431 Class 21

github.com/THOMASELOVE/2019-431

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Today's Agenda

Analysis of Variance adjusting for a covariate (intro to Part C)

- Fitting the model
- Interpreting the result
- Checking assumptions

On Contingency Tables (Chapter 29)

- Building a $J \times K$ Table
- χ^2 Tests of Independence
  - Cochran Conditions and Checking Assumptions
- Stratifying a Table by a Third Categorical Variable
  - The Cochran-Mantel-Haenszel Test for a Three-Way Table
  - The Woolf test to check assumptions

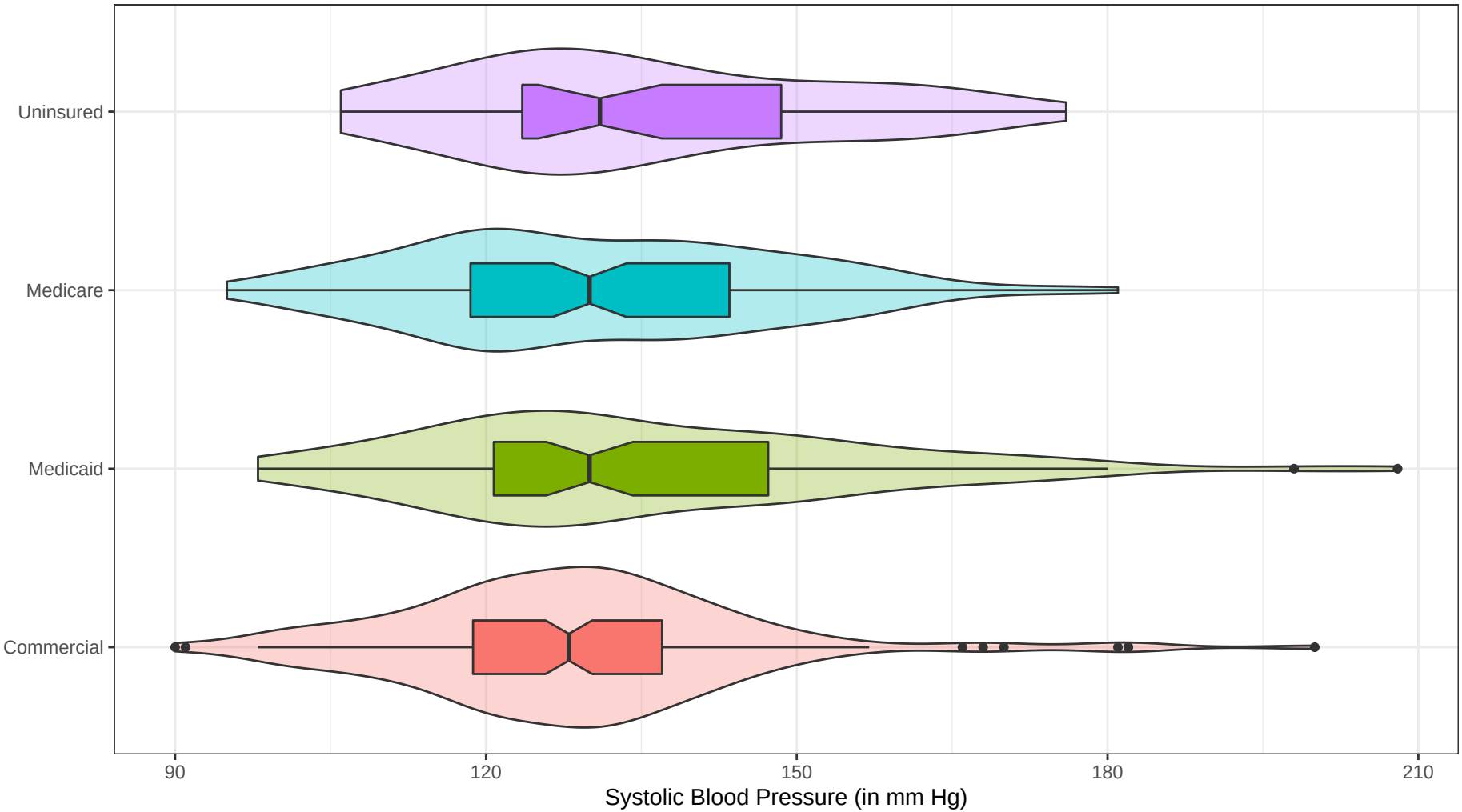
Today's Setup

```
library(vcd) # new today

library(here); library(magrittr); library(janitor)
library(patchwork); library(broom); library(tidyverse)

source(here("R", "Love-boost.R"))
dm431 <- readRDS(here("data", "dm431.Rds"))
```

Running a Regression Model to Compare Means

Returning to `dm431` data

We want to compare systolic blood pressure levels for four groups, defined by insurance.



