Tool Use Analysis

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```
#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()
* Learn how to get started at https://www.tidymodels.org/start/
```

```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")
```
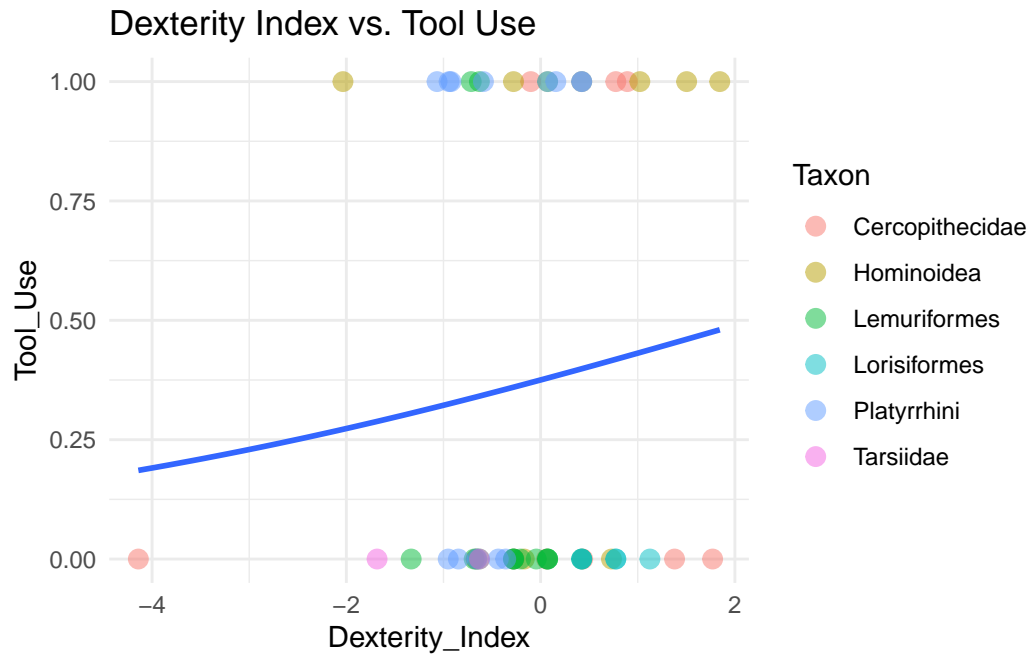
```
#EDA
set.seed(13)

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)") +
  theme_minimal()
```
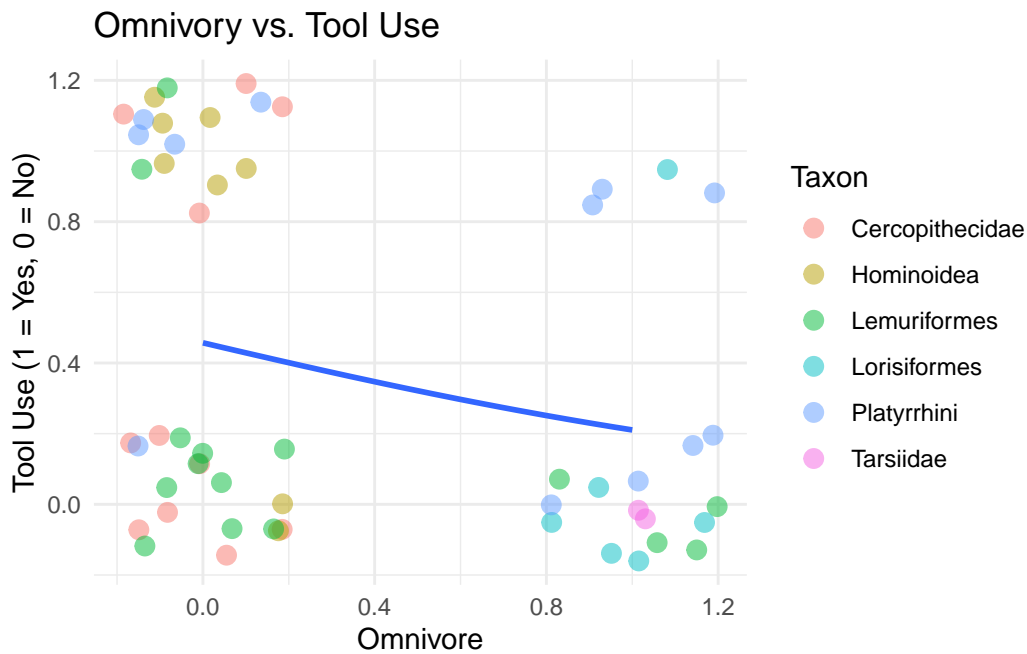


