Package ‘rphylopic’

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Title  Get Silhouettes of Organisms from PhyloPic

Description  Work with the PhyloPic Web Service (<http://api-docs.phylopic.org/v2/>)

to fetch silhouette images of organisms. Includes functions for adding
silhouettes to both base R plots and ggplot2 plots.

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    https://palaeoverse.org

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Description

Specify existing images, taxonomic names, or PhyloPic uuids to add PhyloPic silhouettes as a separate layer to an existing ggplot plot.

Usage

```r
add_phylopic(
  img = NULL,
  name = NULL,
  uuid = NULL,
  filter = NULL,
  x,
  y,
  ysize = Inf,
  alpha = 1,
  color = NA,
  fill = "black",
  horizontal = FALSE,
  vertical = FALSE,
  angle = 0,
  remove_background = TRUE,
  verbose = FALSE
)
```
**add_phylopic**

**Arguments**

- **img**
  A Picture or png array object, e.g., from using `get_phylopic()`.

- **name**
  character. A taxonomic name to be passed to `get_uuid()`.

- **uuid**
  character. A valid uuid for a PhyloPic silhouette (such as that returned by `get_uuid()` or `pick_phylopic()`).

- **filter**
  character. Filter by usage license if name is defined. Use "by" to limit results to images which do not require attribution, "nc" for images which allows commercial usage, and "sa" for images without a ShareAlike clause. The user can also combine these filters as a vector.

- **x**
  numeric. x value of the silhouette center.

- **y**
  numeric. y value of the silhouette center.

- **ysize**
  numeric. Height of the silhouette. The width is determined by the aspect ratio of the original image. If "Inf", the default, the height will be as tall as will fit within the plot area.

- **alpha**
  numeric. A value between 0 and 1, specifying the opacity of the silhouette (0 is fully transparent, 1 is fully opaque).

- **color**
  character. Color of silhouette outline. If "original" or NA is specified, the original color of the silhouette outline will be used (usually the same as "transparent"). To remove the outline, you can set this to "transparent".

- **fill**
  character. Color of silhouette. If "original" is specified, the original color of the silhouette will be used (usually the same as "black"). If color is specified and fill is NA, color will be used as the fill color (for backwards compatibility). To remove the fill, you can set this to "transparent".

- **horizontal**
  logical. Should the silhouette be flipped horizontally?

- **vertical**
  logical. Should the silhouette be flipped vertically?

- **angle**
  numeric. The number of degrees to rotate the silhouette clockwise. The default is no rotation.

- **remove_background**
  logical. Should any white background be removed from the silhouette(s)? See `recolor_phylopic()` for details.

- **verbose**
  logical. Should the attribution information for the used silhouette(s) be printed to the console (see `get_attribution()`)?

**Details**

One (and only one) of img, name, or uuid must be specified. Use parameters x, y, and ysize to place the silhouette at a specified position on the plot. The aspect ratio of the silhouette will always be maintained.

x and/or y may be vectors of numeric values if multiple silhouettes should be plotted at once. In this case, any other arguments (except for remove_background) may also be vectors of values, which will be recycled as necessary.

When specifying a horizontal and/or vertical flip and a rotation, the flip(s) will always occur first. If you would like to customize this behavior, you can flip and/or rotate the image within your own workflow using `flip_phylopic()` and `rotate_phylopic()`.
Note that png array objects can only be rotated by multiples of 90 degrees. Also, outline colors do not currently work for png array objects.

Examples

```r
# Not run:
# Put a silhouette behind a plot based on a taxonomic name
library(ggplot2)
ggplot(iris) +
  add_phylopic(x = 6.1, y = 3.2, name = "Iris", alpha = 0.2) +
  geom_point(aes(x = Sepal.Length, y = Sepal.Width))

# Put a silhouette in several places based on UUID
posx <- runif(10, 0, 10)
posy <- runif(10, 0, 10)
sizexy <- runif(10, 0.4, 2)
angle <- runif(10, 0, 360)
hor <- sample(c(TRUE, FALSE), 10, TRUE)
ver <- sample(c(TRUE, FALSE), 10, TRUE)
fills <- sample(c("black", "darkorange", "grey42", "white"), 10,
  replace = TRUE)
alpha <- runif(10, 0.3, 1)
p <- ggplot(data.frame(cat.x = posx, cat.y = posy), aes(cat.x, cat.y)) +
  geom_blank() +
  add_phylopic(uuid = "23cd6aa4-9587-4a2e-8e26-de42885004c9",
    x = posx, y = posy, ysize = sizexy,
    fill = fills, alpha = alpha, angle = angle,
    horizontal = hor, vertical = ver)
p + ggtitle("R Cat Herd!!")
```

