

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

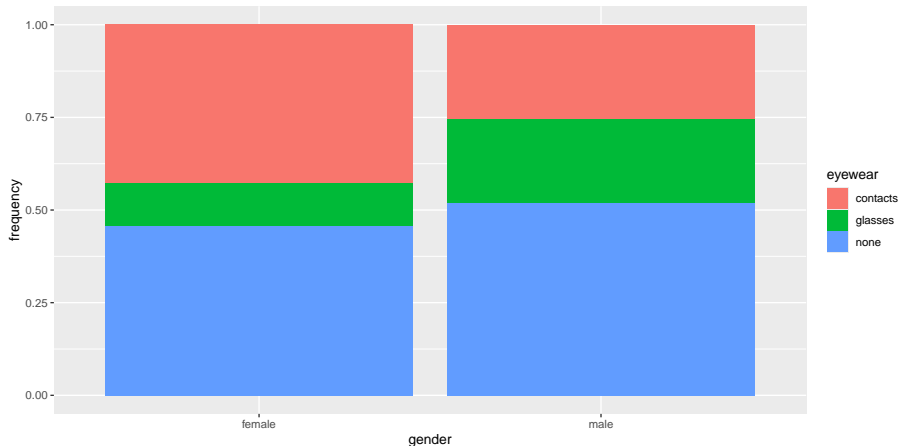
nothing!

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

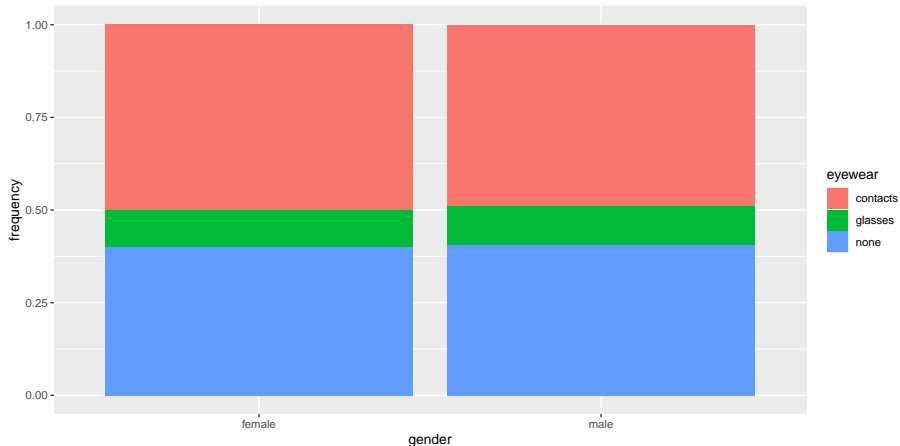
	Df	Deviance	AIC	LRT	Pr(>Chi)
<none>		0.047	43.515		
gender	1	48.624	90.091	48.577	3.176e-12 ***
eyewear	2	138.130	177.598	138.083	< 2.2e-16 ***

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

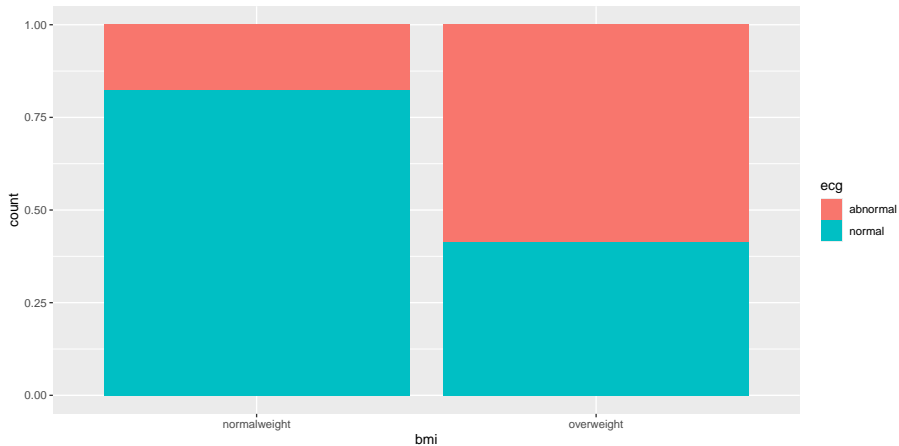
- ecg:smoke has become significant. So we have to stop.
- ecg is associated with both bmi and smoke, but separately (it doesn't depend on the combination of bmi and smoke).

