

# 432 Class 18 Slides

[github.com/THOMASELOVE/2020-432](https://github.com/THOMASELOVE/2020-432)

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# Multinomial Logistic Regression: An Introduction

# Setup

```
library(here); library(magrittr); library(janitor)
library(knitr); library(naniar); library(broom)
library(rms)
library(nnet)
library(tidyverse)
```

# 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.

## Working with gator1

# The gator1 data: 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<sup>1</sup>.

The data include the following data for 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,)
  - Other (which includes reptiles, amphibians, mammals, plant material and stones or other debris.)

We'll be trying to predict primary food choice using length.

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<sup>1</sup>My 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.

# 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 <- read_csv(here("data/gator1.csv")) %>%  
  mutate(choice = fct_relevel(factor(choice), "Other"))
```

# Alligator Food Choice, Part 1

```
gator1
```

```
# A tibble: 59 x 3
```

```
      id length choice
  <dbl>  <dbl> <fct>
1      1    1.24 Invertebrates
2      2    1.3  Invertebrates
3      3    1.3  Invertebrates
4      4    1.32 Fish
5      5    1.32 Fish
6      6    1.4  Fish
7      7    1.42 Invertebrates
8      8    1.42 Fish
9      9    1.45 Invertebrates
10     10    1.45 Other
# ... with 49 more rows
```



## Summarizing the gator1 data

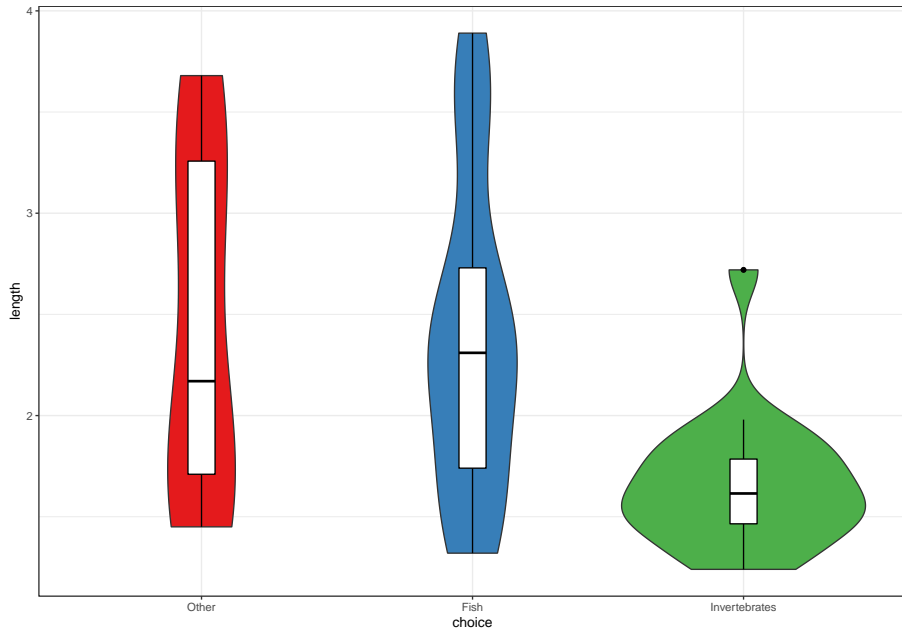
```
mosaic::favstats(length ~ choice, data = gator1) %>%  
  kable(digits = 2)
```

choice	min	Q1	median	Q3	max	mean	sd	n	missi
Other	1.45	1.71	2.17	3.26	3.68	2.42	0.88	8	
Fish	1.32	1.74	2.31	2.73	3.89	2.36	0.76	31	
Invertebrates	1.24	1.47	1.62	1.78	2.72	1.66	0.33	20	

```
n_miss(gator1)
```

```
[1] 0
```

# Plotting Length by Primary Food Choice



## Plotting Length by Primary Food Choice (code)

```
ggplot(gator1, aes(x = choice, y = length, fill = choice)) +  
  geom_violin(trim = TRUE) +  
  geom_boxplot(fill = "white", col = "black",  
               width = 0.1) +  
  scale_fill_brewer(palette = "Set1") +  
  theme_bw() +  
  guides(fill = FALSE)
```

# Fitting a Multinomial Logistic Regression

- We'll start by setting "Other" as the first (reference) level for the choice outcome