Analysis of Variance Table

```
model_1 <- lm(sbp ~ insurance, data = dm431)

anova(model_1)
```

```
Analysis of Variance Table

Response: sbp
           Df Sum Sq Mean Sq F value  Pr(>F)
insurance   3   3403 1134.44  3.3619 0.01874 *
Residuals 427 144089  337.44
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Model 1 $\eta^2 = \frac{3403}{3403+144089} = \frac{3403}{147492} = 0.023$

Summary of Model One (edited to fit the screen)

```
Call: lm(formula = sbp ~ insurance, data = dm431)

Residuals:     Min      1Q  Median      3Q     Max
          -38.421 -11.844  -2.421   9.579  72.970

Coefficients:       Estimate Std. Error t value Pr(>|t|)
(Intercept)          128.421      1.434  89.527  < 2e-16 ***
insuranceMedicaid      6.609      2.331   2.836  0.00479 **
insuranceMedicare      2.238      2.191   1.021  0.30769
insuranceUninsured     6.579      3.119   2.110  0.03548 *
---
Sig. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 18.37 on 427 degrees of freedom
Multiple R-squared:  0.02307,   Adjusted R-squared:  0.01621
F-statistic: 3.362 on 3 and 427 DF,  p-value: 0.01874
```

What if we adjusted for SBP two years ago?

```
model_2 <- lm(sbp ~ insurance + sbp_old, data = dm431)

anova(model_2)
```

```
Analysis of Variance Table

Response: sbp
           Df Sum Sq Mean Sq F value    Pr(>F)
insurance   3   3403  1134.4  3.7137   0.01167 *
sbp_old     1  13958 13957.7 45.6924 4.569e-11 ***
Residuals 426 130131   305.5
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Model 2 $\eta^2 = \frac{3403+13958}{3403+13958+130131} = \frac{17361}{147492} = 0.118$

This ANOVA table runs tests sequentially

```
model_2rev <- lm(sbp ~ sbp_old + insurance, data = dm431)

anova(model_2rev)
```

```
Analysis of Variance Table

Response: sbp
           Df Sum Sq Mean Sq F value   Pr(>F)
sbp_old     1  14994 14993.8 49.0841 9.63e-12 ***
insurance   3   2367   789.1  2.5832   0.0529 .
Residuals 426 130131   305.5
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Model 2 $\eta^2 = \frac{14994+2367}{14994+2367+130131} = \frac{17361}{147492} = 0.118$

Summary of Model Two (edited to fit the screen)

```
summary(model_2)
```

```
Call: lm(formula = sbp ~ insurance + sbp_old, data = dm431)

Residuals:     Min      1Q  Median      3Q     Max
          -41.030 -11.737  -2.301  10.386  74.136

Coefficients:       Estimate Std. Error t value Pr(>|t|)
(Intercept)          86.9253     6.2886  13.823  < 2e-16 ***
insuranceMedicaid     5.5800     2.2227   2.510   0.0124 *
insuranceMedicare     1.7207     2.0861   0.825   0.4099
insuranceUninsured    5.3081     2.9733   1.785   0.0749 .
sbp_old               0.3245     0.0480   6.760 4.57e-11 ***