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")
```

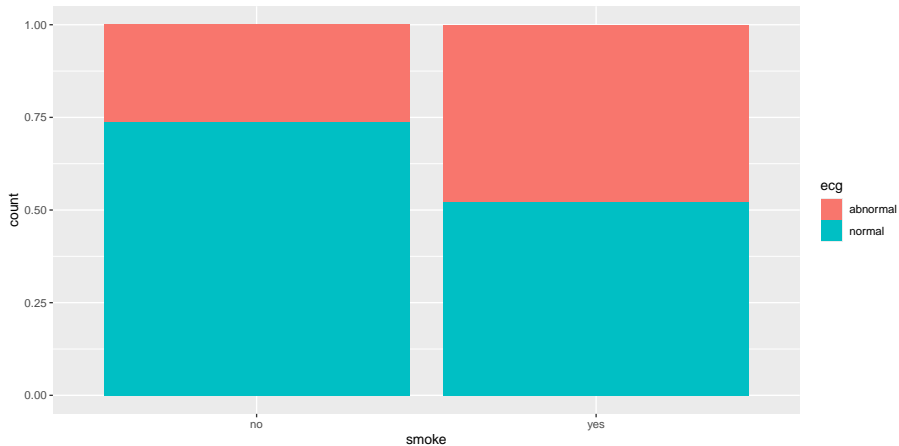


Comment

- 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

Airport	Alaska Airlines		America West	
	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
```

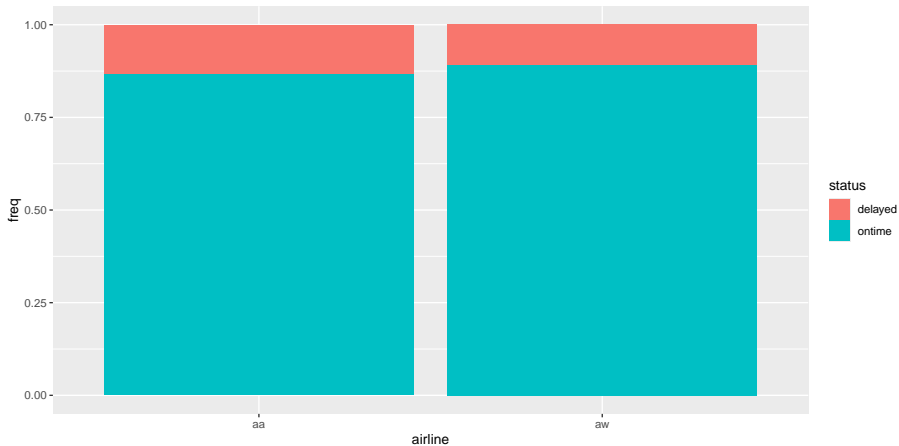
The data frame punctual

```
# 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

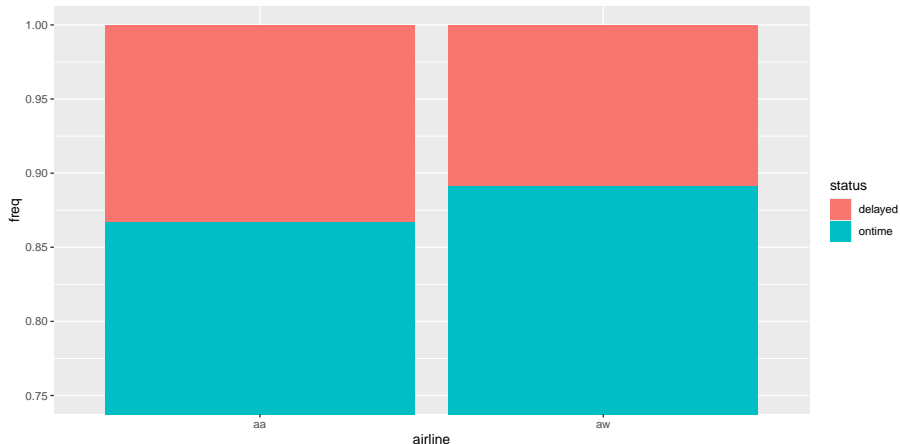
Proportions delayed by airline