```
gator1 <- gator1 %>%  
  mutate(choice = fct_relevel(choice, "Other"))
```

For our first try, we'll use the `multinom` function 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
Invertebrates	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 =  $1.62 - 0.110 \text{ Length}$
- log odds of Invertebrates rather than Other =  $5.70 - 2.465 \text{ Length}$

# Estimating Response Probabilities from our First Try

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

$$\pi_j = \frac{\exp(\beta_{0j} + \beta_{1j}x)}{\sum_j \exp(\beta_{0j} + \beta_{1j}x)}$$

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

- log odds of Fish rather than Other = 1.62 - 0.110 Length
- log odds of Invertebrates rather than Other = 5.70 - 2.465 Length
- For the reference category we use  $\beta_{0j} = 0$  and  $\beta_{1j} = 0$  so that  $\exp(\beta_{0j} + \beta_{1j}x) = 1$  for that category.

## Estimated Response Probabilities

- log odds of Fish rather than Other =  $1.62 - 0.110 \text{ Length}$
- log odds of Invertebrates rather than Other =  $5.70 - 2.465 \text{ Length}$

and so our estimates (which will sum to 1) are:

$$Pr(\text{Fish} | \text{Length} = L) = \frac{\exp(1.62 - 0.110L)}{1 + \exp(1.62 - 0.110L) + \exp(5.70 - 2.465L)}$$

$$Pr(\text{Invert.} | \text{Length} = L) = \frac{\exp(5.70 - 2.465L)}{1 + \exp(1.62 - 0.110L) + \exp(5.70 - 2.465L)}$$

$$Pr(\text{Other} | \text{Length} = L) = \frac{1}{1 + \exp(1.62 - 0.110L) + \exp(5.70 - 2.465L)}$$

# Making a Prediction

For an alligator of 3.9 meters, for instance, the estimated probability that primary food choice is “other” equals:

$$\hat{\pi}(\textit{Other}) = \frac{1}{1 + \exp(1.62 - 0.110[3.9]) + \exp(5.70 - 2.465[3.9])} = 0.232$$



# Storing Predicted Probabilities from try1

```
try1_fits <-  
  predict(try1, newdata = gator1, type = "probs")  
  
gator1_try1 <- cbind(gator1, try1_fits)  
  
head(gator1_try1, 3)
```

	id	length	choice	Other	Fish
1	1	1.24	Invertebrates	0.05150117	0.2265417
2	2	1.30	Invertebrates	0.05727232	0.2502677
3	3	1.30	Invertebrates	0.05727232	0.2502677

	Invertebrates
1	0.7219571
2	0.6924600
3	0.6924600

# Tabulating Response Probabilities

```
gator1_try1 %>% group_by(choice) %>%  
  summarize(mean(Other), mean(Fish), mean(Invertebrates))
```

```
# A tibble: 3 x 4
```

choice	`mean(Other)`	`mean(Fish)`	`mean(Invertebrate`
<fct>	<dbl>	<dbl>	<dbl>
1 Other	0.155	0.580	0.265
2 Fish	0.155	0.590	0.255
3 Invertebra~	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", "Invertebrates"),  
               names_to = "preference",  
               values_to = "probability") %>%  
  mutate(preference = factor(preference))
```

