

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()
* Use tidymodels_prefer() to resolve common conflicts.
```

```
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")
```

```
#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

```

```

#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
#so there are 63 modelitos

#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

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) +
  + 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

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,
  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,
  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"),
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_F0 <- -1.61035
odds_F0 <- exp(logodds_F0)
```

```
odds_BW
```

```
[1] 1.815408
```

```
odds_F0
```

```
[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.