432 Class 19

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## Today’s Topic

**Multinomial Logistic Regression: An Introduction**

* Two Examples about Alligators
* Fitting Multinomial Logistic Regression Models

Chapter 28 of the Course Notes describes an additional example discussing this material.

## Setup

knitr::opts\_chunk$set(comment=NA)  
options(width = 60)  
  
library(janitor)  
library(broom)  
library(mosaic)  
library(gt)  
library(naniar)  
library(nnet)  
library(rms)  
library(conflicted)  
library(tidyverse)  
  
conflicts\_prefer(base::mean, dplyr::filter, dplyr::select, dplyr::summarize)  
  
theme\_set(theme\_bw())

## Regression on Multi-categorical Outcomes

Suppose we have a nominal, multi-categorical outcome of interest. Multinomial (also called multicategory or polychotomous) logistic regression models describe the odds of response in one category instead of another.

* Such models pair each outcome category with a baseline category, the choice of which is arbitrary.
* The model consists of J-1 logit equations (for an outcome with J categories) with separate parameters for each.

# A small example: gator1 on Alligator Food Choices

## Today’s Data

Today’s data relates to alligator food choices. We’ll actually work with two different data sets.

In each case, we’ll read in the data, and set some key variables to be factors and, if needed, actively select the baseline category.

## gator1: Alligator Food Choice

The gator1 data are from a study by the Florida Game and Fresh Water Fish Commission of factors influencing the primary food choice of alligators[[1]](#footnote-24).

We’ll be trying to predict primary food choice using the alligator’s length.

## gator1 has data on 59 alligators

* length (in meters)
* choice = primary food type, in volume, found in the alligator’s stomach, specifically…
  + Fish,
  + Invertebrates (mostly apple snails, aquatic insects and crayfish, and I’ll abbreviate this category as Inverts in what follows)
  + Other (which includes reptiles, amphibians, mammals, plant material and stones or other debris.)

## Ingesting the gator1 data

gator1 <- read\_csv("c19/data/gator1.csv",   
 show\_col\_types = FALSE) |>  
 mutate(choice = fct\_relevel(factor(choice), "Other"),  
 choice = fct\_recode(choice,   
 "Inverts" = "Invertebrates"))  
  
gator1

# A tibble: 59 × 3  
 id length choice   
 <dbl> <dbl> <fct>   
 1 1 1.24 Inverts  
 2 2 1.3 Inverts  
 3 3 1.3 Inverts  
 4 4 1.32 Fish   
 5 5 1.32 Fish   
 6 6 1.4 Fish   
 7 7 1.42 Inverts  
 8 8 1.42 Fish   
 9 9 1.45 Inverts  
10 10 1.45 Other   
# ℹ 49 more rows

## Summarizing length by choice

Note that I’ve set up choice so that “Other” is the baseline (first) category, while ingesting the data.

favstats(length ~ choice, data = gator1) |>  
 gt() |> fmt\_number(min:sd, decimals = 2) |>  
 tab\_options(table.font.size = 20)

| choice | min | Q1 | median | Q3 | max | mean | sd | n | missing |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Other | 1.45 | 1.71 | 2.17 | 3.26 | 3.68 | 2.42 | 0.88 | 8 | 0 |
| Fish | 1.32 | 1.74 | 2.31 | 2.73 | 3.89 | 2.36 | 0.76 | 31 | 0 |
| Inverts | 1.24 | 1.47 | 1.61 | 1.78 | 2.72 | 1.66 | 0.33 | 20 | 0 |

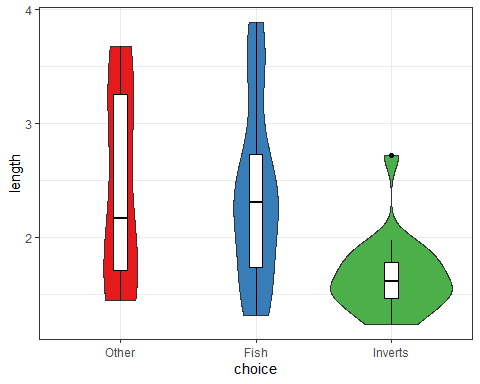
There is no missing data in gator1.

n\_miss(gator1)

[1] 0

## Length and Primary Food Choice

ggplot(gator1, aes(x = choice, y = length, fill = choice)) +  
 geom\_violin() +  
 geom\_boxplot(fill = "white", col = "black", width = 0.1) +  
 scale\_fill\_brewer(palette = "Set1") + guides(fill = "none")