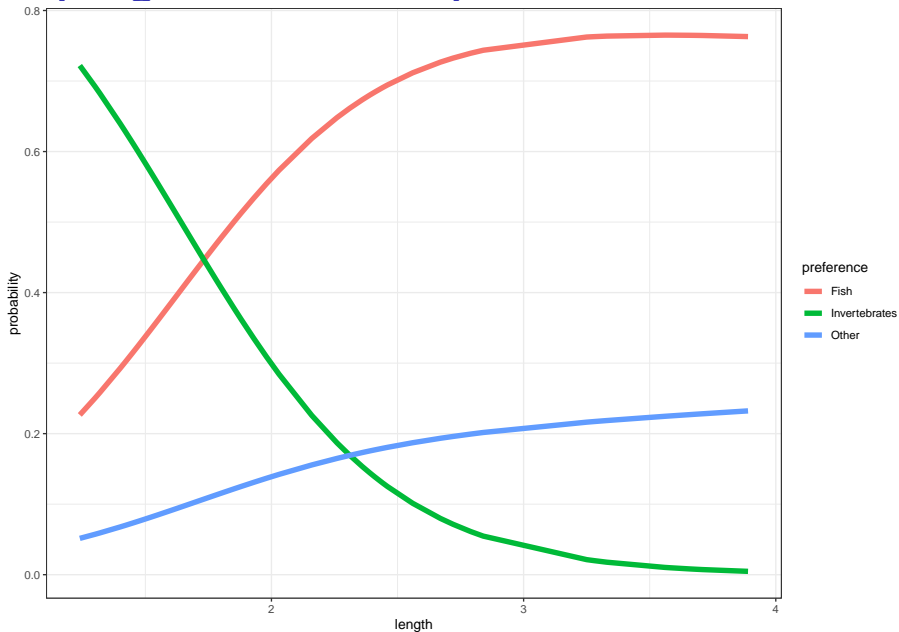
# What does this pivoting accomplish?

```
head(gator1_try1long)
```

```
# A tibble: 6 x 5
```

	id	length	choice	preference	probability
	<dbl>	<dbl>	<fct>	<fct>	<dbl>
1	1	1.24	Invertebrates	Other	0.0515
2	1	1.24	Invertebrates	Fish	0.227
3	1	1.24	Invertebrates	Invertebrates	0.722
4	2	1.3	Invertebrates	Other	0.0573
5	2	1.3	Invertebrates	Fish	0.250
6	2	1.3	Invertebrates	Invertebrates	0.692

# Graphing the Model's Response Probabilities



## Graphing the Response Probabilities (code)

```
ggplot(gator1_try1long, aes(x = length, y = probability,  
                             col = preference)) +  
  geom_line(size = 2) +  
  scale_fill_brewer(palette = "Set1") +  
  theme_bw()
```

## summary of try1

Call:

```
multinom(formula = choice ~ length, data = gator1)
```

Coefficients:

	(Intercept)	length
Fish	1.617952	-0.1101836
Invertebrates	5.697543	-2.4654695

Std. Errors:

	(Intercept)	length
Fish	1.307291	0.5170838
Invertebrates	1.793820	0.8996485

Residual Deviance: 98.34124

AIC: 106.3412

# Assess the try1 model as a whole with a drop in deviance test

Compare the model (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
```



# ANOVA to compare try0 to try1

```
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 significantly better fit to the data than simply fitting an intercept?

# Wald Z tests for individual predictors

By default, tidy exponentiates multinomial coefficients. . .

```
tidy(try1) %>% kable(digits = 3)
```

y.level	term	estimate	std.error	statistic	p.value
Fish	(Intercept)	5.043	1.307	1.238	0.216
Fish	length	0.896	0.517	-0.213	0.831
Invertebrates	(Intercept)	298.134	1.794	3.176	0.001
Invertebrates	length	0.085	0.900	-2.740	0.006

## Working with a larger example: gator2

# A Larger Alligator Food Choice Example

The `gator2.csv` data<sup>2</sup> 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)

The 219 alligators are also categorized by sex, and by length ( $< 2.3$  and  $\geq 2.3$  meters) and by which of four lakes they were captured in (Hancock, Oklawaha, Trafford or George.) Table on next slide.

