

# Package ‘charisma’

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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](https://doi.org/10.1111/ele.14378)>) for spatial-color binning, and integrates with 'pavo' (Maia et al. 2019 <[doi:10.1111/2041-210X.13174](https://doi.org/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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**Author** Shawn Schwartz [aut, cre, cph] (ORCID: <https://orcid.org/0000-0001-6444-8451>),  
 Whitney Tsai [aut] (ORCID: <https://orcid.org/0000-0003-3274-2829>),  
 Elizabeth Karan [aut] (ORCID: <https://orcid.org/0000-0003-1942-0307>),  
 Mark Juhn [aut],  
 Allison Shultz [aut] (ORCID: <https://orcid.org/0000-0002-2089-4086>),  
 John McCormack [aut] (ORCID: <https://orcid.org/0000-0002-0912-1461>),  
 Thomas Smith [aut] (ORCID: <https://orcid.org/0000-0002-5978-6912>),  
 Michael Alfaro [aut] (ORCID: <https://orcid.org/0000-0002-8898-8230>)

**Maintainer** Shawn Schwartz <shawn.t.schwartz@gmail.com>

**Repository** CRAN

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## Contents

charisma . . . . .	2
charisma2 . . . . .	5
clut . . . . .	7
color2label . . . . .	8
mosaic . . . . .	9
plot.charisma . . . . .	11
summarize . . . . .	13
validate . . . . .	14

<b>Index</b>	<b>16</b>
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charisma	<i>Characterize color classes in biological images</i>
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## 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

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

## Details

The `charisma` pipeline consists of three main stages:

- Image preprocessing:** Uses `recolorize::recolorize2()` to perform spatial-color binning, removing noisy pixels and creating a smoothed representation of dominant colors.
- 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()`.
- 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

<code>charisma.obj</code>	A charisma object to be re-analyzed. Cannot be a charisma2 object (attempting to run charisma2 on a charisma2 object will produce an error).
<code>interactive</code>	Logical. If TRUE, enters interactive mode for manual color adjustments. Default is TRUE.
<code>new.threshold</code>	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.
<code>which.state</code>	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".
<code>state.index</code>	Integer specifying which state index to revert to when <code>which.state</code> is "merge" or "replace". Must be provided if <code>which.state</code> is not "none". Default is NULL.
<code>k.override</code>	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	<i>Convert RGB color triplets to discrete color labels</i>
-------------	--

---

### 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 <code>charisma::clut</code> .

### 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)
```

---

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

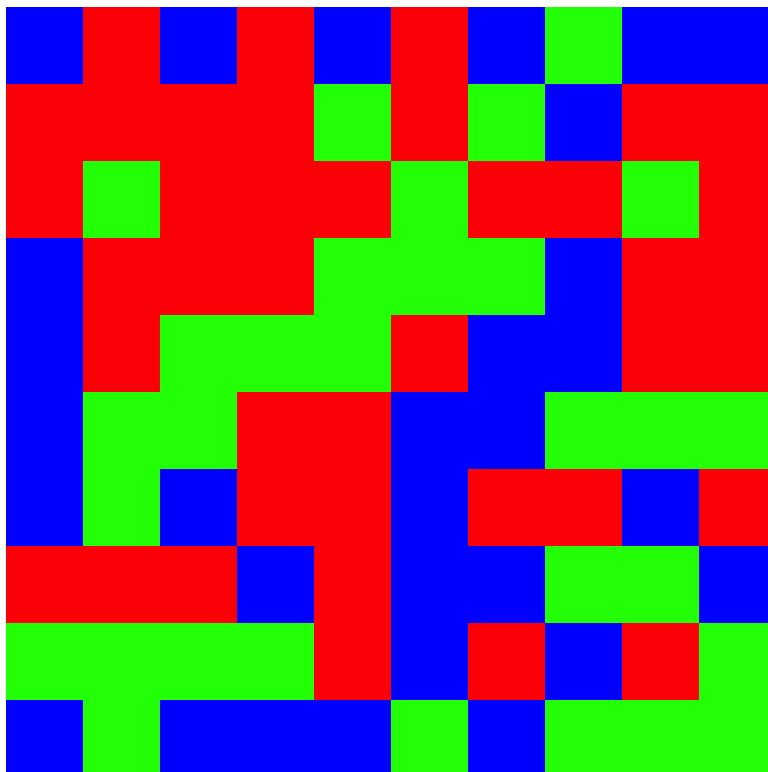
<code>color.props</code>	List of color proportion objects, where each element contains: <ul style="list-style-type: none"><li>• <code>hex</code>: Hex color code (e.g., "#FF0000")</li><li>• <code>color</code>: Color name</li><li>• <code>prop</code>: Proportion value (all proportions must sum to 1)</li></ul>
<code>size</code>	Integer specifying the dimensions of the mosaic grid ( <code>size x size</code> ). Default is 10 (resulting in a 10 x 10 = 100 cell mosaic).
<code>out.path</code>	Character string specifying the directory path for saving the output PNG file. Default is the user's home directory.
<code>out.prefix</code>	Character string prefix for the output filename. Default is "charisma_mosaic".
<code>verbose</code>	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

<code>x</code>	A charisma object (output from <code>charisma</code> or <code>charisma2</code> ).
<code>plot.all</code>	Logical. If TRUE, plots all available visualizations. Default is TRUE.
<code>plot.original</code>	Logical. If TRUE, plots the original image. Default is FALSE.
<code>plot.recolored</code>	Logical. If TRUE, plots the recolored image showing discrete color classifications. Default is FALSE.
<code>plot.masked</code>	Logical. If TRUE, plots the masked image after background removal. Default is FALSE.
<code>plot.props</code>	Logical. If TRUE, plots a bar chart showing the proportion of pixels in each color category. Default is FALSE.
<code>plot.pavo.img</code>	Logical. If TRUE, plots the image used for <b>pavo</b> color pattern geometry analysis. Default is FALSE. Only available if pavo analysis was performed.
<code>plot.pavo.classes</code>	Logical. If TRUE, plots the color palette from <b>pavo</b> k-means clustering. Default is FALSE. Only available if pavo analysis was performed.
<code>font.size</code>	Numeric. Size multiplier for plot text elements. Default is 1.75.
<code>props.x.cex</code>	Numeric. Size multiplier for x-axis labels in the proportions plot. Default is 1.5.
<code>real.bar.colors</code>	Logical. If TRUE, uses actual color values for bars in the proportions plot. If FALSE, uses a default color scheme. Default is TRUE.
<code>...</code>	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 <code>charisma::clut</code> .
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)
```

# Index

## \* datasets

clut, 7

charisma, 2, 6, 8, 9, 11–13, 15

charisma2, 4, 5, 12, 13

clut, 7

color2label, 4, 8, 15

mosaic, 9

plot.charisma, 4, 6, 11

recolorize::recolorize2(), 3

summarise (summarize), 13

summarize, 13

validate, 4, 8, 9, 13, 14