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

```r
library(MASS, exclude = "select")
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
```

This doesn't work

```
status.0 <- glm(status ~ dose, family = "binomial", data = rats)
```

```
Error in eval(family$initialize): y values must be 0 <= y <= 1
```

- Values of response variable (here `status`) must be either:
  - 1 = "success", 0 = "failure"
  - a `factor` (not text) with two levels.
- The error message doesn't say that the second is a possibility.

Basic logistic regression

- So, make response into a factor first:

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

```
# A tibble: 6 x 2
   dose status
  <dbl> <fct>
1     0 lived
2     1 died
3     2 lived
4     3 lived
5     4 died
6     5 died
```

- then fit model:

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

Output

```r
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
```

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.

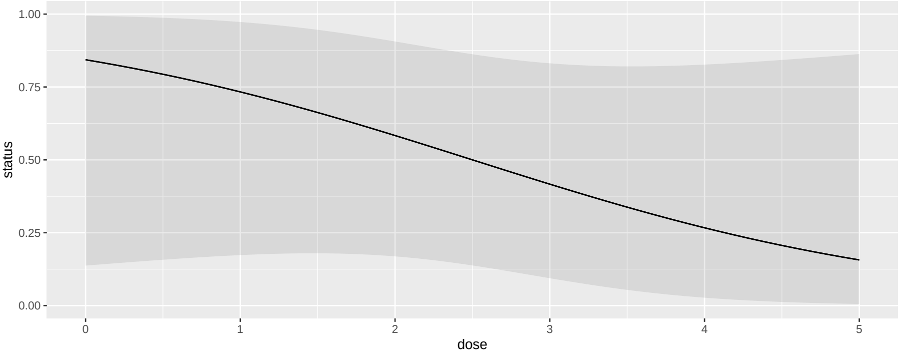
Output part 2: predicted survival probs

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

```
  dose  estimate    conf.low conf.high
1    0 0.8434490 0.137095792 0.9945564
2    1 0.7331122 0.173186479 0.9729896
3    2 0.5834187 0.168847561 0.9061463
4    3 0.4165813 0.093853682 0.8311524
5    4 0.2668878 0.027010413 0.8268135
6    5 0.1565510 0.005443589 0.8629042
```

On a graph

```
plot_predictions(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
```

Response matrix:

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

```
with(rat2, cbind(lived, died))
```

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

Fit logistic regression

- constructing the response in the `glm`:

```r
rat2.1 <- glm(cbind(lived, died) ~ dose,
              family = "binomial", data = rat2)
```

Output

Significant effect of dose now:

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

```
Call:
glm(formula = cbind(lived, died) ~ 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)
```

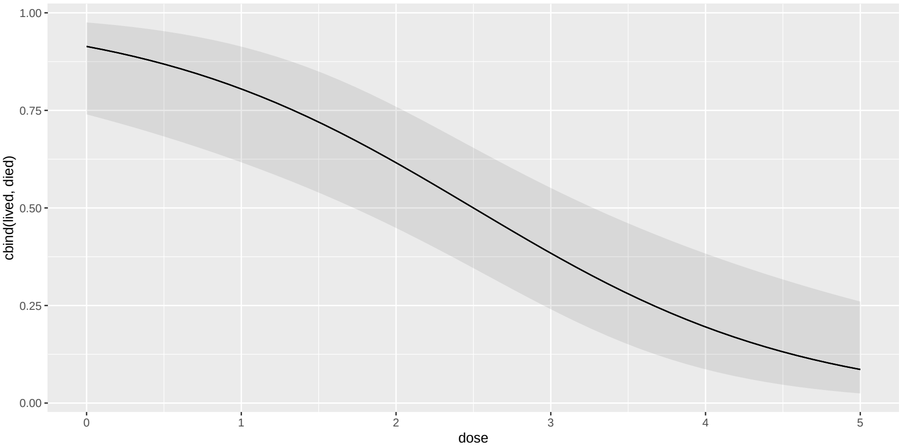
Predicted survival probs

```
new <- datagrid(model = rat2.1, dose = 0:5)
cbind(predictions(rat2.1, newdata = new)) %>%
  select(estimate, dose, conf.low, conf.high)
```

```
   estimate dose   conf.low conf.high
1 0.9138762    0 0.73983042 0.9753671
2 0.8048905    1 0.61695841 0.9135390
3 0.6159474    2 0.44876099 0.7595916
4 0.3840526    3 0.24040837 0.5512390
5 0.1951095    4 0.08646093 0.3830417
6 0.0861238    5 0.02463288 0.2601697
```