```
ggplot(tool_use_expanded, aes(x = Frugivore, y = Tool_Use)) +
  geom_jitter(width = 0.2, height = 0.2, aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args= list(family="binomial")) +
  labs(title = "Frugivory vs. Tool Use") +
  theme_minimal()
```
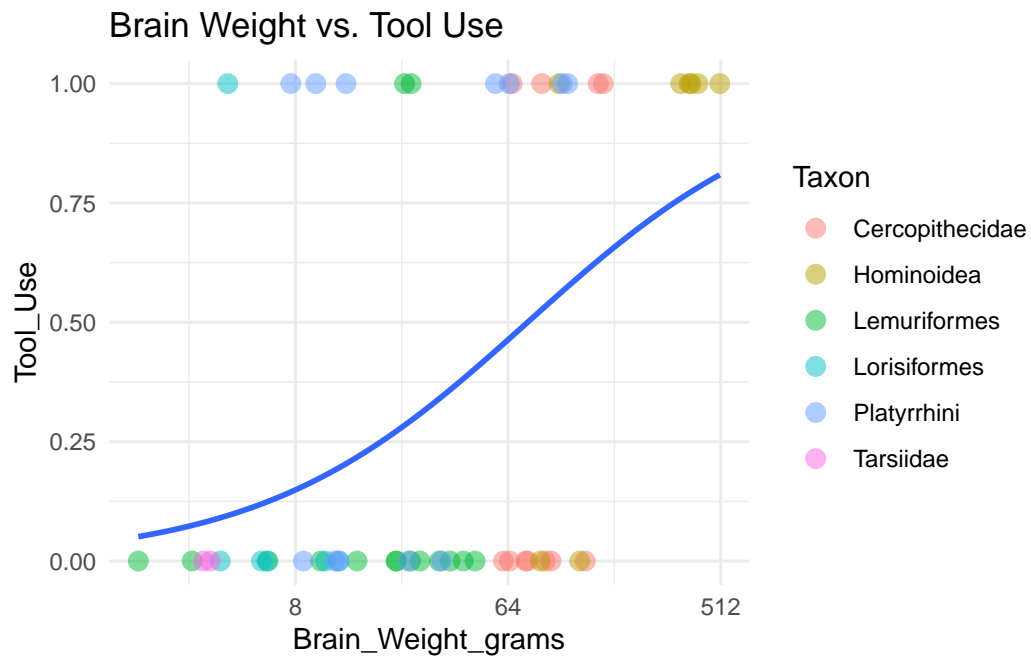
Frugivory vs. Tool Use