Description

Specify existing images, taxonomic names, or PhyloPic uuids to add PhyloPic silhouettes on top of an existing base R plot (like `points()`).

Usage

```r
add_phylopic_base(
  img = NULL,
  name = NULL,
  uuid = NULL,
  filter = NULL,
  x = NULL,
  y = NULL,
  ysize = NULL,
  fill = NULL,
  alpha = NULL,
  angle = NULL,
  horizontal = FALSE,
  vertical = FALSE)
```

Arguments

**img**
A `Picture` or png array object, e.g., from using `get_phylopic()`.

**name**
character. A taxonomic name to be passed to `get_uuid()`.

**uuid**
character. A valid uuid for a PhyloPic silhouette (such as that returned by `get_uuid()` or `pick_phylopic()`).

**filter**
character. Filter by usage license if `name` is defined. Use "by" to limit results to images which do not require attribution, "nc" for images which allows commercial usage, and "sa" for images without a ShareAlike clause. The user can also combine these filters as a vector.

**x**
numeric. x value of the silhouette center. Ignored if `y` and `ysize` are not specified.

**y**
numeric. y value of the silhouette center. Ignored if `x` and `ysize` are not specified.

**ysize**
numeric. Height of the silhouette. The width is determined by the aspect ratio of the original image. Ignored if `x` and `y` are not specified.

**alpha**
numeric. A value between 0 and 1, specifying the opacity of the silhouette (0 is fully transparent, 1 is fully opaque).

**color**
character. Color of silhouette outline. If "original" or NA is specified, the original color of the silhouette outline will be used (usually the same as "transparent"). To remove the outline, you can set this to "transparent".

**fill**
character. Color of silhouette. If "original" is specified, the original color of the silhouette will be used (usually the same as "black"). If color is specified and fill is NA, color will be used as the fill color (for backwards compatibility). To remove the fill, you can set this to "transparent".

**horizontal**
logical. Should the silhouette be flipped horizontally?

**vertical**
logical. Should the silhouette be flipped vertically?

**angle**
numeric. The number of degrees to rotate the silhouette clockwise. The default is no rotation.

**remove_background**
logical. Should any white background be removed from the silhouette(s)? See `recolar_phylopic()` for details.

**verbose**
logical. Should the attribution information for the used silhouette(s) be printed to the console (see `get_attribution()`)?
add_phylopic_base

Details

One (and only one) of img, name, or uuid must be specified. Use parameters x, y, and ysize to place the silhouette at a specified position on the plot. If all three of these parameters are unspecified, then the silhouette will be plotted to the full height and width of the plot. The aspect ratio of the silhouette will always be maintained (even when a plot is resized). However, if the plot is resized after plotting the silhouette, the absolute size and/or position of the silhouette may change.

Any argument (except for remove_background) may be a vector of values if multiple silhouettes should be plotted. In this case, all other arguments may also be vectors of values, which will be recycled as necessary to the length of the longest vector argument.

When specifying a horizontal and/or vertical flip and a rotation, the flip(s) will always occur first. If you would like to customize this behavior, you can flip and/or rotate the image within your own workflow using flip_phylopic() and rotate_phylopic().

Note that png array objects can only be rotated by multiples of 90 degrees. Also, outline colors do not currently work for png array objects.