# Fitting a Multinomial Logistic Regression

## Multinomial Logistic Regression Fit

* “Other” is the first (reference) level for choice

gator1 |> tabyl(choice)

choice n percent  
 Other 8 0.1355932  
 Fish 31 0.5254237  
 Inverts 20 0.3389831

Let’s try using multinom() from the nnet package

try1 <- multinom(choice ~ length, data=gator1)

# weights: 9 (4 variable)  
initial value 64.818125   
iter 10 value 49.170785  
final value 49.170622   
converged

## Looking over the first try

try1

Call:  
multinom(formula = choice ~ length, data = gator1)  
  
Coefficients:  
 (Intercept) length  
Fish 1.617952 -0.1101836  
Inverts 5.697543 -2.4654695  
  
Residual Deviance: 98.34124   
AIC: 106.3412

Our R output suggests the following models:

* log odds of Fish rather than Other = 1.62 - 0.110 Length
* log odds of Inverts. rather than Other = 5.70 - 2.465 Length

## Estimating Response Probabilities

We can express the multinomial logistic regression model directly in terms of outcome probabilities:

Our models contrast “Fish” and “Invertebrates” to “Other” as the reference category.

## Estimating Response Probabilities

In our try1, we have:

* log odds of Fish rather than Other = 1.62 - 0.110 Length
* log odds of Inverts rather than Other = 5.70 - 2.465 Length
* For the reference category we use and so that for that category (here, Other.)

## try1 Response Probabilities

Our estimates (which will sum to 1) are:

## Making a Prediction with try1

For an alligator of 3.9 meters, for instance, we have:

$$
denominator = {1 + exp(1.62 - 0.110 (3.9)) + exp(5.70 - 2.465 (3.9))} = 4.31 \\
Pr(Fish) = \frac{exp(1.62 - 0.110 (3.9))}{4.31} = \frac{3.29}{4.31} = 0.7633\\
Pr(Invert.) = \frac{exp(5.70 - 2.465 (3.9)}{4.31} = \frac{0.02}{4.31} = 0.0046\\
Pr(Other) = \frac{1}{4.31} = 0.2320
$$

## Predicted Probabilities from try1

try1\_fits <-   
 predict(try1, newdata = gator1, type = "probs")  
  
gator1\_try1 <- cbind(gator1, try1\_fits)  
  
head(gator1\_try1); tail(gator1\_try1)

id length choice Other Fish Inverts  
1 1 1.24 Inverts 0.05150117 0.2265417 0.7219571  
2 2 1.30 Inverts 0.05727232 0.2502677 0.6924600  
3 3 1.30 Inverts 0.05727232 0.2502677 0.6924600  
4 4 1.32 Fish 0.05927999 0.2584705 0.6822495  
5 5 1.32 Fish 0.05927999 0.2584705 0.6822495  
6 6 1.40 Fish 0.06770167 0.2925999 0.6396985

id length choice Other Fish Inverts  
54 54 3.56 Fish 0.2245916 0.7650815 0.010326935  
55 55 3.58 Fish 0.2250825 0.7650659 0.009851557  
56 56 3.66 Fish 0.2270070 0.7648358 0.008157239  
57 57 3.68 Other 0.2274793 0.7647398 0.007780920  
58 58 3.71 Fish 0.2281817 0.7645698 0.007248494  
59 59 3.89 Fish 0.2322725 0.7629934 0.004734037

## Tabulating Response Probabilities

gator1\_try1 |> group\_by(choice) |>  
 summarise(mean(Other), mean(Fish), mean(Inverts))

# A tibble: 3 × 4  
 choice `mean(Other)` `mean(Fish)` `mean(Inverts)`  
 <fct> <dbl> <dbl> <dbl>  
1 Other 0.155 0.580 0.265  
2 Fish 0.155 0.590 0.255  
3 Inverts 0.0973 0.404 0.499

## Pivot the Wide data to make it longer

We need to have this data organized differently in order to build the plot I want to build.

gator1\_try1long <-   
 pivot\_longer(gator1\_try1,   
 cols = c("Other", "Fish", "Inverts"),  
 names\_to = "preference",  
 values\_to = "probability") |>  
 mutate(preference = factor(preference))