Residual standard error: 17.48 on 426 degrees of freedom
Multiple R-squared:  0.1177,    Adjusted R-squared:  0.1094
F-statistic: 14.21 on 4 and 426 DF,  p-value: 6.785e-11
```

Comparing Model 1 to Model 2

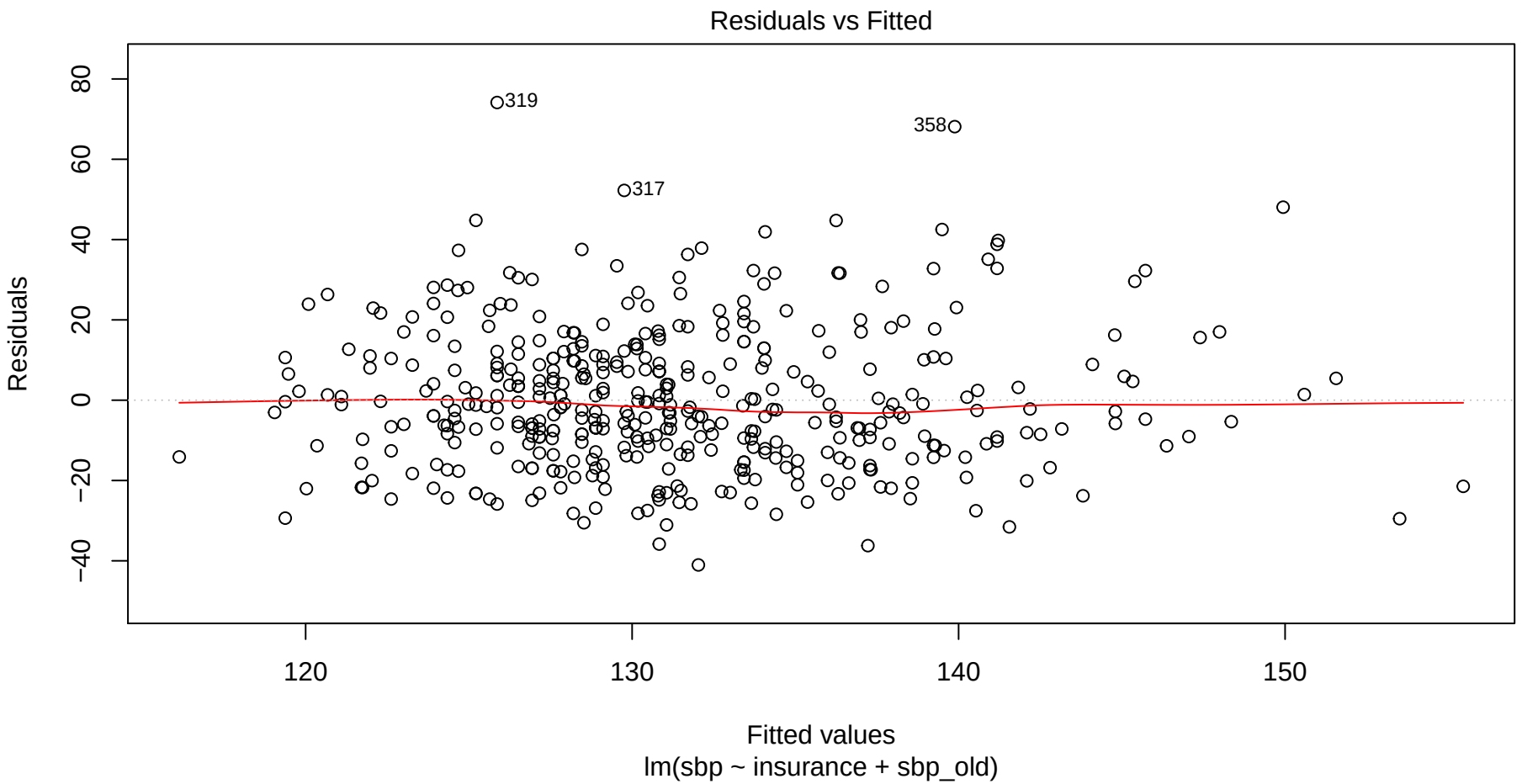
```
g1 <- glance(model_1) %>% mutate(model = "Model 1")
g2 <- glance(model_2) %>% mutate(model = "Model 2")