Examples

```r
## Not run:
# single image
plot(1, 1, type = "n", main = "A cat")
add_phylopic_base(uuid = "23cd6aa4-9587-4a2e-8e26-de42885004c9",
x = 1, y = 1, ysize = 0.4)

# lots of images using a uuid
posx <- runif(10, 0, 1)
posy <- runif(10, 0, 1)
size <- runif(10, 0.1, 0.3)
angle <- runif(10, 0, 360)
hor <- sample(c(TRUE, FALSE), 10, TRUE)
ver <- sample(c(TRUE, FALSE), 10, TRUE)
fills <- sample(c("black", "darkorange", "grey42", "white"), 10, replace = TRUE)
plot(posx, posy, type = "n", main = "A cat herd")
add_phylopic_base(uuid = "23cd6aa4-9587-4a2e-8e26-de42885004c9",
x = posx, y = posy, ysize = size,
fill = fills, angle = angle,
horizontal = hor, vertical = ver)

# Example using a cat background
cat <- get_phylopic("23cd6aa4-9587-4a2e-8e26-de42885004c9")
# setup plot area
plot(posx, posy, type = "n", main = "A cat herd, on top of a cat",
xlim = c(0, 1), ylim = c(0, 1))
# plot background cat
add_phylopic_base(img = cat, alpha = 0.2)
# overlay smaller cats
add_phylopic_base(img = cat, x = posx, y = posy, ysize = size, alpha = 0.8)

## End(Not run)
```
add_phylopic_legend

Add a PhyloPic legend for a base R plot

Description

Specify existing images, taxonomic names, or PhyloPic uuids to add PhyloPic silhouettes as a legend to an existing base R plot (like `legend()`).

Usage

```r
add_phylopic_legend(
  x,
  y = NULL,
  legend,
  img = NULL,
  name = NULL,
  uuid = NULL,
  ysize = NULL,
  color = NA,
  fill = "black",
  ...
)
```

Arguments

- **x** numeric or character. Either the x coordinate to be used to position the legend or a keyword accepted by `legend()` such as "topleft", "topright", "bottomleft", and "bottomright".
- **y** numeric. The y coordinate to be used to position the legend. Can be NULL (default) if using keywords in x.
- **legend** character. A character vector of the labels to appear in the legend.
- **img** A Picture or png array object, e.g., from using `get_phylopic()`.
- **name** character. A taxonomic name to be passed to `get_uuid()`.
- **uuid** character. A valid uuid for a PhyloPic silhouette (such as that returned by `get_uuid()` or `pick_phylopic()`).
- **ysize** numeric. Height of the legend silhouette(s). The width is determined by the aspect ratio of the original image.
- **color** character. Color of silhouette outline. If "original" or NA is specified, the original color of the silhouette outline will be used (usually the same as "transparent"). To remove the outline, you can set this to "transparent".
- **fill** character. Color of silhouette. If "original" is specified, the original color of the silhouette will be used (usually the same as "black"). If color is specified and fill is NA, color will be used as the fill color (for backwards compatibility). To remove the fill, you can set this to "transparent".
- **...** Additional arguments passed to `legend()`.
Details
This function can be used to add PhyloPic silhouettes as a legend to a base R plot. Arguments available in `legend()` can be used and passed via `. . .`. Note that not all arguments in `legend()` are compatible with `add_phylopic_legend()`. These include arguments for modifying lines (e.g. `lty`, `lwd`, `seg.len`), points (e.g. `pch`, `pt.lwd`), and shading (e.g. `angle` and `density`). This is due to `add_phylopic_legend()` using `add_phylopic_base()` to generate the legend symbols. However, arguments for adjusting the legend appearance such as text (e.g. `cex`), legend box (e.g. `bg`), and color (e.g. `border`) are compatible.

Examples
```r
# Get UUIDs
uuids <- get_uuid(name = "Canis lupus", n = 2)
# Generate empty plot
plot(0:10, 0:10, type = "n", main = "Wolves")
# Add data points
add_phylopic_base(uuid = uuids,
                   color = "black", fill = c("blue", "green"),
                   x = c(2.5, 7.5), y = c(2.5, 7.5), ysize = 2)
# Add legend
add_phylopic_legend(uuid = uuids,
                     ysize = 0.5, color = "black", fill = c("blue", "green"),
                     x = "bottomright", legend = c("Wolf 1", "Wolf 2"),
                     bg = "lightgrey")
```

browse_phylopic
Browse PhyloPic for a given taxonomic name or uuid

Description
This function provides a convenient way to browse PhyloPic for a given taxonomic name of uuid.

