

Logistic Regression

Logistic regression

- ▶ When response variable is measured/counted, regression can work well.
- ▶ But what if response is yes/no, lived/died, success/failure?
- ▶ Model *probability* of success.
- ▶ Probability must be between 0 and 1; need method that ensures this.
- ▶ *Logistic regression* does this. In R, is a *generalized linear model* with binomial “family”:

```
glm(y ~ x, family="binomial")
```

- ▶ Begin with simplest case.

Packages

```
library(MASS)
library(tidyverse)
library(marginaleffects)
library(broom)
library(nnet)
library(conflicted)
conflict_prefer("select", "dplyr")
conflict_prefer("filter", "dplyr")
conflict_prefer("rename", "dplyr")
conflict_prefer("summarize", "dplyr")
```

The rats, part 1

► Rats given dose of some poison; either live or die:

| dose | status |
|------|--------|
|------|--------|

| | |
|---|-------|
| 0 | lived |
|---|-------|

| | |
|---|------|
| 1 | died |
|---|------|

| | |
|---|-------|
| 2 | lived |
|---|-------|

| | |
|---|-------|
| 3 | lived |
|---|-------|

| | |
|---|------|
| 4 | died |
|---|------|

| | |
|---|------|
| 5 | died |
|---|------|

Read in:

```
my_url <- "http://ritsokiguess.site/datafiles/rat.txt"
rats <- read_delim(my_url, " ")
rats
```

```
# A tibble: 6 x 2
```

```
  dose status
```

```
<dbl> <chr>
```

```
1     0 lived
```

```
2     1 died
```

```
3     2 lived
```

```
4     3 lived
```

```
5     4 died
```

```
6     5 died
```

Basic logistic regression

- ▶ Make response into a factor first:

```
rats2 <- rats %>% mutate(status = factor(status))
```

- ▶ then fit model:

```
status.1 <- glm(status ~ dose, family = "binomial", data = rats2)
```

Output

```
summary(status.1)
```

Call:

```
glm(formula = status ~ dose, family = "binomial", data = rats2)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 1.6841 | 1.7979 | 0.937 | 0.349 |
| dose | -0.6736 | 0.6140 | -1.097 | 0.273 |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 8.3178 on 5 degrees of freedom
Residual deviance: 6.7728 on 4 degrees of freedom
AIC: 10.773

Number of Fisher Scoring iterations: 4

Interpreting the output

- ▶ Like (multiple) regression, get tests of significance of individual x 's
- ▶ Here not significant (only 6 observations).
- ▶ “Slope” for dose is negative, meaning that as dose increases, probability of event modelled (survival) decreases.

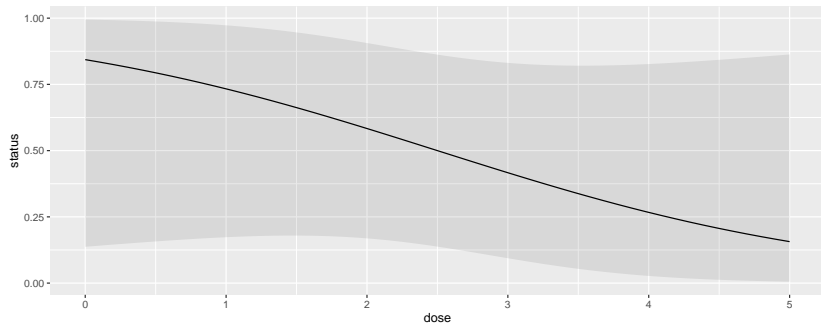
Output part 2: predicted survival probs

```
cbind(predictions(status.1)) %>%  
  select(dose, estimate)
```

| | dose | estimate |
|---|------|-----------|
| 1 | 0 | 0.8434490 |
| 2 | 1 | 0.7331122 |
| 3 | 2 | 0.5834187 |
| 4 | 3 | 0.4165813 |
| 5 | 4 | 0.2668878 |
| 6 | 5 | 0.1565510 |

On a graph

```
plot_cap(status.1, condition = "dose")
```



The rats, more

- ▶ More realistic: more rats at each dose (say 10).
- ▶ Listing each rat on one line makes a big data file.
- ▶ Use format below: dose, number of survivals, number of deaths.

| dose | lived | died |
|------|-------|------|
| 0 | 10 | 0 |
| 1 | 7 | 3 |
| 2 | 6 | 4 |
| 3 | 4 | 6 |
| 4 | 2 | 8 |
| 5 | 1 | 9 |

- ▶ 6 lines of data correspond to 60 actual rats.
- ▶ Saved in rat2.txt.

These data

```
my_url <- "http://ritsokiguess.site/datafiles/rat2.txt"
rat2 <- read_delim(my_url, " ")
rat2
```

```
# A tibble: 6 x 3
  dose lived died
  <dbl> <dbl> <dbl>
1     0    10     0
2     1     7     3
3     2     6     4
4     3     4     6
5     4     2     8
6     5     1     9
```

Create response matrix:

- ▶ Each row contains *multiple* observations.
- ▶ Create *two-column* response:
 - ▶ #survivals in first column,
 - ▶ #deaths in second.