bind_rows(g1, g2) %>%
    select(model, r.squared, adjr2 = adj.r.squared, sigma,
           df, anova_F = statistic, p.value, AIC) %>%
    knitr::kable(digits = c(0, 3, 3, 2, 0, 2, 3, 1))
```

model	r.squared	adjr2	sigma	df	anova_F	p.value	AIC
Model 1	0.023	0.016	18.37	4	3.36	0.019	3738.1
Model 2	0.118	0.109	17.48	5	14.21	0.000	3696.2

Model 2 Assumption Checking: Residual Plot 1

- Residuals vs. Fitted (predicted) values should show fuzzy football. . .

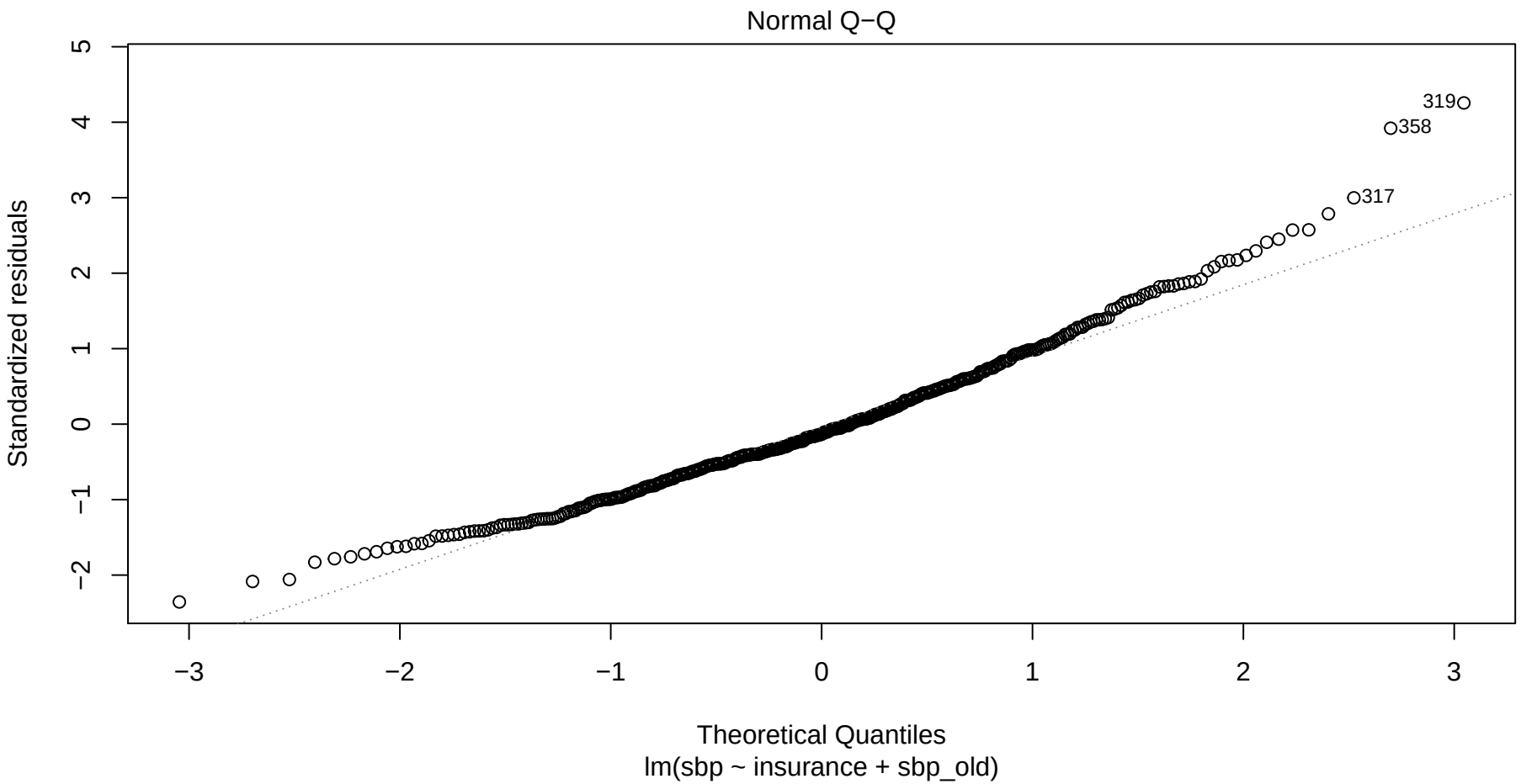
```
plot(model_2, which = 1)
```



Model 2 Assumption Checking: Residual Plots

- Normal Q-Q plot of Standardized Residuals. . .