Usage
```r
browse_phylopic(name = NULL, uuid = NULL)
```

Arguments
- **name**: character. A taxonomic name. Various taxonomic levels are supported (e.g. species, genus, family).
- **uuid**: character. A PhyloPic image uuid, as acquired by `get_uuid()`.

Details
This function returns a PhyloPic url for an input name or uuid and opens the user’s default web browser at this url. If no name or uuid is supplied, the base url of PhyloPic images is returned and opened instead.
flip_phylopic

Value

A character vector of a valid PhyloPic url for the specified name or uuid. If no name or uuid is supplied, the base url of PhyloPic images is returned.

Examples

```r
## Not run:
url <- browse_phylopic(name = "Acropora cervicornis")
## End(Not run)
```

flip_phylopic

Flip a PhyloPic silhouette along its horizontal and/or vertical axis

Description

The picture can be a Picture or png array object, e.g., from using get_phylopic().

Usage

`flip_phylopic(img, horizontal = TRUE, vertical = FALSE)`

Arguments

- `img`: A Picture or png array object, e.g., from using get_phylopic().
- `horizontal`: logical. Should the silhouette be flipped horizontally?
- `vertical`: logical. Should the silhouette be flipped vertically?

Value

A Picture or png array object (matching the type of `img`)

See Also

Other transformations: `recolor_phylopic()`, `rotate_phylopic()`
Description

This geom acts like `ggplot2::geom_point()`, except that the specified silhouettes are used as points. Silhouettes can be specified by their name, uuid, or image objects (img).

Usage

```r
geom_phylopic(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  remove_background = TRUE,
  verbose = FALSE,
  filter = NULL
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **stat**: The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. "count" rather than "stat_count")

- **position**: Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
geom_phylopic

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? FALSE, the default, never includes, NA includes if any aesthetics are mapped, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

remove_background logical. Should any white background be removed from the silhouette(s)? See recolor_phylopic() for details.

verbose logical. Should the attribution information for the used silhouette(s) be printed to the console (see get_attribution())?

filter character. Filter by usage license if using the name aesthetic. Use "by" to limit results to images which do not require attribution, "nc" for images which allows commercial usage, and "sa" for images without a ShareAlike clause. The user can also combine these filters as a vector.

Details

One (and only one) of the img, name, or uuid aesthetics must be specified. The img aesthetic can be Picture objects or png array objects, e.g., from using get_phylopic(). Use the x and y aesthetics to place the silhouettes at specified positions on the plot. The size aesthetic specifies the height of the silhouettes in the units of the y axis. The aspect ratio of the silhouettes will always be maintained.

The color (default: NA), fill (default: "black"), and alpha (default: 1) aesthetics can be used to change the outline color, fill color, and transparency (outline and fill) of the silhouettes, respectively. If color is specified and fill is NA color will be used as the fill color (for backwards compatibility). If "original" is specified for the color aesthetic, the original color of the silhouette outline will be used (usually the same as "transparent"). If "original" is specified for the fill aesthetic, the original color of the silhouette body will be used (usually the same as "black"). To remove the fill or outline, you can set fill or color to "transparent", respectively.

The horizontal and vertical aesthetics can be used to flip the silhouettes. The angle aesthetic can be used to rotate the silhouettes. When specifying a horizontal and/or vertical flip and a rotation, the flip(s) will always occur first. If you would like to customize this behavior, you can flip and/or rotate the image within your own workflow using flip_phylopic() and rotate_phylopic().

Note that png array objects can only be rotated by multiples of 90 degrees. Also, outline colors do not currently work for png array objects.

Aesthetics

geom_phylopic understands the following aesthetics:

- x (required)
• y (required)
• **img/uuid/name** (one, and only one, required)
• size
• color/colour
• fill
• alpha
• horizontal
• vertical
• angle

Learn more about setting these aesthetics in `add_phylopic()`.

### Examples

