

Visualizations

```
#load packages
library(tidyverse)
```

```
-- Attaching packages ----- tidyverse 1.3.2 --
v ggplot2 3.3.6      v purrr  0.3.4
v tibble  3.1.8      v dplyr  1.0.10
v tidyr   1.2.0      v stringr 1.4.1
v readr   2.1.2      v forcats 0.5.2
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

```
library(tidymodels)
```

```
-- Attaching packages ----- tidymodels 1.0.0 --
v broom      1.0.1      v rsample      1.1.0
v dials      1.0.0      v tune         1.0.0
v infer      1.0.3      v workflows    1.0.0
v modeldata  1.0.0      v workflowsets 1.0.0
v parsnip    1.0.1      v yardstick    1.0.0
v recipes    1.0.1
-- Conflicts ----- tidymodels_conflicts() --
x scales::discard() masks purrr::discard()
x dplyr::filter()   masks stats::filter()
x recipes::fixed()  masks stringr::fixed()
x dplyr::lag()      masks stats::lag()
x yardstick::spec() masks readr::spec()
x recipes::step()   masks stats::step()
* Use suppressPackageStartupMessages() to eliminate package startup messages
```

```
library(knitr)
library(ape)
```

Attaching package: 'ape'

The following object is masked from 'package:rsample':

complement

The following object is masked from 'package:dials':

degree

```
library(caper)
```

Loading required package: MASS

Attaching package: 'MASS'

The following object is masked from 'package:dplyr':

select

Loading required package: mvtnorm

```
library(phytools)
```

Loading required package: maps

Attaching package: 'maps'

The following object is masked from 'package:purrr':

map

```
library(nlme)
```

Attaching package: 'nlme'

The following object is masked from 'package:dplyr':

collapse

```
library(gee)
library(TreeTools)
```

Attaching package: 'TreeTools'

The following object is masked from 'package:phytools':

as.multiPhylo

```
library(patchwork)
```

Attaching package: 'patchwork'

The following object is masked from 'package:MASS':

area

```
library(phyloilm)
library(broom)
library(readxl)
```

```
#load data and phylogenetic tree
```

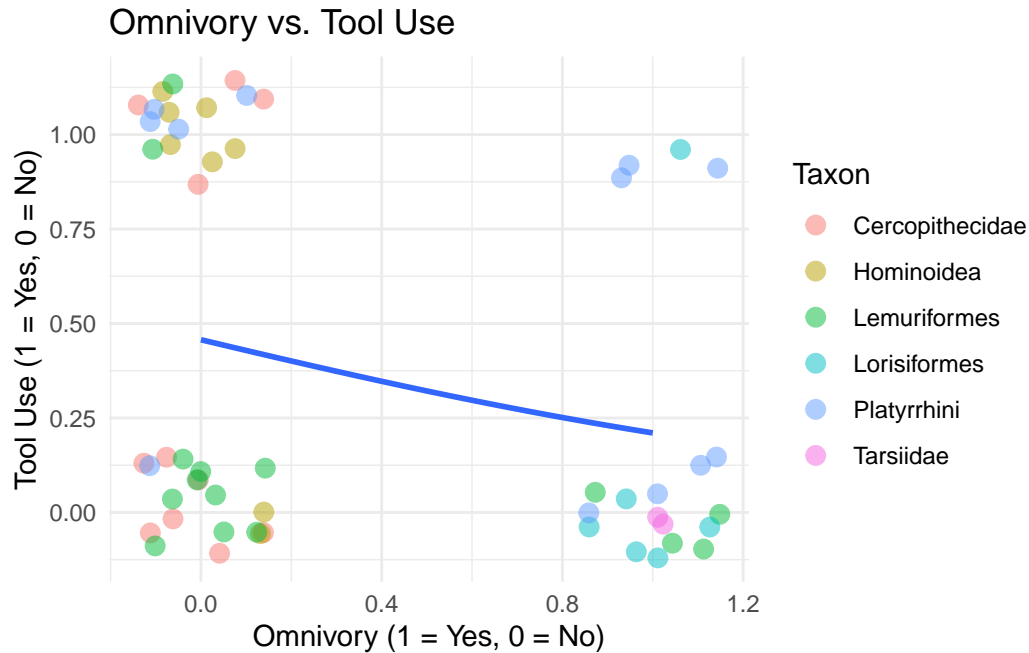
```
tool_use_expanded <- read_xlsx("PrimateToolUseDataset.xlsx", sheet = "Dataset")
```