```
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 = "Folivory vs. Tool Use") +
  theme_minimal()
```

Folivory vs. Tool Use
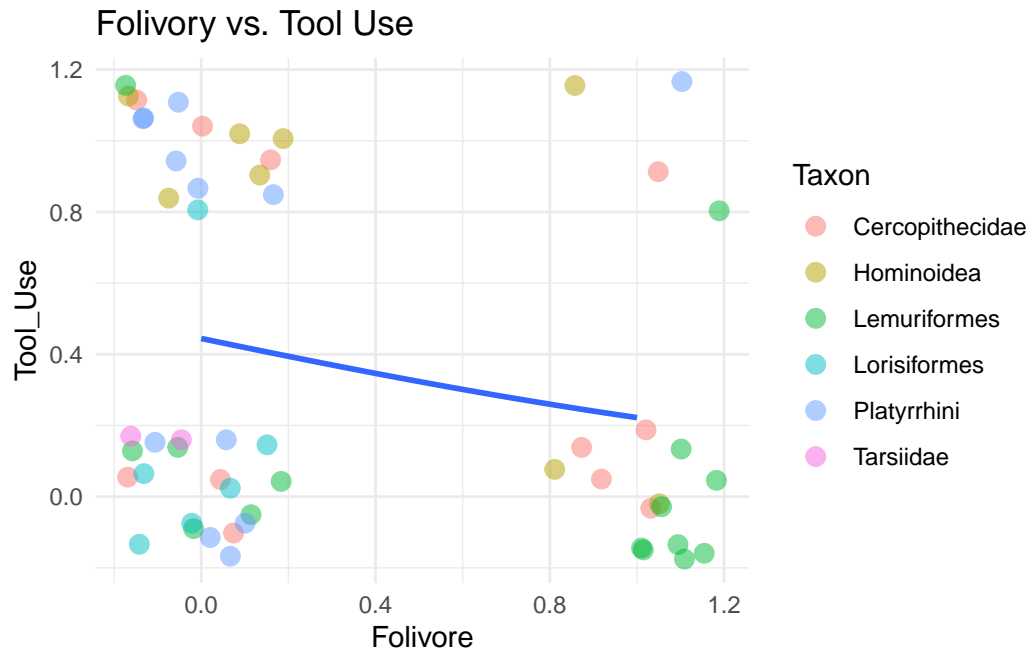
```
ggplot(tool_use_expanded, aes(Dexterity_Index, Tool_Use)) +
  geom_point(aes(color = Taxon), size = 3, alpha = 0.5) +
  geom_smooth(method = glm, se = F, method.args= list(family="binomial"))  +
  labs(title = "Dexterity Index vs. Tool Use") +
  theme_minimal()
```

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")  +
  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, method.args= list(family="binomial"))  +
  labs(title = "Group Size vs. Tool Use")  +
  scale_x_continuous(trans='log2') +
  theme_minimal()
```

Group Size vs. Tool Use
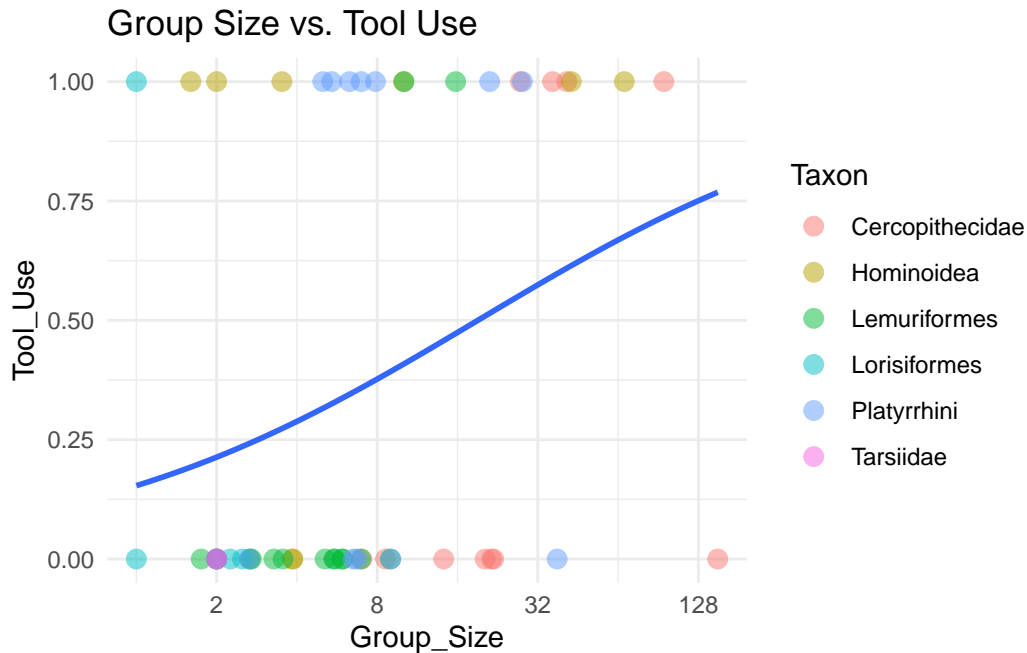

```r
#this ensures that phylogeny and data have species in the same order
species <- tibble(TipLabels(tooluse.tree, single = TRUE)) |>
  rename("Species" = 1)

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)


row.names(tool_use_expanded2) <- tool_use_expanded2$Species
rownames(tool_use_expanded2) == tooluse.tree$tip.label
```

```
 [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[16] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[31] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[46] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```r
#row names in the database matchup with tree tip labels ??
```

```
#this is the global model with all variables included
set.seed(1)
model <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
            log(Group_Size, 2) + Omnivore + Folivore + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached
        log.alpha.bound = 8) #increased so alpha doesn't reach bound
```