## What does this pivoting accomplish?

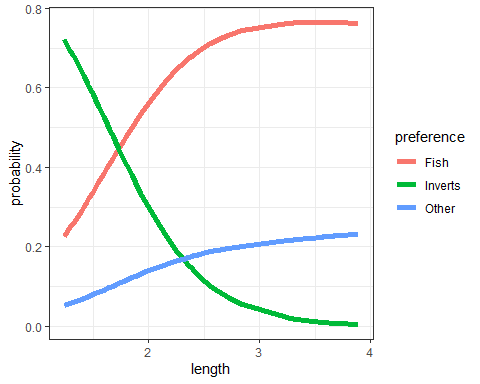
gator1\_try1long

# A tibble: 177 × 5  
 id length choice preference probability  
 <dbl> <dbl> <fct> <fct> <dbl>  
 1 1 1.24 Inverts Other 0.0515  
 2 1 1.24 Inverts Fish 0.227   
 3 1 1.24 Inverts Inverts 0.722   
 4 2 1.3 Inverts Other 0.0573  
 5 2 1.3 Inverts Fish 0.250   
 6 2 1.3 Inverts Inverts 0.692   
 7 3 1.3 Inverts Other 0.0573  
 8 3 1.3 Inverts Fish 0.250   
 9 3 1.3 Inverts Inverts 0.692   
10 4 1.32 Fish Other 0.0593  
# ℹ 167 more rows

## try1 Response Probabilities

ggplot(gator1\_try1long, aes(x = length, y = probability,   
 col = preference)) +  
 geom\_line(size = 2) + scale\_fill\_brewer(palette = "Set1")

Warning: Using `size` aesthetic for lines was deprecated in ggplot2  
3.4.0.  
ℹ Please use `linewidth` instead.



## try1 model summary

summary(try1)

Call:  
multinom(formula = choice ~ length, data = gator1)  
  
Coefficients:  
 (Intercept) length  
Fish 1.617952 -0.1101836  
Inverts 5.697543 -2.4654695  
  
Std. Errors:  
 (Intercept) length  
Fish 1.307291 0.5170838  
Inverts 1.793820 0.8996485  
  
Residual Deviance: 98.34124   
AIC: 106.3412

glance(try1) |> gt() |> tab\_options(table.font.size = 20)

| edf | deviance | AIC | nobs |
| --- | --- | --- | --- |
| 4 | 98.34124 | 106.3412 | 59 |

## Compare to intercept-only model

Compare try1 to the null model with only an intercept (try0)

try0 <- multinom(choice ~ 1, data=gator1)

# weights: 6 (2 variable)  
initial value 64.818125   
final value 57.570928   
converged

AIC(try0, try1)

df AIC  
try0 2 119.1419  
try1 4 106.3412

BIC(try0, try1)

df BIC  
try0 2 123.2969  
try1 4 114.6514

Does the inclusion of length produce a meaningfully better fit to the data than simply fitting an intercept?

## ANOVA for try0 vs. try1

* If you’d prefer a hypothesis testing approach, use anova…

anova(try0, try1)

Likelihood ratio tests of Multinomial Models  
  
Response: choice  
 Model Resid. df Resid. Dev Test Df LR stat.  
1 1 116 115.14186   
2 length 114 98.34124 1 vs 2 2 16.80061  
 Pr(Chi)  
1   
2 0.0002247985

Does the inclusion of length produce a meaningfully better fit to the data than simply fitting an intercept?

## Wald Z tests for individual predictors

By default, tidy exponentiates multinomial coefficients…

tidy(try1) |>   
 gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| Fish | (Intercept) | 1.618 | 1.307 | 1.238 | 0.216 |
| Fish | length | -0.110 | 0.517 | -0.213 | 0.831 |
| Inverts | (Intercept) | 5.698 | 1.794 | 3.176 | 0.001 |
| Inverts | length | -2.465 | 0.900 | -2.740 | 0.006 |

# Working with a larger example: gator2

## gator2 describes 219 alligators

The gator2.csv data[[2]](#footnote-53) considers the stomach contents of 219 alligators, aggregated into 5 categories by primary food choice:

* fish
* invertebrates
* reptiles
* birds
* other (including amphibians, plants, household pets, stones, and debris)