```
plot(model_2, which = 2)
```



New Topic: Larger Contingency Tables

A 2×3 contingency table

This table displays the count of patients who show *complete*, *partial*, or *no response* after treatment with either **active** medication or a **placebo** in our study of 100 patients. . .

Group	None	Partial	Complete
Active	8	24	20
Placebo	12	26	10

Is there a statistically detectable association here, at $\alpha = 0.10$?

- H_0: Response Distribution is the same, regardless of Treatment.
- H_A: There is an association between Treatment and Response.

The Pearson Chi-Square Test

The Pearson χ^2 test assumes the null hypothesis is true (rows and columns are independent.) That is a model for our data. How does it work? Here's the table, with marginal totals added.

–	None	Partial	Complete	**TOTAL**
Active	8	24	20	**52**
Placebo	12	26	10	**48**
TOTAL	**20**	**50**	**30**	**100**

The test needs to estimate the expected frequency in each of the six cells under the assumption of independence. If the rows and columns are in fact independent of each other, then what is the expected number of subjects that will fall in the Active/None cell?

The Independence Model

The independence model means the overall rate of "Response = None" or "Partial" or "Complete" applies to both "Active" and "Placebo" subjects.

–	None	Partial	Complete	**TOTAL**
Active	–	–	–	**52**
Placebo	–	–	–	**48**
TOTAL	**20**	**50**	**30**	**100**

If the rows and columns were independent, then:

- 20/100 or 20% of subjects would have the response "None"
  - That means 20% of the 52 Active, and 20% of the 48 Placebo subjects.
- 50% would have a "Partial" response in each exposure group, and
- 30% would have a "Complete" response in each group.

So, can we fill in the expected frequencies under our independence model?

Observed (*Expected*) Cell Counts

–	None	Partial	Complete	**TOTAL**
Active	8 (*10.4*)	24 (*26.0*)	20 (*15.6*)	**52**
Placebo	12 (*9.6*)	26 (*24.0*)	10 (*14.4*)	**48**
TOTAL	**20**	**50**	**30**	**100**

General Formula for Expected Frequencies under Independence

$$\text{Expected Frequency} = \frac{\text{Row total} \times \text{Column total}}{\text{Grand Total}}$$

This assumes that the independence model holds: the probability of being in a particular column is exactly the same in each row, and vice versa.

Chi-Square Assumptions

- Expected Frequencies: We assume that the expected frequency, under the null hypothesized model of independence, will be **at least 5** (and ideally at least 10) in each cell. If that is not the case, then the χ^2 test is likely to give unreliable results. The *Cochran conditions* require us to have no cells with zero and at least 80% of the cells in our table with expected counts of 5 or higher. That's what R uses to warn you of trouble.
- Don't meet the standards? Consider collapsing categories.

Observed (Expected) Cell Counts

–	None	Partial	Complete	**TOTAL**
Active	8 (**10.4**)	24 (**26.0**)	20 (**15.6**)	52
Placebo	12 (**9.6**)	26 (**24.0**)	10 (**14.4**)	48
TOTAL	20	50	30	100

Getting the Table into R

We'll put the table into a matrix in R. Here's one approach. . .

```
T1 <- matrix(c(8, 24, 20, 12, 26, 10),
             ncol=3, nrow=2, byrow=TRUE)
rownames(T1) <- c("Active", "Placebo")
colnames(T1) <- c("None", "Partial", "Complete")
T1
```

```
        None Partial Complete
Active     8      24       20
Placebo   12      26       10
```

Chi-Square Test Results in R

- H_0: Response Distribution is the same, regardless of Treatment.
  - Rows and Columns of the table are *independent*
- H_A: There is an association between Treatment and Response.
  - Rows and Columns of the table are *associated*.

```
chisq.test(T1)
```

```
    Pearson's Chi-squared test

data:  T1
X-squared = 4.0598, df = 2, p-value = 0.1313
```

What is the conclusion?

Does Sample Size Affect The χ^2 Test?

- T1 results were: $\chi^2 = 4.0598$, df $= 2$, $p = 0.1313$
- What if we had the same pattern, but twice as much data?

```
T1_doubled <- T1*2
T1_doubled
```

```
        None Partial Complete
Active    16      48       40
Placebo   24      52       20
```

```
chisq.test(T1_doubled)
```

```
    Pearson's Chi-squared test

data:  T1_doubled
X-squared = 8.1197, df = 2, p-value = 0.01725
```

Can we run Fisher's exact test instead?

Yes, but . . . if the Pearson assumptions don't hold, then the Fisher's test is not generally an improvement.