#WARNING: the following code chunks will take a long time to run

There are 63 different ways to include 6 different variables in the model.

```
#modelito means little model
#modelitos do not include all the variables
#there are 63 ways to choose which variables to include/exclude

#excluding 1 variable

modelito101 <- phyloglm(Tool_Use ~
            log(Group_Size, 2) + Omnivore + Folivore + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito102 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
            Omnivore + Folivore + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito103 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
            log(Group_Size, 2) + Folivore + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
```

```
                         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito104 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                    log(Group_Size, 2) + Omnivore + Frugivore + Dexterity_Index,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito105 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                    log(Group_Size, 2) + Omnivore + Folivore + Dexterity_Index,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito106 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                    log(Group_Size, 2) + Omnivore + Folivore + Frugivore,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito107 <- phyloglm(Tool_Use ~
                    log(Group_Size, 2) + Omnivore + Folivore + Frugivore,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito108 <- phyloglm(Tool_Use ~
                    Omnivore + Folivore + Frugivore + Dexterity_Index,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound
```

```r
modelito109 <- phyloglm(Tool_Use ~
              Omnivore + Folivore + Frugivore + Dexterity_Index,
      data = tool_use_expanded2,
      phy = tooluse.tree,
      method = c("logistic_IG10"),
      btol = 20, #the limit had been reached somewhere
      log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito110 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Folivore + Frugivore + Dexterity_Index,
      data = tool_use_expanded2,
      phy = tooluse.tree,
      method = c("logistic_IG10"),
      btol = 20, #the limit had been reached somewhere
      log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito111 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Omnivore + Frugivore + Dexterity_Index,
      data = tool_use_expanded2,
      phy = tooluse.tree,
      method = c("logistic_IG10"),
      btol = 20, #the limit had been reached somewhere
      log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito112 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Omnivore + Folivore + Dexterity_Index,
      data = tool_use_expanded2,
      phy = tooluse.tree,
      method = c("logistic_IG10"),
      btol = 20, #the limit had been reached somewhere
      log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito113 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              Folivore + Frugivore + Dexterity_Index,
      data = tool_use_expanded2,
      phy = tooluse.tree,
      method = c("logistic_IG10"),
      btol = 20, #the limit had been reached somewhere
      log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito114 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
```

```r
               + Omnivore + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito115 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
               + Omnivore + Folivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito116 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
               + Omnivore + Folivore + Frugivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito117 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
               log(Group_Size, 2) + Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito118 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
               log(Group_Size, 2) + Folivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito119 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
               log(Group_Size, 2) + Folivore + Frugivore,
```

```
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito120 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              log(Group_Size, 2) + Omnivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito121 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              log(Group_Size, 2) + Omnivore + Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito122 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              log(Group_Size, 2) + Omnivore + Folivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito123 <- phyloglm(Tool_Use ~ Folivore + Frugivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito124 <- phyloglm(Tool_Use ~ Omnivore + Frugivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