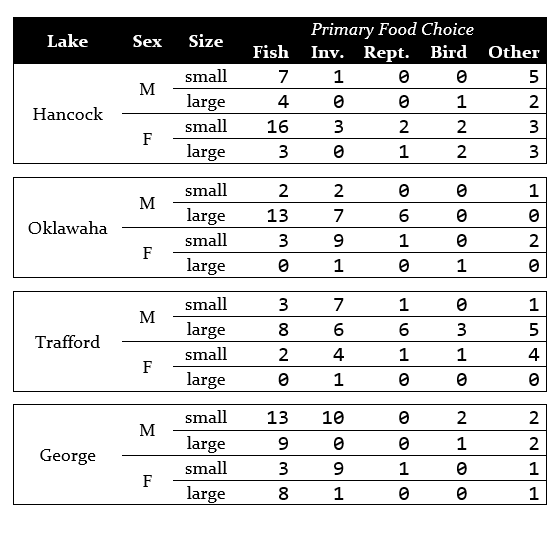
## gator2 has additional predictors

The 219 alligators are also categorized by:

* sex (m or f), and
* by length (< 2.3 and 2.3 meters) and
* by which of four lakes they were captured in (Hancock, Oklawaha, Trafford or George.)

We’ll use as our baseline: fish as a choice, sex as m, length >= 2.3 and lake george.

See the Table on next slide.



## Model Setup

We’ll use Fish as the baseline, so our regression equations take the form

for .

## How many coefficients do we estimate?

* We have six coefficients to estimate in each of four logit equations (one each for ) so there are 24 parameters to estimate.

## Ingesting the gator2 data

gator2 <- read\_csv("c19/data/gator2.csv", show\_col\_types = FALSE) |>  
 mutate(across(where(is\_character), as\_factor),  
 id = as.character(id))

We re-level the factors to put our reference categories first.

gator2 <- gator2 |>  
 mutate(food = fct\_relevel(food, "fish", "invert",   
 "rep", "bird", "other"),  
 size = fct\_relevel(size, ">=2.3"),  
 gender = fct\_relevel(gender, "m"),  
 lake = fct\_relevel(lake, "george"))  
  
summary(gator2 |> select(-id))

food size gender lake   
 fish :94 >=2.3: 95 m:130 george :63   
 invert:61 <2.3 :124 f: 89 hancock :55   
 rep :19 oklawaha:48   
 bird :13 trafford:53   
 other :32

## The Models We Will Fit

We’ll fit (using multinom() from nnet)

* A *saturated* model, including all three predictors and all two-way interactions and the three-way interaction
* A *null* model, with the intercept alone
* Simple logistic regression models for each of the three predictors as a main effect alone
* The model including both L(ake) and S(ize) but nothing else
* The model including all three predictors as main effects, but no interactions

## The Models We Will Fit (code only)

options(contrasts=c("contr.treatment", "contr.poly"))  
fit\_SAT <- multinom(food ~ lake\*size\*gender, data=gator2) # saturated  
fit\_1 <-multinom(food~1,data=gator2) # null  
fit\_G <-multinom(food~gender,data=gator2) # G  
fit\_L <-multinom(food~lake,data=gator2) # L  
fit\_S <-multinom(food~size,data=gator2) # S  
fit\_LS <-multinom(food~lake+size,data=gator2) # L+S  
fit\_GLS <-multinom(food~gender+lake+size,data=gator2) # G+L+S

## What You’ll See When Fitting the models

options(contrasts=c("contr.treatment", "contr.poly"))  
fit\_SAT <- multinom(food ~ lake\*size\*gender, data=gator2)

# weights: 85 (64 variable)  
initial value 352.466903   
iter 10 value 261.200857  
iter 20 value 245.788420  
iter 30 value 244.090612  
iter 40 value 243.812122  
iter 50 value 243.801212  
final value 243.800899   
converged

and we’ll see something similar for each of the other models…

fit\_1<-multinom(food~1,data=gator2) # null

# weights: 10 (4 variable)  
initial value 352.466903   
final value 302.181462   
converged

fit\_G<-multinom(food~gender,data=gator2) # G

# weights: 15 (8 variable)  
initial value 352.466903   
iter 10 value 301.286320  
final value 301.129428   
converged

fit\_L<-multinom(food~lake,data=gator2) # L

# weights: 25 (16 variable)  
initial value 352.466903   
iter 10 value 281.030560  
iter 20 value 280.583926  
final value 280.583844   
converged

fit\_S<-multinom(food~size,data=gator2) # S

# weights: 15 (8 variable)  
initial value 352.466903   
iter 10 value 294.670879  
final value 294.606678   
converged

fit\_LS<-multinom(food~lake+size,data=gator2) # L+S

# weights: 30 (20 variable)  
initial value 352.466903   
iter 10 value 271.607785  
iter 20 value 270.046051  
final value 270.040140   
converged

fit\_GLS<-multinom(food~gender+lake+size,data=gator2) # G+L+S

# weights: 35 (24 variable)  
initial value 352.466903   
iter 10 value 271.128034  
iter 20 value 268.936875  
final value 268.932741   
converged

