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(broom)
library(nnet)
```

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://www.utsc.utoronto.ca/~butler/d29/rat.txt"
rats <- read_delim(my_url, " ")
```

```
##
## -- Column specification --------------------------
## cols(
##   dose = col_double(),
##   status = col_character()
## )
```

```
rats
```

dose	status
0	lived
1	died
2	lived
3	lived

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)
##
## Deviance Residuals:
##       1        2        3        4        5
##  0.5835  -1.6254   1.0381   1.3234  -0.7880
##       6
## -0.5835
##
## 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

```
p <- predict(status.1, type = "response")
cbind(rats, p)
```

dose	status	p
0	lived	0.8434490
1	died	0.7331122
2	lived	0.5834187
3	lived	0.4165813
4	died	0.2668878
5	died	0.1565510

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://www.utsc.utoronto.ca/~butler/d29/rat2.txt"
rat2 <- read_delim(my_url, " ")
```

```
##
## -- Column specification --------------------------
## cols(
##   dose = col_double(),
##   lived = col_double(),
##   died = col_double()
## )
```

```
rat2
```

dose	lived	died
0	10	0
1	7	3
2	6	4
3	4	6
4	2	8
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" "arrav"
```

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)
##
## Deviance Residuals:
##       1        2        3        4        5
##  1.3421  -0.7916  -0.1034   0.1034   0.0389
##       6
##  0.1529
##
## 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
##
## (Intercept) ***
## dose        ***
## ---
## Signif. codes:
## 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
```

Predicted survival probs

```
p <- predict(rat2.1, type = "response")
cbind(rat2, p)
```

dose	lived	died	p
0	10	0	0.9138762
1	7	3	0.8048905
2	6	4	0.6159474
3	4	6	0.3840526
4	2	8	0.1951095
5	1	9	0.0861238

Comments

- Significant effect of dose.
- Effect of larger dose is to *decrease* survival probability ("slope" negative; also see in decreasing predictions.)

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://www.utsc.utoronto.ca/~butler/d29/sepsis.txt"
sepsis <- read_delim(my_url, " ")
```

```
##
## -- Column specification --------------------------
## cols(
##   death = col_double(),
##   shock = col_double(),
##   malnut = col_double(),
##   alcohol = col_double(),
##   age = col_double(),
##   bowelinf = col_double()
## )
```

The data

```
sepsis
```

death	shock	malnut	alcohol	age	bowelinf
0	0	0	0	56	0
0	0	0	0	80	0
0	0	0	0	61	0
0	0	0	0	26	0
0	0	0	0	53	0
1	0	1	0	87	0
0	0	0	0	21	0
1	0	0	1	69	0
0	0	0	0	57	0
0	0	1	0	76	0
1	0	0	1	66	1
0	0	0	0	48	0
0	0	0	0	18	0

Fit model

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

Output part 1

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

term	estimate	std.error	statistic	p.value
(Intercept)	-9.7539056	2.5416952	-3.837559	0.0001243
shock	3.6738658	1.1648114	3.154044	0.0016103
malnut	1.2165811	0.7282236	1.670615	0.0947978
alcohol	3.3548846	0.9821026	3.416022	0.0006354
age	0.0921527	0.0303237	3.038968	0.0023739
bowelinf	2.7975864	1.1639717	2.403483	0.0162397

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

Removing malnut

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

term	estimate	std.error	statistic	p.value
(Intercept)	-8.8945899	2.3168948	-3.839013	0.0001235
shock	3.7011932	1.1035347	3.353944	0.0007967
alcohol	3.1859040	0.9172457	3.473338	0.0005140
age	0.0898318	0.0292153	3.074821	0.0021063
bowelinf	2.3864685	1.0722662	2.225631	0.0260389

- 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 chosen at random:

```
sepsis.pred <- predict(sepsis.2, type = "response")
d <- data.frame(sepsis, sepsis.pred)
myrows <- c(4, 1, 2, 11, 32)
slice(d, myrows)
```

	death	shock	malnut	alcohol	age	bowelinf	sepsis.pred
4	0	0	0	0	26	0	0.0014153
1	0	0	0	0	56	0	0.0205524
2	0	0	0	0	80	0	0.1534168
11	1	0	0	1	66	1	0.9312901
32	1	0	0	1	49	0	0.2130010

