Multiway Frequency Tables

Packages

```
library(tidyverse)
```

Multi-way frequency analysis

- A study of gender and eyewear-wearing finds the following frequencies:

```
gender  contacts  glasses  none
female  121       32       129
male    42        37       85
```

- Is there association between eyewear and gender?
- Normally answer this with chisquare test (based on observed and expected frequencies from null hypothesis of no association).
- Two categorical variables and a frequency.
- We assess in way that generalizes to more categorical variables.

The data file

```
gender contacts glasses none
female 121      32      129
male   42       37      85
```

- This is *not tidy!*
- Two variables are gender and *eyewear*, and those numbers all frequencies.

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

```
# A tibble: 2 x 4
  gender contacts glasses  none
  <chr>     <dbl>   <dbl> <dbl>
1 female      121      32   129
2 male         42      37    85
```

Tidying the data

```
eyewear %>%
  pivot_longer(contacts:none, names_to="eyewear",
               values_to="frequency") -> eyes
eyes
```

```
# A tibble: 6 x 3
  gender eyewear  frequency
  <chr>  <chr>        <dbl>
1 female contacts       121
2 female glasses         32
3 female none           129
4 male   contacts        42
5 male   glasses         37
6 male   none            85
```

Modelling

- Predict frequency from other factors and combos.
- glm with poisson family.

```
eyes.1 <- glm(frequency ~ gender * eyewear,
  data = eyes,
  family = "poisson"
)
```

- Called **log-linear model**.

What can we get rid of?

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

```
Single term deletions

Model:
frequency ~ gender * eyewear
              Df Deviance    AIC    LRT   Pr(>Chi)
<none>               0.000 47.958
gender:eyewear  2   17.829 61.787 17.829 0.0001345 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
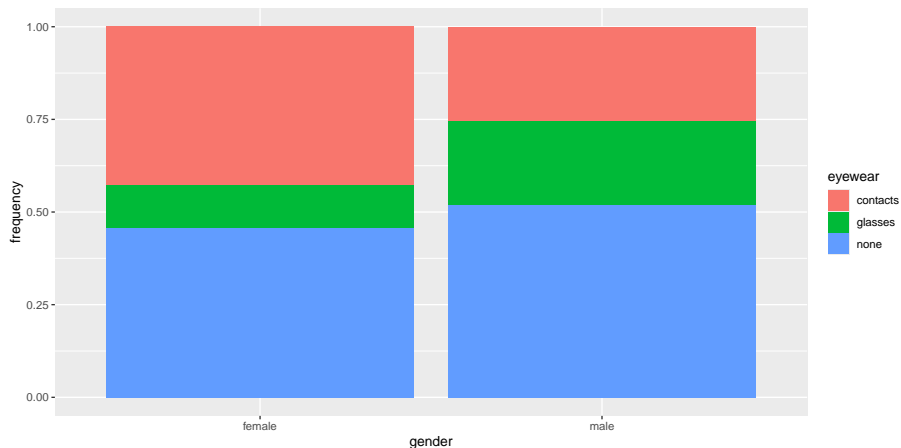
nothing!

Conclusions

- `drop1` says what we can remove at this step. Significant = must stay.
- Cannot remove anything.
- Frequency depends on `gender-eye wear` *combination*, cannot be simplified further.
- Gender and eyewear are *associated*.
- For modelling, stop here.

Making a graph

```
ggplot(eyes, aes(x = gender, y = frequency, fill = eyewear)) +
  geom_col(position = "fill")
```

Conclusions

- Females are more likely to wear contacts than males are.
- Females are *less* likely to wear glasses than males are.
- The previous two comments are the reasons for the significant association.

Code comments 1/2

- The code again:

```
ggplot(eyes, aes(x = gender, y = frequency, fill = eyewear))
  geom_col(position = "fill")
```

- Variation on two-variable bar chart that we saw in C32.
- Comparing (most easily) *proportions*, so fill clearer than dodge.
- Each row of dataframe represents many people (the number in frequency), so use geom_col rather than geom_bar.
- geom_col takes a y that should be the frequency.

Code comments 2/2

```
ggplot(eyes, aes(x = gender, y = frequency, fill = eyewear)) +
  geom_col(position = "fill")
```

- Often in this work, one variable in association is explanatory rather than response. Have that as x (here gender); eyewear is response and goes in fill.
- Interpretation: out of each category of explanatory ("out of females"), what proportion in each response category and where do they differ?

No association

- Suppose table had been as shown below:

```
my_url <- "http://ritsokiguess.site/datafiles/eyewear2.txt"
eyewear2 <- read_table(my_url)
eyewear2
```

```
# A tibble: 2 x 4
  gender contacts glasses  none
  <chr>     <dbl>   <dbl> <dbl>
1 female      150      30   120
2 male         75      16    62
```