```

```
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito125 <- phyloglm(Tool_Use ~ Omnivore + Folivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito126 <- phyloglm(Tool_Use ~ Omnivore + Folivore + Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito127 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Frugivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito128 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Folivore + Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito129 <- phyloglm(Tool_Use ~
              log(Group_Size, 2) + Folivore + Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound
```

```r
modelito130 <- phyloglm(Tool_Use ~
            log(Group_Size, 2) + Omnivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito131 <- phyloglm(Tool_Use ~
            log(Group_Size, 2) + Omnivore + Frugivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito132 <- phyloglm(Tool_Use ~
            log(Group_Size, 2) + Omnivore + Folivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito133 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                Frugivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito134 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                Folivore + Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito135 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
```

```
                    Folivore + Frugivore,
         data = tool_use_expanded2,
         phy = tooluse.tree,
         method = c("logistic_IG10"),
         btol = 20, #the limit had been reached somewhere
         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito136 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                   Omnivore + Dexterity_Index,
         data = tool_use_expanded2,
         phy = tooluse.tree,
         method = c("logistic_IG10"),
         btol = 20, #the limit had been reached somewhere
         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito137 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                   Omnivore + Frugivore,
         data = tool_use_expanded2,
         phy = tooluse.tree,
         method = c("logistic_IG10"),
         btol = 20, #the limit had been reached somewhere
         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito138 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                   Omnivore + Folivore,
         data = tool_use_expanded2,
         phy = tooluse.tree,
         method = c("logistic_IG10"),
         btol = 20, #the limit had been reached somewhere
         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito139 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                 log(Group_Size, 2)  + Dexterity_Index,
         data = tool_use_expanded2,
         phy = tooluse.tree,
         method = c("logistic_IG10"),
         btol = 20, #the limit had been reached somewhere
         log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito140 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
                 log(Group_Size, 2)  + Omnivore,
```

```
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito141 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
             log(Group_Size, 2)  + Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito142 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
             log(Group_Size, 2)  + Folivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito143 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
             log(Group_Size, 2),
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito144 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
             Omnivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito145 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
             Folivore,
          data = tool_use_expanded2,
```

```r
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito146 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito147 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2) +
              Dexterity_Index,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito148 <- phyloglm(Tool_Use ~ log(Group_Size, 2) +
              Omnivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito149 <- phyloglm(Tool_Use ~ log(Group_Size, 2) +
              Folivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
          method = c("logistic_IG10"),
          btol = 20, #the limit had been reached somewhere
          log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito150 <- phyloglm(Tool_Use ~ log(Group_Size, 2) +
              Frugivore,
          data = tool_use_expanded2,
          phy = tooluse.tree,
```

```r
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito151 <- phyloglm(Tool_Use ~ log(Group_Size, 2) +
            Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito152 <- phyloglm(Tool_Use ~ Omnivore +
            Folivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito153 <- phyloglm(Tool_Use ~ Omnivore +
            Frugivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito154 <- phyloglm(Tool_Use ~ Omnivore +
            Dexterity_Index,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
        btol = 20, #the limit had been reached somewhere
        log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito155 <- phyloglm(Tool_Use ~ Folivore +
            Frugivore,
        data = tool_use_expanded2,
        phy = tooluse.tree,
        method = c("logistic_IG10"),
```

```r
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito156 <- phyloglm(Tool_Use ~ Dexterity_Index +
                Folivore,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito157 <- phyloglm(Tool_Use ~ Frugivore +
                Dexterity_Index,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito158 <- phyloglm(Tool_Use ~ log(Brain_Weight_grams, 2),
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito159 <- phyloglm(Tool_Use ~ log(Group_Size, 2),
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito160 <- phyloglm(Tool_Use ~ Omnivore,
            data = tool_use_expanded2,
            phy = tooluse.tree,
            method = c("logistic_IG10"),
            btol = 20, #the limit had been reached somewhere
            log.alpha.bound = 8) #increased so alpha doesn't reach bound

modelito161 <- phyloglm(Tool_Use ~ Folivore,
```

```
                data = tool_use_expanded2,
                phy = tooluse.tree,
                method = c("logistic_IG10"),
                btol = 20, #the limit had been reached somewhere
                log.alpha.bound = 8) #increased so alpha doesn't reach bound

    modelito162 <- phyloglm(Tool_Use ~ Frugivore,
                data = tool_use_expanded2,
                phy = tooluse.tree,
                method = c("logistic_IG10"),
                btol = 20, #the limit had been reached somewhere
                log.alpha.bound = 8) #increased so alpha doesn't reach bound

    modelito163 <- phyloglm(Tool_Use ~ Dexterity_Index,
                data = tool_use_expanded2,
                phy = tooluse.tree,
                method = c("logistic_IG10"),
                btol = 20, #the limit had been reached somewhere
                log.alpha.bound = 8) #increased so alpha doesn't reach bound


    a <- rbind(modelito101$aic) |> rbind(modelito102$aic) |> rbind(modelito103$aic) |> rbind(m

    min(a)
```

```
[1] 62.04777
```

```
    a
```

```
          [,1]
 [1,]  72.06131
 [2,]  67.20482
 [3,]  67.23089
 [4,]  68.77598
 [5,]  67.70063
 [6,]  67.37822
 [7,]  70.08271
 [8,]  70.83898
 [9,]  70.83898
[10,]  71.03872
[11,]  70.97915
```

```
[12,] 70.09444
[13,] 65.27118
[14,] 66.88412
[15,] 65.76854
[16,] 65.42540
[17,] 67.71183
[18,] 65.70288
[19,] 65.36395
[20,] 70.72570
[21,] 67.12630
[22,] 65.80816
[23,] 70.14790
[24,] 70.59843
[25,] 69.00292
[26,] 69.06482
[27,] 69.87550
[28,] 73.31505
[29,] 68.99828
[30,] 74.76383
[31,] 69.06367
[32,] 68.17402
[33,] 65.76874
[34,] 63.86774
[35,] 63.37047
[36,] 69.40315
[37,] 65.21036
[38,] 63.84676
[39,] 69.30241
[40,] 68.89107
[41,] 65.96523
[42,] 63.91473
[43,] 67.32900
[44,] 67.49131
[45,] 62.04777
[46,] 64.16565
[47,] 67.89266
[48,] 72.84509
[49,] 71.31938
[50,] 67.51660
[51,] 73.88661
[52,] 67.27844
[53,] 68.63641
[54,] 75.28354
```

```
[55,] 68.35958
[56,] 76.07649
[57,] 69.28363
[58,] 65.90761
[59,] 71.95937
[60,] 72.11663
[61,] 74.55256
[62,] 67.25434
[63,] 76.59433
```

```
#modelito 145 has the lowest AIC, so it is selected and presented
set.seed(1)
summary(modelito145)
```

```
Call:
phyloglm(formula = Tool_Use ~ log(Brain_Weight_grams, 2) + Folivore,
    data = tool_use_expanded2, phy = tooluse.tree, method = c("logistic_IG10"),
    btol = 20, log.alpha.bound = 8)
      AIC     logLik Pen.logLik
    62.05    -27.02     -23.91

Method: logistic_IG10
Mean tip height: 73.00302
Parameter estimate(s):
alpha: 17.59341

Coefficients:
                             Estimate   StdErr z.value   p.value
(Intercept)                  -3.09370  1.00232 -3.0865  0.002025 **
log(Brain_Weight_grams, 2)    0.59631  0.18844  3.1645  0.001553 **
Folivore1                    -1.61035  0.74985 -2.1476  0.031749 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Note: Wald-type p-values for coefficients, conditional on alpha=17.59341
```

Interpreting results:

```
logodds_BW <- 0.59631
odds_BW <- exp(logodds_BW)
```

```
logodds_FO <- -1.61035
odds_FO <- exp(logodds_FO)

odds_BW
```

[1] 1.815408

```
odds_FO
```

[1] 0.1998177

Holding all other variables constant, we expect that, on average, every doubling in brain mass increases the odds of observed tool use behavior by a factor of 1.82.

Holding all other variables constant, we expect that, on average, the odds of observed tool use behavior in folivores is lower than in other primates by a factor of 0.200.