## The Intercept only Model fit\_1

summary(fit\_1)

Call:  
multinom(formula = food ~ 1, data = gator2)  
  
Coefficients:  
 (Intercept)  
invert -0.4324211  
rep -1.5988558  
bird -1.9783458  
other -1.0775589  
  
Std. Errors:  
 (Intercept)  
invert 0.1644133  
rep 0.2515350  
bird 0.2959078  
other 0.2046663  
  
Residual Deviance: 604.3629   
AIC: 612.3629

## Tidying this summary

tidy(fit\_1, exponentiate = FALSE) |>   
 gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| invert | (Intercept) | -0.432 | 0.164 | -2.630 | 0.009 |
| rep | (Intercept) | -1.599 | 0.252 | -6.356 | 0.000 |
| bird | (Intercept) | -1.978 | 0.296 | -6.686 | 0.000 |
| other | (Intercept) | -1.078 | 0.205 | -5.265 | 0.000 |

glance(fit\_1) |> gt() |>   
 tab\_options(table.font.size = 20)

| edf | deviance | AIC | nobs |
| --- | --- | --- | --- |
| 4 | 604.3629 | 612.3629 | 219 |

## Size only model

tidy(fit\_S, exponentiate = FALSE) |> gt() |>   
 fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| invert | (Intercept) | -1.034 | 0.291 | -3.553 | 0.000 |
| invert | size<2.3 | 0.949 | 0.357 | 2.659 | 0.008 |
| rep | (Intercept) | -1.242 | 0.315 | -3.944 | 0.000 |
| rep | size<2.3 | -0.858 | 0.535 | -1.604 | 0.109 |
| bird | (Intercept) | -1.727 | 0.384 | -4.502 | 0.000 |
| bird | size<2.3 | -0.555 | 0.606 | -0.916 | 0.360 |
| other | (Intercept) | -1.242 | 0.315 | -3.944 | 0.000 |
| other | size<2.3 | 0.294 | 0.415 | 0.709 | 0.478 |

## Size only model

glance(fit\_S) |> gt() |> tab\_options(table.font.size = 20)

| edf | deviance | AIC | nobs |
| --- | --- | --- | --- |
| 8 | 589.2134 | 605.2134 | 219 |

## Gender only model

tidy(fit\_G, exponentiate = FALSE) |> gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| invert | (Intercept) | -0.581 | 0.217 | -2.673 | 0.008 |
| invert | genderf | 0.358 | 0.334 | 1.072 | 0.284 |
| rep | (Intercept) | -1.513 | 0.306 | -4.937 | 0.000 |
| rep | genderf | -0.251 | 0.538 | -0.467 | 0.641 |
| bird | (Intercept) | -2.132 | 0.400 | -5.332 | 0.000 |
| bird | genderf | 0.368 | 0.596 | 0.618 | 0.537 |
| other | (Intercept) | -1.187 | 0.269 | -4.409 | 0.000 |
| other | genderf | 0.271 | 0.415 | 0.652 | 0.514 |

## Gender only model

glance(fit\_G) |> gt() |> tab\_options(table.font.size = 20)

| edf | deviance | AIC | nobs |
| --- | --- | --- | --- |
| 8 | 602.2589 | 618.2589 | 219 |

## Lake only model (part 1 of 2)

tidy(fit\_L, exponentiate = FALSE) |> slice(1:10) |>   
 gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| invert | (Intercept) | -0.501 | 0.283 | -1.767 | 0.077 |
| invert | lakehancock | -1.514 | 0.603 | -2.511 | 0.012 |
| invert | lakeoklawaha | 0.555 | 0.434 | 1.278 | 0.201 |
| invert | laketrafford | 0.826 | 0.461 | 1.791 | 0.073 |
| rep | (Intercept) | -3.496 | 1.015 | -3.445 | 0.001 |
| rep | lakehancock | 1.194 | 1.182 | 1.010 | 0.312 |
| rep | lakeoklawaha | 2.552 | 1.108 | 2.302 | 0.021 |
| rep | laketrafford | 3.011 | 1.110 | 2.713 | 0.007 |
| bird | (Intercept) | -2.398 | 0.603 | -3.976 | 0.000 |
| bird | lakehancock | 0.607 | 0.773 | 0.785 | 0.432 |