```
eyewear2 %>%
  pivot_longer(contacts:none, names_to = "eyewear",
               values_to = "frequency") -> eyes2
```

Comments

- Females and males wear contacts and glasses *in same proportions*
    - ▶ though more females and more contact-wearers.
- No *association* between gender and eyewear.

Analysis for revised data

```
eyes.2 <- glm(frequency ~ gender * eyewear,
  data = eyes2,
  family = "poisson"
)
drop1(eyes.2, test = "Chisq")


Single term deletions

Model:
frequency ~ gender * eyewear
              Df Deviance    AIC     LRT Pr(>Chi)
<none>           0.000000 47.467
gender:eyewear  2 0.047323 43.515 0.047323   0.9766
```

No longer any association. Take out interaction.

No interaction

```
eyes.3 <- update(eyes.2, . ~ . - gender:eyewear)
drop1(eyes.3, test = "Chisq")
```

```
Single term deletions

Model:
frequency ~ gender + eyewear
        Df Deviance    AIC     LRT  Pr(>Chi)
<none>         0.047  43.515
gender   1   48.624  90.091  48.577 3.176e-12 ***
eyewear  2  138.130 177.598 138.083 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
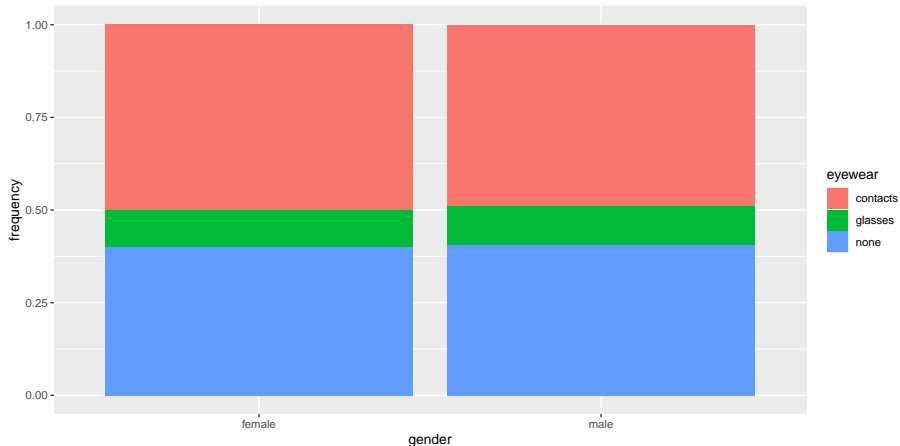
- More females (gender effect) over all eyewear
- fewer glasses-wearers (eyewear effect) over both genders
- no association (no interaction).

Graph shows no association

```
ggplot(eyes2, aes(x = gender, y = frequency, fill = eyewear)) +
  geom_col(position = "fill")
```

Chest pain, being overweight and being a smoker

- In a hospital emergency department, 176 subjects who attended for acute chest pain took part in a study.
- Each subject had a normal or abnormal electrocardiogram reading (ECG), were overweight (as judged by BMI) or not, and were a smoker or not.
- How are these three variables related, or not?

The data

In modelling-friendly format:

```
ecg bmi smoke count
abnormal overweight yes 47
abnormal overweight no 10
abnormal normalweight yes 8
abnormal normalweight no 6
normal overweight yes 25
normal overweight no 15
normal normalweight yes 35
normal normalweight no 30
```

First step

```
my_url <- "http://ritsokiguess.site/datafiles/ecg.txt"
chest <- read_delim(my_url, " ")
chest.1 <- glm(count ~ ecg * bmi * smoke,
  data = chest,
  family = "poisson"
)
drop1(chest.1, test = "Chisq")


Single term deletions

Model:
count ~ ecg * bmi * smoke
              Df Deviance    AIC    LRT Pr(>Chi)
<none>            0.0000 53.707
ecg:bmi:smoke  1  1.3885 53.096 1.3885   0.2387
```

That 3-way interaction comes out.

Removing the 3-way interaction

```
chest.2 <- update(chest.1, . ~ . - ecg:bmi:smoke)
drop1(chest.2, test = "Chisq")
```

```
Single term deletions

Model:
count ~ ecg + bmi + smoke + ecg:bmi + ecg:smoke + bmi:smoke
          Df Deviance    AIC     LRT   Pr(>Chi)
<none>          1.3885 53.096
ecg:bmi    1  29.0195 78.727 27.6310 1.468e-07 ***
ecg:smoke  1   4.8935 54.601  3.5050   0.06119 .
bmi:smoke  1   4.4689 54.176  3.0803   0.07924 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

At $\alpha = 0.05$, bmi:smoke comes out.

Removing bmi:smoke

```
chest.3 <- update(chest.2, . ~ . - bmi:smoke)
drop1(chest.3, test = "Chisq")


Single term deletions

Model:
count ~ ecg + bmi + smoke + ecg:bmi + ecg:smoke
          Df Deviance    AIC    LRT  Pr(>Chi)
<none>         4.469 54.176
ecg:bmi    1  36.562 84.270 32.094 1.469e-08 ***
ecg:smoke  1  12.436 60.144  7.968  0.004762 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- ecg:smoke has become significant. So we have to stop.
- ecg is associated with both bmi and smoke, but separately (it doesn't depend on the combination of bmi and smoke).

