

APPLICATION

Methods in Ecology and Evolution



rphylopic: An R package for fetching, transforming, and visualising PhyloPic silhouettes

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Handling Editor: Will Pearse**Abstract**

1. Effective data visualisation is vital for data exploration, analysis and communication in research. In ecology and evolutionary biology, data are often associated with various taxonomic entities. Graphics of organisms associated with these taxa are valuable for framing results within a broader biological context. However, acquiring and using such resources can be challenging due to availability and licensing constraints. The PhyloPic database solves many of these issues by making organism silhouettes freely available. Tools that integrate this database with existing research workflows are needed to remove hurdles associated with data visualisation in the biological sciences.
2. Here, we introduce rphylopic, an R package for fetching, transforming and visualising silhouettes of organisms from the PhyloPic database. In addition to making over 8000 organism silhouettes available within the R programming language, rphylopic empowers users to modify the appearance of these silhouettes for ultimate customisability when coding production-quality visualisations in both base R and ggplot2 workflows.
3. In this work, we provide details about how the package can be installed, its implementation and potential use cases. For the latter, we showcase three examples across the ecology and evolutionary biology spectrum.
4. Our hope is that rphylopic will make it easier for biologists to develop more accessible and engaging data visualisations by making external resources readily accessible, customisable and usable within R. In turn, by integrating into existing workflows, rphylopic helps to ensure that science is reproducible and accessible.

KEYWORDS

accessible, data visualisation, database, R programming, reproducible

1 | INTRODUCTION

Data visualisation is a key component of any scientific data analysis workflow (Ali et al., 2016) and is vital for the summarisation and dissemination of complex ideas and results (Ware, 2019). In ecology and evolutionary biology, data are often associated with taxonomic

entities. However, taxonomic nomenclature, which is fundamental to the biological sciences, is often unfamiliar to nonspecialists. Therefore, it has become commonplace to utilise visual representations of organisms, including photographs, illustrations and silhouettes, to make results more accessible and visually engaging (e.g. Cooke et al., 2022; Farina et al., 2023; Hirt et al., 2017). However,

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the taxonomic affinity, availability and licensing of such resources can be hurdles to incorporating them into research articles.

PhyloPic (<https://www.phylopic.org>) solves many of the aforementioned hurdles by providing an online open-access database of silhouette images of animals, plants and other life forms. To date, the silhouettes have been created by over 500 volunteer contributors, are available for reuse under various Creative Commons licences and are stored within a taxonomic/phylogenetic framework (e.g. phylum Mollusca and clade pan-Mollusca are both valid). While PhyloPic is almost never cited within scientific publications, silhouettes from the database have been utilised to convey taxonomic information effectively and simply for innumerable scientific articles, conference contributions and much more. However, despite this already wide array of applications, usage hurdles exist due to its platform-agnostic nature. For example, while silhouettes can be downloaded in raster or vector formats, these can still be difficult to integrate into a coding-based scientific workflow, especially when the user is trying to maintain reproducibility. Often, custom code and/or postproduction editing are required to accommodate these images.

Here, we describe rphylopic, a dedicated R package for interfacing with the PhyloPic database. The package contains functions for accessing, transforming and visualising PhyloPic silhouettes. We first provide instructions for installing the package and details on its implementation. Second, we demonstrate the functionality available in rphylopic through usage examples. Finally, we provide details about the resources we have made available to the community and to support rphylopic users.

2 | INSTALLATION

The rphylopic package can be installed from CRAN using the `install.packages` function in R (R Core Team, 2023):

```
install.packages("rphylopic")
```

If preferred, the development version of rphylopic can be installed from GitHub via the `remotes` R package (Csárdi et al., 2023):

```
remotes::install_github("palaeoverse-community/rphylopic")
```

Following installation, rphylopic can be loaded via the `library` function in R:

```
library("rphylopic")
```

2.1 | Dependencies

The rphylopic package depends on R (>4.0) (R Core Team, 2023) and imports functions from: `curl` (Ooms, 2023), `ggplot2`

TABLE 1 Summary table of the functions currently available in the rphylopic R package.