```
response <- with(rat2, cbind(lived, died))  
response
```

| | lived | died |
|------|-------|------|
| [1,] | 10 | 0 |
| [2,] | 7 | 3 |
| [3,] | 6 | 4 |
| [4,] | 4 | 6 |
| [5,] | 2 | 8 |
| [6,] | 1 | 9 |

- ▶ Response is R matrix:

```
class(response)
```

```
[1] "matrix" "array"
```

Fit logistic regression

► using response you just made:

```
rat2.1 <- glm(response ~ dose,  
  family = "binomial",  
  data = rat2  
)
```

Output

```
summary(rat2.1)
```

Call:

```
glm(formula = response ~ dose, family = "binomial", data = rat2)
```

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) | |
|-------------|----------|------------|---------|----------|-----|
| (Intercept) | 2.3619 | 0.6719 | 3.515 | 0.000439 | *** |
| dose | -0.9448 | 0.2351 | -4.018 | 5.87e-05 | *** |

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 27.530 on 5 degrees of freedom
Residual deviance: 2.474 on 4 degrees of freedom
AIC: 18.94

Number of Fisher Scoring iterations: 4

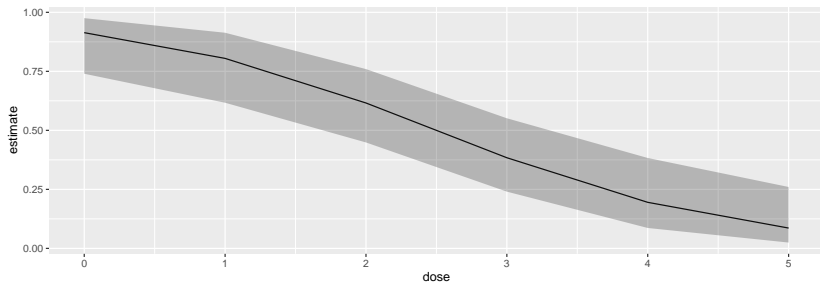
Predicted survival probs

```
new <- datagrid(model = rat2.1, dose = 0:5)
cbind(predictions(rat2.1, newdata = new))
```

| | rowid | estimate | p.value | s.value | conf.low | conf.hi |
|---|-------|-----------|--------------|-----------|------------|---------|
| 1 | 1 | 0.9138762 | 0.0004389651 | 11.153606 | 0.73983042 | 0.97536 |
| 2 | 2 | 0.8048905 | 0.0031438277 | 8.313262 | 0.61695841 | 0.91353 |
| 3 | 3 | 0.6159474 | 0.1721141940 | 2.538562 | 0.44876099 | 0.75959 |
| 4 | 4 | 0.3840526 | 0.1721142921 | 2.538561 | 0.24040837 | 0.55123 |
| 5 | 5 | 0.1951095 | 0.0031438384 | 8.313257 | 0.08646093 | 0.38304 |
| 6 | 6 | 0.0861238 | 0.0004389668 | 11.153600 | 0.02463288 | 0.26016 |

On a picture

```
cbind(predictions(rat2.1, newdata = new)) %>%  
  select(estimate, conf.low, conf.high, dose) %>%  
  ggplot(aes(x = dose, y = estimate,  
             ymin = conf.low, ymax = conf.high)) +  
    geom_line() + geom_ribbon(alpha = 0.3)
```



Comments

- ▶ Significant effect of dose.
- ▶ Effect of larger dose is to *decrease* survival probability (“slope” negative; also see in decreasing predictions.)
- ▶ Confidence intervals around prediction narrower (more data).

Multiple logistic regression

- ▶ With more than one x , works much like multiple regression.
- ▶ Example: study of patients with blood poisoning severe enough to warrant surgery. Relate survival to other potential risk factors.
- ▶ Variables, 1=present, 0=absent:
 - ▶ survival (death from sepsis=1), response
 - ▶ shock
 - ▶ malnutrition
 - ▶ alcoholism
 - ▶ age (as numerical variable)
 - ▶ bowel infarction
- ▶ See what relates to death.

Read in data

```
my_url <-  
  "http://ritsokiguess.site/datafiles/sepsis.txt"  
sepsis <- read_delim(my_url, " ")
```

Make sure categoricals really are

```
sepsis %>%  
  mutate(across(-age, \(x) factor(x))) -> sepsis
```

The data (some)

```
sepsis
```

```
# A tibble: 106 x 6
```

| | death | shock | malnut | alcohol | age | bowelinf |
|----|-------|-------|--------|---------|-------|----------|
| | <fct> | <fct> | <fct> | <fct> | <dbl> | <fct> |
| 1 | 0 | 0 | 0 | 0 | 56 | 0 |
| 2 | 0 | 0 | 0 | 0 | 80 | 0 |
| 3 | 0 | 0 | 0 | 0 | 61 | 0 |
| 4 | 0 | 0 | 0 | 0 | 26 | 0 |
| 5 | 0 | 0 | 0 | 0 | 53 | 0 |
| 6 | 1 | 0 | 1 | 0 | 87 | 0 |
| 7 | 0 | 0 | 0 | 0 | 21 | 0 |
| 8 | 1 | 0 | 0 | 1 | 69 | 0 |
| 9 | 0 | 0 | 0 | 0 | 57 | 0 |
| 10 | 0 | 0 | 1 | 0 | 76 | 0 |

```
# i 96 more rows
```

Fit model

```
sepsis.1 <- glm(death ~ shock + malnut + alcohol + age +  
  bowelinf,  
  family = "binomial",  
  data = sepsis  
)
```

Output part 1

```
tidy(sepsis.1)
```

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

| | term <chr> | estimate <dbl> | std.error <dbl> | statistic <dbl> | p.value <dbl> |
|---|---------------|-------------------|--------------------|--------------------|------------------|
| 1 | (Intercept) | -9.75 | 2.54 | -3.84 | 0.000124 |
| 2 | shock1 | 3.67 | 1.16 | 3.15 | 0.00161 |
| 3 | malnut1 | 1.22 | 0.728 | 1.67 | 0.0948 |
| 4 | alcohol1 | 3.35 | 0.982 | 3.42 | 0.000635 |
| 5 | age | 0.0922 | 0.0303 | 3.04 | 0.00237 |
| 6 | bowelinf1 | 2.80 | 1.16 | 2.40 | 0.0162 |

- ▶ All P-values fairly small
- ▶ but malnut not significant: remove.

Removing malnut