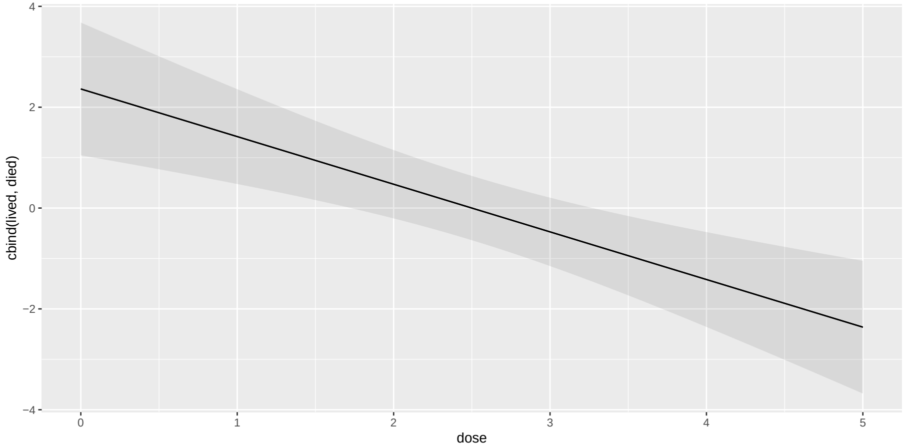
On a picture

```
plot_predictions(rat2.1, condition = "dose")
```



Dose and predicted log-odds

```
plot_predictions(rat2.1, condition = "dose", type = "link")
```



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

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

```
# A tibble: 106 x 6
   death shock malnut alcohol   age bowelinf
   <dbl> <dbl>  <dbl>   <dbl> <dbl>    <dbl>
 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
```

Make sure categoricals really are

```r
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

```r
summary(sepsis.1)
```

```

Call:
glm(formula = death ~ shock + malnut + alcohol + age + bowelinf,
    family = "binomial", data = sepsis)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -9.75391    2.54170  -3.838 0.000124 ***
shock1       3.67387    1.16481   3.154 0.001610 **
malnut1      1.21658    0.72822   1.671 0.094798 .
alcohol1     3.35488    0.98210   3.416 0.000635 ***
age          0.09215    0.03032   3.039 0.002374 **
bowelinf1    2.79759    1.16397   2.403 0.016240 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

Or, with tidy (from broom)

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

```
# A tibble: 6 x 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <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)
summary(sepsis.2)
```

```

Call:
glm(formula = death ~ shock + alcohol + age + bowelinf, family = "bi
    data = sepsis)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -8.89459    2.31689  -3.839 0.000124 ***
shock1       3.70119    1.10353   3.354 0.000797 ***
alcohol1     3.18590    0.91725   3.473 0.000514 ***
age          0.08983    0.02922   3.075 0.002106 **
bowelinf1    2.38647    1.07227   2.226 0.026039 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

Comments

- Everything significant now.
- 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” 1/2

- 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
```

Predictions from model without “malnut” 2/2

```
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
```

```
  shock alcohol bowelinf age rowid
1     0       0        0  30     1
2     0       0        0  40     2
3     0       0        0  50     3
4     0       0        0  60     4
5     0       0        0  70     5
```

Assessing age effect

```r
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

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