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<sup>2</sup>Source: <https://onlinecourses.science.psu.edu/stat504/node/226>

Lake	Sex	Size	Primary Food Choice				
			Fish	Inv.	Rept.	Bird	Other
Hancock	M	small	7	1	0	0	5
		large	4	0	0	1	2
	F	small	16	3	2	2	3
		large	3	0	1	2	3
Oklawaha	M	small	2	2	0	0	1
		large	13	7	6	0	0
	F	small	3	9	1	0	2
		large	0	1	0	1	0
Trafford	M	small	3	7	1	0	1
		large	8	6	6	3	5
	F	small	2	4	1	1	4
		large	0	1	0	0	0
George	M	small	13	10	0	2	2
		large	9	0	0	1	2
	F	small	3	9	1	0	1
		large	8	1	0	0	1

# Model Setup

$$\pi_1 = Pr(Fish), \pi_2 = Pr(Invert.), \pi_3 = Pr(Reptiles), \\ \pi_4 = Pr(Birds), \pi_5 = Pr(Other)$$

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

$$\log\left(\frac{\pi_j}{\pi_1}\right) = \beta_0 + \beta_1[Lake = Hancock] + \beta_2[Lake = Oklawaha] + \\ \beta_3[Lake = Trafford] + \beta_4[Length \geq 2.3] + \beta_5[Sex = Female]$$

for  $j = 2, 3, 4, 5$ .

- We have six coefficients to estimate in each of four logit equations (one each for  $j = 2, 3, 4, 5$ ) so there are 24 parameters to estimate.

## Loading the gator2 data

```
gator2 <- read_csv(here("data/gator2.csv")) %>%  
  type.convert() # converts characters to factors
```

```
summary(gator2)
```

	id	food	size	gender
Min.	: 1.0	bird :13	<2.3 :124	f: 89
1st Qu.:	55.5	fish :94	>=2.3: 95	m:130
Median	:110.0	invert:61		
Mean	:110.0	other :32		
3rd Qu.:	164.5	rep :19		
Max.	:219.0			
	lake			
	george :63			
	hancock :55			
	oklawaha:48			
	trafford:53			

## Rearranging the gator2 data

We rearrange factor levels as needed to get our reference categories to appear first.

```
gator2 <- gator2 %>%  
  mutate(food = fct_relevel(food, "fish", "invert",  
                             "rep", "bird", "other"),  
         size = fct_relevel(size, ">=2.3"),  
         gender = fct_relevel(gender, "m"))
```



## Now, gator2 matches our order...

```
summary(gator2)
```

id	food	size	gender
Min. : 1.0	fish :94	>=2.3: 95	m:130
1st Qu.: 55.5	invert:61	<2.3 :124	f: 89
Median :110.0	rep :19		
Mean :110.0	bird :13		
3rd Qu.:164.5	other :32		
Max. :219.0			
lake			
george :63			
hancock :55			
oklawaha:48			
trafford:53			

# Complete Set of Models We Will Fit

- Response: Category of Primary Food Choice
- Predictors: L = lake, G = gender, S = size

Specifically, we'll fit (using the `multinom` function in the `nnet` package)

- 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

# Our Models (Code)

```
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...

etc.

etc.

etc.

## Summarizing the Models: Intercept only

```
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

## Tidying this summary

```
tidy(fit_1, exponentiate = FALSE) %>% kable(digits = 3)
```

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) %>% kable()
```

edf	deviance	AIC
4	604.3629	612.3629

# Summarizing the Models: Size only

```
summary(fit_S)
```

Call:

```
multinom(formula = food ~ size, data = gator2)
```

Coefficients:

	(Intercept)	size<2.3
invert	-1.034070	0.9489120
rep	-1.241705	-0.8583649
bird	-1.727214	-0.5551882
other	-1.241709	0.2943162

Std. Errors:

	(Intercept)	size<2.3
invert	0.2910708	0.3568648
rep	0.3148729	0.5349960
bird	0.3836949	0.6063277
other	0.3148735	0.4149523

## Size only model

```
tidy(fit_S, exponentiate = FALSE) %>% kable(digits = 3)
```

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

```
glance(fit_S) %>% kable()
```

edf	deviance	AIC
8	589.2134	605.2134



## Gender only model

```
tidy(fit_G, exponentiate = FALSE) %>% kable(digits = 3)
```

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

```
glance(fit_G) %>% kable()
```

edf	deviance	AIC
8	602.2589	618.2589

## Lake only model (part 1 of 2)

```
tidy(fit_L, exponentiate = FALSE) %>% slice(1:12) %>% kable(d
```

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
bird	lakeoklawaha	-0.492	1.191	-0.413	0.680
bird	laketrafford	1.220	0.831	1.468	0.142

## Lake only model (part 2 of 2)