```
fisher.test(T1)
```

```
    Fisher's Exact Test for Count Data

data:  T1
p-value = 0.1358
alternative hypothesis: two.sided
```

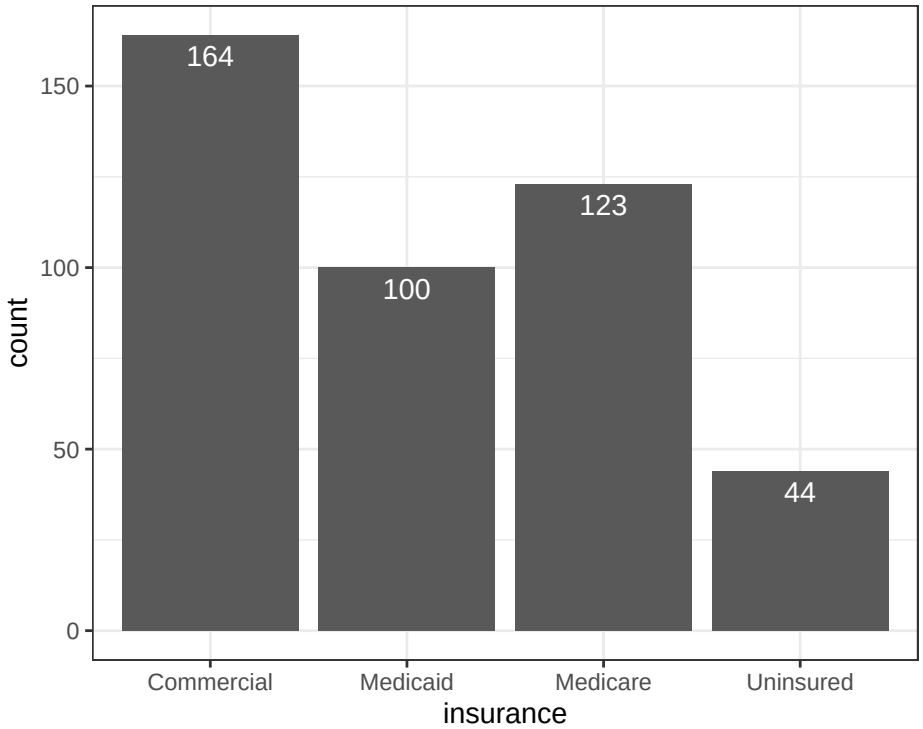
- It's also really meant more for square tables, with the same number of rows as columns, and relatively modest sample sizes.

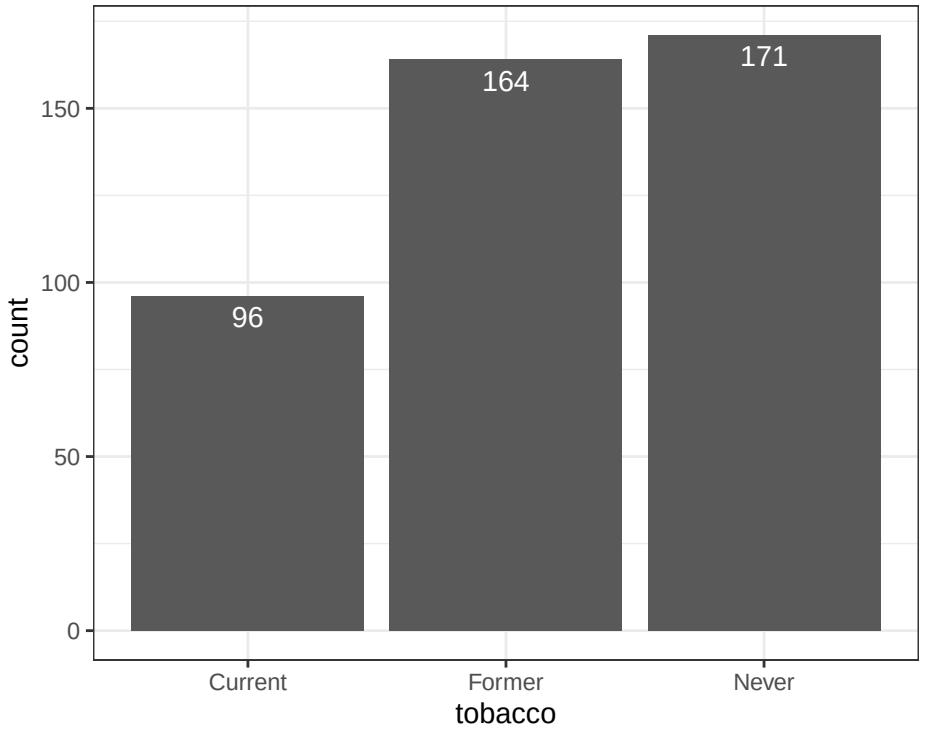
OK. Back to dm431

What am I plotting here?