## Lake only model (part 2 of 2)

tidy(fit\_L, exponentiate = FALSE) |> slice(11:16) |>   
 gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| bird | lakeoklawaha | -0.492 | 1.191 | -0.413 | 0.680 |
| bird | laketrafford | 1.220 | 0.831 | 1.468 | 0.142 |
| other | (Intercept) | -1.705 | 0.444 | -3.841 | 0.000 |
| other | lakehancock | 0.869 | 0.554 | 1.567 | 0.117 |
| other | lakeoklawaha | -0.087 | 0.765 | -0.114 | 0.910 |
| other | laketrafford | 1.443 | 0.611 | 2.359 | 0.018 |

glance(fit\_L) |> gt() |> tab\_options(table.font.size = 20)

| edf | deviance | AIC | nobs |
| --- | --- | --- | --- |
| 16 | 561.1677 | 593.1677 | 219 |

## The Saturated Model

fit\_SAT

Call:  
multinom(formula = food ~ lake \* size \* gender, data = gator2)  
  
Coefficients:  
 (Intercept) lakehancock lakeoklawaha laketrafford  
invert -22.731435 -7.6997047 22.11245 22.443706  
rep -29.030622 4.5446124 28.25748 28.742943  
bird -2.196705 0.8106289 -18.76043 1.215771  
other -1.503884 0.8107459 -25.23128 1.033839  
 size<2.3 genderf lakehancock:size<2.3  
invert 22.4691578 20.6519880 6.0160287  
rep -2.1497924 -1.5018889 -15.0175978  
bird 0.3248760 -17.2683965 -22.8201143  
other -0.3675892 -0.5756885 0.7242536  
 lakeoklawaha:size<2.3 laketrafford:size<2.3  
invert -21.85028 -21.3342850  
rep -17.43950 1.3387310  
bird -25.18859 -25.8829682  
other 26.40938 -0.2614093  
 lakehancock:genderf lakeoklawaha:genderf  
invert -3.946342 4.226498  
rep 24.889170 -13.585689  
bird 18.248790 62.485154  
other 1.268734 -1.758853  
 laketrafford:genderf size<2.3:genderf  
invert 25.465169 -19.2913107  
rep -18.078274 31.5836415  
bird 16.978562 0.6638064  
other -7.586589 1.3479978  
 lakehancock:size<2.3:genderf  
invert 2.857688  
rep -15.396895  
bird 20.157737  
other -3.378585  
 lakeoklawaha:size<2.3:genderf  
invert -4.488351  
rep 2.767887  
bird -24.265617  
other 1.274620  
 laketrafford:size<2.3:genderf  
invert -26.979637  
rep -11.597631  
bird 25.472087  
other 8.606604  
  
Residual Deviance: 487.6018   
AIC: 615.6018

## Building a Model Comparison Table

For a model fitX, we find the:

* Effective degrees of freedom with fitX$edf
* Deviance with deviance(fitX) or by listing or summarizing the model
* AIC and BIC with AIC(fitX) and BIC(fitX)

fit\_SAT$edf; deviance(fit\_SAT); AIC(fit\_SAT); BIC(fit\_SAT)

[1] 64

[1] 487.6018

[1] 615.6018

[1] 832.5024

Note that for these models, AIC = Deviance + 2(edf)

## Results across all models we’ve fit

| fit | Model | edf | Deviance | AIC | BIC |
| --- | --- | --- | --- | --- | --- |
| 1 | Intercept only | 4 | 604.4 | 612.4 | 625.9 |
| G | Gender only | 8 | 602.3 | 618.3 | 645.4 |
| S | Size only | 8 | 589.2 | 605.2 | 632.3 |
| L | Lake only | 16 | 561.2 | 593.2 | 647.4 |
| LS | Lake and Size | 20 | 540.1 | 580.1 | 647.9 |
| GLS | G, L, S main effects | 24 | 537.9 | 585.9 | 667.2 |
| SAT | G\*S\*L (saturated) | 64 | 487.6 | 615.6 | 615.6 |

Which model looks like it fits the data best?