```
tidy(fit_L, exponentiate = FALSE) %>% slice(13:16) %>% kable()
```

y.level	term	estimate	std.error	statistic	p.value
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)
```

```
# A tibble: 1 x 3
  edf deviance  AIC
  <dbl>   <dbl> <dbl>
1    16    561.  593.
```

# 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	

# 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 with `AIC(fitX)` or by listing or summarizing the model

```
fit_SAT$edf
```

```
[1] 64
```

```
deviance(fit_SAT)
```

```
[1] 487.6018
```

```
AIC(fit_SAT)
```

```
[1] 615.6018
```

Label	Model	Effective df	Deviance	AIC
fit_SAT	G*S*L (saturated)	64	487.6	615.6

## Results across all of the models we've fit

fit	Model	Effective df	Deviance	AIC
1	Intercept only	4	604.4	612.4
G	Gender only	8	602.3	618.3
S	Size only	8	589.2	605.2
L	Lake only	16	561.2	593.2
LS	Lake and Size	20	540.1	580.1
GLS	G, L, S main effects	24	537.9	585.9
SAT	G*S*L (saturated)	64	487.6	615.6

Which model looks like it fits the data best?

- Here,  $AIC = Deviance + 2(EDF)$

# 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	<i>p</i> -value
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 looks like it fits the data best?

## Results of testing

fit	Model	edf	Deviance	versus	p-value
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 looks like it fits the data best?
- The best model (of these) is apparently the model which collapses on Gender, and uses only Lake and Size as predictors for Food Choice.

## The start of the L+S Model

```
tidy(fit_LS, exponentiate = FALSE) %>%  
  slice(1:5) %>% kable(digits = 3)
```

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

- So, for instance, log odds of invertebrates rather than fish are:

-1.54 + 1.46 Small - 1.66 Hancock  
+ 0.94 Oklawaha + 1.12 Trafford

etc. For the baseline category, log odds of fish = 0, so  $\exp(\log \text{ odds}) = 1$ .

## Response Probabilities in the L+S Model

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:

$$\begin{aligned}\hat{\pi}(Fish) &= \frac{1}{1 + \exp(-1.54) + \exp(-3.31) + \exp(-2.09) + \exp(-1.90)} \\ &= \frac{1}{1.524} = 0.66\end{aligned}$$

## Response Probabilities in the L+S Model

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

$$\begin{aligned}\hat{\pi}(\text{Inv.}) &= \frac{\exp(-1.54)}{1 + \exp(-1.54) + \exp(-3.31) + \exp(-2.09) + \exp(-1.90)} \\ &= \frac{0.214}{1.524} = 0.14\end{aligned}$$

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

- 0.02 for Reptiles, 0.08 for Birds, and 0.10 for Other
- And the five probabilities will sum to 1, at least within rounding error.

# Comparing Model Estimates to Observed Counts

For large size alligators in Lake George, we have. . .

Food Type	Fish	Invertebrates	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.

## Storing Predicted Probabilities from fit\_LS

```
fitLS_fits <-  
  predict(fit_LS, newdata = gator2, type = "probs")  
  
gator2_fit_LS <- cbind(gator2, fitLS_fits)  
  
head(gator2_fit_LS, 3)
```

	id	food	size	gender	lake	fish	invert
1	1	fish	<2.3	m	hancock	0.5352844	0.09311221
2	2	fish	<2.3	m	hancock	0.5352844	0.09311221
3	3	fish	<2.3	m	hancock	0.5352844	0.09311221

	rep	bird	other
1	0.04745855	0.07040277	0.2537421
2	0.04745855	0.07040277	0.2537421
3	0.04745855	0.07040277	0.2537421