```
sepsis.2 <- update(sepsis.1, . ~ . - malnut)
tidy(sepsis.2)
```

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

| | term <chr> | estimate <dbl> | std.error <dbl> | statistic <dbl> | p.value <dbl> |
|---|---------------|-------------------|--------------------|--------------------|------------------|
| 1 | (Intercept) | -8.89 | 2.32 | -3.84 | 0.000124 |
| 2 | shock1 | 3.70 | 1.10 | 3.35 | 0.000797 |
| 3 | alcohol1 | 3.19 | 0.917 | 3.47 | 0.000514 |
| 4 | age | 0.0898 | 0.0292 | 3.07 | 0.00211 |
| 5 | bowelinf1 | 2.39 | 1.07 | 2.23 | 0.0260 |

► Everything significant now.

Comments

- ▶ Most of the original x 's helped predict death. Only `malnut` seemed not to add anything.
- ▶ Removed `malnut` and tried again.
- ▶ Everything remaining is significant (though `bowelinf` actually became *less* significant).
- ▶ All coefficients are *positive*, so having any of the risk factors (or being older) *increases* risk of death.

Predictions from model without “malnut”

► A few (rows of original dataframe) chosen “at random”:

```
sepsis %>% slice(c(4, 1, 2, 11, 32)) -> new  
new
```

```
# A tibble: 5 x 6  
  death shock malnut alcohol   age bowelinf  
  <fct> <fct> <fct> <fct>   <dbl> <fct>  
1 0      0      0      0      26 0  
2 0      0      0      0      56 0  
3 0      0      0      0      80 0  
4 1      0      0      1      66 1  
5 1      0      0      1      49 0
```

```
cbind(predictions(sepsis.2, newdata = new)) %>%  
  select(estimate, conf.low, conf.high, shock:bowelinf)
```

| | estimate | conf.low | conf.high | shock | malnut | alcohol | age | bowelinf |
|---|-------------|--------------|------------|-------|--------|---------|-----|----------|
| 1 | 0.001415347 | 6.272642e-05 | 0.03103047 | 0 | 0 | 0 | 26 | 0 |
| 2 | 0.020552383 | 4.102504e-03 | 0.09656596 | 0 | 0 | 0 | 56 | 0 |
| 3 | 0.153416834 | 5.606838e-02 | 0.35603441 | 0 | 0 | 0 | 80 | 0 |
| 4 | 0.931290137 | 5.490986e-01 | 0.99341482 | 0 | 0 | 1 | 66 | 1 |
| 5 | 0.213000997 | 7.639063e-02 | 0.46967947 | 0 | 0 | 1 | 49 | 0 |

Comments

- ▶ Survival chances pretty good if no risk factors, though decreasing with age.
- ▶ Having more than one risk factor reduces survival chances dramatically.
- ▶ Usually good job of predicting survival; sometimes death predicted to survive.

Another way to assess effects

of age:

```
new <- datagrid(model = sepsis.2, age = seq(30, 70, 10))  
new
```

| | death | shock | alcohol | bowelinf | age |
|---|-------|-------|---------|----------|-----|
| 1 | 0 | 0 | 0 | 0 | 30 |
| 2 | 0 | 0 | 0 | 0 | 40 |
| 3 | 0 | 0 | 0 | 0 | 50 |
| 4 | 0 | 0 | 0 | 0 | 60 |
| 5 | 0 | 0 | 0 | 0 | 70 |

Assessing age effect

```
cbind(predictions(sepsis.2, newdata = new)) %>%  
  select(estimate, shock:age)
```

| | estimate | shock | alcohol | bowelinf | age |
|---|-------------|-------|---------|----------|-----|
| 1 | 0.002026053 | 0 | 0 | 0 | 30 |
| 2 | 0.004960283 | 0 | 0 | 0 | 40 |
| 3 | 0.012092515 | 0 | 0 | 0 | 50 |
| 4 | 0.029179226 | 0 | 0 | 0 | 60 |
| 5 | 0.068729752 | 0 | 0 | 0 | 70 |

Assessing shock effect

```
new <- datagrid(shock = c(0, 1), model = sepsis.2)
new
```

| | death | alcohol | age | bowelinf | shock |
|---|-------|---------|----------|----------|-------|
| 1 | 0 | 0 | 51.28302 | 0 | 0 |
| 2 | 0 | 0 | 51.28302 | 0 | 1 |

```
cbind(predictions(sepsis.2, newdata = new)) %>%
  select(estimate, death:shock)
```

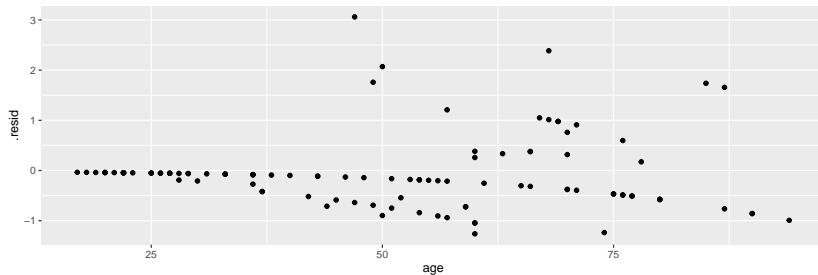
| | estimate | death | alcohol | age | bowelinf | shock |
|---|------------|-------|---------|----------|----------|-------|
| 1 | 0.01354973 | 0 | 0 | 51.28302 | 0 | 0 |
| 2 | 0.35742607 | 0 | 0 | 51.28302 | 0 | 1 |

Assessing proportionality of odds for age

- ▶ An assumption we made is that log-odds of survival depends linearly on age.
- ▶ Hard to get your head around, but basic idea is that survival chances go continuously up (or down) with age, instead of (for example) going up and then down.
- ▶ In this case, seems reasonable, but should check:

Residuals vs. age