```
p1 <- ggplot(dm431, aes(x = insurance)) + geom_bar() +
    theme_bw() +
    geom_text(aes(label = ..count..), stat = "count",
              vjust = 1.5, col = "white")

p2 <- ggplot(dm431, aes(x = tobacco)) + geom_bar() +
    theme_bw() +
    geom_text(aes(label = ..count..), stat = "count",
              vjust = 1.5, col = "white")

p1 + p2 # requires patchwork package
```

dm431: Two Categorical Variables of interest





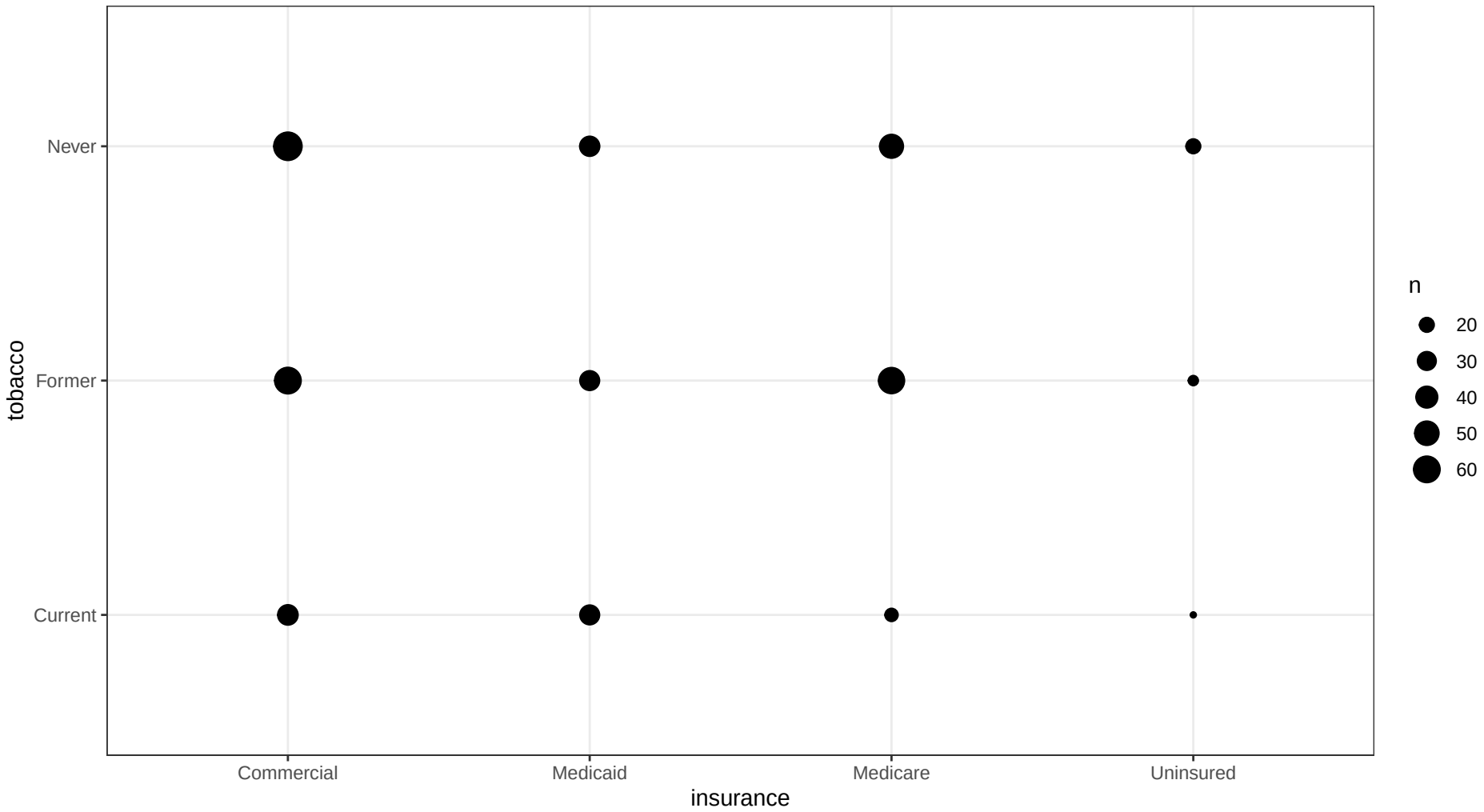
A 4×3 table with the dm431 data