```
  alcohol      age bowelinf shock rowid
1       0 51.28302        0     0     1
2       0 51.28302        0     1     2
```

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

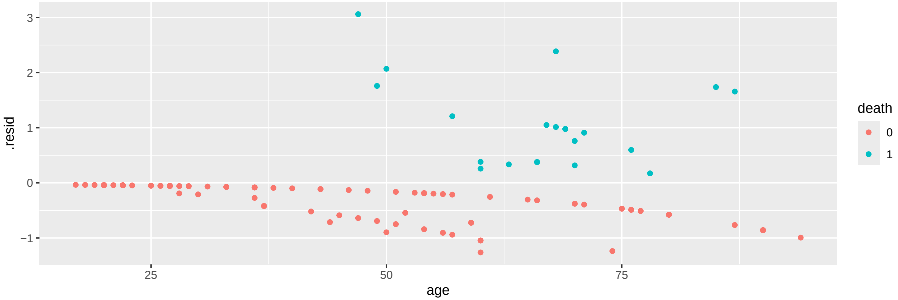
```
    estimate alcohol      age bowelinf shock
1 0.01354973       0 51.28302        0     0
2 0.35742607       0 51.28302        0     1
```

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, colour = death)) +
  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	Words
0.5	$0.5 / 0.5 = 1.00$	0.00	even money
0.1	$0.1 / 0.9 = 0.11$	-2.20	9 to 1
0.4	$0.4 / 0.6 = 0.67$	-0.41	1.5 to 1
0.8	$0.8 / 0.2 = 4.00$	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.
- Thus, predict *log-odds of probability* from explanatory variable(s), rather than probability itself.

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
```

```
# 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
```

Multiplying the odds

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

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

```
# 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
```

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 = '
  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
```

```
levels(miners$Severity)
```

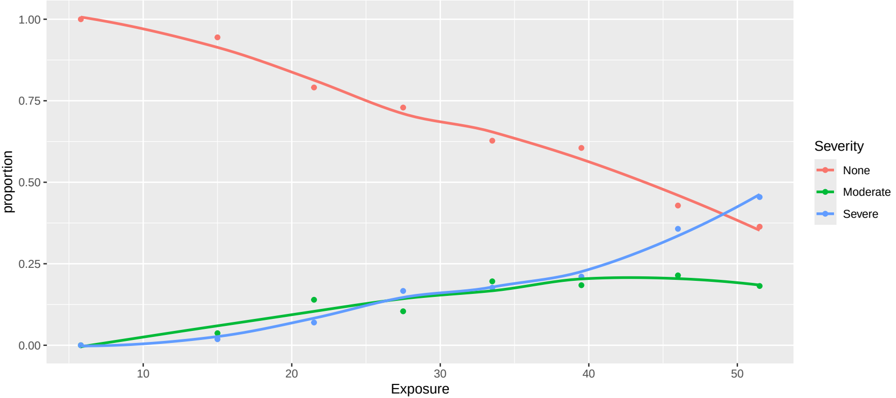
Plot proportions against exposure 1/2

```
miners %>%
  group_by(Exposure) %>%
  mutate(proportion = Freq / sum(Freq)) -> prop
prop
```

```
# A tibble: 24 x 4
# Groups:   Exposure [8]
   Exposure Severity  Freq proportion
      <dbl> <fct>    <dbl>      <dbl>
 1      5.8 None        98     1
 2      5.8 Moderate     0     0
 3      5.8 Severe       0     0
 4     15   None        51     0.944
 5     15   Moderate     2     0.0370
 6     15   Severe       1     0.0185
 7     21.5 None        34     0.791
 8     21.5 Moderate     6     0.140
 9     21.5 Severe       3     0.0698
10     27.5 None        35     0.729
# i 14 more rows
```

Plot proportions against exposure 2/2

```
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

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

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

```
Call:
polr(formula = Severity ~ Exposure, data = miners, weights = Freq)

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. Pr(Chi)
1        1       369   505.1621                              
2 Exposure       368   416.9188 1 vs 2     1 88.24324       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
```

