

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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License GPL (>= 3)

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Depends R (>= 4.0)

Imports ggplot2, jsonlite, grid, graphics, png, grImport2, rsvg, httr, curl, methods

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Config/testthat/edition 3

URL <https://rphylopic.palaeoverse.org>,
<https://github.com/palaeoverse-community/rphylopic>,
<https://palaeoverse.org>

BugReports <https://github.com/palaeoverse-community/rphylopic/issues>

NeedsCompilation no

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R topics documented:

add_phylopic	2
add_phylopic_base	3
get_attribution	5
get_phylopic	6
get_uuid	6
pick_phylopic	7
save_phylopic	8

Index	10
--------------	-----------

add_phylopic	<i>Add a PhyloPic to a ggplot plot</i>
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Description

Specify an existing image, taxonomic name, or PhyloPic uuid to add a PhyloPic silhouette as a separate layer to an existing ggplot plot.

Usage

```
add_phylopic(
  img = NULL,
  name = NULL,
  uuid = NULL,
  x = NULL,
  y = NULL,
  ysize = NULL,
  alpha = 1,
  color = "black"
)
```

Arguments

img	A Picture or png array object, e.g., from using get_phylopic() .
name	A taxonomic name to be passed to get_uuid() .
uuid	A valid uuid for a PhyloPic silhouette (such as that returned by get_uuid() or pick_phylopic()).
x	x value of the silhouette center. Ignored if y and ysize are not specified.
y	y value of the silhouette center. Ignored if x and ysize are not specified.
ysize	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	A value between 0 and 1, specifying the opacity of the silhouette (0 is fully transparent, 1 is fully opaque).
color	Color to plot the silhouette in.

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.

Examples

```
# Put a silhouette behind a plot based on a taxonomic name
library(ggplot2)
ggplot(iris) +
  add_phylopic(name = "Iris", alpha = .2) +
  geom_point(aes(x = Sepal.Length, y = Sepal.Width))

# Put a silhouette anywhere based on UUID
posx <- runif(10, 0, 10)
posy <- runif(10, 0, 10)
sizey <- runif(10, 0.4, 2)
cols <- sample(c("black", "darkorange", "grey42", "white"), 10,
  replace = TRUE)

# Since we are plotting a lot of the same image, we should just save
# the image in our environment first
cat <- get_phylopic("23cd6aa4-9587-4a2e-8e26-de42885004c9")
p <- ggplot(data.frame(cat.x = posx, cat.y = posy), aes(cat.x, cat.y))
for (i in 1:10) {
  p <- p + add_phylopic(cat, x = posx[i], y = posy[i],
    ysize = sizey[i], color = cols[i])
}
p + ggtitle("R Cat Herd!!")
```

add_phylopic_base	<i>Add a PhyloPic to a base R plot</i>
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Description

Specify an existing image, taxonomic name, or PhyloPic uuid to add a PhyloPic silhouette on top of an existing base R plot.

Usage

```
add_phylopic_base(
  img = NULL,
  name = NULL,
  uuid = NULL,
  x = NULL,
  y = NULL,
  ysize = NULL,
```

```

    alpha = 1,
    color = "black"
  )

```

Arguments

img	A Picture or png array object, e.g., from using <code>get_phylopic()</code> .
name	A taxonomic name to be passed to <code>get_uuid()</code> .
uuid	A valid uuid for a PhyloPic silhouette (such as that returned by <code>get_uuid()</code> or <code>pick_phylopic()</code>).
x	x value of the silhouette center. Ignored if y and ysize are not specified.
y	y value of the silhouette center. Ignored if x and ysize are not specified.
ysize	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	A value between 0 and 1, specifying the opacity of the silhouette.
color	Color to plot the silhouette in.

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 figure is resized). However, if the plot is resized afterwards, the absolute position of the silhouette may change.

Examples

```

# single image
plot(1, 1, type="n", main="A cat")
add_phylopic_base(name = "Cat", x = 1, y = 1, ysize = .4)

# lots of images using a uuid
posx <- runif(50, 0, 1)
posy <- runif(50, 0, 1)
size <- runif(50, 0.01, 0.2)

# Since we are plotting a lot of the same image, we should just save
# the image in our environment first
cat <- get_phylopic("23cd6aa4-9587-4a2e-8e26-de42885004c9")

plot(posx, posy, type="n", main="A cat herd")
for (i in 1:50) {
  add_phylopic_base(cat, x = posx[i], y = posy[i], ysize = size[i])
}

# Example using a cat background
# 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(cat, alpha=0.2)
# overlay smaller cats
for (i in 1:50) {
  add_phylopic_base(cat, x = posx[i], y = posy[i], ysize = size[i], alpha=.8)
}
```

get_attribution	<i>Get PhyloPic attribution data</i>
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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)
```

Arguments

uuid character. A valid uuid for a PhyloPic silhouette such as that returned by [get_uuid\(\)](#) or [pick_phylopic\(\)](#).

Details

This function returns image uuid specific attribution data, including: contributor name, contributor uuid, contributor contact, image uuid and license.

Value

A list of PhyloPic attribution data for an image uuid.

Examples

```
# Get valid uuid
uuid <- get_uuid(name = "Acropora cervicornis")
# Get attribution data for uuid
attri <- get_attribution(uuid = uuid)
```

get_phylopic	<i>Retrieve an image for a given PhyloPic uuid</i>
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Description

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

Usage

```
get_phylopic(uuid = NULL, format = "vector")
```

Arguments

uuid	A PhyloPic image uuid.
format	Format of the image. To return a vectorized image, use "vector". To return a rasterized image, use one of 512, 1024, or 1536. Rasterized thumbnails can be returned by using 64, 128, or 192. Finally, using "twitter" will return a rasterized image that includes the PhyloPic logo and is formatted for posting on social media.

Value

If format is "vector", a [Picture](#) object is returned. Otherwise, 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 = "512") # raster format
```

get_uuid	<i>Get a PhyloPic uuid</i>
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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, n = 1, 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.
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.
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)
```

pick_phylopic	<i>Pick a PhyloPic image from available options</i>
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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 species in PhyloPic, this function is useful for choosing the right image/uuid for the user.

Usage

```
pick_phylopic(name = NULL, n = 5, 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.

`auto` numeric. This argument allows the user to automate input into the menu choice. If the input value is 1, requested images will be automatically cycled through with the final image returned. If the input value is 2, the first returned image will be selected. 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.

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:
img <- pick_phylopic(name = "Canis lupus", n = 5)

## End(Not run)
```

save_phylopic	<i>Save a PhyloPic image</i>
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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, ...)
```

Arguments

<code>img</code>	picture. A Picture object. For PhyloPic silhouettes, this is generated by get_phylopic and pick_phylopic .
<code>path</code>	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.
<code>...</code>	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

```
## 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)
```

Index

add_phylopic, 2
add_phylopic_base, 3

get_attribution, 5
get_phylopic, 6, 8, 9
get_phylopic(), 2, 4
get_uuid, 6
get_uuid(), 2, 4, 5
grDevices, 8, 9

pick_phylopic, 7, 7, 8
pick_phylopic(), 2, 4, 5
Picture, 2, 6, 8
png, 8

save_phylopic, 8