```r
## Not run:
library(ggplot2)
df <- data.frame(x = c(2, 4), y = c(10, 20),
                 name = c("Felis silvestris catus", "Odobenus rosmarus"))
ggplot(df) +
  geom_phylopic(aes(x = x, y = y, name = name),
                fill = "purple", size = 10) +
  facet_wrap(~name) +
  coord_cartesian(xlim = c(1,6), ylim = c(5, 30))
## End(Not run)
```

---

**get_attribution**

*Get PhyloPic attribution data*

### Description

This function provides a convenient way to obtain attribution data for PhyloPic images via an image uuid returned by `get_uuid()`.

### Usage

```r
get_attribution(uuid = NULL, img = NULL, text = FALSE, permalink = FALSE)
```

### Arguments

- **uuid** character. A vector of valid uuid(s) for PhyloPic silhouette(s) such as that returned by `get_uuid()` or `pick_phylopic()`.
- **img** A `Picture` or png array object from `get_phylopic()`. A list of these objects can also be supplied. If `img` is supplied, `uuid` is ignored. Defaults to NULL.
- **text** logical. Should attribution information be returned as a text paragraph? Defaults to FALSE.
- **permalink** logical. Should a permalink be created for this collection of uuid(s)? Defaults to FALSE.
get_phylopic

Details

This function returns image uuid specific attribution data, including: contributor name, contributor uuid, contributor contact, image uuid, license, and license abbreviation. If text is set to TRUE, a text paragraph with the contributor name, year of contribution, and license type is printed and image attribution data is returned invisibly (i.e. using invisible()). If permalink is set to TRUE, a permanent link (hosted by PhyloPic) will be generated. This link can be used to view and share details about the image silhouettes, including contributors and licenses.

Value

A list of PhyloPic attribution data for an image uuid or a text output of relevant attribution information.

Examples

```r
## Not run:
# Get valid uuid
uuid <- get_uuid(name = "Acropora cervicornis")
# Get attribution data for uuid
attri <- get_attribution(uuid = uuid)

# Get list of valid uuids
uuids <- get_uuid(name = "Scleractinia", n = 5)
# Get attribution data for uuids
get_attribution(uuid = uuids, text = TRUE)
# Get attribution data for uuids and create permalink
get_attribution(uuid = uuids, text = TRUE, permalink = TRUE)
## End(Not run)
```

---

get_phylopic

Retrieves an image for a given PhyloPic uuid

Description

This retrieves a PhyloPic silhouette as a vectorized or rasterized object.

Usage

```
get_phylopic(uuid = NULL, format = "vector", height = 512, preview = FALSE)
```

## S3 method for class 'Picture'
```
print(x, ...)
```

## S3 method for class 'phylopic'
```
print(x, ...)
```
Arguments

- **uuid**: character. A PhyloPic image uuid.
- **format**: character. Format of the image. To return a vectorized image, use "vector". To return a rasterized image, use "raster" and specify a desired height.
- **height**: numeric. If format is "raster", this is the desired height of the raster image in pixels. This is ignored if format is "vector".
- **preview**: logical. If preview is TRUE, the returned image is plotted. Defaults to FALSE.
- **x**: A Picture or png array object, e.g., from using `get_phylopic()`.
- **...**: Ignored

Details

The `height` argument is ignored if the `format` argument is not set to "raster". If `format` is "raster", the `height` argument specifies the height of the desired raster object. The width of this raster object will be determined by the original aspect ratio of the silhouette. If a pre-rendered raster exists with the desired dimensions, it will be downloaded from PhyloPic. If not, the vector image from PhyloPic will be used to render a raster object of the desired size.

Value

If `format` is "vector", a Picture object is returned. If `format` is "raster", a png array representing the rasterized image is returned. Either way, the uuid and download url are included as the "uuid" and "url" attributes, respectively.

Examples

```r
## Not run:
# uuid
uuid <- "9fae30cd-fb59-4a81-a39c-e1826a35f612"

