

# 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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add_phylopic	<i>Annotate a ggplot plot with PhyloPics</i>
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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**

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

**Arguments**

img	A <a href="#">Picture</a> or png array object, e.g., from using <a href="#">get_phylopic()</a> .
name	character. A taxonomic name to be passed to <a href="#">get_uid()</a> .
uid	character. A valid uid for a PhyloPic silhouette (such as that returned by <a href="#">get_uid()</a> or <a href="#">pick_phylopic()</a> ).
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").
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 the outline and fill color will be the same.
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 <a href="#">recolor_phylopic()</a> for details.
verbose	logical. Should the attribution information for the used silhouette(s) be printed to the console (see <a href="#">get_attribution()</a> )?

**Details**

One (and only one) of `img`, `name`, or `uid` 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**

```
# 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)
sizey <- runif(10, 0.4, 2)
angle <- runif(10, 0, 360)
hor <- sample(c(TRUE, FALSE), 10, TRUE)
ver <- sample(c(TRUE, FALSE), 10, TRUE)
cols <- 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 = sizey,
    color = cols, alpha = alpha, angle = angle,
    horizontal = hor, vertical = ver)
p + ggtitle("R Cat Herd!!")
```

---

add\_phylopic\_base

*Add PhyloPics to a base R plot*


---

**Description**

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

**Usage**

```
add_phylopic_base(
  img = NULL,
  name = NULL,
  uuid = NULL,
  filter = NULL,
  x = NULL,
  y = NULL,
  ysize = NULL,
  alpha = 1,
  color = "black",
  fill = NA,
  horizontal = FALSE,
```

```

    vertical = FALSE,
    angle = 0,
    remove_background = TRUE,
    verbose = FALSE
  )

```

### Arguments

img	A <a href="#">Picture</a> or png array object, e.g., from using <a href="#">get_phylopic()</a> .
name	character. A taxonomic name to be passed to <a href="#">get_uuid()</a> .
uuid	character. A valid uuid for a PhyloPic silhouette (such as that returned by <a href="#">get_uuid()</a> or <a href="#">pick_phylopic()</a> ).
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").
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 the outline and fill color will be the same.
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 <a href="#">recolor_phylopic()</a> for details.
verbose	logical. Should the attribution information for the used silhouette(s) be printed to the console (see <a href="#">get_attribution()</a> )?

### 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

```
# 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)
cols <- 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,
                  color = cols, 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)
```

**Description**

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

**Usage**

```
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.

**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**

```
url <- browse_phylopic(name = "Acropora cervicornis")
```

---

flip_phylopic	<i>Flip a PhyloPic silhouette along its horizontal and/or vertical axis</i>
---------------	---

---

**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\(\)](#)

---

 geom\_phylopic

*Geom for adding PhyloPic silhouettes to a plot*


---

**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**

```
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 <a href="#">aes()</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot()</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify()</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
stat	The statistical transformation to use on the data for this layer, either as a <code>ggproto</code> <code>Geom</code> subclass or as a string naming the stat stripped of the <code>stat_</code> prefix (e.g. "count" rather than "stat_count")



position	Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use <code>position_jitter</code> ), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...	Other arguments passed on to <code>layer()</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>colour = "red"</code> or <code>size = 3</code> . 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. <code>borders()</code> .
remove_background	logical. Should any white background be removed from the silhouette(s)? See <code>recolor_phylopic()</code> for details.
verbose	logical. Should the attribution information for the used silhouette(s) be printed to the console (see <code>get_attribution()</code> )?
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: "black"), `fill` (default: NA), 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 the outline and fill color will be the same. 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").

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

```
## 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 = "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

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

**Arguments**

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

**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 returned.

**Value**

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

**Examples**

```
# Get valid uuid
uuid <- get_uuid(name = "Acropora cervicornis")
# Get attribution data for uuid
attri <- get_attribution(uuid = uuid)
## Not run:
# Get list of valid uuids
uuids <- get_uuid(name = "Scleractinia", n = 5)
# Get attribution data for uuids
get_attribution(uuid = uuids, text = TRUE)

## End(Not run)
```

---

get\_phylopic

*Retrieve 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 <a href="#">Picture</a> or png array object, e.g., from using <a href="#">get_phylopic()</a> .
...	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**

```
# 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 <a href="#">Picture</a> or png array object from <a href="#">get_phylopic()</a> . 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**

```
uuid <- get_uuid(name = "Acropora cervicornis")
uuid <- get_uuid(name = "Dinosauria", n = 5, url = TRUE)
```

---

phylopic\_key\_glyph      *Use PhyloPics as legend key glyphs*

---

**Description**

Specify existing images, taxonomic names, or PhyloPic uuids to use PhyloPic silhouettes as legend key glyphs in a ggplot plot.

**Usage**

```
phylopic_key_glyph(img = NULL, name = NULL, uuid = NULL)
```

**Arguments**

img	A <a href="#">Picture</a> or png array object, e.g., from using <a href="#">get_phylopic()</a> .
name	character. A taxonomic name to be passed to <a href="#">get_uuid()</a> .
uuid	character. A valid uuid for a PhyloPic silhouette (such as that returned by <a href="#">get_uuid()</a> or <a href="#">pick_phylopic()</a> ).

## 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

```
## 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)
```

---

pick\_phylopic

*Pick a PhyloPic image from available options*

---

## 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, view = 1, filter = NULL, auto = NULL)
```

## Arguments

<code>name</code>	character. A taxonomic name. Different taxonomic levels are supported (e.g. species, genus, family).
<code>n</code>	numeric. How many uuids should be viewed? Depending on the requested name, multiple silhouettes may exist. If <code>n</code> exceeds the number of available images, all available uuids will be returned. Defaults to 5.

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.
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 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

```
## Not run:
# Defaults pane layout
img <- 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**

```
## 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	<i>Recolor a PhyloPic image</i>
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---

**Description**

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

**Usage**

```
recolor_phylopic(
  img,
  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\(\)](#)

---

rotate_phylopic	<i>Rotate a PhyloPic silhouette</i>
-----------------	-------------------------------------

---

**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**

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

**Arguments**

<code>img</code>	A <a href="#">Picture</a> or png array object, e.g., from using <a href="#">get_phylopic()</a> .
<code>angle</code>	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	<i>Save a PhyloPic image</i>
---------------	------------------------------

---

**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**

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

## Arguments

img	picture. A <a href="#">Picture</a> object. For PhyloPic silhouettes, this is generated by <a href="#">get_phylopic</a> and <a href="#">pick_phylopic</a> .
path	character. The output file path. The name of the file and file extension should be included (e.g. <code>"/phylopic.png"</code> ). 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 <code>grDevices</code> function. The called function is determined by the file extension used in <code>path</code> (e.g. <a href="#">png</a> ).

## 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

```
## 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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