```
tooluse.tree <- read.nexus("ToolUsePhylo54.nex")
```

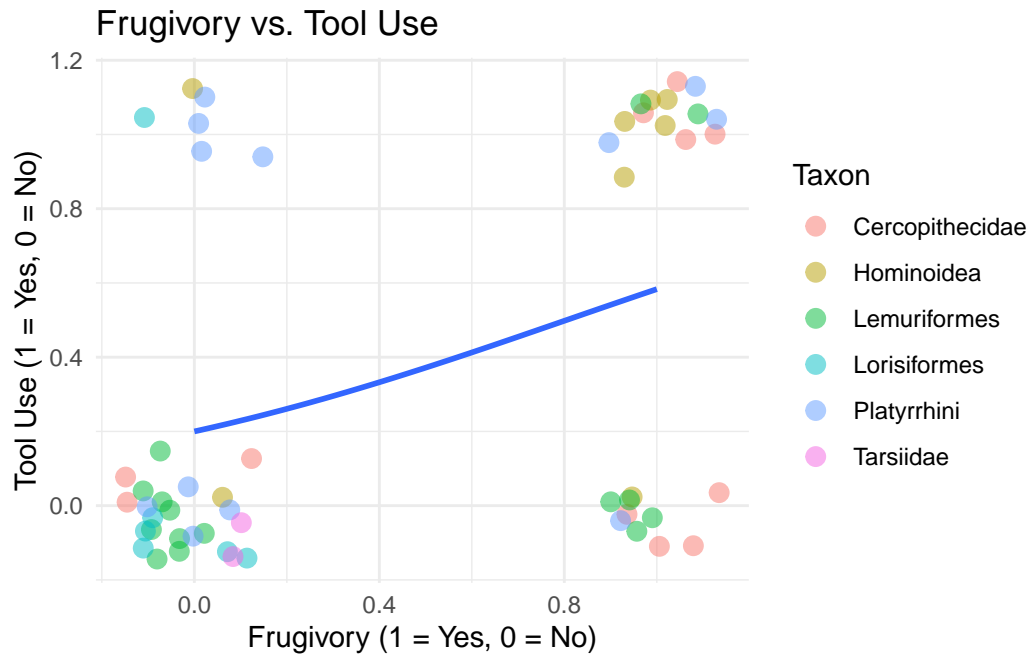
```
#EDA
```