```
sepsis.2 %>% augment(sepsis) %>%  
  ggplot(aes(x = age, y = .resid)) +  
  geom_point()
```



Comments

- ▶ No apparent problems overall.
- ▶ Confusing “line” across: no risk factors, survived.

Probability and odds

- ▶ For probability p , odds is $p/(1 - p)$:

| Prob. | | Odds | log-odds | in words |
|-------|--------------------------|------|----------|--------------|
| 0.5 | $0.5/0.5 = 1/1 = 1.00$ | | 0.00 | “even money” |
| 0.1 | $0.1/0.9 = 1/9 = 0.11$ | | -2.20 | “9 to 1” |
| 0.4 | $0.4/0.6 = 1/1.5 = 0.67$ | | -0.41 | “1.5 to 1” |
| 0.8 | $0.8/0.2 = 4/1 = 4.00$ | | 1.39 | “4 to 1 on” |

- ▶ Gamblers use odds: if you win at 9 to 1 odds, get original stake back plus 9 times the stake.
- ▶ Probability has to be between 0 and 1
- ▶ Odds between 0 and infinity
- ▶ Log-odds can be anything: any log-odds corresponds to valid probability.

Odds ratio

- ▶ Suppose 90 of 100 men drank wine last week, but only 20 of 100 women.
- ▶ Prob of man drinking wine $90/100 = 0.9$, woman $20/100 = 0.2$.
- ▶ Odds of man drinking wine $0.9/0.1 = 9$, woman $0.2/0.8 = 0.25$.
- ▶ Ratio of odds is $9/0.25 = 36$.
- ▶ Way of quantifying difference between men and women: “odds of drinking wine 36 times larger for males than females”.

Sepsis data again

- Recall prediction of probability of death from risk factors:

```
sepsis.2.tidy <- tidy(sepsis.2)
sepsis.2.tidy
```

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

| | term <chr> | estimate <dbl> | std.error <dbl> | statistic <dbl> | p.value <dbl> |
|---|---------------|-------------------|--------------------|--------------------|------------------|
| 1 | (Intercept) | -8.89 | 2.32 | -3.84 | 0.000124 |
| 2 | shock1 | 3.70 | 1.10 | 3.35 | 0.000797 |
| 3 | alcohol1 | 3.19 | 0.917 | 3.47 | 0.000514 |
| 4 | age | 0.0898 | 0.0292 | 3.07 | 0.00211 |
| 5 | bowelinf1 | 2.39 | 1.07 | 2.23 | 0.0260 |

- Slopes in column estimate.

Multiplying the odds

- ▶ Can interpret slopes by taking “exp” of them. We ignore intercept.

```
sepsis.2.tidy %>%  
  mutate(exp_coef=exp(estimate)) %>%  
  select(term, exp_coef)
```

```
# A tibble: 5 x 2  
  term      exp_coef  
  <chr>      <dbl>  
1 (Intercept) 0.000137  
2 shock1      40.5  
3 alcohol1    24.2  
4 age         1.09  
5 bowelinf1   10.9
```

Interpretation

```
# A tibble: 5 x 2
  term          exp_coeff
  <chr>         <dbl>
1 (Intercept)  0.000137
2 shock1       40.5
3 alcohol1     24.2
4 age          1.09
5 bowelinf1    10.9
```

- ▶ These say “how much do you *multiply* odds of death by for increase of 1 in corresponding risk factor?” Or, what is odds ratio for that factor being 1 (present) vs. 0 (absent)?
- ▶ Eg. being alcoholic vs. not increases odds of death by 24 times
- ▶ One year older multiplies odds by about 1.1 times. Over 40 years, about $1.09^{40} = 31$ times.

Odds ratio and relative risk

- ▶ **Relative risk** is ratio of probabilities.
- ▶ Above: 90 of 100 men (0.9) drank wine, 20 of 100 women (0.2).
- ▶ Relative risk $0.9/0.2=4.5$. (odds ratio was 36).
- ▶ When probabilities small, relative risk and odds ratio similar.
- ▶ Eg. prob of man having disease 0.02, woman 0.01.
- ▶ Relative risk $0.02/0.01 = 2$.

Odds ratio vs. relative risk

- Odds for men and for women:

```
(od1 <- 0.02 / 0.98) # men
```

```
[1] 0.02040816
```

```
(od2 <- 0.01 / 0.99) # women
```

```
[1] 0.01010101
```

- Odds ratio

```
od1 / od2
```

```
[1] 2.020408
```

- Very close to relative risk of 2.

More than 2 response categories

- ▶ With 2 response categories, model the probability of one, and prob of other is one minus that. So doesn't matter which category you model.
- ▶ With more than 2 categories, have to think more carefully about the categories: are they
- ▶ *ordered*: you can put them in a natural order (like low, medium, high)
- ▶ *nominal*: ordering the categories doesn't make sense (like red, green, blue).
- ▶ R handles both kinds of response; learn how.

Ordinal response: the miners

- ▶ Model probability of being in given category *or lower*.
- ▶ Example: coal-miners often suffer disease pneumoconiosis. Likelihood of disease believed to be greater among miners who have worked longer.
- ▶ Severity of disease measured on categorical scale: none, moderate, severe.

Miners data

► Data are frequencies:

| Exposure | None | Moderate | Severe |
|----------|------|----------|--------|
| 5.8 | 98 | 0 | 0 |
| 15.0 | 51 | 2 | 1 |
| 21.5 | 34 | 6 | 3 |
| 27.5 | 35 | 5 | 8 |
| 33.5 | 32 | 10 | 9 |
| 39.5 | 23 | 7 | 8 |
| 46.0 | 12 | 6 | 10 |
| 51.5 | 4 | 2 | 5 |

Reading the data

Data in aligned columns with more than one space between, so:

```
my_url <- "http://ritsokiguess.site/datafiles/miners-tab.txt"
freqs <- read_table(my_url)
```

The data

```
freqs
```

```
# A tibble: 8 x 4
```

| | Exposure | None | Moderate | Severe |
|---|----------|-------|----------|--------|
| | <dbl> | <dbl> | <dbl> | <dbl> |
| 1 | 5.8 | 98 | 0 | 0 |
| 2 | 15 | 51 | 2 | 1 |
| 3 | 21.5 | 34 | 6 | 3 |
| 4 | 27.5 | 35 | 5 | 8 |
| 5 | 33.5 | 32 | 10 | 9 |
| 6 | 39.5 | 23 | 7 | 8 |
| 7 | 46 | 12 | 6 | 10 |
| 8 | 51.5 | 4 | 2 | 5 |

Tidying

```
freqs %>%  
  pivot_longer(-Exposure, names_to = "Severity", values_to = "Count")  
  mutate(Severity = fct_inorder(Severity)) -> miners
```

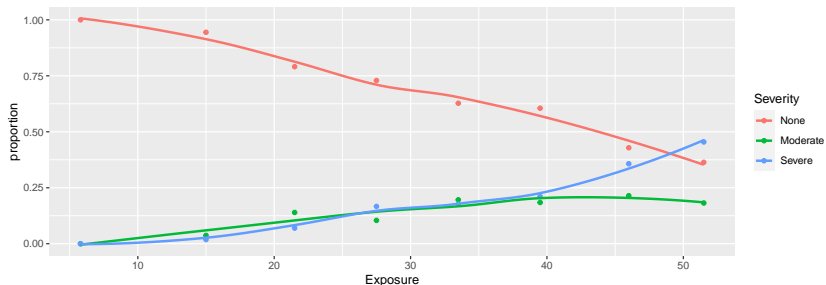
Result

```
miners
```

```
# A tibble: 24 x 3
  Exposure Severity Freq
  <dbl> <fct>    <dbl>
1     5.8 None      98
2     5.8 Moderate    0
3     5.8 Severe     0
4     15 None      51
5     15 Moderate    2
6     15 Severe     1
7    21.5 None     34
8    21.5 Moderate    6
9    21.5 Severe     3
10   27.5 None     35
# i 14 more rows
```


Plot proportions against exposure

```
miners %>%  
  group_by(Exposure) %>%  
  mutate(proportion = Freq / sum(Freq)) -> prop  
ggplot(prop, aes(x = Exposure, y = proportion,  
                  colour = Severity)) +  
  geom_point() + geom_smooth(se = F)
```



Reminder of data setup

```
miners
```

```
# A tibble: 24 x 3
```

| | Exposure | Severity | Freq |
|----|----------|----------|-------|
| | <dbl> | <fct> | <dbl> |
| 1 | 5.8 | None | 98 |
| 2 | 5.8 | Moderate | 0 |
| 3 | 5.8 | Severe | 0 |
| 4 | 15 | None | 51 |
| 5 | 15 | Moderate | 2 |
| 6 | 15 | Severe | 1 |
| 7 | 21.5 | None | 34 |
| 8 | 21.5 | Moderate | 6 |
| 9 | 21.5 | Severe | 3 |
| 10 | 27.5 | None | 35 |

```
# i 14 more rows
```

Fitting ordered logistic model

Use function `polr` from package `MASS`. Like `glm`.

```
sev.1 <- polr(Severity ~ Exposure,  
  weights = Freq,  
  data = miners  
)
```

Output: not very illuminating

```
sev.1 <- polr(Severity ~ Exposure,  
  weights = Freq,  
  data = miners,  
  Hess = TRUE  
)
```

```
summary(sev.1)
```

Call:

```
polr(formula = Severity ~ Exposure, data = miners, weights = Freq,  
     Hess = TRUE)
```

Coefficients:

| | Value | Std. Error | t value |
|----------|--------|------------|---------|
| Exposure | 0.0959 | 0.01194 | 8.034 |

Intercepts:

| | Value | Std. Error | t value |
|-----------------|--------|------------|---------|
| None Moderate | 3.9558 | 0.4097 | 9.6558 |
| Moderate Severe | 4.8690 | 0.4411 | 11.0383 |

Residual Deviance: 416.9188

AIC: 422.9188

Does exposure have an effect?

Fit model without Exposure, and compare using anova. Note 1 for model with just intercept:

```
sev.0 <- polr(Severity ~ 1, weights = Freq, data = miners)
anova(sev.0, sev.1)
```

Likelihood ratio tests of ordinal regression models

Response: Severity

| | Model | Resid. df | Resid. Dev | Test | Df | LR stat. |
|---|----------|-----------|------------|--------|----|----------|
| 1 | 1 | 369 | 505.1621 | | | |
| 2 | Exposure | 368 | 416.9188 | 1 vs 2 | 1 | 88.24324 |
| | Pr(Chi) | | | | | |
| 1 | | | | | | |
| 2 | 0 | | | | | |

Exposure definitely has effect on severity of disease.

Another way

- ▶ What (if anything) can we drop from model with exposure?