Comments

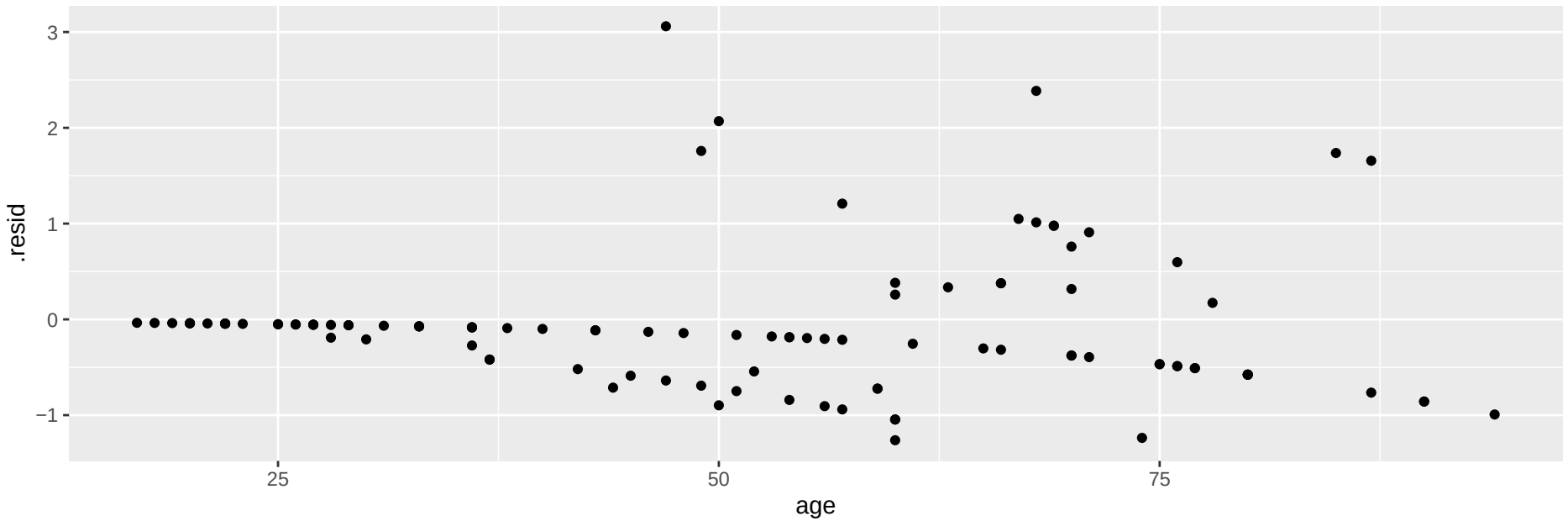
- Survival chances pretty good if no risk factors, though decreasing with age.
- Having more than one risk factor reduces survival chances dramatically.
- Usually good job of predicting survival; sometimes death predicted to survive.

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

```
ggplot(augment(sepsis.2), 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
```

term	estimate	std.error	statistic	p.value
(Intercept)	-8.8945899	2.3168948	-3.839013	0.0001235
shock	3.7011932	1.1035347	3.353944	0.0007967
alcohol	3.1859040	0.9172457	3.473338	0.0005140
age	0.0898318	0.0292153	3.074821	0.0021063
bowelinf	2.3864685	1.0722662	2.225631	0.0260389

- Slopes in column `estimate`.

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)
```

term	exp_coeff
(Intercept)	0.0001371
shock	40.4955951
alcohol	24.1891449
age	1.0939902
bowelinf	10.8750206

Interpretation

term	exp_coeff
(Intercept)	0.0001371
shock	40.4955951
alcohol	24.1891449
age	1.0939902
bowelinf	10.8750206

- 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, 3 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://www.utsc.utoronto.ca/~butler/d29/miners-tab.txt"
freqs <- read_table(my_url)
```

```
##
## -- Column specification --------------------------
## cols(
##   Exposure = col_double(),
##   None = col_double(),
##   Moderate = col_double(),
##   Severe = col_double()
## )
```

The data

```
freqs
```

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

Tidying and row proportions

```
freqs %>%
  gather(Severity, Freq, None:Severe) %>%
  group_by(Exposure) %>%
  mutate(proportion = Freq / sum(Freq)) -> miners
```