Understanding the final model

- For each of the significant associations, make a bar chart (here, two-variable because two-way interactions)
- Here, ecg is response (patients came into the study being smokers or overweight) so use as `fill` in both graphs.
- y is the frequency column.

ecg:bmi

```
ggplot(chest, aes(x = bmi, y = count, fill = ecg)) +
  geom_col(position = "fill")
```
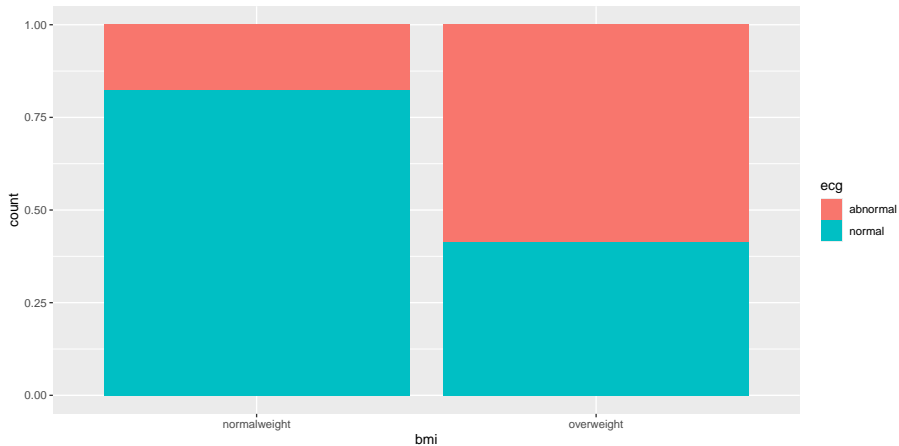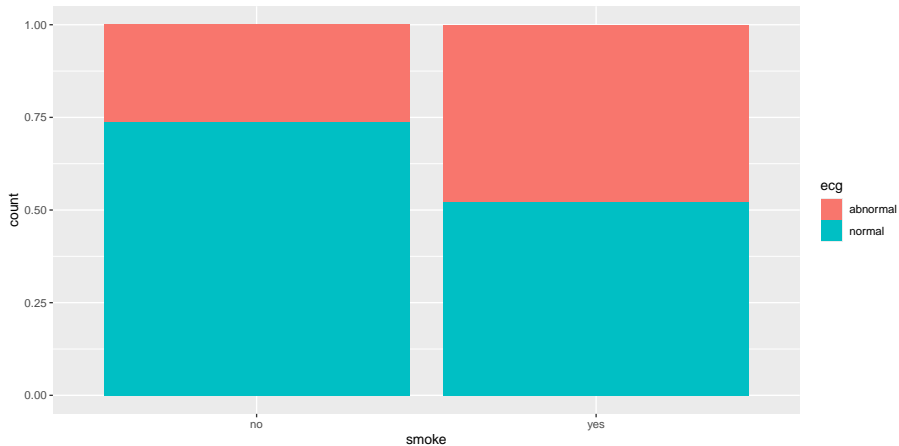
Comment

- Most of the normal weight people had a normal ECG as well, but for the overweight people, a small majority had an abnormal ECG.

ecg:smoke

```
ggplot(chest, aes(x = smoke, y = count, fill = ecg)) +
  geom_col(position = "fill")
```

Comments

- Most nonsmokers have a normal ECG, but smokers are about 50–50 normal and abnormal ECG.
- Don't look at smoke:bmi since not significant.

Simpson's paradox: the airlines example

	Alaska Airlines		America West	
Airport	On time	Delayed	On time	Delayed
Los Angeles	497	62	694	117
Phoenix	221	12	4840	415
San Diego	212	20	383	65
San Francisco	503	102	320	129
Seattle	1841	305	201	61
Total	3274	501	6438	787

Use status as variable name for "on time/delayed".

- Alaska: 13.3% flights delayed $(501/(3274 + 501))$.
- America West: 10.9% $(787/(6438 + 787))$.
- America West more punctual, right?

