Project presentations and rmarkdown example

Contents

1 Project presentations

Ignite format: 5 minutes presentations (20 slides, 15 seconds each)

You can find some advice and examples here and here

Presentations must include:

1. Title
2. Description of main aim or question
3. Brief methods description (Main data sources and methods)
4. A brief description of your data (e.g., table, map, plot showing the number of species, areas, etc.)
5. Primary results and a brief discussion

AVOID to include unnecessary code into the R markdown. Code for data downloading and cleaning should be incorporated into a separate R file. Start the document with the clean, processed and merge data.

2 Project Rmarkdown

3 Example: Life history traits and distribution of Hyraxes

```
# Include here your libraries
library(knitr)
library(tidyverse)
library(maptools)
library(ggpubr)
```

3.1 Introduction

- A brief background
- The main question or aim of the project

3.2 Methods

- Github repository link
- Data sources
- Data cleaning and processing
- Describe main procedures
- Data summary (how many species? which groups? how many records?...)

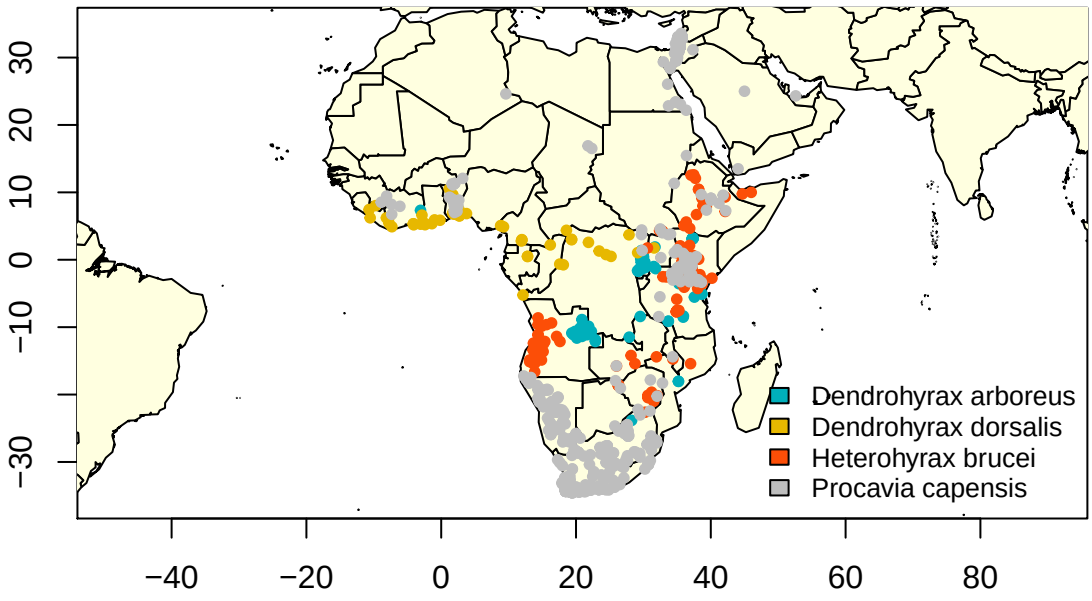
3.2.1 Data description

```
## Data decription
Hyraxes_df<-read.csv("data/processed/Hyracoidea_traits_geo.csv")

Hyraxes_df %>%
  group_by(genus,species) %>%
  tally() %>%
  kable()
```

genus	species	n
Dendrohyrax	arboreus	123
Dendrohyrax	dorsalis	66
Heterohyrax	brucei	132
Procavia	capensis	599