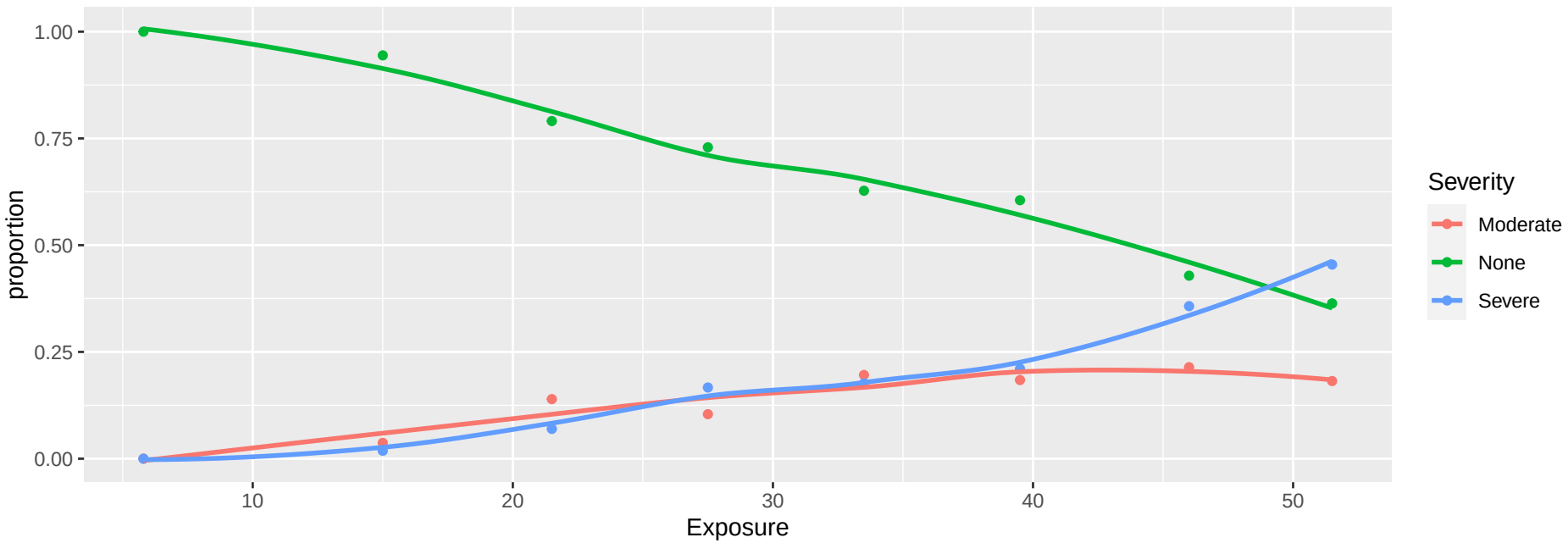
Result

```
miners
```

Exposure	Severity	Freq	proportion
5.8	None	98	1.0000000
15.0	None	51	0.9444444
21.5	None	34	0.7906977
27.5	None	35	0.7291667
33.5	None	32	0.6274510
39.5	None	23	0.6052632
46.0	None	12	0.4285714
51.5	None	4	0.3636364
5.8	Moderate	0	0.0000000
15.0	Moderate	2	0.0370370
21.5	Moderate	6	0.1395349
27.5	Moderate	5	0.1041667
33.5	Moderate	10	0.1960784
39.5	Moderate	7	0.1842105
46.0	Moderate	6	0.2142857

Plot proportions against exposure

```
ggplot(miners, aes(x = Exposure, y = proportion,
                   colour = Severity)) +
  geom_point() + geom_smooth(se = F)
```



Reminder of data setup

```
miners
```

Exposure	Severity	Freq	proportion
5.8	None	98	1.0000000
15.0	None	51	0.9444444
21.5	None	34	0.7906977
27.5	None	35	0.7291667
33.5	None	32	0.6274510
39.5	None	23	0.6052632
46.0	None	12	0.4285714
51.5	None	4	0.3636364
5.8	Moderate	0	0.0000000
15.0	Moderate	2	0.0370370
21.5	Moderate	6	0.1395349
27.5	Moderate	5	0.1041667
33.5	Moderate	10	0.1960784
39.5	Moderate	7	0.1842105
46.0	Moderate	6	0.2142857
51.5	Moderate	2	0.1818182
5.8	Severe	0	0.0000000

Creating an ordered factor

- Problem: on plot, `Severity` categories in *wrong order*.
- *In the data frame*, categories in *correct* order.
- Package `forcats` (in `tidyverse`) has functions for creating factors to specifications.
- `fct_inorder` takes levels *in order they appear in data*:

```
miners %>%
  mutate(sev_ord = fct_inorder(Severity)) -> miners
```

- To check:

```
levels(miners$sev_ord)
```

```
## [1] "None"     "Moderate" "Severe"
```