```
drop1(sev.1, test = "Chisq")
```

Single term deletions

Model:

Severity ~ Exposure

| | Df | AIC | LRT | Pr(>Chi) |
|----------|----|--------|--------|---------------|
| <none> | | 422.92 | | |
| Exposure | 1 | 509.16 | 88.243 | < 2.2e-16 *** |

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- ▶ Nothing. Exposure definitely has effect.

Predicted probabilities 1/2

```
freqs %>% select(Exposure) -> new  
new
```

```
# A tibble: 8 x 1
```

```
  Exposure
```

```
    <dbl>
```

```
1      5.8
```

```
2     15
```

```
3    21.5
```

```
4    27.5
```

```
5    33.5
```

```
6    39.5
```

```
7     46
```

```
8    51.5
```

Predicted probabilities 2/2

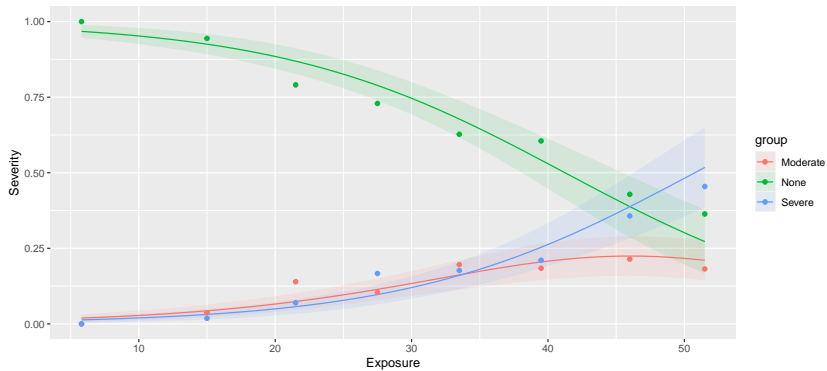
```
cbind(predictions(sev.1, newdata = new)) %>%  
  select(group, estimate, Exposure) %>%  
  pivot_wider(names_from = group, values_from = estimate)
```

```
# A tibble: 8 x 4
```

| | Exposure | None | Moderate | Severe |
|---|----------|-------|----------|--------|
| | <dbl> | <dbl> | <dbl> | <dbl> |
| 1 | 5.8 | 0.968 | 0.0191 | 0.0132 |
| 2 | 15 | 0.925 | 0.0433 | 0.0314 |
| 3 | 21.5 | 0.869 | 0.0739 | 0.0569 |
| 4 | 27.5 | 0.789 | 0.114 | 0.0969 |
| 5 | 33.5 | 0.678 | 0.162 | 0.160 |
| 6 | 39.5 | 0.542 | 0.205 | 0.253 |
| 7 | 46 | 0.388 | 0.224 | 0.388 |
| 8 | 51.5 | 0.272 | 0.210 | 0.517 |

The graph

ggg



Comments

- ▶ Model appears to match data well enough.
- ▶ As exposure goes up, prob of None goes down, Severe goes up (sharply for high exposure).
- ▶ So more exposure means worse disease.

Unordered responses

- ▶ With unordered (nominal) responses, can use *generalized logit*.
- ▶ Example: 735 people, record age and sex (male 0, female 1), which of 3 brands of some product preferred.
- ▶ Data in `mlogit.csv` separated by commas (so `read_csv` will work):

```
my_url <- "http://ritsokiguess.site/datafiles/mlogit.csv"
brandpref <- read_csv(my_url)
```

The data (some)

```
brandpref
```

```
# A tibble: 735 x 3  
  brand    sex  age  
  <dbl> <dbl> <dbl>  
1     1     0   24  
2     1     0   26  
3     1     0   26  
4     1     1   27  
5     1     1   27  
6     3     1   27  
7     1     0   27  
8     1     0   27  
9     1     1   27  
10    1     0   27  
# i 725 more rows
```

Bashing into shape

- ▶ sex and brand not meaningful as numbers, so turn into factors:

```
brandpref %>%  
  mutate(sex = ifelse(sex == 1, "female", "male"),  
         sex = factor(sex),  
         brand = factor(brand)  
  ) -> brandpref
```

Fitting model

- ▶ We use multinom from package nnet. Works like polr.

```
brands.1 <- multinom(brand ~ age + sex, data = brandpref)
```

```
# weights:  12 (6 variable)
initial  value 807.480032
iter   10 value 702.990572
final   value 702.970704
converged
```

Can we drop anything?

- ▶ Unfortunately drop1 seems not to work:

```
drop1(brands.1, test = "Chisq", trace = 0)
```

```
trying - age
```

```
Error in if (trace) {: argument is not interpretable as logical}
```

- ▶ So, fall back on fitting model without what you want to test, and comparing using anova.

Do age/sex help predict brand? 1/3

Fit models without each of age and sex:

```
brands.2 <- multinom(brand ~ age, data = brandpref)
```

```
# weights:  9 (4 variable)
initial  value 807.480032
iter   10 value 706.796323
iter   10 value 706.796322
final   value 706.796322
converged
```