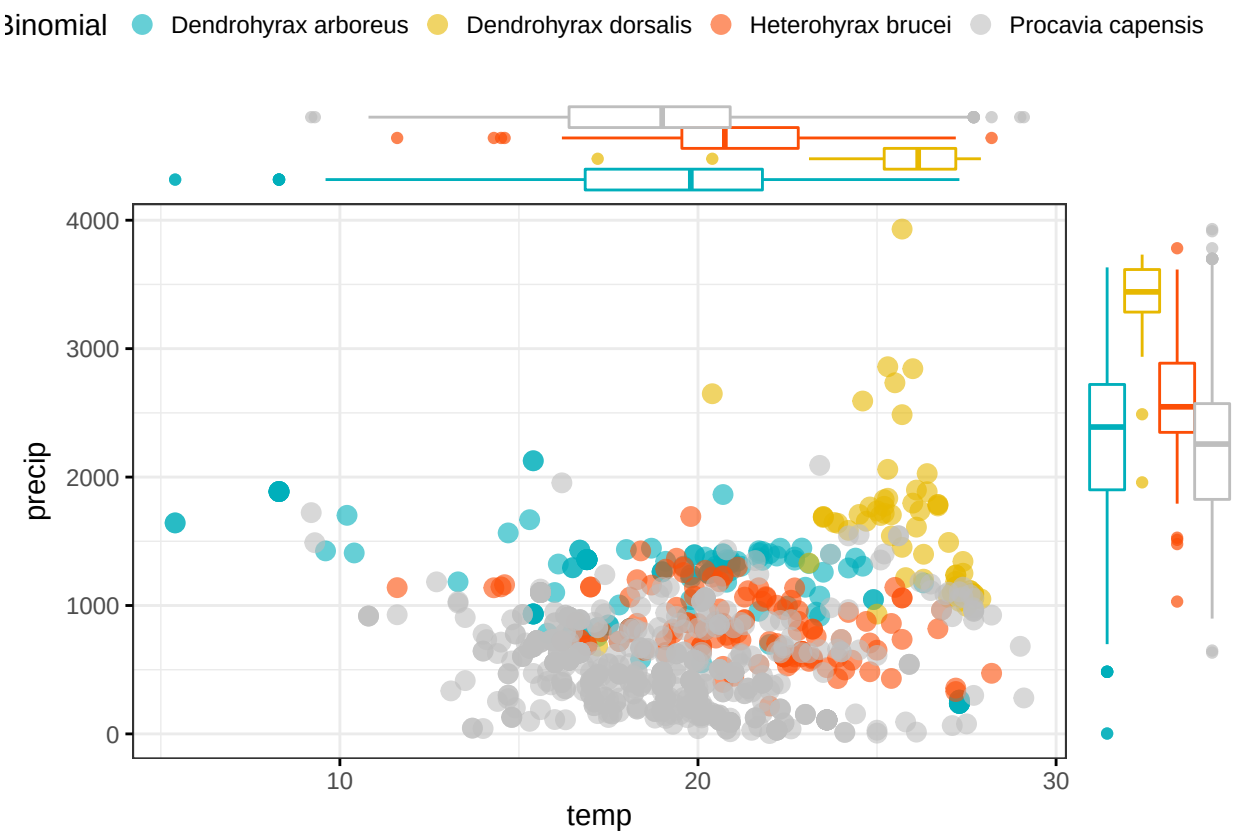
3.2.2 Data distribution

```
# Distribution
Hyraxes_df_geo<-Hyraxes_df
coordinates(Hyraxes_df_geo)<-~lon + lat

# Get map and change projection
data(wrld_simpl)
proj4string(wrld_simpl)<-proj4string(Hyraxes_df_geo)

# Colour vector
cols<-c("#00AFBB", "#E7B800", "#FC4E07","grey")
cols_sp<-cols[Hyraxes_df$Binomial]

# Plot map and species distribution
plot(wrld_simpl, xlim=c(min(Hyraxes_df$lon)-1,max(Hyraxes_df$lon)+1),
     ylim=c(min(Hyraxes_df$lat)-1,max(Hyraxes_df$lat)+1), axes=TRUE, col="light yellow")

points(Hyraxes_df_geo,col=cols_sp, pch=20)
legend('bottomright', bty='n', legend=unique(Hyraxes_df$Binomial),
cex=0.8, fill=unique(cols_sp))
```



3.3 Results and Discussion

```
p <- ggplot(Hyraxes_df, aes(temp, precip)) +
  geom_point(aes(color = Binomial), size = 3, alpha = 0.7) +
  scale_color_manual(values = c("#00AFBB", "#E7B800", "#FC4E07","grey"))+
  xlab("Temperature C") +
  ylab("Precipitation")

# Grouped Scatter plot with marginal density plots
ggscatterhist(
  Hyraxes_df, x = "temp", y = "precip",
  color = "Binomial", size = 3, alpha = 0.6,
  palette = c("#00AFBB", "#E7B800", "#FC4E07","grey"),
  margin.plot = "boxplot",
  ggtheme = theme_bw()
  )
```


Binomial
Dendrohyrax arboreus
Dendrohyrax dorsalis
Heterohyrax brucei
Procavia capensis
precip
4000
3000
2000
1000
0
10
20
30
temp