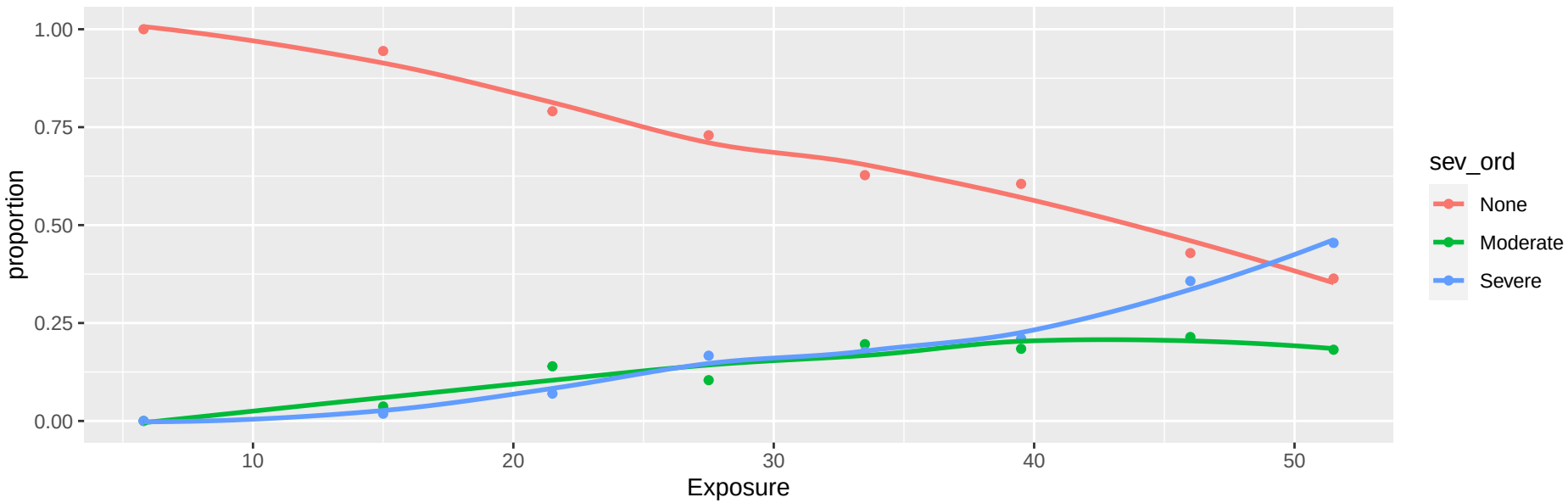
New data frame

```
miners
```

Exposure	Severity	Freq	proportion	sev_ord
5.8	None	98	1.0000000	None
15.0	None	51	0.9444444	None
21.5	None	34	0.7906977	None
27.5	None	35	0.7291667	None
33.5	None	32	0.6274510	None
39.5	None	23	0.6052632	None
46.0	None	12	0.4285714	None
51.5	None	4	0.3636364	None
5.8	Moderate	0	0.0000000	Moderate
15.0	Moderate	2	0.0370370	Moderate
21.5	Moderate	6	0.1395349	Moderate
27.5	Moderate	5	0.1041667	Moderate
33.5	Moderate	10	0.1960784	Moderate
39.5	Moderate	7	0.1842105	Moderate
46.0	Moderate	6	0.2142857	Moderate

Improved plot

```
ggplot(miners, aes(x = Exposure, y = proportion,
                   colour = sev_ord)) +
  geom_point() + geom_smooth(se = F)
```



Fitting ordered logistic model

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

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

Output: not very illuminating

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

```
##
## Re-fitting to get Hessian

## Call:
## polr(formula = sev_ord ~ 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(sev_ord ~ 1, weights = Freq, data = miners)
anova(sev.0, sev.1)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
1	369	505.1621		NA	NA	NA
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")
```

	Df	AIC	LRT	Pr(>Chi)
	NA	422.9188	NA	NA
Exposure	1	509.1621	88.24324	0

- Nothing. Exposure definitely has effect.

Predicted probabilities

Make new data frame out of all the exposure values (from original data frame), and predict from that:

```
sev.new <- tibble(Exposure = freqs$Exposure)
pr <- predict(sev.1, sev.new, type = "p")
miners.pred <- cbind(sev.new, pr)
miners.pred
```

Exposure	None	Moderate	Severe
5.8	0.9676920	0.0190891	0.0132189
15.0	0.9253445	0.0432993	0.0313561
21.5	0.8692003	0.0738586	0.0569411
27.5	0.7889290	0.1141300	0.0969409
33.5	0.6776641	0.1620715	0.1602644
39.5	0.5418105	0.2048420	0.2533476
46.0	0.3879962	0.2244155	0.3875883
51.5	0.2732543	0.2102501	0.5174956

Comments

- Model appears to match data: as exposure goes up, prob of None goes down, Severe goes up (sharply for high exposure).
- Like original data frame, this one nice to look at but *not tidy*. We want to make graph, so tidy it.
- Also want the severity values in right order.
- Usual `gather`, plus a bit:

```
miners.pred %>%
  gather(Severity, probability, -Exposure) %>%
  mutate(sev_ord = fct_inorder(Severity)) -> preds
```

