 128), verbose = TRUE)
```

---

launch_clut_editor *Launch the CLUT Editor*

Description

Opens the interactive Color Lookup Table (CLUT) Editor in your web browser. The CLUT Editor allows you to visually design and customize HSV color space partitions for color classification, with 3D visualizations and coverage statistics.

Usage

```
launch_clut_editor(online = TRUE)
```

Arguments

online	Logical. If TRUE (default), opens the hosted version at https://charisma.shawnschwartz.com/app. If FALSE, opens the local version bundled with the package.

Details

The CLUT Editor provides:

- Visual editing of HSV color space boundaries for each color category
- Real-time coverage statistics showing gaps and overlaps
- Multiple visualization modes: hue slices, 3D cone, 3D scatter, hue wheel
- Export to R code or JSON for use with `charisma()`
- Import/export functionality for sharing custom CLUTs

Custom CLUTs created with the editor can be validated using `validate()` and then used in `charisma()` analyses via the `clut` parameter.

Value

Invisibly returns the URL that was opened. Called primarily for its side effect of opening the CLUT Editor in the default web browser.

See Also

`validate` for validating custom CLUTs, `charisma` for using custom CLUTs in analyses, `clut` for the default Color Look-Up Table

Examples

```
## Not run:
# Open the online CLUT Editor (recommended)
launch_clut_editor()

# Open the local version bundled with the package
launch_clut_editor(online = FALSE)

## End(Not run)
```

`mosaic` *Create a color mosaic visualization from color proportions*

Description

This function generates a randomized mosaic grid visualization representing the proportions of different colors, useful for visually displaying color composition in a standardized format.

Usage

```
mosaic(
  color.props,
  size = 10,
  out.path = normalizePath("~"),
  out.prefix = "charisma_mosaic",
  verbose = TRUE
)
```

Arguments

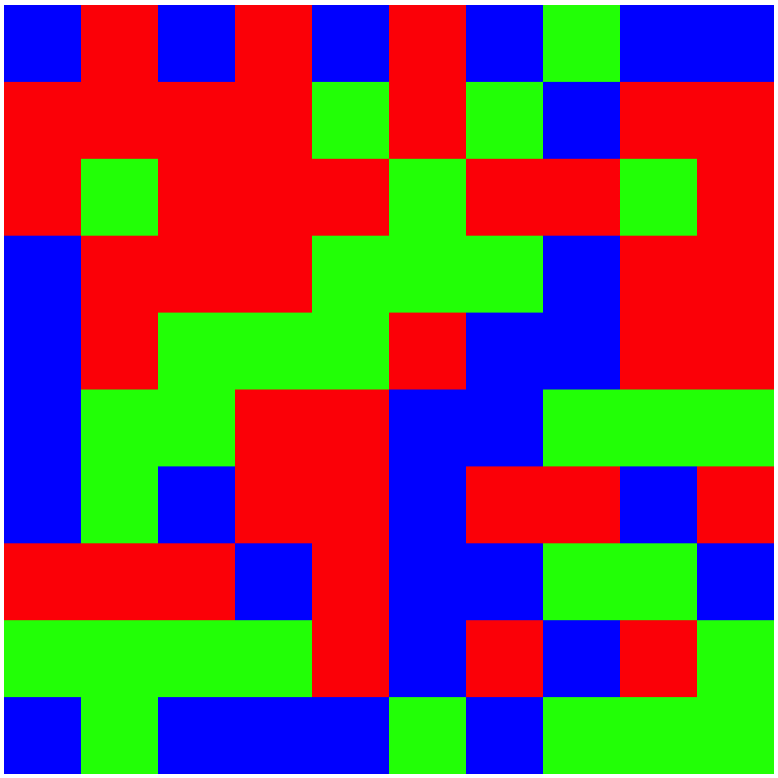
`color.props`	List of color proportion objects, where each element contains: • `hex`: Hex color code (e.g., "#FF0000") • `color`: Color name • `prop`: Proportion value (all proportions must sum to 1)
`size`	Integer specifying the dimensions of the mosaic grid (size x size). Default is 10 (resulting in a 10 x 10 = 100 cell mosaic).
`out.path`	Character string specifying the directory path for saving the output PNG file. Default is the user's home directory.
`out.prefix`	Character string prefix for the output filename. Default is `"charisma_mosaic"`.
`verbose`	Logical. If `TRUE`, prints the full output path. Default is `TRUE`.

Details

The mosaic function creates a visual representation of color proportions by:

1. Allocating grid cells proportional to each color's proportion
2. Randomly shuffling cell positions to create a mosaic pattern
3. Saving the result as a PNG file with an informative filename

The output filename automatically encodes the hex codes, color names, and proportions for documentation purposes.



Value

Character string containing the full path to the saved PNG file.

See Also

charisma for generating color classifications

Examples

```
# Create a mosaic from color proportions
colors <- list(
  list(hex = "#FF0000", color = "red", prop = 0.4),
  list(hex = "#00FF00", color = "green", prop = 0.3),
  list(hex = "#0000FF", color = "blue", prop = 0.3)
)
mosaic(colors, size = 10, out.path = tempdir())
```

---

plot.charisma *Plot method for charisma objects*

Description

This function creates visualizations of color classification results from a charisma analysis. It can display the original image, recolored image, masked image, color proportions, and pavo color pattern geometry results.

Usage