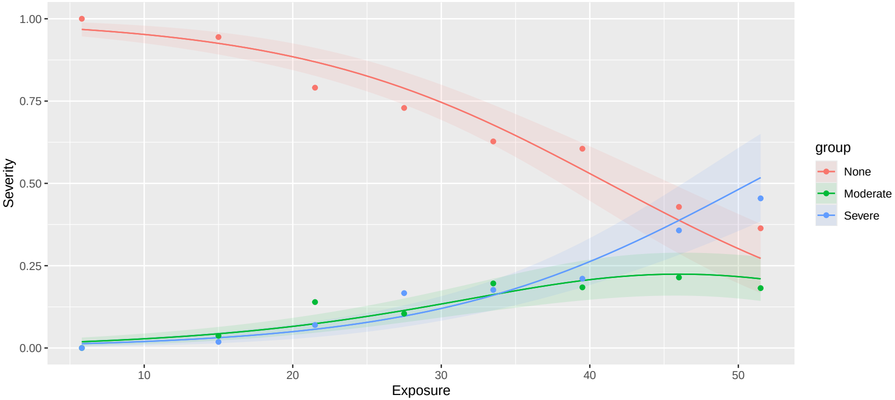
Plot of predicted probabilities

- Wider for looking at, longer for graph:

```
plot_predictions(model = sev.1,
                 condition = c("Exposure", "group"),
                 type = "probs") +
  geom_point(data = prop, aes(x = Exposure, y = proportion,
                              colour = Severity)) -> ggg
```

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
```

```
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
```

Fitting model

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

```
library(nnet)
# levels(brandpref$sex)

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
```

- summary output not helpful.

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 logica
```

- 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.    Pr(Chi)
1       age      1466   1413.593
2 age + sex      1464   1405.941 1 vs 2     2 7.651236 0.02180496
```

Do age/sex help predict brand? 3/3

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

```
Likelihood ratio tests of Multinomial Models

Response: brand
      Model Resid. df Resid. Dev   Test    Df LR stat. Pr(Chi)
1       sex      1466   1583.723                              
2 age + sex      1464   1405.941 1 vs 2     2 177.7811       0
```

Comments

- 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

```r
new <- datagrid(age = seq(24, 40, 4), # cover age range
                sex = c("female", "male"), model = brands.1)
new
```

```
   age    sex rowid
1   24 female     1
2   24   male     2
3   28 female     3
4   28   male     4
5   32 female     5
6   32   male     6
7   36 female     7
8   36   male     8
9   40 female     9
10  40   male    10
```

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    28 female 0.696   0.271  0.0329
 4    28 male   0.793   0.183  0.0236
 5    32 female 0.291   0.495  0.214
 6    32 male   0.405   0.408  0.187
 7    36 female 0.0503  0.374  0.576
 8    36 male   0.0795  0.350  0.571
 9    40 female 0.00473 0.153  0.842
10    40 male   0.00759 0.146  0.847
```

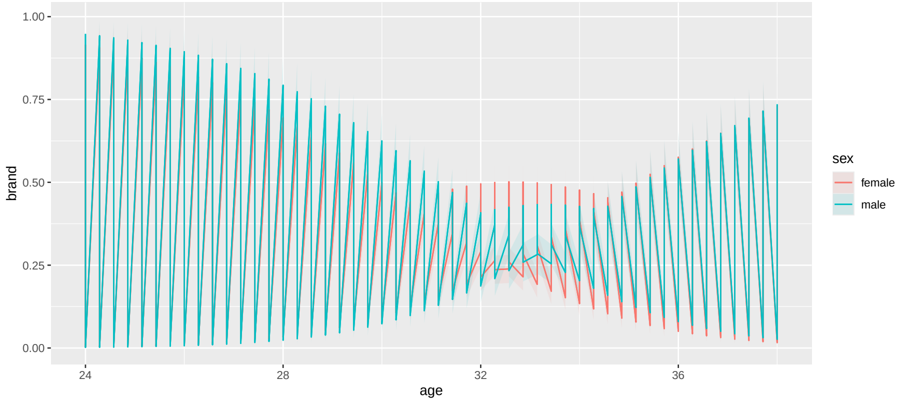
Comments

- 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

- I thought `plot_predictions` doesn't work as we want, but I was (sort of) wrong about that:

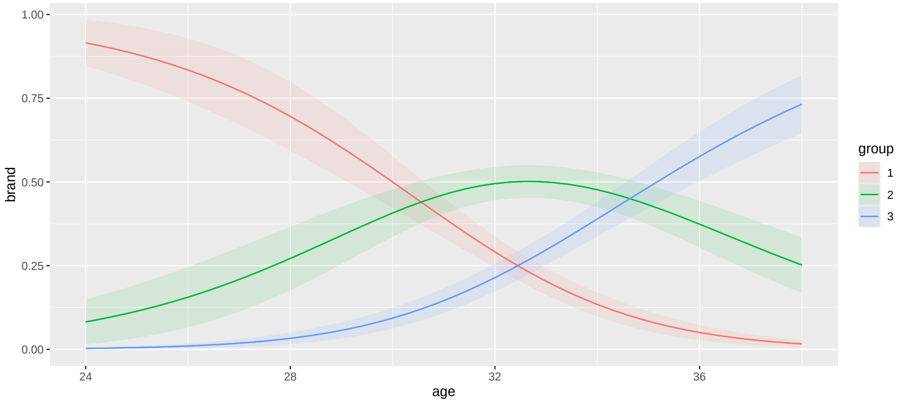
```
plot_predictions(brands.1, condition = c("age", "sex"),
          type = "probs")
```



Making it go

- We have to include group in the condition:

```
plot_predictions(brands.1, condition = c("age", "group"))
```



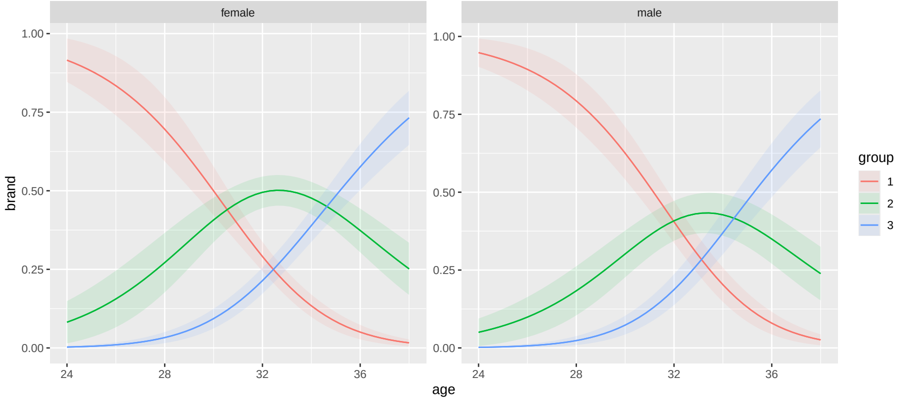
Comments

- This picks the most common `sex` in the data (females).
- See younger females prefer brand 1, older ones preferring brand 3.

For each sex

If we add the other variable to the *end*, we get facets for sex:

```
plot_predictions(brands.1, condition = c("age", "group", "sex"))
```



Not actually much difference between males and females.