# Get data for an image
img_svg <- get_phylopic(uuid, format = "vector") # vector format
img_png <- get_phylopic(uuid, format = "raster") # raster format
```

---

**get_uuid**

*Get a PhyloPic uuid*

**Description**

This function provides a convenient way to obtain a valid uuid or image url for an input taxonomic name. As multiple silhouettes can exist for each species in PhyloPic, this function extracts the primary image.
Usage

get_uuid(name = NULL, img = NULL, n = 1, filter = NULL, url = FALSE)

Arguments

name character. A taxonomic name. Various taxonomic levels are supported (e.g. species, genus, family). NULL can also be supplied which will skip the taxonomic filtering of the PhyloPic database.

img A Picture or png array object from get_phylopic(). A list of these objects can also be supplied. If img is supplied, name and n are ignored. Defaults to NULL.

n numeric. How many uuids should be returned? Depending on the requested name, multiple silhouettes might exist. If n exceeds the number of available images, all available uuids will be returned. This argument defaults to 1.

filter character. Filter uuid(s) by usage license. Use "by" to limit results to image uuids which do not require attribution, "nc" for image uuids which allow commercial usage, and "sa" for image uuids without a ShareAlike clause. The user can also combine these filters as a vector.

url logical. If FALSE (default), only the uuid is returned. If TRUE, a valid PhyloPic image url of the uuid is returned.

Details

This function returns uuid(s) or image url (svg) for an input name. If a specific image is desired, the user can make use of pick_phylopic to visually select the desired uuid/url.

Value

A character vector of a valid PhyloPic uuid or svg image url.

Examples

## Not run:
uid <- get_uuid(name = "Acropora cervicornis")
uid <- get_uuid(name = "Dinosauria", n = 5, url = TRUE)

## End(Not run)
Usage
phylopic_key_glyph(img = NULL, name = NULL, uuid = NULL)

Arguments
- **img**: A Picture or png array object, e.g., from using `get_phylopic()`.
- **name**: character. A taxonomic name to be passed to `get_uuid()`.
- **uuid**: character. A valid uuid for a PhyloPic silhouette (such as that returned by `get_uuid()` or `pick_phylopic()`).

Details
One (and only one) of img, name, or uuid must be specified.
This argument may also be a vector/list of valid values if multiple silhouettes should be used as key glyphs. In this case, the specified silhouettes will be used as ordered as key glyphs one by one, with recycling as necessary.
Note that the sizes of the silhouettes in the legend are currently maximized based on the size of the key. This size can be modified using the `legend.key.size` argument in `ggplot2::theme()`. Therefore, the silhouettes will not reflect the size aesthetic, and this function should not be used for size legends.

Examples
```r
## Not run:
library(ggplot2)
df <- data.frame(x = c(2, 4), y = c(10, 20),
                 name = c("Felis silvestris catus", "Odobenus rosmarus"))

ggplot(df) +
  geom_phylopic(aes(x = x, y = y, name = name, color = name), size = 10,
                show.legend = TRUE,
                key_glyph = phylopic_key_glyph(name =
                  c("Felis silvestris catus",
                    "Odobenus rosmarus"))) +

  coord_cartesian(xlim = c(1,6), ylim = c(5, 30))
## End(Not run)
```

Description
This function provides a visually interactive way to pick an image and valid uuid for an input taxonomic name. As multiple silhouettes can exist for each organism in PhyloPic, this function is useful for choosing the right image/uuid for the user.
Usage

pick_phylopic(
    name = NULL,
    n = 5,
    uuid = NULL,
    view = 1,
    filter = NULL,
    auto = NULL
)

Arguments

name character. A taxonomic name. Different taxonomic levels are supported (e.g. species, genus, family).

n numeric. How many uuids should be viewed? Depending on the requested name, multiple silhouettes may exist. If n exceeds the number of available images, all available uuids will be returned. Defaults to 5. Only relevant if name supplied.

uuid character. A vector (or list) of valid PhyloPic silhouette uuids, such as that returned by get_uuid() or resolve_phylopic().

view numeric. Number of silhouettes that should be plotted at the same time. Defaults to 1.

filter character. Filter uuid(s) by usage license. Use "by" to limit results to image uuids which do not require attribution, "nc" for image uuids which allow commercial usage, and "sa" for image uuids without a ShareAlike clause. The user can also combine these filters. Only relevant if name supplied.

auto numeric. This argument allows the user to automate input into the menu choice. If the input value is 1, the first returned image will be selected. If the input value is 2, requested images will be automatically cycled through with the final image returned. If the input value is 3, a list of attribution information for each image is returned (this functionality is principally intended for testing). If NULL (default), the user must interactively respond to the called menu.

Details

This function allows the user to visually select the desired image from a pool of silhouettes available for the input name.

Note that while the view argument can be any positive integer, weaker/older computers may have issues displaying very large numbers of images at the same time (i.e. view > 9). If no images are displayed in your plotting environment, try decreasing the value of view.

Value

A Picture object is returned. The uuid of the selected image is saved as the "uuid" attribute of the returned object and is also printed to console.
Examples