```
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

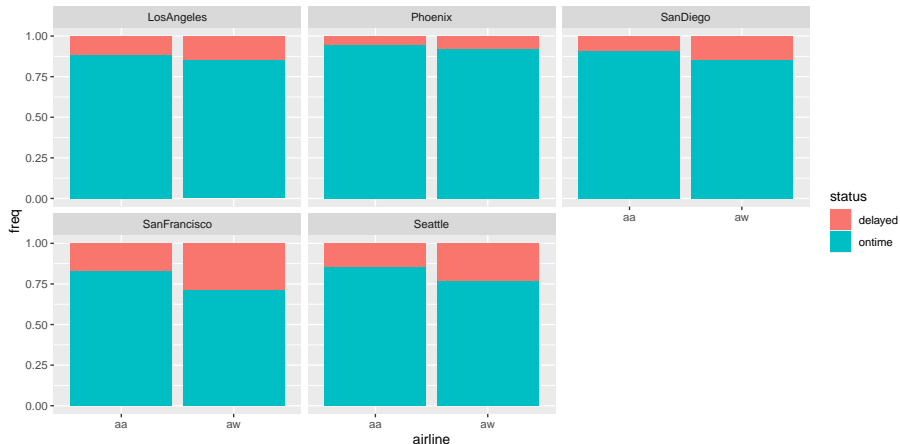
- Most flights are on time, but Alaska Airlines is late a little more often.

Proportion delayed by airport, for each airline

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

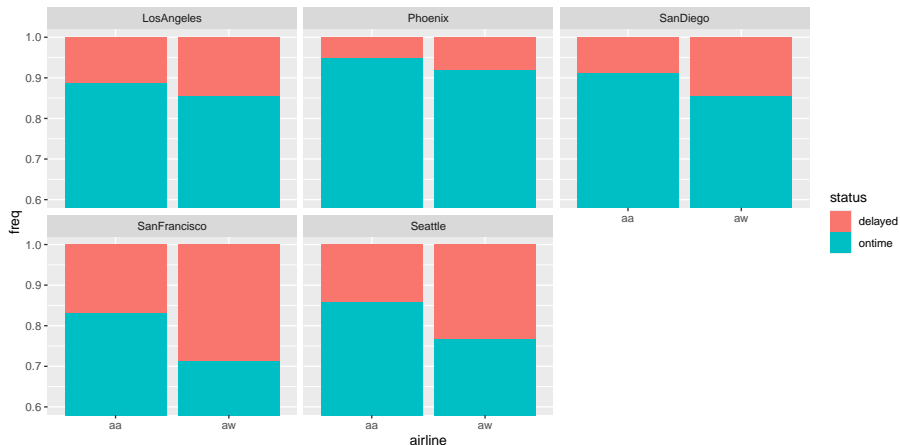
The graph(s)

```
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
```

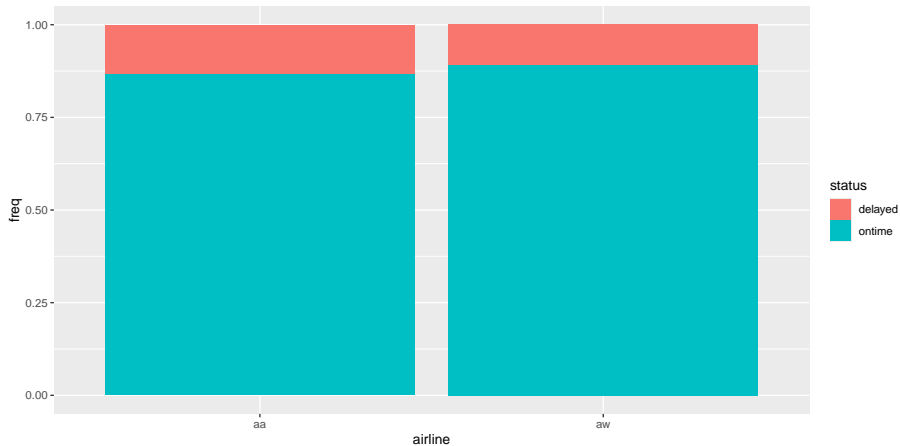
	Df	Deviance	AIC	LRT	Pr(>Chi)
<none>		3.2	178.7		
airport:airline	4	6432.5	6599.9	6429.2	< 2.2e-16 ***
airport:status	4	240.1	407.5	236.9	< 2.2e-16 ***
airline:status	1	45.5	218.9	42.2	8.038e-11 ***

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")
```

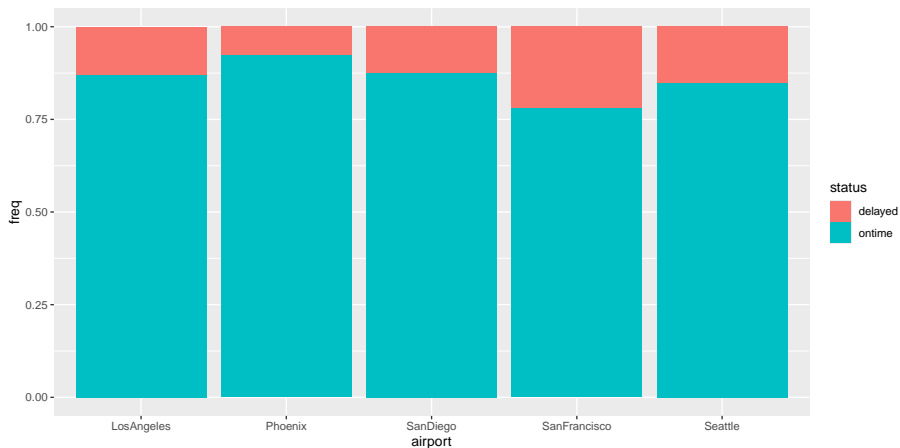


Comments

- 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")
```