Function	Description
<code>add_phylopic</code>	Adds PhyloPic silhouette(s) layer to ggplot2 plots
<code>add_phylopic_base</code>	Adds PhyloPic silhouette(s) to base R plots
<code>browse_phylopic</code>	Browse PhyloPic for a given taxonomic name or unique identifier
<code>flip_phylopic</code>	Flips a PhyloPic silhouette along a horizontal or vertical axis
<code>geom_phylopic</code>	Plots data points as PhyloPic silhouette(s) for ggplot2
<code>get_attribution</code>	Gets the attribution data for a given PhyloPic silhouette
<code>get_phylopic</code>	Gets the image data for a given PhyloPic silhouette
<code>get_uuid</code>	Gets the unique identifier for a given PhyloPic silhouette
<code>phylopic_key_glyph</code>	Use PhyloPics as legend key glyphs
<code>plot</code>	Preview a PhyloPic silhouette
<code>pick_phylopic</code>	Enables visual selection of PhyloPic silhouettes
<code>print</code>	Print key information about a PhyloPic silhouette
<code>recolor_phylopic</code>	Recolours a given PhyloPic silhouette
<code>rotate_phylopic</code>	Rotates a given PhyloPic silhouette
<code>save_phylopic</code>	Saves a given PhyloPic silhouette

(Wickham, 2016), `graphics` (R Core Team, 2023), `grid` (R Core Team, 2023), `grImport2` (Potter & Murrell, 2019), `httr` (Wickham, 2023), `jsonlite` (Ooms, 2014), `knitr` (Xie, 2014), `lifecycle` (Henry & Wickham, 2022), `methods` (R Core Team, 2023), `pbapply` (Solymos & Zawadzki, 2023), `png` (Urbanek, 2022) and `rsvg` (Ooms, 2022). The package was developed with the support of the R packages `devtools` (Wickham, Hester, et al., 2022), `testthat` (Wickham, 2011) and `roxygen2` (Wickham, Danenberg, et al., 2022).

3 | IMPLEMENTATION

A summary of the functions currently available in rphylopic is provided in Table 1. Detailed description is provided below followed by usage examples to demonstrate the functionality and versatility of the package.

3.1 | Fetching

Image data (i.e. silhouettes) are fetched from the PhyloPic application programming interface service via the `get_phylopic` function. The function requires an image universally unique identifier (UUID), which can be provided by the user for a known silhouette. If the

user does not know the UUID for the desired image, the `get_uuid` function can be used to retrieve the image UUID associated with a specific taxonomic name:

```
# Get image uuid
uuid <- get_uuid(name = "Acropora cervicornis")
# Get data for an image
img_vec <- get_phylopic(uuid = uuid, format = "vector") # vector
format
img_ras <- get_phylopic(uuid = uuid, format = "raster") # raster format
```

Silhouettes can be returned as both Scalable Vector Graphics (SVG) and Portable Network Graphics (PNG), depending on the user-defined format ('vector' and 'raster', respectively). An additional argument (height) can be defined for the 'raster' format to control the image height in pixels (larger height values result in higher resolutions). However, in most cases, we encourage users to use the default 'vector' format to maintain the highest quality possible.

Multiple silhouettes can exist for a single taxonomic name in PhyloPic, particularly at higher taxonomic levels. To help facilitate user selection from various image silhouettes, we provide the `pick_phylopic` function to enable users to interactively pick an image through visualising the available options (Figure 1):

```
img_pick <- pick_phylopic(name = "Scleractinia", view = 4)
```

The function `save_phylopic` is provided to allow users to conveniently save any vector silhouettes in a range of formats, including the following: Portable Document Format (PDF), Portable Network Graphics (PNG), Scale Vector Graphics (SVG), Tag Image File Format (TIFF), Joint Photographic Experts Group (JPEG) and bit-map (BMP). Note, this is not required if all further transformations and visualisations will be conducted within R; however, we include this function for users who may still need to use these silhouettes outside R.

```
# Save file
save_phylopic(img = img_vec, path = "img.png", width = 500, height = 500)
```

3.2 | Transformation

Once a silhouette is picked and saved in the user's R environment, it may be useful to transform the image to better suit the particular visualisation of interest. We have implemented three user-friendly functions to accommodate three transformations that might be