```r
## Not run:
# Defaults pane layout
ing <- pick_phylopic(name = "Canis lupus", n = 5)
# 3 x 3 pane layout
img <- pick_phylopic(name = "Scleractinia", n = 9, view = 9)
## End(Not run)
```

---

**plot.Picture**

*Preview a PhyloPic silhouette*

**Description**

Preview a raster or vector representation of a PhyloPic silhouette. This will plot the silhouette on a new page in your default plotting device.

**Usage**

```r
## S3 method for class 'Picture'
plot(x, ...)
## S3 method for class 'phylopic'
plot(x, ...)
```

**Arguments**

- `x` A `Picture` or `png` array object, e.g., from using `get_phylopic()`.
- `...` Other arguments passed on to `grImport2::grid.picture()` or `grid::grid.raster()`.

---

**recolor_phylopic**

*Recolor a PhyloPic image*

**Description**

Function to recolor and change alpha levels of a PhyloPic image.

**Usage**

```r
recolor_phylopic(
ing, 
  alpha = 1,
  color = NULL,
  fill = NULL,
  remove_background = TRUE
)
```
Arguments

- **img**: A `Picture` or `png` array object, e.g., from using `get_phylopic()`.
- **alpha**: numeric. A value between 0 and 1, specifying the opacity of the silhouette.
- **color**: character. Color to make the outline of the silhouette. If NULL, the outline color is not changed.
- **fill**: character. Color to make the body of the silhouette. If NULL, the body color is not changed.
- **remove_background**: logical. Should any white background be removed? Only useful if `img` is a `Picture` object. See details.

Details

Some PhyloPic silhouettes do not have a transparent background. Consequently, when color is used with vectorized versions of these images, the entire image—including the background—is recolored. Setting `remove_background` to `TRUE` (the default) will remove any white parts of the image (which should only be the background).

Value

A `Picture` or `png` array object (matching the type of `img`)

See Also

Other transformations: `flip_phylopic()`, `rotate_phylopic()`

---

**resolve_phylopic**

*Use a taxonomic name from another database to get a PhyloPic image UUID*

Description

This function takes a supplied taxonomic name, queries it via the specified external API, resolves the API’s returned taxonomic ID to the PhyloPic taxonomic node database, then retrieves PhyloPic image uuids (or urls) for that node.

Usage

