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
```

```r
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

```r
library(caper)
```

Loading required package: MASS

Attaching package: 'MASS'

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

    select

Loading required package: mvtnorm

```r
library(phytools)
```

Loading required package: maps

Attaching package: 'maps'

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

    map

```r
library(nlme)
```

```
Attaching package: 'nlme'

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

    collapse
```

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

```
Attaching package: 'TreeTools'

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

    as.multiPhylo
```

```r
library(patchwork)
```

```
Attaching package: 'patchwork'

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

    area
```

```r
library(phylolm)
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)
```
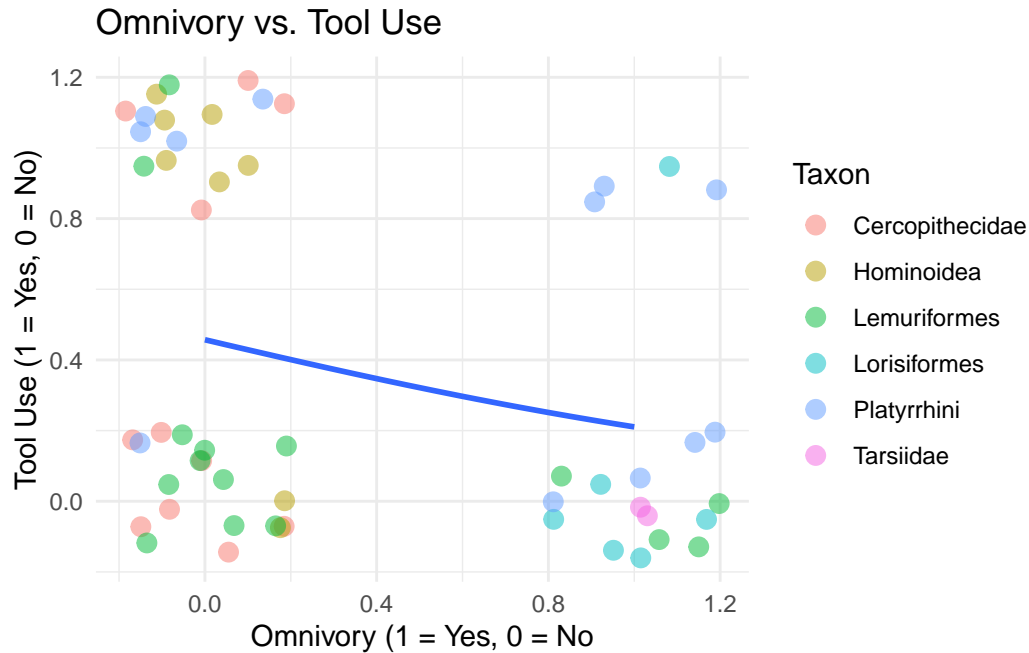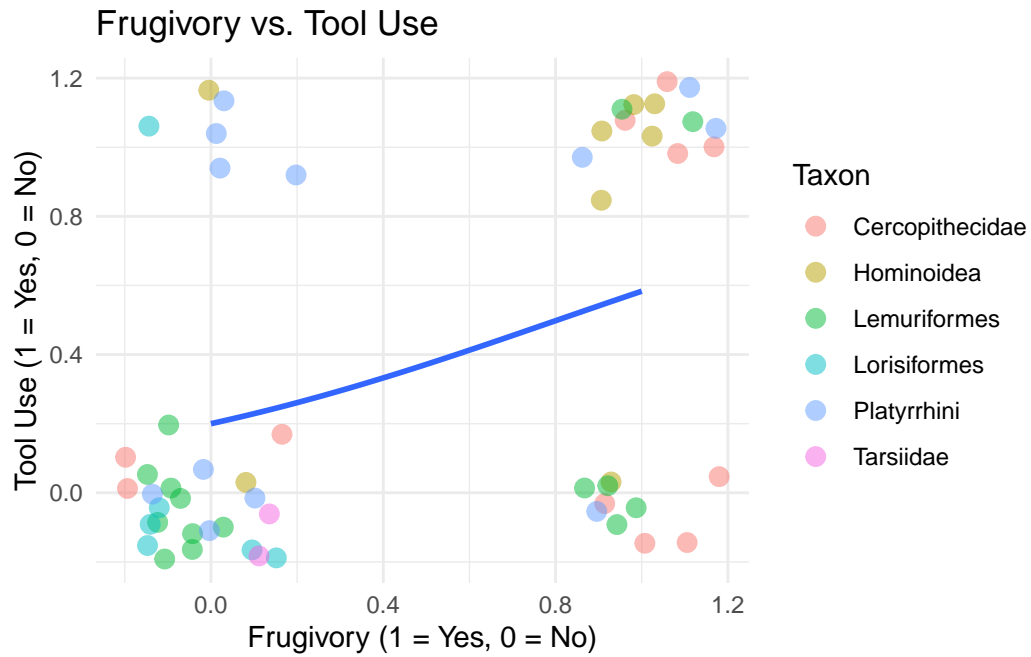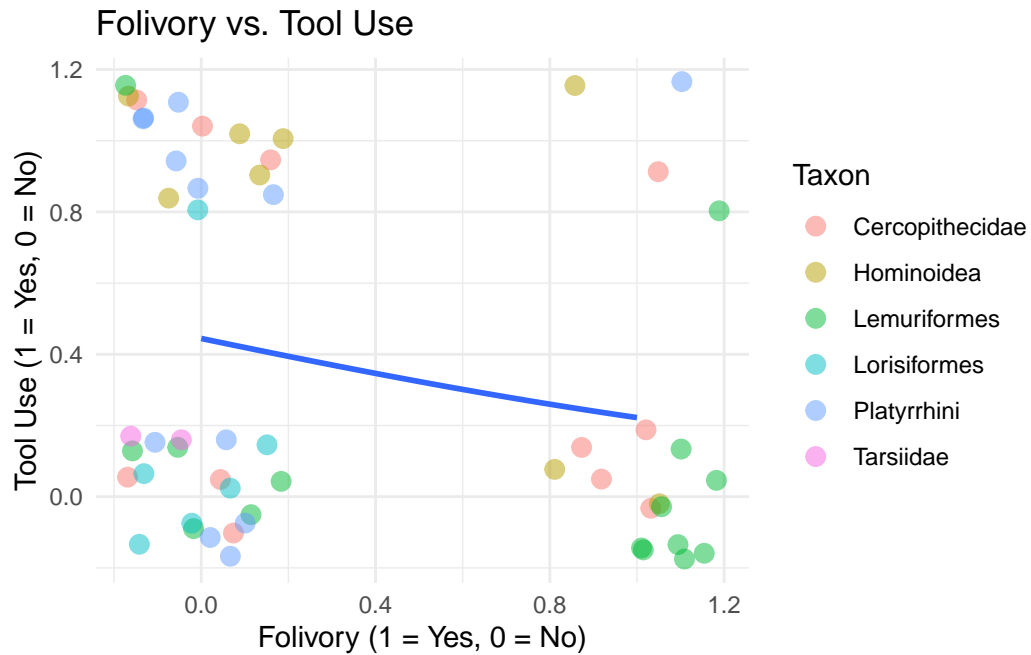
```
ggplot(tool_use_expanded, aes(x = Omnivore, y = Tool_Use)) +
  geom_jitter(width = 0.2, height = 0.2,
              aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args = list(family="binomial")) +
  labs(title = "Omnivory vs. Tool Use",
       y = "Tool Use (1 = Yes, 0 = No)",
       x = "Omnivory (1 = Yes, 0 = No") +
  theme_minimal()
```
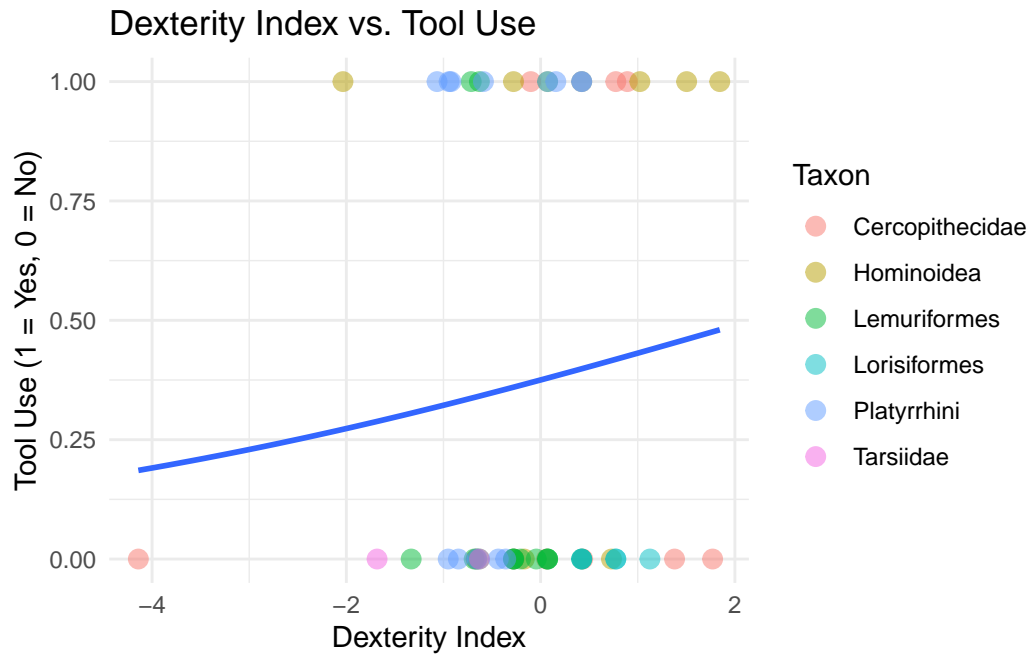


```
ggplot(tool_use_expanded, aes(x = Frugivore, y = Tool_Use)) +
