

Add silhouettes with rphylopic :: CHEAT SHEET



Install rphylopic

rphylopic allows you to add species' silhouettes from phylopic to ggplot2 or base plots:

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

Development version
install.packages("remotes")
remotes::install_github("sckott/rphylopic")

library('rphylopic')
```

uuid

Universally unique identifier (uuid) is a 128-bit number. It has 32 alphanumeric characters in the form of 8-4-4-4-12. Every silhouette has a uuid to uniquely identify it.

Find silhouettes

1. Work with names.

- **name_search**(text, options)[[1]]
Searches the uuid code based on common name or taxonomy of a species. The options can be namebankID, type, names, root, uri.
- **name_get**(uuid, options)
Get information on a name using the uuid code. The options can be citationStart, html, namebankID, root.
- **name_images**(uuid, options = 'credit')
Searches for different images for a taxonomic name.
- **name_taxonomy**(uuid, options, as)
Returns taxonomic name based on uuid code. Options can be string, and as can be list, table, json.
- **name_taxonomy_many**(uuid, options, as)
Returns taxonomic names for two or more concatenated (c()) uuid codes.
- **name_taxonomy_sources**(uuid)
Gives information on the sources for a name's taxonomy given a uuid.

2. Work with uBio data

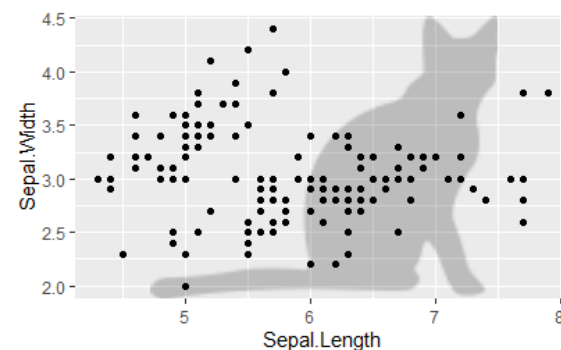
- **ubio_get**(namebankID)
Retrieve the uuid code based on the namebankID number.

Plot silhouettes

1. Plot a silhouette behind a plot

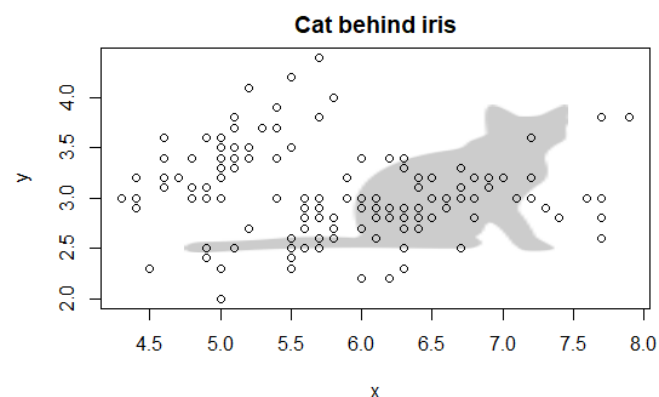
```
• ggplot
library(ggplot2)
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]
```

```
ggplot(data = iris,
       aes(x = Sepal.Length,
           y = Sepal.Width)) +
  geom_point() +
  add_phylopic(cat, alpha = 0.2)
```



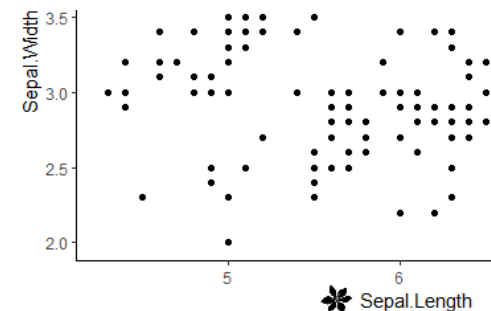
```
• Base plot
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]
```

```
plot(1, 1,
     type = 'n',
     main = "Cat behind iris")
add_phylopic_base(cat,
                  x = 0.5,
                  y = 0.5,
                  ysize = 0.8,
                  alpha = 0.2)
```



2. Plot a silhouette anywhere in a plot

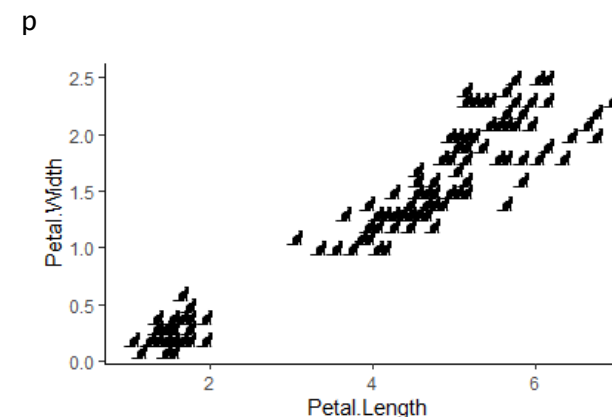
```
ggpubr::ggarrange(plot) +
  add_phylopic(irisimg,
               alpha = 1,
               x = 0.43,
               y = 0.05,
               ysize = 0.06)
```



3. Plot silhouettes as points in a plot

```
• ggplot2
p <- ggplot(iris,
            aes(Petal.Length,
                Petal.Width)) +
  geom_blank() +
  theme_classic()

for (i in 1:nrow(iris)) {
  p <- p +
    add_phylopic(cat,
                 alpha = 1,
                 iris$Petal.Length[i],
                 iris$Petal.Width[i],
                 ysize = 0.2)
}
```

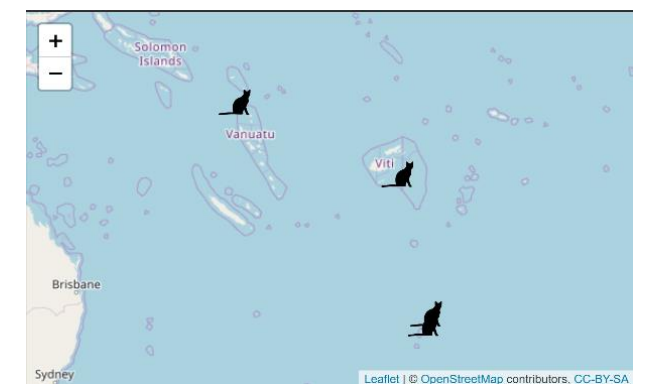


4. Save PNG file to disk

- Download a silhouette from <http://phylopic.org/> and save it in your working directory.
img <- png::readPNG("img.png")

5. Use silhouettes as icons in leaflet plots

```
library(leaflet)
data(quakes) ## this is a table
# get an image
cat <- image_data("23cd6aa4-9587-4a2e-8e26-de42885004c9", size = 128)[[1]]
# save to disk
cating <- save_png(cat)
# make an icon. See ?makeIcon for more
# iconwidth is in pixels
cat_icon <- makeIcon(iconUrl = cating,
                     iconwidth = 30)
# make the plot, just 7:10 rows
leaflet(data = quakes[7:10,]) %>%
  addTiles() %>%
  addMarkers(~long, ~lat,
             icon = cat_icon)
```



Citation
Don't forget to cite rphylopic. See how here:

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