```r
resolve_phylopic(
  name,
  api = "gbif.org",
  hierarchy = FALSE,
  max_ranks = 5,
  n = 1,
  filter = NULL,
  url = FALSE
)
```
Arguments

- **name** character. A full or partial taxonomic name to be queried via the specified api.
- **api** character. The API in which to query name. See Details for the available options.
- **hierarchy** logical. Whether the taxonomic hierarchy of name should be retrieved from the API and used to get several sets of PhyloPic image uuids (or urls).
- **max_ranks** numeric. The maximum number of taxonomic ranks that should be included if hierarchy is TRUE.
- **n** numeric. How many uuids should be returned? Depending on the requested name, multiple silhouettes might exist. If n exceeds the number of available images, all available uuids will be returned. This argument defaults to 1.
- **filter** character. Filter uuid(s) by usage license. Use "by" to limit results to image uuids which do not require attribution, "nc" for image uuids which allow commercial usage, and "sa" for image uuids without a ShareAlike clause. The user can also combine these filters as a vector.
- **url** logical. If FALSE (default), only the uuid is returned. If TRUE, a valid PhyloPic image url of the uuid is returned.

Details

If hierarchy is FALSE, the specified name is queried via the specified api. The matched id is then resolved to the matching taxonomic node in the PhyloPic database. If hierarchy is TRUE, the full taxonomic hierarchy for name is retrieved from the specified api, those taxonomic names are subset to max_ranks ranks (starting from the specified name and ascending the hierarchy). Then each of those names is resolved to the matching taxonomic node in the PhyloPic database (where possible). In either case, get_uuid() is then used to retrieve n image UUID(s) for each taxonomic name.

Note that while the names of the returned list are the taxonomic names as reported by the specified api, the PhyloPic images that are returned are associated with whatever taxonomic node that taxonomic name resolves to in the PhyloPic database. This means that, if hierarchy is TRUE, the same images may be returned for multiple taxonomic names. Also, if a particular taxonomic name does not resolve to any node in the PhyloPic database, no images will be returned for that name.

The following APIs are available for querying (api):

- "eol.org": the Encyclopedia of Life (note: hierarchy = TRUE is not currently available for this API) ("eol" is also allowed)
- "gbif.org": the Global Biodiversity Information Facility ("gbif" is also allowed)
- "marinespecies.org": the World Register of Marine Species ("worms" is also allowed)
- "opentreeoflife.org": the Open Tree of Life ("otol" is also allowed)
- "paleobiodb.org": the Paleobiology Database ("pbdb" is also allowed)

Value

A list where each value is n (or fewer) PhyloPic image uuids (or urls if url = TRUE) and each name is the taxonomic name as matched and reported by the specified api. If hierarchy is FALSE, the list has length 1. If hierarchy is TRUE, the list has maximum length max_ranks.
**Examples**

```r
## Not run:
# get a uuid for a single name
resolve_phylopic(name = "Canis lupus")
# get uuids for the taxonomic hierarchy
resolve_phylopic(name = "Velociraptor mongoliensis", api = "paleobiodb.org",
                 hierarchy = TRUE, max_ranks = 3)
## End(Not run)
```

---

**rotate_phylopic**  
*Rotate a PhyloPic silhouette*

**Description**

The picture can be a `Picture` or png array object, e.g., from using `get_phylopic()`. Note that png array objects can only be rotated by multiples of 90 degrees.

**Usage**

```r
rotate_phylopic(img, angle = 90)
```

**Arguments**

- `img`  
  A `Picture` or png array object, e.g., from using `get_phylopic()`.

- `angle`  
  numeric. The number of degrees to rotate the silhouette clockwise.

**Value**

A `Picture` or png array object (matching the type of `img`)

**See Also**

Other transformations: `flip_phylopic()`, `recolor_phylopic()`

---

**save_phylopic**  
*Save a PhyloPic image*

**Description**

`save_phylopic` is a convenient function for saving a PhyloPic silhouette fetched via `get_phylopic`. Available formats for saving are those available in the `grDevices` package (i.e. pdf, png, svg, tiff, jpeg, and bmp).

**Usage**

```r
save_phylopic(img = NULL, path = NULL, bg = "transparent", ...)
```
save_phylopic

Arguments

- **img** character. A Picture object. For PhyloPic silhouettes, this is generated by `get_phylopic` and `pick_phylopic`.
- **path** character. The output file path. The name of the file and file extension should be included (e.g. "./phylopic.png"). If this argument is NULL (default), the file is automatically saved in the current working directory as a png file.
- **bg** character. The desired background color. By default this argument is set to "transparent". Note: jpeg files are always exported with a background colour.
- **...** Additional arguments available for the called grDevices function. The called function is determined by the file extension used in `path` (e.g. `png`).

Details

This function can be used to save a PhyloPic image obtained via the `get_phylopic` or any object of class `Picture` from the grImport2 package. Any file format available in the grDevices package can be used (i.e. pdf, png, svg, tiff, jpeg, and bmp).

Value

An image is saved. Nothing is returned to the R interface.

Examples

```r
## Not run:
# Get image data
img <- get_phylopic("27356f15-3cf8-47e8-ab41-71c6260b2724")
# Save file
save_phylopic(img = img, path = "./phylopic.png",
width = 500, height = 500)
## End(Not run)
```
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