```
## S3 method for class 'charisma'
plot(
  x,
  plot.all = TRUE,
  plot.original = FALSE,
  plot.recolored = FALSE,
  plot.masked = FALSE,
  plot.props = FALSE,
  plot.pavo.img = FALSE,
  plot.pavo.classes = FALSE,
  font.size = 1.75,
  props.x.cex = 1.5,
  real.bar.colors = TRUE,
  ...
)
```

Arguments

`x`	A charisma object (output from `charisma` or `charisma2`).
`plot.all`	Logical. If `TRUE`, plots all available visualizations. Default is `TRUE`.
`plot.original`	Logical. If `TRUE`, plots the original image. Default is `FALSE`.
`plot.recolored`	Logical. If `TRUE`, plots the recolored image showing discrete color classifications. Default is `FALSE`.
`plot.masked`	Logical. If `TRUE`, plots the masked image after background removal. Default is `FALSE`.
`plot.props`	Logical. If `TRUE`, plots a bar chart showing the proportion of pixels in each color category. Default is `FALSE`.
`plot.pavo.img`	Logical. If `TRUE`, plots the image used for **pavo** color pattern geometry analysis. Default is `FALSE`. Only available if pavo analysis was performed.
`plot.pavo.classes`	Logical. If `TRUE`, plots the color palette from **pavo** k-means clustering. Default is `FALSE`. Only available if pavo analysis was performed.
`font.size`	Numeric. Size multiplier for plot text elements. Default is `1.75`.
`props.x.cex`	Numeric. Size multiplier for x-axis labels in the proportions plot. Default is `1.5`.
`real.bar.colors`	Logical. If `TRUE`, uses actual color values for bars in the proportions plot. If `FALSE`, uses a default color scheme. Default is `TRUE`.
`...`	Additional arguments (currently not used).

Details

When `plot.all = TRUE`, all available plots are displayed in a multi-panel layout. Individual plots can be selected by setting the corresponding `plot.*` parameters to `TRUE`.

The function automatically detects whether **pavo** analysis results are present in the charisma object and adjusts the plot layout accordingly.

Value

This function is called for its side effects (creating plots) and does not return a value.

See Also

`charisma` for the main classification pipeline, `charisma2` for batch processing

Examples

```
# Run charisma on an image
img <- system.file("extdata", "Tangara_fastuosa_LACM60421.png",
                   package = "charisma")
result <- charisma(img)

# Plot all results
plot(result)

# Plot only original and recolored images
plot(result, plot.all = FALSE, plot.original = TRUE, plot.recolored = TRUE)

# Plot color proportions
plot(result, plot.all = FALSE, plot.props = TRUE)
```

---

summarize *Summarize color classification results*

Description

This function takes a charisma object and produces a summary table showing the proportion of pixels classified into each discrete color category.

Usage

```
summarize(charisma_obj)

summarise(charisma_obj)
```

Arguments

charisma_obj	A charisma object (output from charisma or charisma2) containing color classification results.

Details

The summary table shows the percentage of pixels classified into each of the discrete color categories defined in the Color Look-Up Table (CLUT). This provides a quantitative overview of the color composition of the analyzed image.

Value

A data frame with one row per image showing the proportion of pixels assigned to each color category. Row names are set to the basename of the image file path.

See Also

charisma for the main classification pipeline, validate for CLUT validation

Examples

```
# Run charisma on an image
img <- system.file("extdata", "Tangara_fastuosa_LACM60421.png",
                   package = "charisma")
result <- charisma(img)

# Summarize the color classification results
summary_table <- summarize(result)
print(summary_table)
```

---

validate *Validate Color Look-Up Table completeness*

Description

This function validates that a Color Look-Up Table (CLUT) provides complete and non-overlapping coverage of the HSV color space by testing every HSV coordinate against the CLUT definitions. Validation ensures each color maps to exactly one color class.

Usage

```
validate(clut = charisma::clut, simple = TRUE)
```

Arguments

clut	Data frame containing the Color Look-Up Table with HSV boundaries for each color class. Default is charisma::clut.
simple	Logical. If TRUE (default), tests a reduced HSV space with 1-degree increments (361 x 101 x 101 = 3,682,561 coordinates). If FALSE, uses finer 0.5-degree increments, which is more thorough but significantly slower and best suited for cluster computing.

Details

The validation process:

1. Generates a complete grid of HSV color space coordinates
2. Uses parallel processing (all available cores - 1) to classify each coordinate using the CLUT definitions
3. Checks that each coordinate maps to exactly one color class
4. Reports any missing or duplicate classifications

Validation is essential when modifying the CLUT or creating custom CLUTs for different image datasets. The process can take several minutes even with simple = TRUE.

Value

If validation passes, returns 0 and prints a success message. If validation fails, returns a data frame containing all HSV coordinates that either: (1) were not classified to any color, or (2) were classified to multiple colors (indicating overlap).

References

Schwartz, S.T., Tsai, W.L.E., Karan, E.A., Juhn, M.S., Shultz, A.J., McCormack, J.E., Smith, T.B., and Alfaro, M.E. (2025). charisma: An R package to perform reproducible color characterization of digital images for biological studies. (In Review).

See Also

charisma for using validated CLUTs, color2label for color classification

Examples

```
## Not run:
# Validate the default CLUT (takes several minutes with parallel processing)

# Note: These examples are not run during R CMD check due to CRAN build
# limitations. With only 2 cores available during CRAN checks, validation
# can exceed 20 minutes.

result <- validate()

# Validate a custom CLUT
```

```
my_clut <- charisma::clut  # Start with default
# ... modify my_clut ...
result <- validate(clut = my_clut)

# More thorough validation (much slower, recommended for cluster computing)
result <- validate(simple = FALSE)

## End(Not run)
```

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