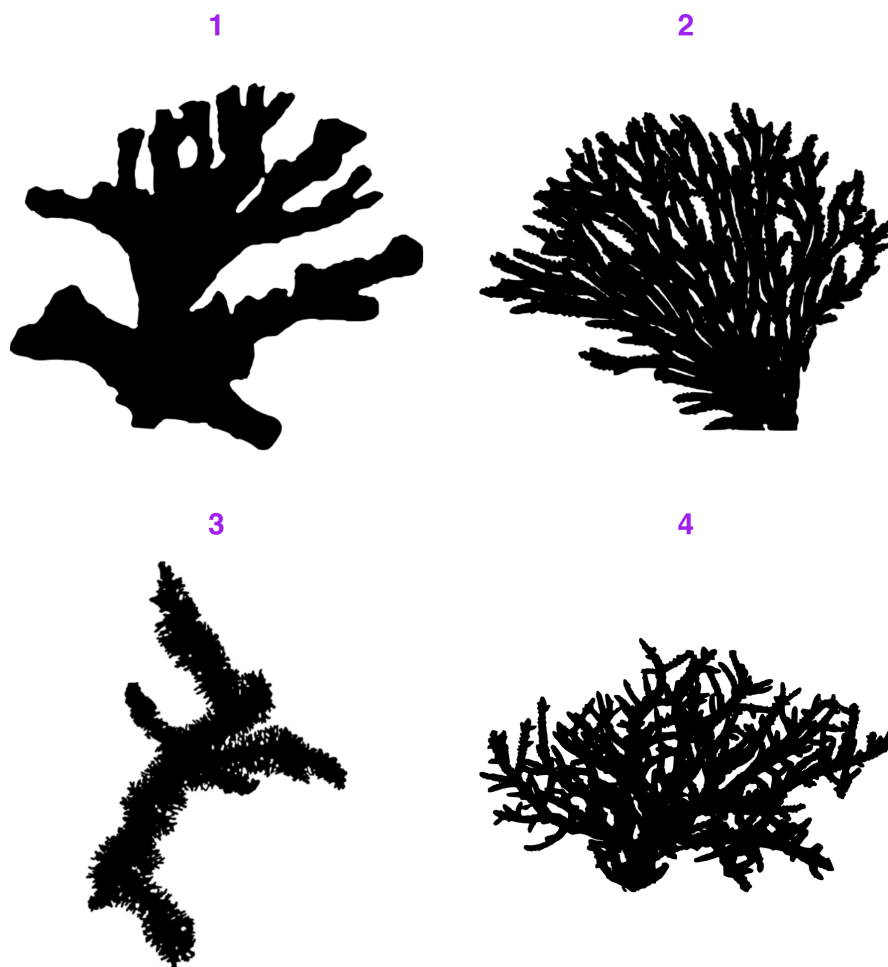


FIGURE 1 An example of the output from `pick_phylopic` for selecting image silhouettes. The image silhouettes are from PhyloPic (<https://www.phylopic.org>; Keesey, 2023). Silhouette 1 was contributed by Víctor Piñon-González (2023; CC0 1.0), and silhouettes 2–4 were contributed by Guillaume Dera (2022; CC0 1.0).

desired by the user: flipping, rotating and recolouring. All three functions work on both vector and raster versions of silhouettes.

The `flip_phylopic` function can be used to flip a silhouette horizontally and/or vertically. This may be useful if, for example, the user wants all of the silhouettes to face the same direction.

```
# Flip silhouette horizontally
img_flip <- flip_phylopic(img = img_vec, horizontal = TRUE, vertical = FALSE)
```

The `rotate_phylopic` function can be used to rotate a silhouette an arbitrary number of degrees. This may be useful when trying to align a silhouette with text or other objects within a figure.

```
# Rotate silhouette by 45 degrees
img_rot <- rotate_phylopic(img = img_vec, angle = 45)
```

Finally, the `recol_phylopic` function can be used to modify the fill colour, outline colour and/or transparency of a silhouette. The vast majority of PhyloPic silhouettes are black and fully opaque by default. However, it may be useful to change this when the user is trying to either match an existing visualisation colour palette or trying to convey extra information, such as categorical data, through colour.

```
# Change colour to blue and transparency to 50%
img_col <- recolor_phylopic(img = img_vec, alpha = 0.5, fill = "blue")
```

For convenience, we have also included these transformation options within all of the visualisation functions discussed in the next section. However, when the same transformed silhouette will be used for multiple visualisations, we suggest transforming the silhouette first, saving it as a new object, then using this new object for visualisation purposes.