```
set.seed(13)
```

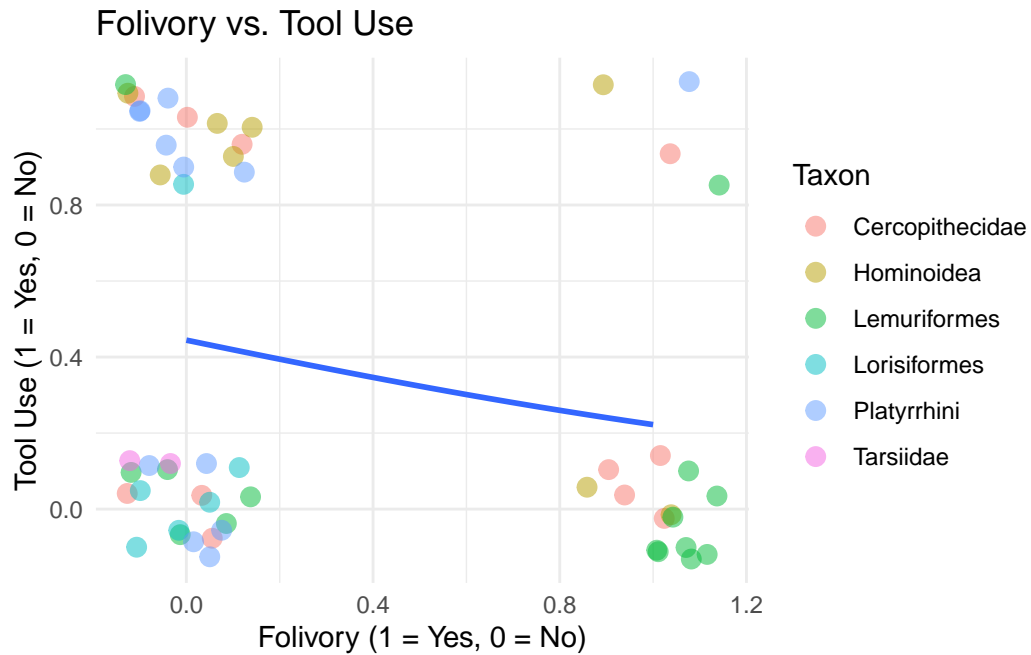
```
ggplot(tool_use_expanded, aes(x = Omnivore, y = Tool_Use)) +
  geom_jitter(width = 0.15, height = 0.15,
             aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args = list(family="binomial")) +
  labs(title = "Omnivory vs. Tool Use",
       y = "Tool Use (1 = Yes, 0 = No)",
       x = "Omnivory (1 = Yes, 0 = No)") +
  theme_minimal()
```



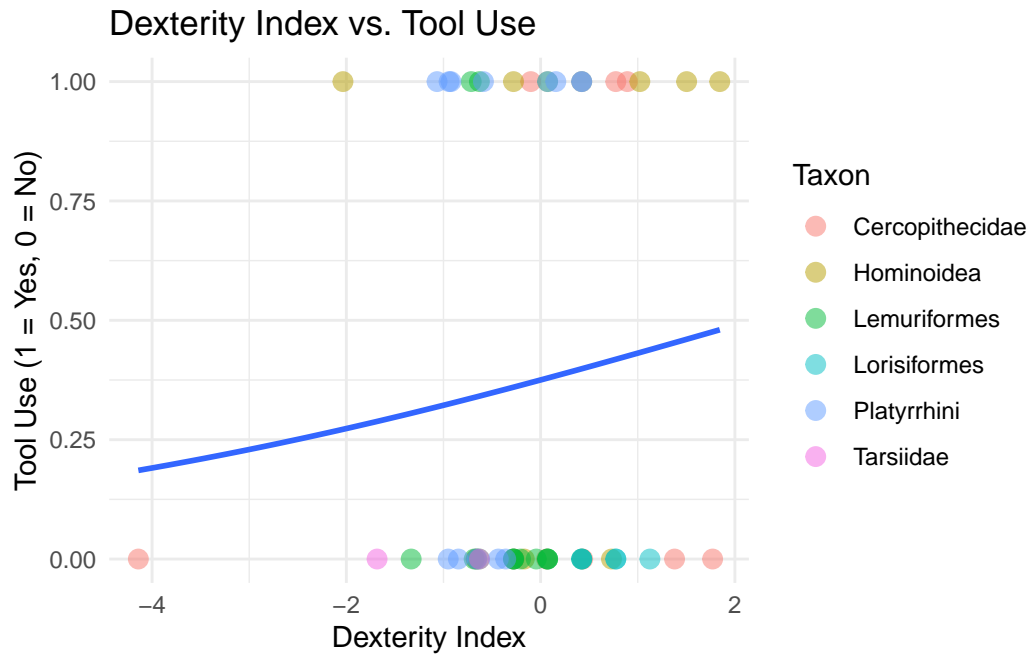
```
ggplot(tool_use_expanded, aes(x = Frugivore, y = Tool_Use)) +
  geom_jitter(width = 0.15, height = 0.15, aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args= list(family="binomial")) + labs(title = "
  y = "Tool Use (1 = Yes, 0 = No)",
  x = "Frugivory (1 = Yes, 0 = No)") +