# Tabulating Response Probabilities

```
gator2_fit_LS %>% group_by(food) %>%  
  summarize(mean(fish), mean(invert), mean(rep),  
             mean(bird), mean(other))
```

```
# A tibble: 5 x 6
```

	food	`mean(fish)`	`mean(invert)`	`mean(rep)`	`mean(bird)`
	<fct>	<dbl>	<dbl>	<dbl>	<dbl>
1	fish	0.481	0.230	0.0763	0.0631
2	inve~	0.361	0.393	0.0858	0.0395
3	rep	0.381	0.258	0.148	0.0641
4	bird	0.452	0.197	0.0960	0.0841
5	other	0.426	0.246	0.0791	0.0733

```
# ... with 1 more variable: `mean(other)` <dbl>
```



## Turn Wide Data into Long (current approach)

```
gator2_fitLSlong <-  
  pivot_longer(gator2_fit_LS,  
               cols = fish:other,  
               names_to = "response",  
               values_to = "prob")  
  
head(gator2_fitLSlong,3)
```

# A tibble: 3 x 7

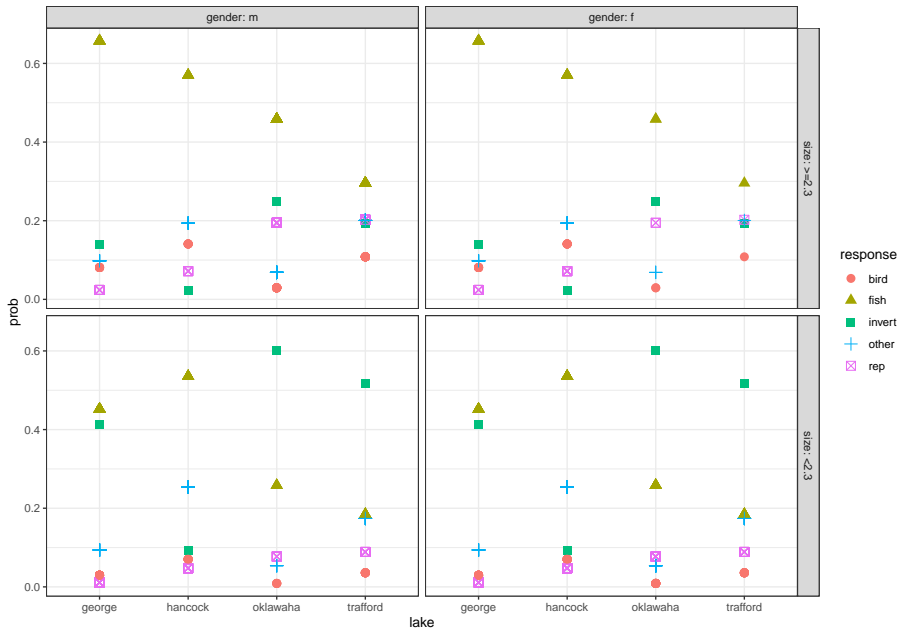
	id	food	size	gender	lake	response	prob
	<int>	<fct>	<fct>	<fct>	<fct>	<chr>	<dbl>
1	1	fish	<2.3	m	hancock	fish	0.535
2	1	fish	<2.3	m	hancock	invert	0.0931
3	1	fish	<2.3	m	hancock	rep	0.0475

## Turn Wide Data into Long (old approach, still in Notes)

```
gator2_fitLSlong_old <-  
  gather(gator2_fit_LS, key = response,  
         value = prob,  
         fish:other, factor_key = TRUE)  
  
head(gator2_fitLSlong_old,3)
```

	id	food	size	gender	lake	response	prob
1	1	fish	<2.3	m	hancock	fish	0.5352844
2	2	fish	<2.3	m	hancock	fish	0.5352844
3	3	fish	<2.3	m	hancock	fish	0.5352844

# Graphing the Model's Response Probabilities



# Graphing the Model's Response Probabilities (code)

```
ggplot(gator2_fitLSlong, aes(x = lake, y = prob,
                             col = response,
                             shape = response)) +
  geom_point(size = 3) +
  scale_fill_brewer(palette = "Set1") +
  theme_bw() +
  facet_grid(size ~ gender, labeller = "label_both")
```

# Some Sources for Multinomial Logistic Regression

In addition to the example found in our Course Notes...

- A good source of information on fitting these models is <https://stats.idre.ucla.edu/r/dae/multinomial-logistic-regression/>
- 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.