Some of the gathered predictions

```
preds %>% slice(1:15)
```

Exposure	Severity	probability	sev_ord
5.8	None	0.9676920	None
15.0	None	0.9253445	None
21.5	None	0.8692003	None
27.5	None	0.7889290	None
33.5	None	0.6776641	None
39.5	None	0.5418105	None
46.0	None	0.3879962	None
51.5	None	0.2722543	None
5.8	Moderate	0.0190891	Moderate
15.0	Moderate	0.0432993	Moderate
21.5	Moderate	0.0738586	Moderate
27.5	Moderate	0.1141300	Moderate
33.5	Moderate	0.1620715	Moderate
39.5	Moderate	0.2048420	Moderate
46.0	Moderate	0.2244155	Moderate

Plotting predicted and observed proportions

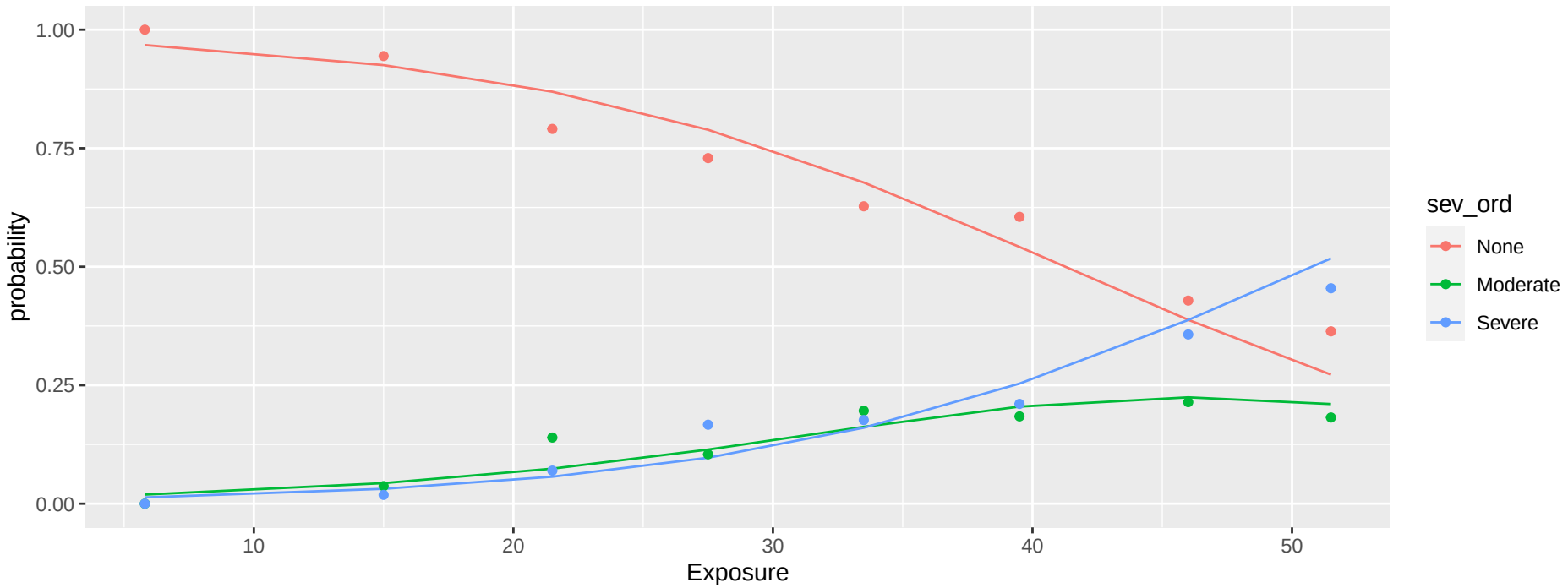
- Plot:
  - predicted probabilities, lines (shown) joining points (not shown)
  - data, just the points.
- Unfamiliar process: data from two *different* data frames:

```
g <- ggplot(preds, aes(
  x = Exposure, y = probability,
  colour = sev_ord
)) + geom_line() +
  geom_point(data = miners, aes(y = proportion))
```

- Idea: final `geom_point` uses data in `miners` rather than `preds`, y-variable for plot is `proportion` from that data frame, but x-coordinate is `Exposure`, as it was before, and `colour` is `Severity` as before. The final `geom_point` "inherits" from the first `aes` as needed.

The plot: data match model

```
g
```



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://www.utsc.utoronto.ca/~butler/d29/mlogit.csv"
brandpref <- read_csv(my_url)
```

```
##
## -- Column specification --------------------------------
## cols(
##   brand = col_double(),
##   sex = col_double(),
##   age = col_double()
## )
```

The data

`brandpref`

brand	sex	age
1	0	24
1	0	26
1	0	26
1	1	27
1	1	27
3	1	27
1	0	27
1	0	27
1	1	27
1	0	27
1	0	27
1	1	27
2	1	28

Bashing into shape, and fitting model

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

```
brandpref <- brandpref %>%
  mutate(sex = factor(sex)) %>%
  mutate(brand = factor(brand))
```

- 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 702.976983
## 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 log
```

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

Do age/sex help predict brand? 1/2

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? 2/2

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

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age	1466	1413.593		NA	NA	NA
age + sex	1464	1405.941	1 vs 2	2	7.651236	0.021805

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

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

Do age/sex help predict brand? 3/3

- age definitely significant (second `anova`)
- `sex` seems significant also (first `anova`)
- Keep both.