  theme_minimal()
```



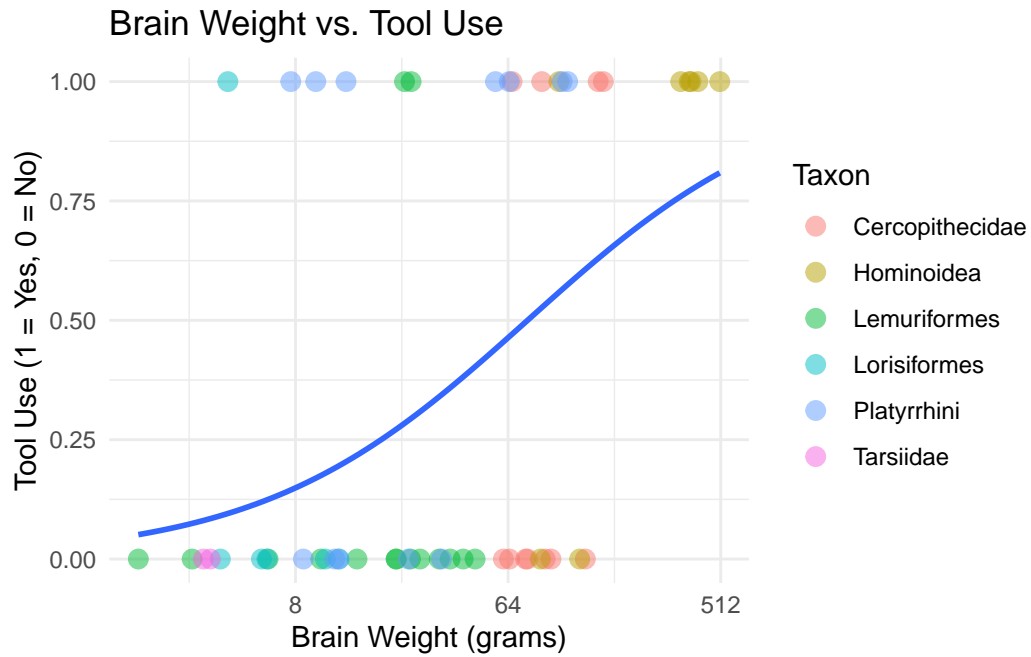
```
ggplot(tool_use_expanded, aes(x = Folivore, y = Tool_Use)) +
  geom_jitter(width = 0.15, height = 0.15, aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args= list(family="binomial")) + labs(title =
    y = "Tool Use (1 = Yes, 0 = No)",
    x = "Folivory (1 = Yes, 0 = No)") + theme_minimal()
```



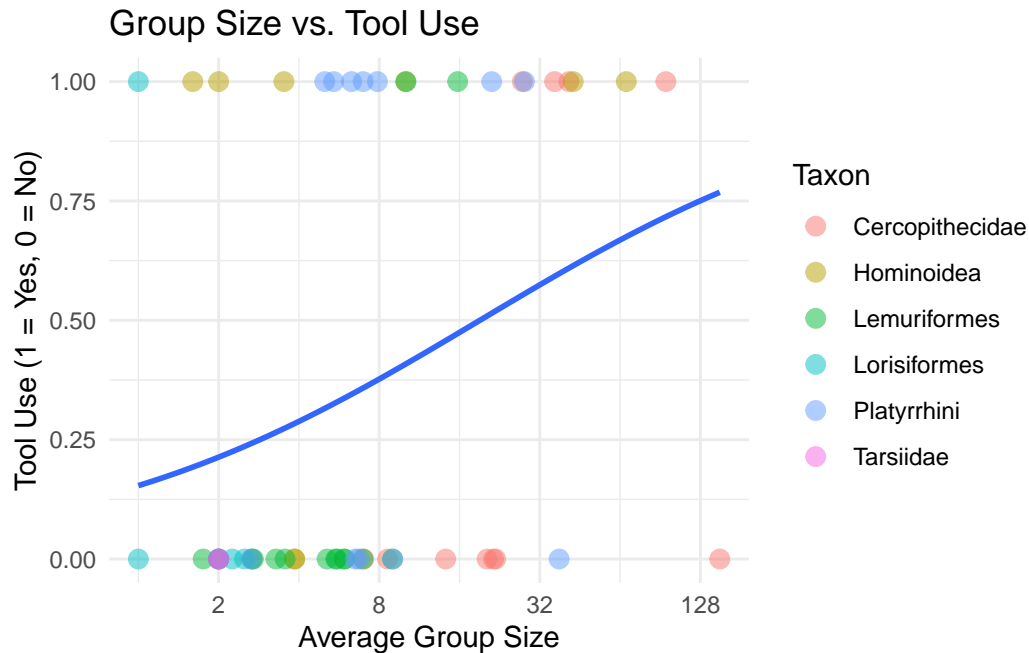
```
ggplot(tool_use_expanded, aes(Dexterity_Index, Tool_Use)) +
  geom_point(aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F,
              method.args = list(family="binomial")) +
  labs(title = "Dexterity Index vs. Tool Use",
       y = "Tool Use (1 = Yes, 0 = No)",
       x = "Dexterity Index") +
  theme_minimal()
```