Arranging the data

- Can only have single thing in columns, so we have to construct column names like this:

```
airport     aa_ontime aa_delayed aw_ontime aw_delayed
LosAngeles   497         62        694        117
Phoenix      221         12       4840        415
SanDiego     212         20        383         65
SanFrancisco 503        102        320        129
Seattle     1841        305        201         61
```

- Read in:

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

Data, as read in

```
airlines
```

```
# A tibble: 5 x 5
  airport      aa_ontime aa_delayed aw_ontime aw_delayed
  <chr>            <dbl>      <dbl>     <dbl>      <dbl>
1 LosAngeles         497         62       694        117
2 Phoenix            221         12      4840        415
3 SanDiego           212         20       383         65
4 SanFrancisco       503        102       320        129
5 Seattle           1841        305       201         61
```

Tidying

- Some tidying gets us the right layout, with frequencies all in one
  column and the airline and delayed/on time status separated out.
  This uses one of the fancy versions of `pivot_longer`:

```
airlines %>%
  pivot_longer(-airport,
               names_to = c("airline", "status"),
               names_sep = "_",
               values_to = "freq" ) -> punctual
```

The data frame punctual

```
# A tibble: 20 x 4
   airport     airline status   freq
   <chr>       <chr>   <chr>   <dbl>
 1 LosAngeles  aa      ontime    497
 2 LosAngeles  aa      delayed    62
 3 LosAngeles  aw      ontime    694
 4 LosAngeles  aw      delayed   117
 5 Phoenix     aa      ontime    221
 6 Phoenix     aa      delayed    12
 7 Phoenix     aw      ontime   4840
 8 Phoenix     aw      delayed   415
 9 SanDiego    aa      ontime    212
10 SanDiego    aa      delayed    20
11 SanDiego    aw      ontime    383
12 SanDiego    aw      delayed    65
13 SanFrancisco aa     ontime    503
14 SanFrancisco aa     delayed   102
```
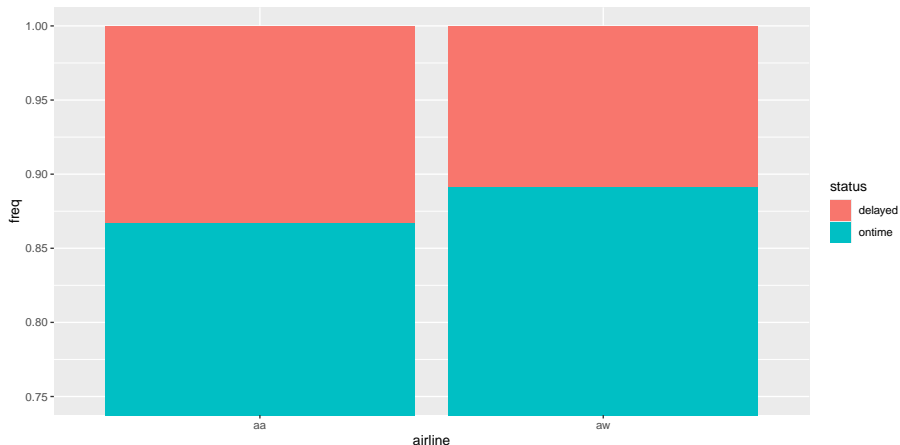
Proportions delayed by airline

```
ggplot(punctual, aes(x = airline, y = freq, fill = status)) +
  geom_col(position = "fill")
```
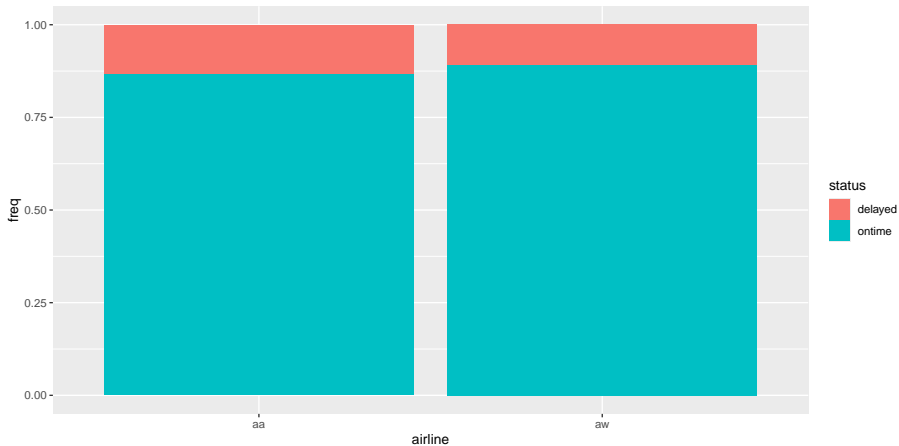
Shrinking the y-axis

```
ggplot(punctual, aes(x = airline, y = freq, fill = status)) +
  geom_col(position = "fill") +
  coord_cartesian(ylim = c(0.75, 1))
```
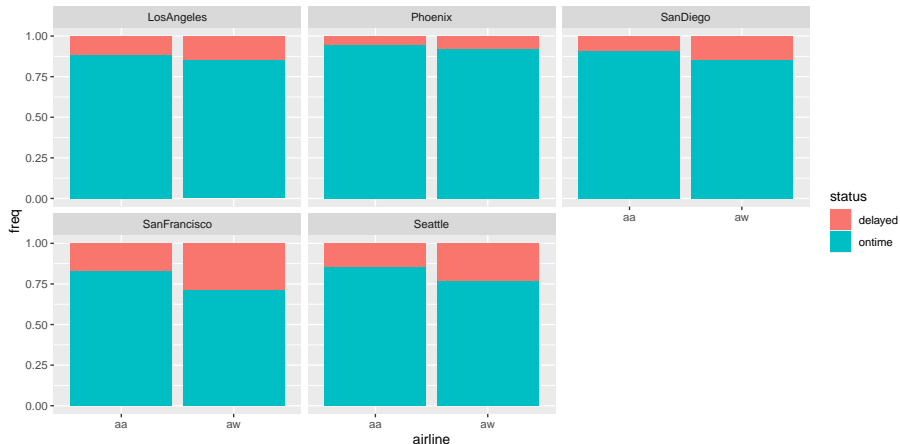
Comment