```
brands.3 <- multinom(brand ~ sex, data = brandpref)
```

```
# weights:  9 (4 variable)
initial  value 807.480032
final   value 791.861266
converged
```

Do age/sex help predict brand? 2/3

```
anova(brands.2, brands.1)
```

Likelihood ratio tests of Multinomial Models

Response: brand

| | Model | Resid. df | Resid. Dev | Test | Df | LR stat. |
|---|-----------|-----------|------------|--------|----|----------|
| 1 | age | 1466 | 1413.593 | | | |
| 2 | age + sex | 1464 | 1405.941 | 1 vs 2 | 2 | 7.651236 |

Pr(Chi)

| | |
|---|------------|
| 1 | |
| 2 | 0.02180496 |

```
anova(brands.3, brands.1)
```

Likelihood ratio tests of Multinomial Models

Response: brand

| | Model | Resid. df | Resid. Dev | Test | Df | LR stat. |
|---|-----------|-----------|------------|--------|----|----------|
| 1 | sex | 1466 | 1583.723 | | | |
| 2 | age + sex | 1464 | 1405.941 | 1 vs 2 | 2 | 177.7811 |

Pr(Chi)

| | |
|---|---|
| 1 | |
| 2 | 0 |

Do age/sex help predict brand? 3/3

- ▶ age definitely significant (second anova)
- ▶ sex significant also (first anova), though P-value less dramatic
- ▶ Keep both.
- ▶ Expect to see a large effect of age, and a smaller one of sex.

Another way to build model

- ▶ Start from model with everything and run step:

```
step(brands.1, trace = 0)
```

```
trying - age
```

```
trying - sex
```

Call:

```
multinom(formula = brand ~ age + sex)
```

Coefficients:

| | (Intercept) | age | sexmale |
|---|-------------|-----------|------------|
| 2 | -11.25127 | 0.3682202 | -0.5237736 |
| 3 | -22.25571 | 0.6859149 | -0.4658215 |

Residual Deviance: 1405.941

AIC: 1417.941

- ▶ Final model contains both age and sex so neither could be removed.

Making predictions

Find age 5-number summary, and the two sexes:

```
summary(brandpref)
```

| brand | sex | age |
|-------|------------|--------------|
| 1:207 | female:466 | Min. :24.0 |
| 2:307 | male :269 | 1st Qu.:32.0 |
| 3:221 | | Median :32.0 |
| | | Mean :32.9 |
| | | 3rd Qu.:34.0 |
| | | Max. :38.0 |

Space the ages out a bit for prediction (see over).

Combinations

```
new <- datagrid(age = c(24, 30, 33, 35, 38),  
                sex = c("female", "male"), model = brands.1  
new
```

| | brand | age | sex |
|----|-------|-----|--------|
| 1 | 2 | 24 | female |
| 2 | 2 | 24 | male |
| 3 | 2 | 30 | female |
| 4 | 2 | 30 | male |
| 5 | 2 | 33 | female |
| 6 | 2 | 33 | male |
| 7 | 2 | 35 | female |
| 8 | 2 | 35 | male |
| 9 | 2 | 38 | female |
| 10 | 2 | 38 | male |

The predictions

```
cbind(predictions(brands.1, newdata = new)) %>%  
  select(group, estimate, age, sex) %>%  
  pivot_wider(names_from = group, values_from = estimate)
```

A tibble: 10 x 5

| | age | sex | `1` | `2` | `3` |
|----|-------|--------|--------|--------|---------|
| | <dbl> | <fct> | <dbl> | <dbl> | <dbl> |
| 1 | 24 | female | 0.915 | 0.0819 | 0.00279 |
| 2 | 24 | male | 0.948 | 0.0502 | 0.00181 |
| 3 | 30 | female | 0.500 | 0.407 | 0.0933 |
| 4 | 30 | male | 0.625 | 0.302 | 0.0732 |
| 5 | 33 | female | 0.203 | 0.500 | 0.297 |
| 6 | 33 | male | 0.296 | 0.432 | 0.272 |
| 7 | 35 | female | 0.0840 | 0.432 | 0.484 |
| 8 | 35 | male | 0.131 | 0.397 | 0.472 |
| 9 | 38 | female | 0.0162 | 0.252 | 0.732 |
| 10 | 38 | male | 0.0260 | 0.239 | 0.735 |

Comments

- ▶ Young males prefer brand 1, but older males prefer brand 3.
- ▶ Females similar, but like brand 1 less and brand 2 more.
- ▶ A clear brand effect, but the sex effect is less clear.

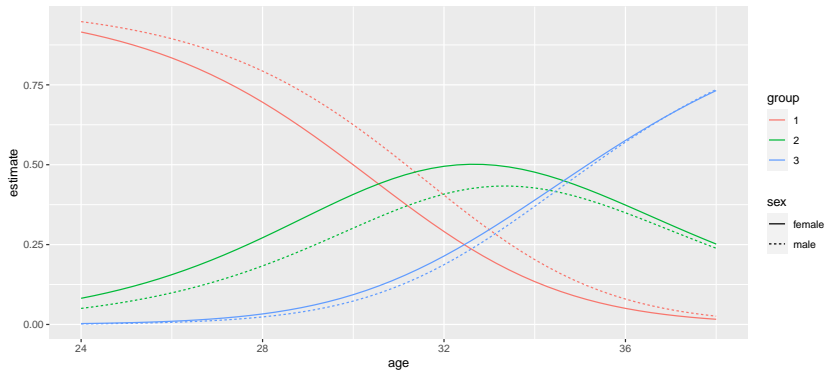
Making a plot

- ▶ `plot_cap` doesn't quite work
- ▶ so don't draw, edit, *then* make graph:

```
plot_cap(brands.1, condition = c("age", "brand", "sex"),  
          type = "probs", draw = FALSE) %>%  
  ggplot(aes(x = age, y = estimate, colour = group,  
             linetype = sex)) +  
  geom_line() -> g
```

The graph

σ_α



Digesting the plot

- ▶ Brand vs. age: younger people (of both genders) prefer brand 1, but older people (of both genders) prefer brand 3. (Explains significant age effect.)
- ▶ Brand vs. sex: females (solid) like brand 1 less than males (dashed), like brand 2 more (for all ages).
- ▶ Not much brand difference between genders (solid and dashed lines of same colours close), but enough to be significant.
- ▶ Model didn't include interaction, so modelled effect of gender on brand same for each age, modelled effect of age same for each gender. (See also later.)

Alternative data format

Summarize all people of same brand preference, same sex, same age on one line of data file with frequency on end:

```
brandpref
```

```
# A tibble: 735 x 3
  brand sex    age
  <fct> <fct> <dbl>
1 1     male    24
2 1     male    26
3 1     male    26
4 1    female    27
5 1    female    27
6 3    female    27
7 1     male    27
8 1     male    27
9 1    female    27
10 1    male    27
# i 725 more rows
```

Getting alternative data format

```
brandpref %>%  
  group_by(age, sex, brand) %>%  
  summarize(Freq = n()) %>%  
  ungroup() -> b  
b
```

A tibble: 65 x 4

| | age | sex | brand | Freq |
|----|-------|--------|-------|-------|
| | <dbl> | <fct> | <fct> | <int> |
| 1 | 24 | male | 1 | 1 |
| 2 | 26 | male | 1 | 2 |
| 3 | 27 | female | 1 | 4 |
| 4 | 27 | female | 3 | 1 |
| 5 | 27 | male | 1 | 4 |
| 6 | 28 | female | 1 | 6 |
| 7 | 28 | female | 2 | 2 |
| 8 | 28 | female | 3 | 1 |
| 9 | 28 | male | 1 | 4 |
| 10 | 28 | male | 3 | 2 |

Fitting models, almost the same

- ▶ Just have to remember weights to incorporate frequencies.
- ▶ Otherwise multinom assumes you have just 1 obs on each line!
- ▶ Again turn (numerical) sex and brand into factors:

```
b %>%  
  mutate(sex = factor(sex)) %>%  
  mutate(brand = factor(brand)) -> bf  
b.1 <- multinom(brand ~ age + sex, data = bf, weights = Freq)  
b.2 <- multinom(brand ~ age, data = bf, weights = Freq)
```

P-value for sex identical

```
anova(b.2, b.1)
```

Likelihood ratio tests of Multinomial Models

Response: brand

| | Model | Resid. df | Resid. Dev | Test | Df | LR stat. |
|---|-----------|-----------|------------|--------|----|----------|
| 1 | age | 126 | 1413.593 | | | |
| 2 | age + sex | 124 | 1405.941 | 1 vs 2 | 2 | 7.651236 |

Pr(Chi)

| | |
|---|------------|
| 1 | |
| 2 | 0.02180496 |

Same P-value as before, so we haven't changed anything important.

Trying interaction between age and gender

```
brands.4 <- update(brands.1, . ~ . + age:sex)
```

```
# weights: 15 (8 variable)
initial value 807.480032
iter 10 value 703.191146
iter 20 value 702.572260
iter 30 value 702.570900
iter 30 value 702.570893
iter 30 value 702.570893
final value 702.570893
converged
```

```
anova(brands.1, brands.4)
```

Likelihood ratio tests of Multinomial Models

Response: brand

| | Model | Resid. df | Resid. Dev | Test | Df |
|---|---------------------|-----------|------------|--------|----|
| 1 | age + sex | 1464 | 1405.941 | | |
| 2 | age + sex + age:sex | 1462 | 1405.142 | 1 vs 2 | 2 |
| | LR stat. | Pr(Chi) | | | |
| 1 | | | | | |
| 2 | 0.7996223 | 0.6704466 | | | |

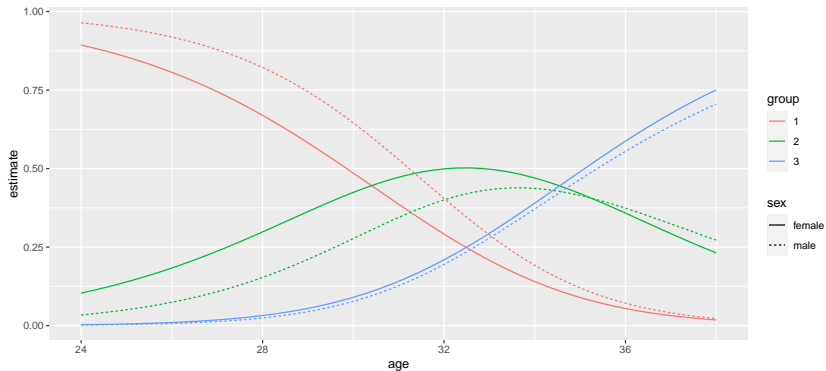
- No evidence that effect of age on brand preference differs for the two genders.

Make graph again

```
plot_cap(brands.4, condition = c("age", "brand", "sex"),  
          type = "probs", draw = FALSE) %>%  
  ggplot(aes(x = age, y = estimate, colour = group,  
             linetype = sex)) +  
  geom_line() -> g4
```

Not much difference in the graph

g4



Compare model without interaction

09