```
ggplot(tool_use_expanded, aes(Brain_Weight_grams, Tool_Use)) +
  geom_point(aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F,
              method.args= list(family="binomial")) +
  labs(title = "Brain Weight vs. Tool Use",
       y = "Tool Use (1 = Yes, 0 = No)",
       x = "Brain Weight (grams)") +
  scale_x_continuous(trans='log2') +
  theme_minimal()
```



```
ggplot(tool_use_expanded, aes(Group_Size, Tool_Use)) +
  geom_point(aes(color = Taxon), size = 3, alpha = 0.5) + geom_smooth(method = glm, se = F)
labs(title = "Group Size vs. Tool Use",
      y = "Tool Use (1 = Yes, 0 = No)",
      x = "Average Group Size") +
scale_x_continuous(trans='log2') + theme_minimal()
```

#phylogeny

```
#this ensures that phylogeny and data have species in the same order
species <- tibble(TipLabels(tooluse.tree, single = TRUE)) |>
  rename("Species" = 1)

tool_use_expanded2 <- merge(species, tool_use_expanded, sort = FALSE)

#this turns dummy variables into factors
tool_use_expanded2$Omnivore <- as.factor(tool_use_expanded2$Omnivore)
tool_use_expanded2$Folivore <- as.factor(tool_use_expanded2$Folivore)
tool_use_expanded2$Frugivore <- as.factor(tool_use_expanded2$Frugivore)
tool_use_expanded2$Brain_Weight_grams <-
  as.numeric(tool_use_expanded2$Brain_Weight_grams)

tool_use_data_only <- tool_use_expanded2 |> dplyr::select(Species, Tool_Use, Brain_Weight_grams)

row.names(tool_use_data_only) <- tool_use_data_only$Species

tool_use_data_only <- tool_use_data_only |>
  dplyr::select(Tool_Use, Brain_Weight_grams, Group_Size, Frugivore, Folivore, Omnivore, D
```

```

x <- as.matrix(tool_use_data_only[,1])

a <- setNames(x , tool_use_expanded2$Species)
row.names(a) <- tool_use_expanded2$Species

fmode<-as.matrix(setNames(tool_use_data_only[,as.factor(1)],
                           rownames(tool_use_expanded2)))

row.names(fmode) <- tool_use_expanded2$Species

tool_use_expanded2$Species

```

[1] "Cercopithecus_diana"	"Cercopithecus_lhoesti"
[3] "Avahi_laniger"	"Cheirogaleus_major"
[5] "Cheirogaleus_medius"	"Daubentonia_madagascariensis"
[7] "Eulemur_coronatus"	"Eulemur_fulvus_fulvus"
[9] "Eulemur_macaco_macaco"	"Eulemur_mongoz"
[11] "Hapalemur_griseus"	"Indri_indri"
[13] "Lemur_catta"	"Microcebus_murinus"
[15] "Propithecus_diadema"	"Propithecus_verreauxi"
[17] "Varecia_variegata_variegata"	"Alouatta_seniculus"
[19] "Ateles_fusciceps"	"Ateles_geoffroyi"
[21] "Callimico_goeldii"	"Callithrix_geoffroyi"
[23] "Callithrix_jacchus"	"Cebus_albifrons"
[25] "Leontopithecus_chrysomelas"	"Leontopithecus_rosalia"
[27] "Saguinus_oedipus"	"Saimiri_sciureus"
[29] "Loris_tardigradus"	"Nycticebus_coucang"
[31] "Gorilla_gorilla_gorilla"	"Hylobates_lar"
[33] "Hylobates_pileatus"	"Pan_paniscus"
[35] "Pan_troglodytes_troglodytes"	"Pongo_abelii"
[37] "Pongo_pygmaeus"	"Symphalangus_syndactylus"
[39] "Pithecia_pithecia"	"Macaca_fascicularis"
[41] "Macaca_mulatta"	"Macaca_sylvanus"
[43] "Mandrillus_sphinx"	"Papio_hamadryas"
[45] "Theropithecus_gelada"	"Colobus_guereza"
[47] "Presbytis_comata"	"Pygathrix_nemaeus"
[49] "Euoticus_elegantulus"	"Galago_moholi"
[51] "Galago_senegalensis"	"Otolemur_crassicaudatus"
[53] "Tarsius_bancanus"	"Tarsius_syrichta"

```

dotTree(tooluse.tree,a,colors=setNames(c("blue","red"), c("tool","no tool")),ftype="i",fsi

```



```

b <- as.matrix(as.factor(a))
row.names(b) <- tool_use_expanded2$Species

b <- tibble(b) |> mutate(Species = row.names(b))
b$b <- as.numeric(b$b)
row.names(b) <- tool_use_expanded2$Species

tool.trees<-make.simmap(tooluse.tree,b,nsim=100)

obj<-densityMap(tool.trees,states=
  c("No Tool Use","Tool Use"),plot=FALSE)

plot(obj,lwd=4,outline=TRUE,fsiz=c(0.7,0.9),legend=50)

```