3.3 | Visualisation

In recognition of the wide range of users who may use the package, we have included functions to add the desired PhyloPic silhouettes to both base R and ggplot2 plots. Furthermore, for convenience, each of the following functions works with the names of species/clades (the `name` argument/aesthetic), UUIDs (the `uuid` argument/aesthetic) or image objects (vector or raster) (the `img` argument/aesthetic). For simplicity, we will only showcase the use of names here.

The `add_phylopic_base` function can be used to add one or more silhouettes to a base R plot. The function behaves very similarly to the base R `points` function, where `x` and `y` coordinates are supplied for the centres of the silhouettes. The `ysize` argument can be used to vary the size of the silhouettes. For convenience, if any of these arguments are vectors, the other arguments will be recycled as necessary. For example, a single silhouette can be plotted at multiple `x`

and `y` coordinates, or multiple silhouettes can be plotted at multiple `y` coordinates but all with the same `x` coordinate.

```
# Make a simple base R plot
plot(x = 0:10, y = 0:10, type = "n", main = "A cat")
# Add a cat in multiple places
add_phylopic_base(name = "Felis catus", x = seq(2, 8, 2),
  y = seq(2, 8, 2), ysize = 2)
```

The equivalent function for ggplot2 usage is the `add_phylopic` function, which adds PhyloPic silhouettes as a separate layer to an existing ggplot object. It works very similarly to the `annotate` function in the ggplot2 package (Wickham, 2016). A common use case for this is to add a PhyloPic silhouette as a background image:

```
# Load the ggplot2 package
library(ggplot2)
# Make a simple ggplot plot with a faded iris flower in the background
ggplot(iris) +
  add_phylopic(x = 6.1, y = 3.2, name = "Iris", alpha = 0.2) +
  geom_point(aes(x = Sepal.Length, y = Sepal.Width))
```

In case the user already has a `data.frame` of data, we have also provided the `geom_phylopic` function, which acts like the `geom_point` function from ggplot2, except the specified silhouettes are used as points. This can be combined with other functions (e.g. `facet_wrap`) from ggplot2 and other packages to create complex visualisations:

```
# Assemble a data.frame
df <- data.frame(x = 2:5, y = seq(10, 25, 5),
  name = c("leopard", "walrus", "house mouse", "iris"))
# Plot each silhouette in its own panel
ggplot(df) +
  geom_phylopic(aes(x = x, y = y, name = name),
  colour = "purple", size = 10) +
  facet_wrap(~name) +
  coord_cartesian(xlim = c(1,6), ylim = c(5, 30))
```

As mentioned above, for convenience, these three functions all allow for transformations during the plotting stage. For the `add_phylopic` and `add_phylopic_base` functions, `horizontal`, `vertical`, `alpha`, `color` and `fill` are arguments. For the `geom_phylopic` function, these are ggplot2 aesthetics. These transformations work whether silhouettes are specified as names, UUIDs or image objects.

3.4 | Attribution

The `rphylopic` package gathers resources (i.e. silhouettes) from the PhyloPic database. The silhouettes are made available under various Creative Commons copyright licences and should

be appropriately attributed when used (see figure captions for examples). To help facilitate this process, including automatic generation of attribution statements, we provide the function `get_attribution`:

```
# Get valid uuid
uuid <- get_uuid(name = "Acropora cervicornis")
# Get attribution data for uuid
att <- get_attribution(uuid = uuid)
# Get attribution data for uuid as text output
get_attribution(uuid = uuid, text = TRUE)
```

This function returns attribution data for a specific image UUID, including the following: contributor name, contributor UUID, contributor contact, image UUID and the type of licence. While not requested by the creator of PhyloPic (T. Michael Keeseey), we also encourage acknowledgement of his work. Note, when requesting a UUID (`get_uuid`) or image (`pick_phylopic`, `geom_phylopic`, `add_phylopic`, `add_phylopic_base`), the results can be filtered to exclude specific copyright licences that might not be appropriate in some instances (e.g. with a ShareAlike clause that is often incompatible with use in journal publications):

```
# Exclude images with a ShareAlike clause
uuid <- get_uuid(name = "Bacteria", filter = "sa")
img <- pick_phylopic(name = "Bacteria", filter = "sa")
```