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, data = brandpref)
##
## Coefficients:
##   (Intercept)       age      sex1
## 2   -11.77469 0.3682075 0.5238197
## 3   -22.72141 0.6859087 0.4659488
##
## Residual Deviance: 1405.941
## AIC: 1417.941
```

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

Predictions: all possible combinations

Create data frame with various age and sex:

```
ages <- c(24, 28, 32, 35, 38)
sexes <- factor(0:1)
new <- crossing(age = ages, sex = sexes)
new
```

age	sex
24	0
24	1
28	0
28	1
32	0
32	1
35	0
35	1
38	0
38	1

Making predictions

```
p <- predict(brands.1, new, type = "probs")
probs <- cbind(new, p)
```

or

```
p %>% as_tibble() %>%
  bind_cols(new) -> probs
```

The predictions

```
probs
```

1	2	3	age	sex
0.9479582	0.0502293	0.0018125	24	0
0.9153208	0.0818904	0.0027888	24	1
0.7931320	0.1832969	0.0235711	28	0
0.6956179	0.2714391	0.0329430	28	1
0.4048727	0.4081032	0.1870241	32	0
0.2908635	0.4950314	0.2141052	32	1
0.1305782	0.3972405	0.4721813	35	0
0.0840413	0.4316859	0.4842727	35	1
0.0259816	0.2385507	0.7354677	38	0
0.0162309	0.2516220	0.7321471	38	1

- Young males (`sex=0`) prefer brand 1, but older males prefer brand 3.
- Females similar, but like brand 1 less and brand 2 more.

Making a plot

- Plot fitted probability against age, distinguishing brand by colour and gender by plotting symbol.
- Also join points by lines, and distinguish lines by gender.
- I thought about facetting, but this seems to come out clearer.
- First need tidy data frame, by familiar process:

```
probs %>%
  gather(brand, probability, -(age:sex)) -> probs.long
```

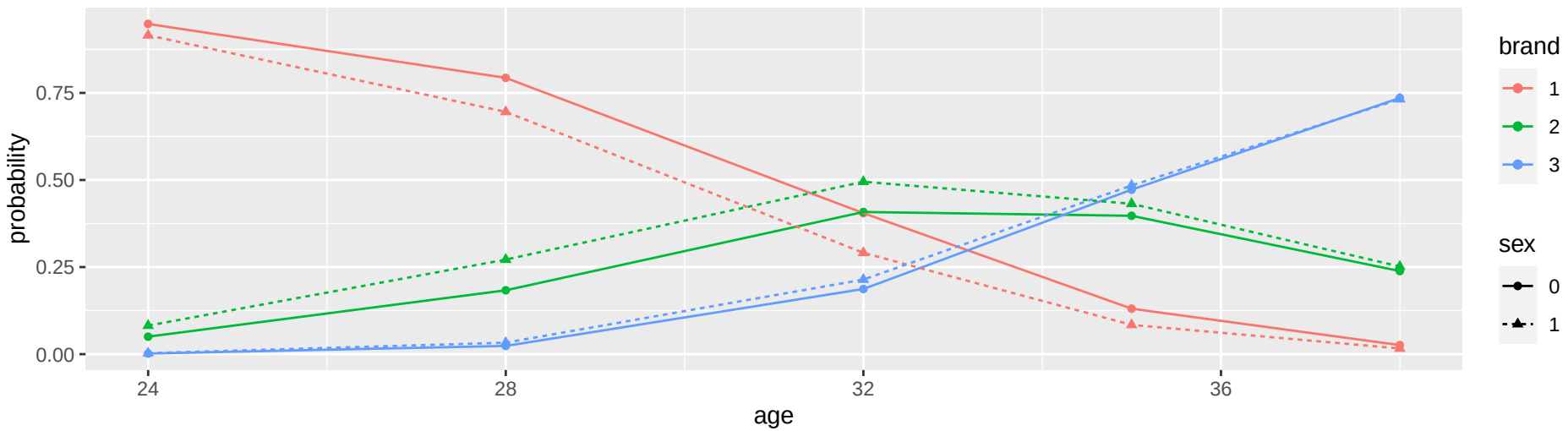
The tidy data (random sample of rows)