  geom_jitter(width = 0.2, height = 0.2, aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args= list(family="binomial")) + labs(title = "
       y = "Tool Use (1 = Yes, 0 = No)",
       x = "Frugivory (1 = Yes, 0 = No)") +
  theme_minimal()
```
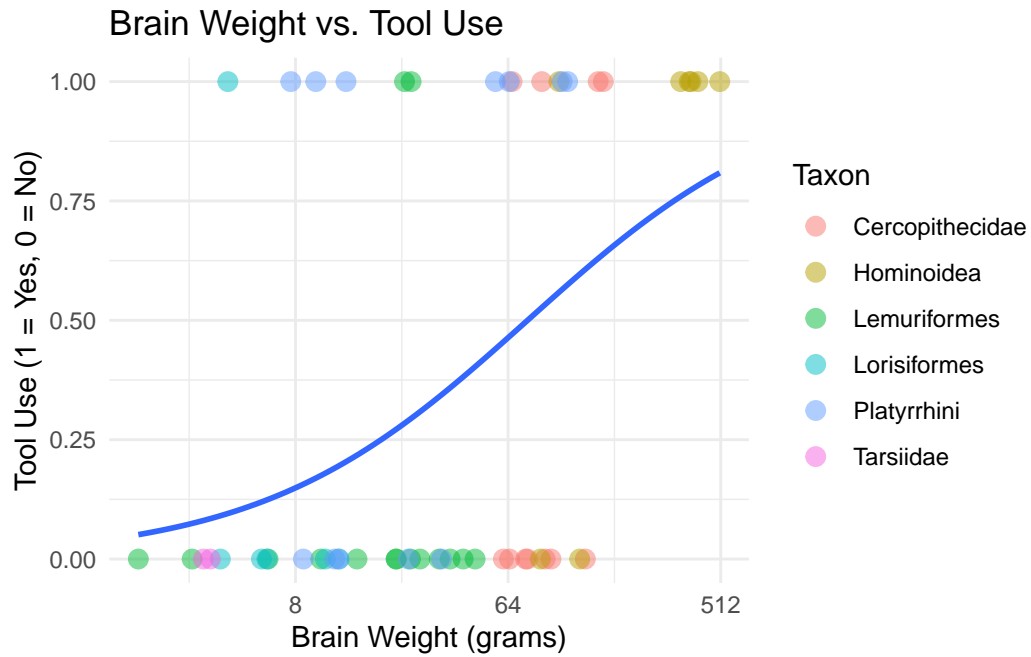
Frugivory vs. Tool Use


```
ggplot(tool_use_expanded, aes(x = Folivore, y = Tool_Use)) +
  geom_jitter(width = 0.2, height = 0.2, 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()
```

Folivory vs. Tool Use


```
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()
```

Dexterity Index vs. Tool Use


```
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()
```

Brain Weight vs. Tool Use


```
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()
```

Group Size vs. Tool Use