## Drop in deviance tests (example 1)

Compare Model G to intercept-only

anova(fit\_G, fit\_1)

Likelihood ratio tests of Multinomial Models  
  
Response: food  
 Model Resid. df Resid. Dev Test Df LR stat.  
1 1 872 604.3629   
2 gender 868 602.2589 1 vs 2 4 2.104069  
 Pr(Chi)  
1   
2 0.7166248

## Drop in deviance tests (example 2)

Compare Model SAT to Model GLS

anova(fit\_SAT, fit\_GLS)

Likelihood ratio tests of Multinomial Models  
  
Response: food  
 Model Resid. df Resid. Dev Test Df  
1 gender + lake + size 852 537.8655   
2 lake \* size \* gender 812 487.6018 1 vs 2 40  
 LR stat. Pr(Chi)  
1   
2 50.26368 0.1281851

## Results of testing

| fit | Model | edf | Deviance | versus | *p* |
| --- | --- | --- | --- | --- | --- |
| 1 | Intercept only | 4 | 604.4 | – | – |
| G | Gender only | 8 | 602.3 | 1 | 0.717 |
| S | Size only | 8 | 589.2 | 1 | 0.004 |
| L | Lake only | 16 | 561.2 | 1 | 0 |
| LS | Lake and Size | 20 | 540.1 | L | 0 |
| GLS | G, L, S main effects | 24 | 537.9 | LS | 0.696 |
| SAT | G\*S\*L (saturated) | 64 | 487.6 | GLS | 0.128 |

## Which model fits the data best?

The model with the lowest AIC is the model which collapses on Gender, and uses only Lake and Size as predictors for Food Choice. (fit\_LS).

* This (fit\_LS) is also the model which has the most evidence in its favor from the drop in deviance testing.

The model with the lowest BIC is the model which collapses on both Gender and Lake, and uses only Size as a predictor for Food Choice. (fit\_S)

## fit\_LS coefficients

coef(fit\_LS)

(Intercept) lakehancock lakeoklawaha laketrafford  
invert -1.549021 -1.6581178 0.937237973 1.122002  
rep -3.314512 1.2428408 2.458913302 2.935262  
bird -2.093358 0.6954256 -0.652622721 1.088098  
other -1.904343 0.8263115 0.005792737 1.516461  
 size<2.3  
invert 1.4581457  
rep -0.3512702  
bird -0.6306329  
other 0.3315514

## The start of the L+S Model

tidy(fit\_LS, exponentiate = FALSE) |>   
 slice(1:5) |> gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| y.level | term | estimate | std.error | statistic | p.value |
| --- | --- | --- | --- | --- | --- |
| invert | (Intercept) | -1.549 | 0.425 | -3.645 | 0.000 |
| invert | lakehancock | -1.658 | 0.613 | -2.706 | 0.007 |
| invert | lakeoklawaha | 0.937 | 0.472 | 1.986 | 0.047 |
| invert | laketrafford | 1.122 | 0.491 | 2.287 | 0.022 |
| invert | size<2.3 | 1.458 | 0.396 | 3.683 | 0.000 |

* log odds of invertebrates rather than fish are:

-1.549 - 1.658 (Hancock) + 0.937 (Oklahawa) + 1.122 (Trafford) + 1.458 (size < 2.3)

For baseline category, log odds of fish = 0, so exp(log odds) = 1.

## Response Probabilities in fit\_LS

To keep things relatively simple, we’ll look at the class of Large size alligators (so the small size indicator is 0), in Lake George, (so the three Lake indicators are all 0, also).

* The estimated probability of Fish in Large size alligators in Lake George according to our model is:

## Response Probabilities in fit\_LS

* The estimated probability of Invertebrates in Large size alligators in Lake George according to our model is:

The estimated probabilities for the other categories in Large size Lake George alligators are:

* 0.024 for Reptiles, 0.081 for Birds, and 0.098 for Other
* And the five probabilities will sum to 1, at least within rounding error.

## Model Estimates vs. Observed Counts

For large size alligators in Lake George, we have…

| Food Type | Fish | Inverts | Reptiles | Birds | Other |
| --- | --- | --- | --- | --- | --- |
| Observed # | 17 | 1 | 0 | 1 | 3 |
| Observed Prob. | 0.77 | 0.045 | 0 | 0.045 | 0.14 |
| L+S Model Prob. | 0.66 | 0.14 | 0.02 | 0.08 | 0.10 |

We could perform similar calculations for all other combinations of size and lake, but I’ll leave that to the dedicated.