If you use the `rphylopic` package in your workflow, we also ask that you cite the package appropriately. A citation for the package can be accessed via the function `citation`:

```
citation("rphylopic")
```

4 | APPLICATION

Herein, we provide three example applications of the `rphylopic` package in combination with `ggplot2` (Wickham, 2016). These examples are greatly expanded in an associated step-by-step vignette of the package. All of this demonstrated functionality is also available for base R and showcased in a separate step-by-step vignette of the package. The vignettes are available online (<https://rphylopic.palaeoverse.org/articles/>) and are also bundled with the package:

```
browseVignettes("rphylopic")
```

4.1 | Basic accession and transformation

The `rphylopic` package provides robust and flexible tools to access and transform PhyloPic silhouettes. Here, we demonstrate this

using the example data set of Antarctic penguins from the `palm-erpenguins` R package (Horst et al., 2020). Since we do not know which silhouette we want to use, we first use `pick_phylopic` to identify a suitable silhouette for *Pygoscelis*. We then rotate this silhouette and use it instead of points for a standard x-y plot showing the relationship between bill length and flipper length (Figure 2). Note that we modify the size and fill of the silhouette based on the mass and sex of each penguin, respectively. The fill aesthetic can be used to modify the body colour of the silhouette, while the colour aesthetic is used for modifying the outline colour. Here, we specify `colour = NA` to leave the outline transparent. As with all `ggplot`-related functions, `geom_phylopic` accepts both 'color' and 'colour' as aesthetic names.

```
# Load libraries
library(rphylopic)
library(ggplot2)
library(palmerpenguins)
# Get penguin data and clean it
data(penguins)
penguins_subset <- subset(penguins, !is.na(sex))
# Pick a silhouette for Pygoscelis (here we pick #2)
penguin_vec <- pick_phylopic("Pygoscelis", n = 3, view = 3)
# It's a little slanted, so let's rotate it a little bit
penguin_rot <- rotate_phylopic(penguin_vec, 15)
# Now use the silhouette for an x-y plot
ggplot(penguins_subset) +
  geom_phylopic(img = penguin_rot,
    aes(x = bill_length_mm, y = flipper_length_mm,
      size = body_mass_g, fill = sex), colour = NA,
    show.legend = TRUE,
    key_glyph = phylopic_key_glyph(img = penguin_rot)) +
  labs(x = "Bill length (mm)", y = "Flipper length (mm)") +
  scale_size_continuous(guide = "none") +
  scale_fill_manual("Sex", values = c("orange", "blue"),
    labels = c("Female", "Male")) +
  facet_wrap(~species, ncol = 1) +
  theme_bw(base_size = 15) +
  theme(legend.position = c(0.9, 0.9))
```

4.2 | Geographic distribution

In much the same way as generic x-y plotting, the `rphylopic` package can be used in combination with `ggplot2` (Wickham, 2016) to plot organism silhouettes on a map (Figure 3). That is, to plot data points (e.g. species occurrences) as silhouettes. We provide an example here of how this might be achieved for individuals who wish to do so. For this application, we use the example occurrence data set of early (Carboniferous to Early Triassic) tetrapods from the `palaeoverse` R package (Jones et al., 2023) to visualise the geographic distribution of *Diplocaulus* fossils.

FIGURE 2 Relationship between bill length and flipper length in Antarctic penguins. Each panel represents a different species of *Pygoscelis*. Silhouette sizes represent relative body masses and silhouette colours represent the sex of measured individuals (orange: female; blue: male). The image silhouette is from PhyloPic (<https://www.phylopic.org>; Keesey, 2023) and was contributed by Alexandre Vong (2018; CC0 1.0).