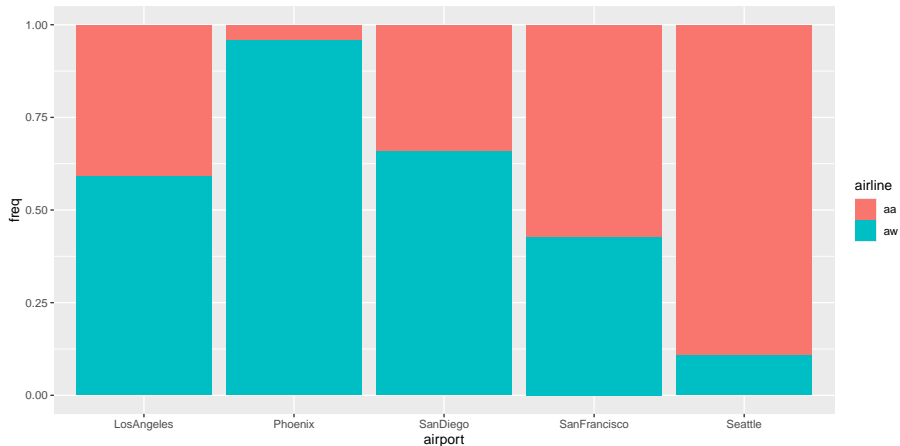


Comments

- 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

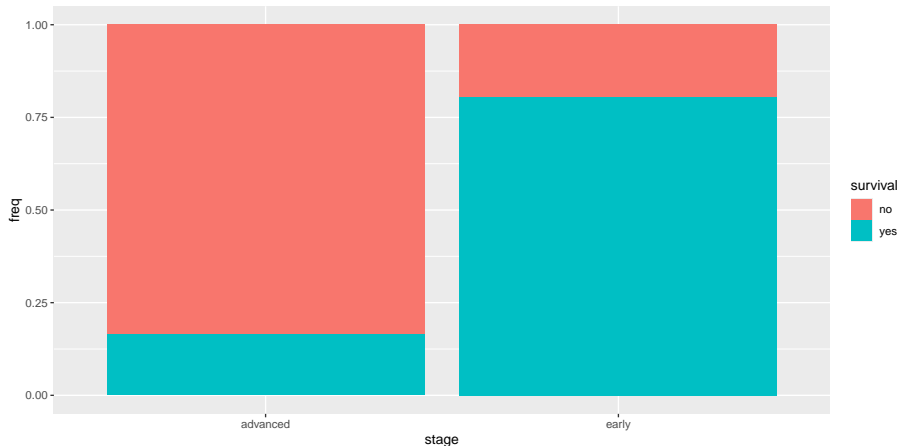
Finally done!

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")
```

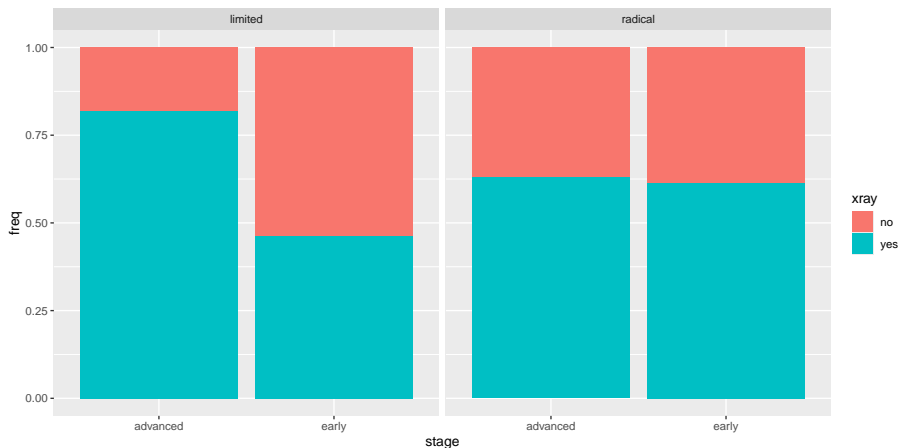


Comments

- 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.