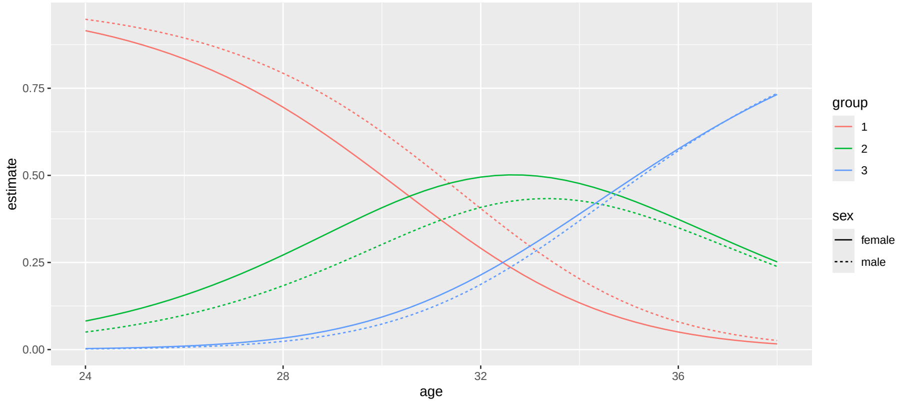
A better graph

- but the male-female difference *was* significant. How?
- *don't* actually plot the graph, then plot the right things:

```
plot_predictions(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

```
g
```



estimate
0.00
0.25
0.50
0.75
24
28
32
36
age
group
1
2
3
sex
female
male

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:

```
1 0 24 1
1 0 26 2
1 0 27 4
1 0 28 4
1 0 29 7
1 0 30 3
...
```

Whole data set in 65 lines not 735! But how?

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
```

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.    Pr(Chi)
1       age       126   1413.593
2 age + sex       124   1405.941 1 vs 2     2 7.651236 0.02180496
```

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

Trying interaction between age and sex

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

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

```
Likelihood ratio tests of Multinomial Models

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

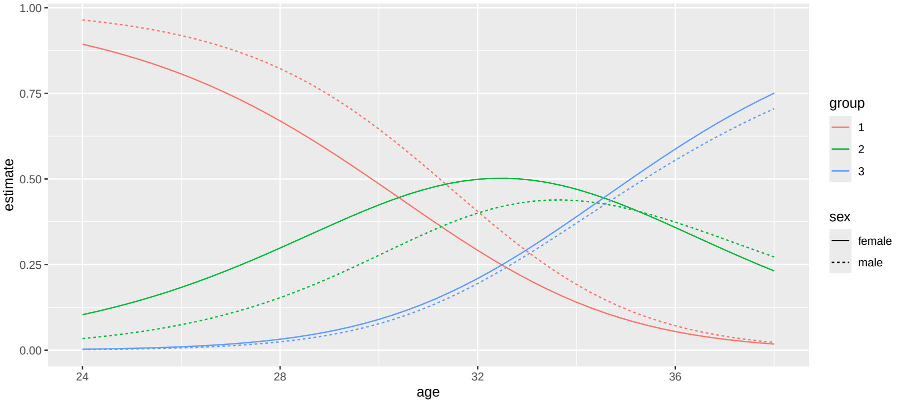
- No evidence that effect of age on brand preference differs for the two genders.

Make graph again

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

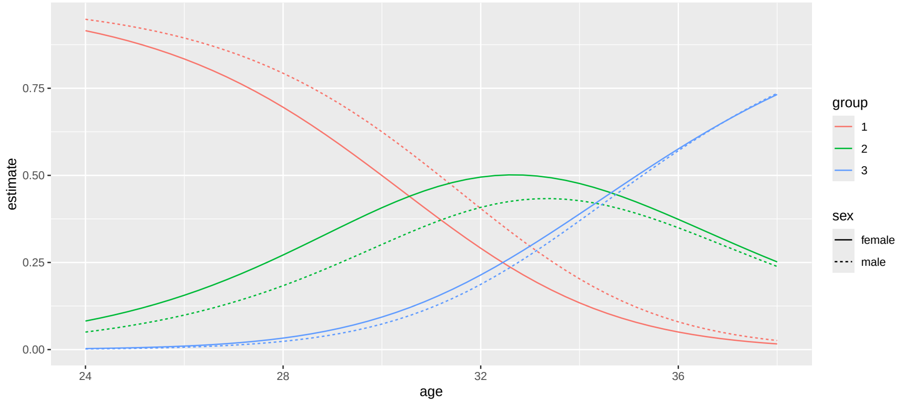
Not much difference in the graph

```
g4
```



Compare model without interaction

```
g
```


estimate
age
group
sex
female
male