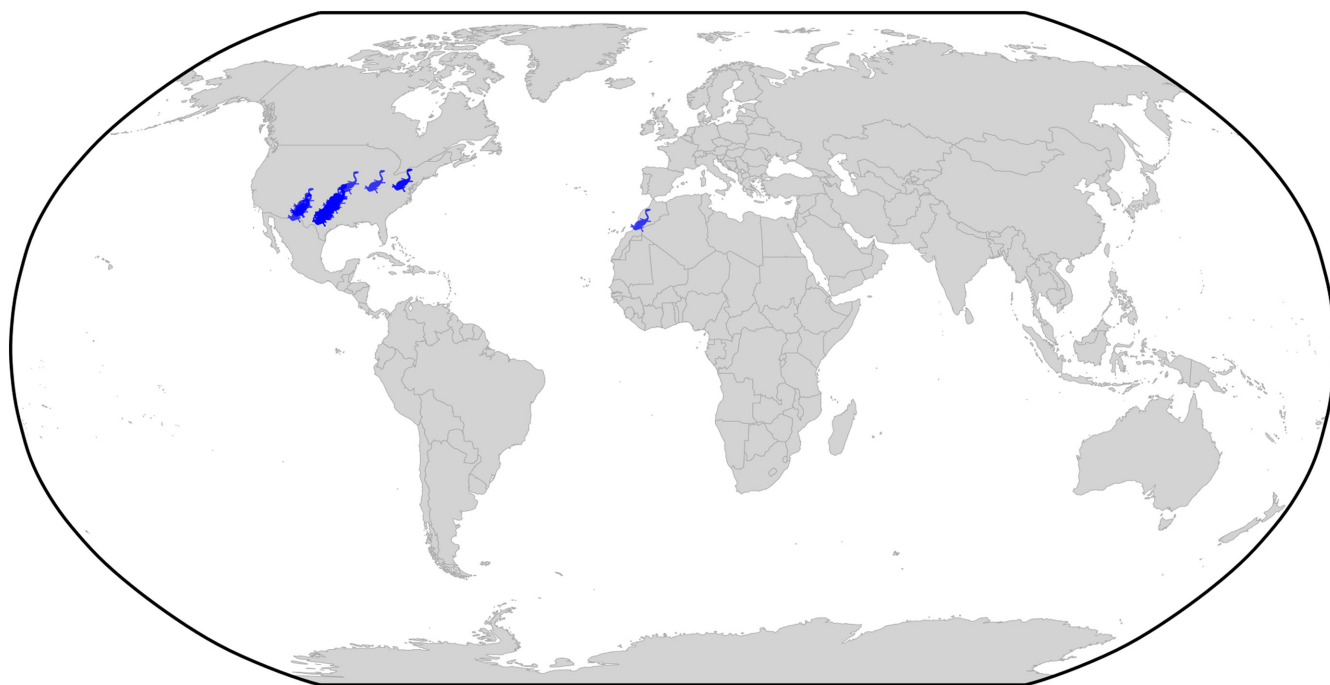
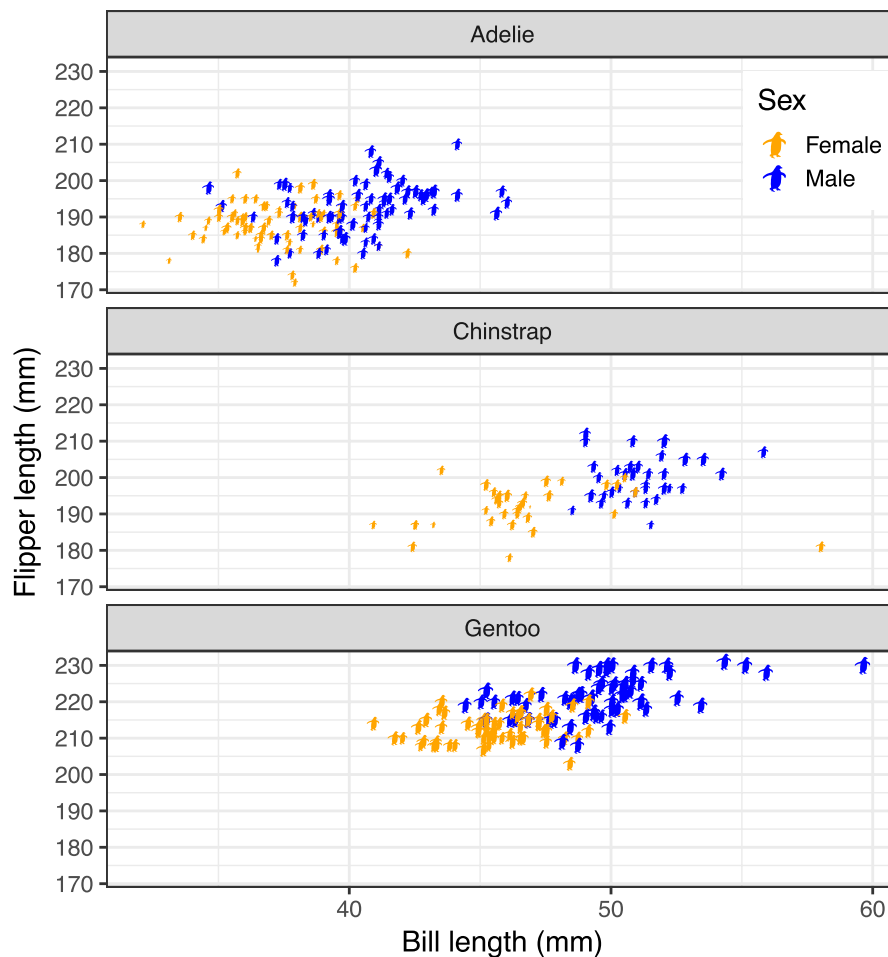