- Most flights are on time, but Alaska Airlines is late a little more often.

Proportion delayed by airport, for each airline

We now have *three* categorical variables, so use one of the explanatories
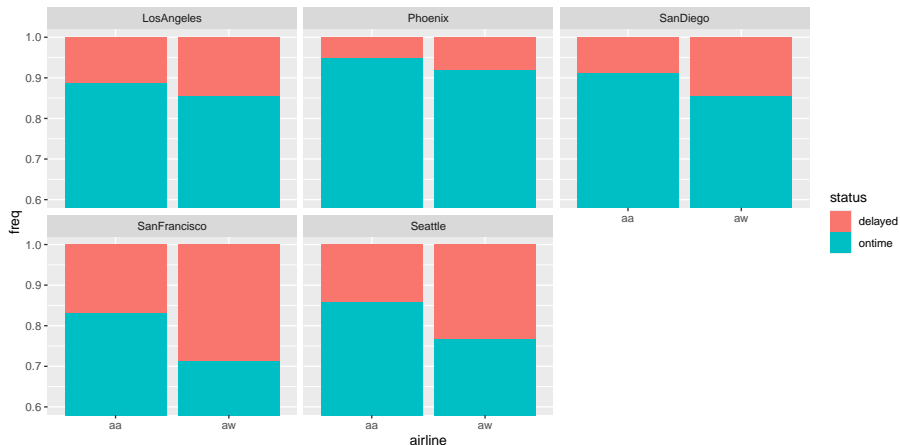(for me, airport) as facets:

The graph(s)

```
ggplot(punctual, aes(x = airline, y = freq, fill = status)) +
  geom_col(position = "fill") + facet_wrap(~ airport)
```

Zoom in on the y-scale

```
ggplot(punctual, aes(x = airline, y = freq, fill = status)) +
  geom_col(position = "fill") + facet_wrap(~ airport) +
  coord_cartesian(ylim = c(0.6, 1))
```

Simpson's Paradox

- America West more punctual overall,
- but worse at *every single* airport!
- How is that possible?
- Log-linear analysis sheds some light.

Model 1 and output

```
punctual.1 <- glm(freq ~ airport * airline * status,
  data = punctual, family = "poisson"
)
drop1(punctual.1, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ airport * airline * status
                      Df Deviance    AIC    LRT Pr(>Chi)
<none>                      0.0000 183.44
airport:airline:status  4   3.2166 178.65 3.2166   0.5223
```