```
probs.long %>% sample_n(10)
```

age	sex	brand	probability
32	0	1	0.4048727
28	0	2	0.1832969
24	1	2	0.0818904
24	0	2	0.0502293
24	0	1	0.9479582
38	1	1	0.0162309
28	1	3	0.0329430
35	1	3	0.4842727
32	1	1	0.2908635
38	0	3	0.7354677

The plot

```
ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_point() + geom_line(aes(linetype = sex))
```



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 (dashed) like brand 1 less than males (solid), 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.

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
```

```
## `summarise()` regrouping output by 'age', 'sex' (override w
```

```
b %>% slice(1:6)
```

age	sex	brand	Freq
24	0	1	1
26	0	1	2
27	0	1	4
27	1	1	4
27	1	3	1
28	0	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)
```

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age	126	1413.593		NA	NA	NA
age + sex	124	1405.941	1 vs 2	2	7.651236	0.021805

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

Including data on plot

- Everyone's age given as whole number, so maybe not too many different ages with sensible amount of data at each:

```
b %>%
  group_by(age) %>%
  summarize(total = sum(Freq))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

age	total
24	1
26	2
27	9
28	15
29	19
30	23
31	40
32	333
33	55
34	64
35	35
36	85

Comments and next

- Not great (especially at low end), but live with it.
- Need proportions of frequencies in each brand for each age-gender combination. Mimic what we did for miners:

```
b %>%
  group_by(age, sex) %>%
  mutate(proportion = Freq / sum(Freq)) -> brands
```

Checking proportions for age 32

```
brands %>% filter(age == 32)
```

age	sex	brand	Freq	proportion
32	0	1	48	0.4067797
32	0	2	51	0.4322034
32	0	3	19	0.1610169
32	1	1	62	0.2883721
32	1	2	117	0.5441860
32	1	3	36	0.1674419

- First three proportions (males) add up to 1.
- Last three proportions (females) add up to 1.
- So looks like proportions of right thing.

Attempting plot

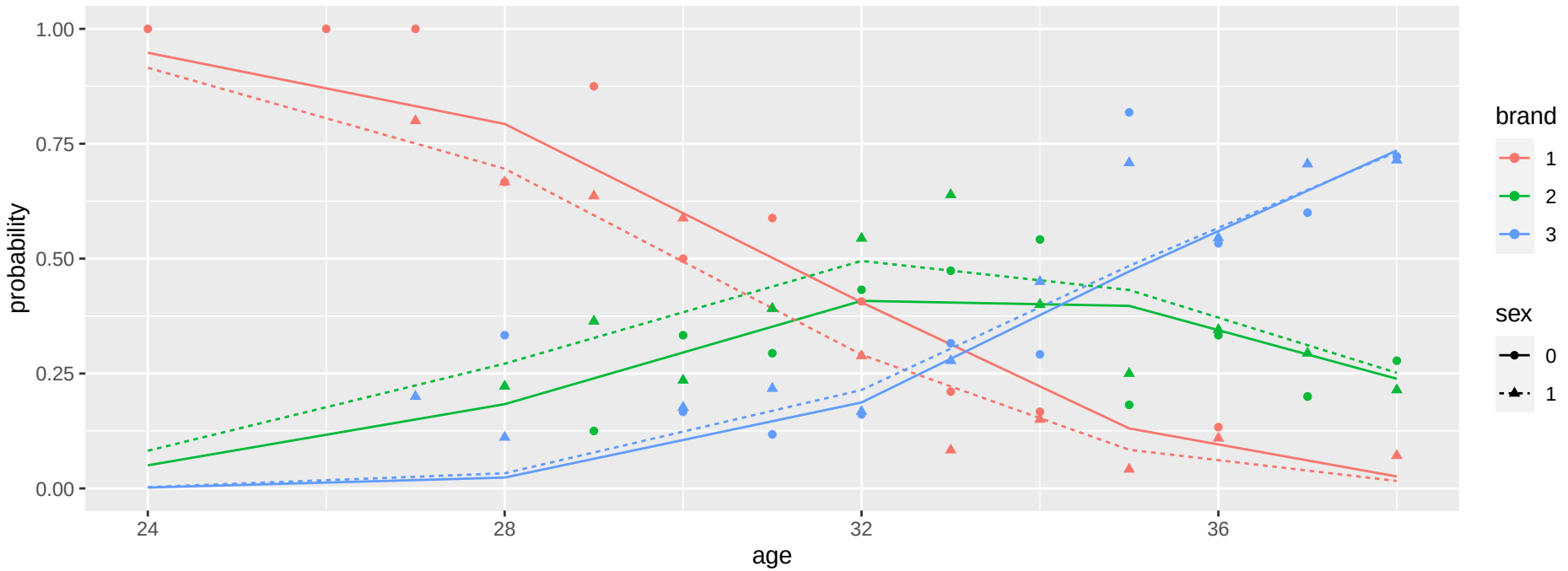
- Take code from previous plot and:
- remove `geom_point` for fitted values
- add `geom_point` with correct `data=` and `aes` to plot data.

```
g <- ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_line(aes(linetype = sex)) +
  geom_point(data = brands, aes(y = proportion))
```