FIGURE 3 Geographic distribution of Carboniferous to Early Triassic *Diplocaulus* fossil occurrences. Organism silhouettes are from PhyloPic (<https://www.phylopic.org>; Keesey, 2023). Silhouette was contributed by Gareth Monger, 2013 (CC BY 3.0). The original silhouette has been modified in colour from black to blue. Map is depicted in the Robinson projection (ESRI:54030). Note that the value of size must be large in such cases to scale with the y-axis range of the map units.


```

# Load libraries
library(rphylopic)
library(ggplot2)
library(palaeoverse)
library(sf)
library(rnaturalearth)
library(rnaturalearthdata)
# Get map data
world <- ne_countries(scale = "medium", returnclass = "sf")
# Get occurrence data
data(tetrapods)
# Subset to desired group
tetrapods <- subset(tetrapods, genus == "Diplocaulus")
# Set up a bounding box
bbox <- st_graticule(crs = st_crs("ESRI:54030"),
  lat = c(-89.9, 89.9), lon = c(-179.9, 179.9))
# Make map
ggplot(data = world) +
  geom_sf(fill = "lightgray", colour = "darkgrey", linewidth = 0.1) +
  geom_phylopic(data = tetrapods, aes(x = lng, y = lat, name = genus),
    size = 6E5, alpha = 0.75, colour = NA, fill = "blue") +
  geom_sf(data = bbox) +
  theme_void() +
  coord_sf(default_crs = st_crs(4326), crs = st_crs("ESRI:54030"))

```

4.3 | Phylogenetics

Another common use case of PhyloPic silhouettes is to represent taxonomic information. In this example, we demonstrate how to use silhouettes within a phylogenetic framework (Figure 4). In this case, the phylogeny, from the *phytools* R package (Revell, 2012), includes taxa across all vertebrates. Even many taxonomic experts are unlikely to know the scientific names of these 11 disparate taxa, so we replace the names with PhyloPic silhouettes. We use the *ggtree* R package (Yu et al., 2017) to plot the phylogeny and the *deephime* R package (Gearty, 2023) to add a geological timescale to the background. We use a vectorised version of the *get_uuid* function to retrieve UUID values for all of the species at once; however, one of the scientific names is not matched in the PhyloPic database so we need to use a higher taxonomic name. We also choose to use the *pick_phylopic* function to select a specific image for the boar. Note that only a single size is specified, and aspect ratio is always maintained, hence why the silhouettes all have the same height but different widths.

```

# Load libraries
library(rphylopic)
library(ggplot2)
library(ggtree)
library(phytools)
library(deephime)
# Get vertebrate phylogeny and data