Remove 3-way interaction

```
punctual.2 <- update(punctual.1, ~ . - airport:airline:status)
drop1(punctual.2, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ airport + airline + status + airport:airline + airport:status +
    airline:status
               Df Deviance    AIC    LRT  Pr(>Chi)
<none>                 3.2  178.7
airport:airline  4  6432.5 6599.9 6429.2 < 2.2e-16 ***
airport:status   4   240.1  407.5  236.9 < 2.2e-16 ***
airline:status   1    45.5  218.9   42.2 8.038e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
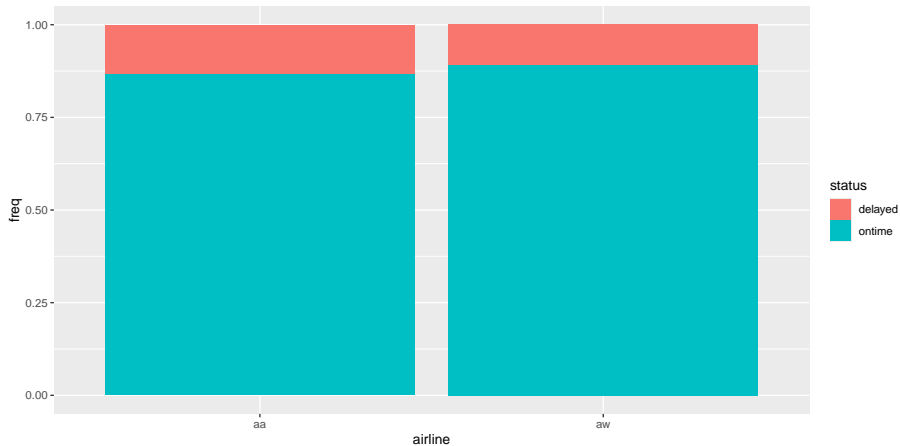
Stop here, and draw graphs to understand significant results.

airline:status:

```
ggplot(punctual, aes(x = airline, y = freq, fill = status)) +
  geom_col(position = "fill")
```
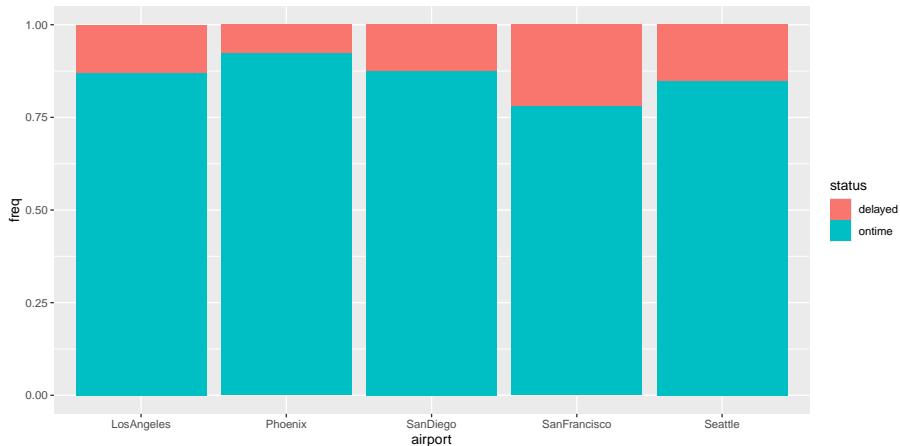
Comments

- We did this one before.
- Slightly more of Alaska Airlines' flights delayed overall.

airport:status:

```
ggplot(punctual, aes(x = airport, y = freq, fill = status)) +
  geom_col(position = "fill")
```
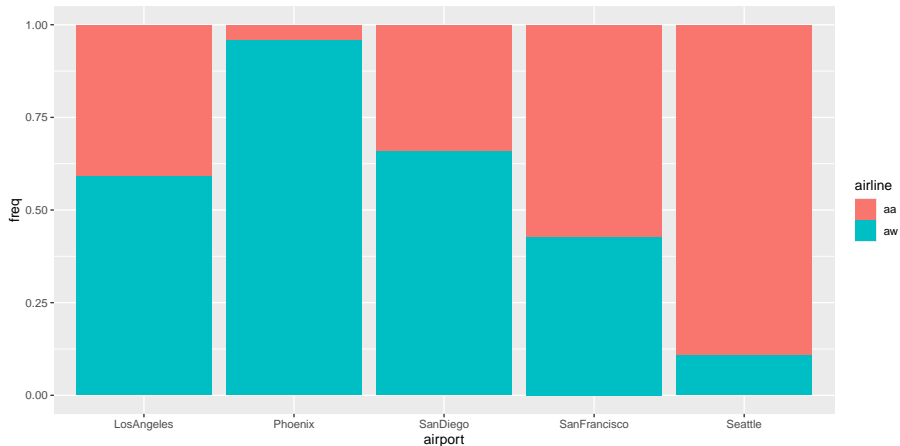
Comments

- Flights into San Francisco (and maybe Seattle) are often late, and flights into Phoenix are usually on time.
- Considerable variation among airports.

airport:airline:

```
ggplot(punctual, aes(x = airport, y = freq, fill = airline)) +
  geom_col(position = "fill")
```

Comments

- What fraction of each airline's flights are to each airport.
- Most of Alaska Airlines' flights to Seattle and San Francisco.
- Most of America West's flights to Phoenix.

The resolution

- Most of America West's flights to Phoenix, where it is easy to be on time.
- Most of Alaska Airlines' flights to San Francisco and Seattle, where it is difficult to be on time.
- Overall comparison looks bad for Alaska because of this.
- But, *comparing like with like*, if you compare each airline's performance *to the same airport*, Alaska does better.
- Aggregating over the very different airports was a (big) mistake: that was the cause of the Simpson's paradox.
- Alaska Airlines is *more* punctual when you do the proper comparison.

Ovarian cancer: a four-way table

- Retrospective study of ovarian cancer done in 1973.
- Information about 299 women operated on for ovarian cancer 10 years previously.
- Recorded:
  - stage of cancer (early or advanced)
  - type of operation (radical or limited)
  - X-ray treatment received (yes or no)
  - 10-year survival (yes or no)
- Survival looks like response (suggests logistic regression).
- Log-linear model finds any associations at all.

The data

after tidying:

```
stage operation xray survival freq
early radical no no 10
early radical no yes 41
early radical yes no 17
early radical yes yes 64
early limited no no 1
early limited no yes 13
early limited yes no 3
early limited yes yes 9
advanced radical no no 38
advanced radical no yes 6
advanced radical yes no 64
advanced radical yes yes 11
advanced limited no no 3
advanced limited no yes 1
advanced limited yes no 13
advanced limited yes yes 5
```

Reading in data

```
my_url <- "http://ritsokiguess.site/datafiles/cancer.txt"
cancer <- read_delim(my_url, " ")
cancer %>% slice(1:6)
```

```
# A tibble: 6 x 5
  stage operation xray  survival  freq
  <chr> <chr>     <chr> <chr>    <dbl>
1 early radical   no    no          10
2 early radical   no    yes         41
3 early radical   yes   no          17
4 early radical   yes   yes         64
5 early limited   no    no           1
6 early limited   no    yes         13
```

Model 1

hopefully looking familiar by now:

```
cancer.1 <- glm(freq ~ stage * operation * xray * survival,
  data = cancer, family = "poisson")
```

Output 1

See what we can remove:

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

```
Single term deletions

Model:
freq ~ stage * operation * xray * survival
                             Df Deviance    AIC    LRT Pr(>Chi)
<none>                          0.00000 98.130
stage:operation:xray:survival  1 0.60266 96.732 0.60266   0.4376
```

Non-significant interaction can come out.

Model 2

```
cancer.2 <- update(cancer.1, . ~ . - stage:operation:xray:survival)
drop1(cancer.2, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + operation:survival +
    xray:survival + stage:operation:xray + stage:operation:survival +
    stage:xray:survival + operation:xray:survival
                          Df Deviance    AIC     LRT Pr(>Chi)
<none>                        0.60266 96.732
stage:operation:xray      1  2.35759 96.487 1.75493   0.1853
stage:operation:survival  1  1.17730 95.307 0.57465   0.4484
stage:xray:survival       1  0.95577 95.085 0.35311   0.5524
operation:xray:survival   1  1.23378 95.363 0.63113   0.4269
```

Least significant term is `stage:xray:survival`: remove.

Take out stage:xray:survival

```
cancer.3 <- update(cancer.2, . ~ . - stage:xray:survival)
drop1(cancer.3, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + operation:survival +
    xray:survival + stage:operation:xray + stage:operation:survival +
    operation:xray:survival
                        Df Deviance    AIC     LRT Pr(>Chi)
<none>                     0.95577 95.085
stage:operation:xray     1 3.08666 95.216 2.13089   0.1444
stage:operation:survival 1 1.56605 93.696 0.61029   0.4347
operation:xray:survival  1 1.55124 93.681 0.59547   0.4403
```

operation:xray:survival comes out next.

Remove operation:xray:survival

```
cancer.4 <- update(cancer.3, . ~ . - operation:xray:survival)
drop1(cancer.4, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + operation:survival +
    xray:survival + stage:operation:xray + stage:operation:survival
                        Df Deviance    AIC    LRT Pr(>Chi)
<none>                      1.5512 93.681
xray:survival            1  1.6977 91.827 0.1464  0.70196
stage:operation:xray     1  6.8420 96.972 5.2907  0.02144 *
stage:operation:survival 1  1.9311 92.061 0.3799  0.53768
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Comments

- `stage:operation:xray` has now become significant, so won't remove that.
- Shows value of removing terms one at a time.
- There are no higher-order interactions containing both `xray` and `survival`, so now we get to test (and remove) `xray:survival`.

Remove xray:survival

```
cancer.5 <- update(cancer.4, . ~ . - xray:survival)
drop1(cancer.5, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + operation:survival +
    stage:operation:xray + stage:operation:survival
                        Df Deviance    AIC    LRT Pr(>Chi)
<none>                      1.6977 91.827
stage:operation:xray     1  6.9277 95.057 5.2300   0.0222 *
stage:operation:survival 1  2.0242 90.154 0.3265   0.5677
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Remove stage:operation:survival

```
cancer.6 <- update(cancer.5, . ~ . - stage:operation:survival)
drop1(cancer.6, test = "Chisq")
```

```
Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + operation:survival +
    stage:operation:xray
                     Df Deviance    AIC    LRT Pr(>Chi)
<none>                   2.024  90.154
stage:survival        1 135.198 221.327 133.173   <2e-16 ***
operation:survival    1   4.116  90.245   2.092   0.1481
stage:operation:xray  1   7.254  93.384   5.230   0.0222 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Last step?