## Predicted fit\_LS Probabilities

fitLS\_fits <-   
 predict(fit\_LS, newdata = gator2, type = "probs")  
  
gator2\_fit\_LS <- cbind(gator2, fitLS\_fits)  
  
tail(gator2\_fit\_LS, 3)

id food size gender lake fish invert  
217 217 fish >=2.3 f george 0.6574619 0.1396817  
218 218 invert >=2.3 f george 0.6574619 0.1396817  
219 219 other >=2.3 f george 0.6574619 0.1396817  
 rep bird other  
217 0.02389991 0.08104695 0.09790956  
218 0.02389991 0.08104695 0.09790956  
219 0.02389991 0.08104695 0.09790956

## Tabulating Response Probabilities

gator2\_fit\_LS |> group\_by(food) |>  
 summarize(mean(fish), mean(invert), mean(rep),   
 mean(bird), mean(other)) |>  
 gt() |> fmt\_number(decimals = 3) |>  
 tab\_options(table.font.size = 20)

| food | mean(fish) | mean(invert) | mean(rep) | mean(bird) | mean(other) |
| --- | --- | --- | --- | --- | --- |
| fish | 0.481 | 0.230 | 0.076 | 0.063 | 0.149 |
| invert | 0.361 | 0.393 | 0.086 | 0.040 | 0.121 |
| rep | 0.381 | 0.258 | 0.148 | 0.064 | 0.148 |
| bird | 0.452 | 0.197 | 0.096 | 0.084 | 0.171 |
| other | 0.426 | 0.246 | 0.079 | 0.073 | 0.175 |

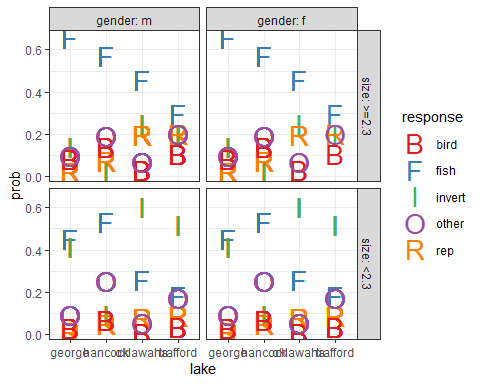
## Turn Wide Data into Long

gator2\_fitLSlong <-  
 pivot\_longer(gator2\_fit\_LS,   
 cols = fish:other,   
 names\_to = "response",  
 values\_to = "prob")  
  
head(gator2\_fitLSlong)

# A tibble: 6 × 7  
 id food size gender lake response prob  
 <chr> <fct> <fct> <fct> <fct> <chr> <dbl>  
1 1 fish <2.3 m hancock fish 0.535   
2 1 fish <2.3 m hancock invert 0.0931  
3 1 fish <2.3 m hancock rep 0.0475  
4 1 fish <2.3 m hancock bird 0.0704  
5 1 fish <2.3 m hancock other 0.254   
6 2 fish <2.3 m hancock fish 0.535

## fit\_LS Response Probabilities

ggplot(gator2\_fitLSlong, aes(x = lake, y = prob,   
 col = response,  
 shape = response)) +  
 geom\_point(size = 7) +  
 scale\_color\_brewer(palette = "Set1") +  
 facet\_grid(size ~ gender, labeller = "label\_both") +  
 scale\_shape\_manual(values = c("B", "F", "I", "O", "R"))



## Other Sources

In addition to the example found in our Course Notes (Chapter 28)…

* A good source of information on fitting these models is <https://stats.idre.ucla.edu/r/dae/multinomial-logistic-regression/>
* Using the tidymodels structure to fit these models is another good idea. Julia Silge has a very nice example at <https://juliasilge.com/blog/multinomial-volcano-eruptions/>
* More mathematically oriented sources include the following texts:
  + Hosmer DW Lemeshow S Sturdivant RX (2013) Applied Logistic Regression, 3rd Edition, Wiley
  + Agresti A (2007) An Introduction to Categorical Data Analysis, 2nd Edition, Wiley.

## Next Time

A *very* brief introduction to hierarchical models for data

1. Source: Agresti’s 1996 first edition of An Introduction to Categorical Data Analysis, Table 8.1. These were provided by Delany MF and Moore CT. [↑](#footnote-ref-24)
2. Source: <https://online.stat.psu.edu/stat504/lesson/8> [↑](#footnote-ref-53)