```

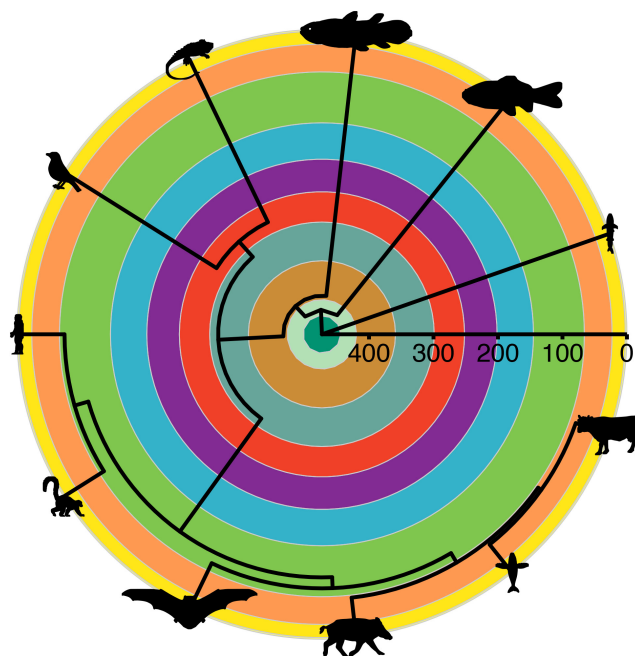


FIGURE 4 A very simplified phylogeny showing the relationships between a selection of extant vertebrates. The coloured background represents geological periods as defined by the International Commission on Stratigraphy, and the axis represents time in millions of years before present. The image silhouettes are from PhyloPic (<https://www.phylopic.org>; Keesey, 2023) and were contributed as follows: *Carcharodon carcharias* by Guillaume Dera (2022; CC0 1.0); *Carassius auratus* by Corrine Avidan (2022; CC0 1.0); *Latimeria chalumnae* by Chuanxin Yu (2021; CC0 1.0); *Homo sapiens* by T. Michael Keesey (2011; CC0 1.0); *Lemur catta* by Ferran Sayoi (2015; CC0 1.0); *Lasiurus cinereus* by Andy Wilson (2022; CC0 1.0); *Sus scrofa* by Steven Traver (2012; CC0 1.0); *Megaptera novaeangliae* by Guillaume Dera (2022; CC0 1.0); *Bos taurus* by Steven Traver (2012; CC0 1.0); *Iguana iguana* by Jack Mayer Wood (2014; CC0 1.0); and *Turdus migratorius* by Karina Garcia (2022; CC BY-NC 3.0).

```

data(vertebrate.tree)
# Make a data.frame for the PhyloPic names
vertebrate.data <- data.frame(species = vertebrate.tree$tip.label,
  uuid = NA)
# Try to get PhyloPic UUIDs for the species names
vertebrate.data$uuid <- sapply(vertebrate.tree$tip.label,
  function(x) tryCatch(get_uuid(x,
    filter = "sa",
    error = function(e) NA))
# We're still missing one for the bat, let's use the subfamily
vertebrate.data$uuid[vertebrate.data$species == "Myotis lucifugus"]
<-
  get_uuid("Vespertilioninae", filter = "sa")
# Pick a different boar image; e.g. #2
boar_vec <- pick_phylopic("Sus scrofa", view = 5, filter = "sa")
# Extract the UUID
vertebrate.data$uuid[vertebrate.data$species == "Sus scrofa"] <-
  get_uuid(img = boar_vec)

```

```
# Plot the tree with a geological timescale in the background
revts(ggtree(vertebrate.tree, size = 1)) %<+% vertebrate.data +
geom_phylopic(aes(uuid = uuid), size = 25) +
scale_x_continuous(breaks = seq(-500, 0, 100),
labels = seq(500, 0, -100)) +
coord_geo_polar(dat = "periods") +
theme(line = element_line(linewidth = 1),
axis.text.r = element_text(size = 5, hjust = -0.5, vjust = -1.5))
```

5 | RESOURCES

We have made several resources available for our users. First, we have built a package website (<http://rphylopic.palaeoverse.org>) that provides information on how to contribute to rphylopic, report issues and bugs, and a contributor code of conduct. We have also made available a cheat sheet and three vignettes/tutorials for the package, which provide user-friendly usage guides (<https://rphylopic.palaeoverse.org>).

AUTHOR CONTRIBUTIONS

William Gearty and Lewis A. Jones developed the source code for the software and contributed to the writing of the manuscript. Both authors gave final approval for publication.

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CONFLICT OF INTEREST STATEMENT

We declare we have no conflict of interest.

PEER REVIEW

The peer review history for this article is available at <https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/2041-210X.14221>.

DATA AVAILABILITY STATEMENT

The rphylopic R package can be installed via the Comprehensive R Archive Network (CRAN) using the `install.packages("rphylopic")` function. The package has been tested on Windows, Mac and Linux (Ubuntu) operating systems using GitHub actions. Source code for the package is available at <https://github.com/palaeoverse-community/rphylopic>. The code is also archived in Zenodo through continuous integration (Gearty et al., 2023). All code is released under a GPL (≥3) licence.

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