Remove `operation:survival`.

```
cancer.7 <- update(cancer.6, . ~ . - operation:survival)
drop1(cancer.7, test = "Chisq")


Single term deletions

Model:
freq ~ stage + operation + xray + survival + stage:operation +
    stage:xray + operation:xray + stage:survival + stage:operation:xray
                    Df Deviance     AIC    LRT Pr(>Chi)
<none>                    4.116  90.245
stage:survival        1 136.729 220.859 132.61   <2e-16 ***
stage:operation:xray  1   9.346  93.475   5.23   0.0222 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
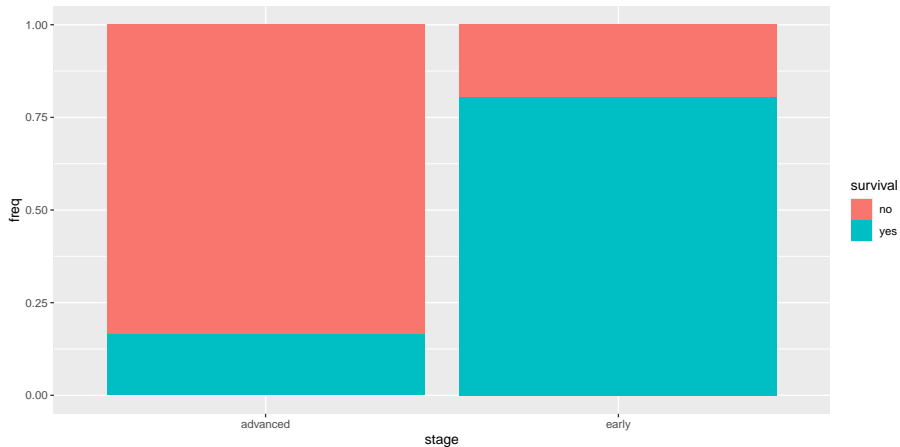
Finally done!

Conclusions

- What matters is things associated with `survival` (`survival` is "response").
- Only significant such term is `stage:survival`.

The graph

```
ggplot(cancer, aes(x = stage, y = freq, fill = survival)) +
  geom_col(position = "fill")
```
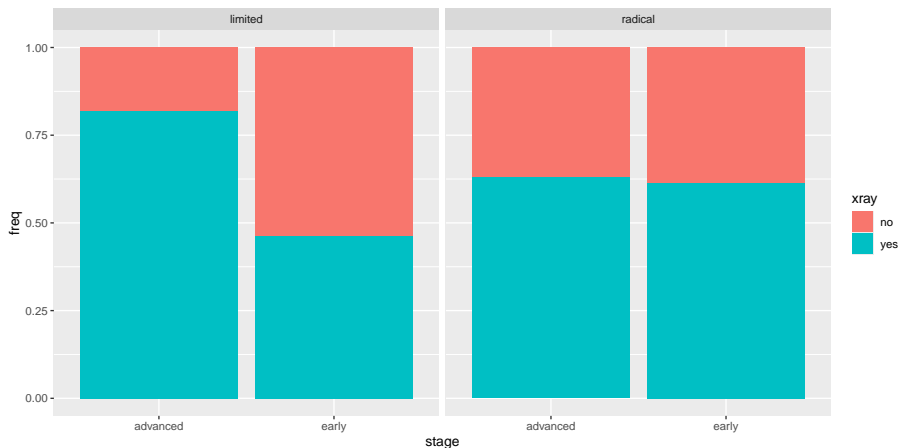
Comments

- Most people in early stage of cancer survived, and most people in advanced stage did not survive.
- This true *regardless* of type of operation or whether or not X-ray treatment was received. These things have no impact on survival.

What about that other interaction?

```
ggplot(cancer, aes(x = stage, y = freq, fill = xray)) +
  geom_col(position = "fill") + facet_wrap(~ operation)
```

Comments

- The association is between `stage` and `xray` *only for those who had the limited operation*.
- For those who had the radical operation, there was no association between `stage` and `xray`.
- This is of less interest than associations with `survival`.

General procedure

- Start with "complete model" including all possible interactions.
- `drop1` gives highest-order interaction(s) remaining, remove least non-significant.
- Repeat as necessary until everything significant.
- Look at graphs of significant interactions.
- Main effects not usually very interesting.
- Interactions with "response" usually of most interest: show association with response.