- Data seem to correspond more or less to fitted curves:

The plot

```
g
```


1.00
0.75
0.50
0.25
0.00
probability
24
28
32
36
age
brand
1
2
3
sex
0
1

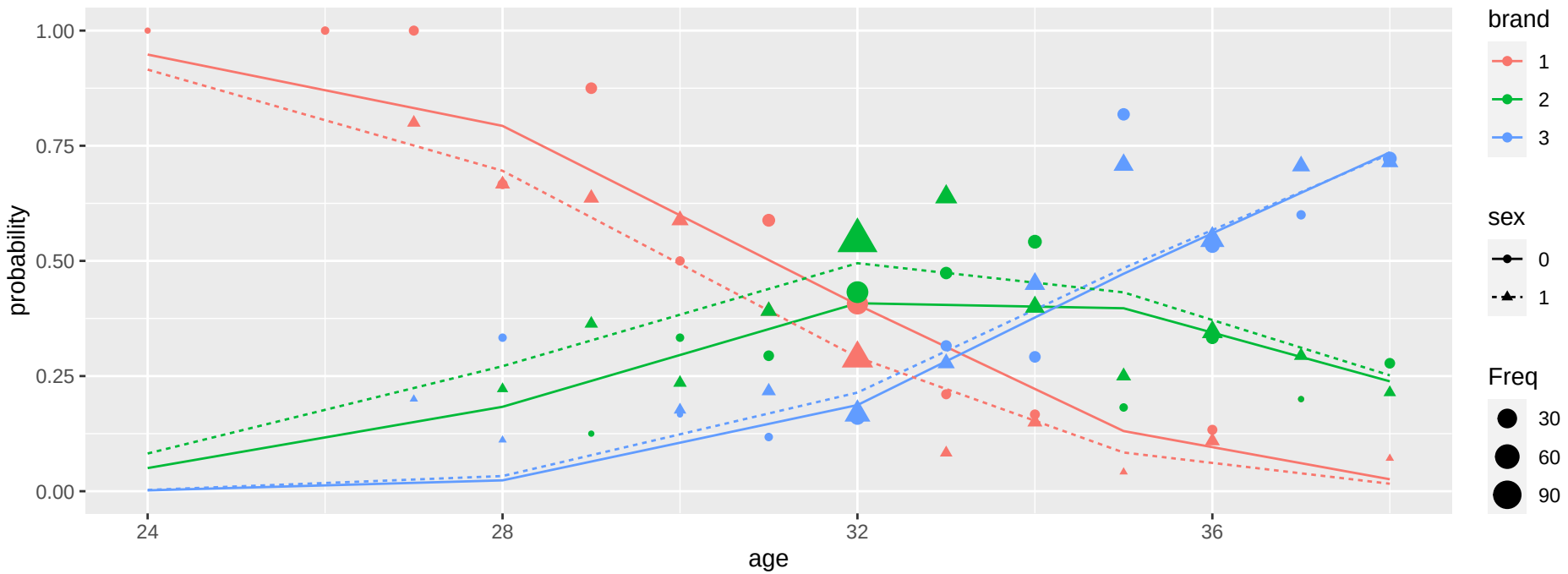
But...

- Some of the plotted points based on a lot of people, and some only a few.
- Idea: make the *size* of plotted point bigger if point based on a lot of people (in `Freq`).
- Hope that larger points then closer to predictions.
- Code:

```
g <- ggplot(probs.long, aes(
  x = age, y = probability,
  colour = brand, shape = sex
)) +
  geom_line(aes(linetype = sex)) +
  geom_point(
    data = brands,
    aes(y = proportion, size = Freq)
  )
```

The plot

```
g
```


1.00
0.75
0.50
0.25
0.00
probability
24
28
32
36
age
brand
1
2
3
sex
0
1
Freq
30
60
90

Trying interaction between age and gender

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

```
## # weights:  15 (8 variable)
## initial  value 807.480032
## iter  10 value 704.811229
## iter  20 value 702.582802
## final  value 702.582761
## converged
```

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

Model	Resid. df	Resid. Dev	Test	Df	LR stat.	Pr(Chi)
age + sex	124	1405.941		NA	NA	NA
age + sex + age:sex	122	1405.166	1 vs 2	2	0.7758861	0.678451

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