```
dm431 %>%
    tabyl(insurance, tobacco) %>%
    adorn_totals(where = c("row", "col"))
```

insurance	Current	Former	Never	Total
Commercial	35	60	69	164
Medicaid	33	33	34	100
Medicare	17	58	48	123
Uninsured	11	13	20	44
Total	96	164	171	431

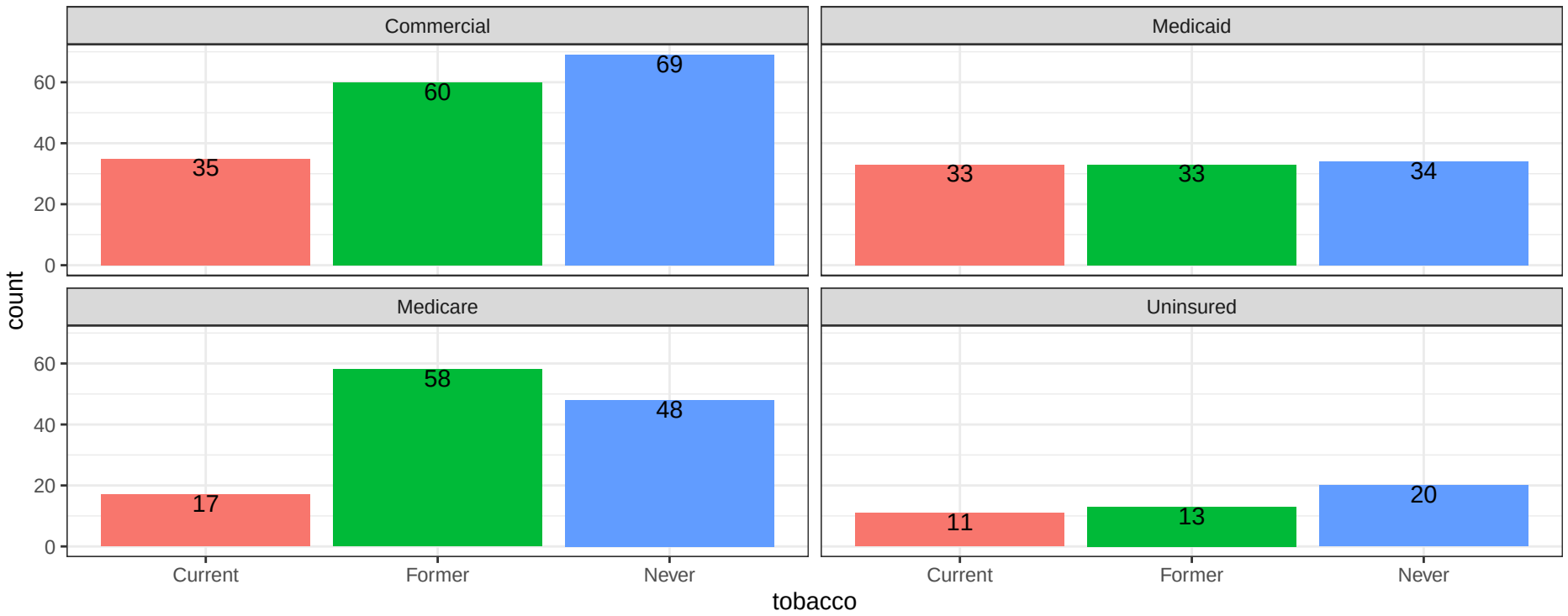
Plotting a Cross-Tabulation?

```
ggplot(dm431, aes(x = insurance, y = tobacco)) +
    geom_count() + theme_bw()
```



Tobacco Bar Chart faceted by Insurance

```
ggplot(dm431, aes(x = tobacco, fill = tobacco)) +
    geom_bar() + theme_bw() + facet_wrap(~ insurance) +
    guides(fill = FALSE) +
    geom_text(aes(label = ..count..), stat = "count",
              vjust = 1, col = "black")
```



Tobacco Status and Insurance in dm431

- H_0: Insurance type and Tobacco status are independent
- H_A: Insurance type and Tobacco status have a detectable association

Pearson χ^2 results?

```
dm431 %>% tabyl(insurance, tobacco) %>% chisq.test()
```

```
    Pearson's Chi-squared test

data:  .
X-squared = 15.033, df = 6, p-value = 0.02
```

Can we check our expected frequencies?

Tobacco Status and Insurance in dm431

Checking Assumptions:

```
res <- dm431 %>% tabyl(insurance, tobacco) %>% chisq.test()

res$observed
```

insurance	Current	Former	Never
Commercial	35	60	69
Medicaid	33	33	34
Medicare	17	58	48
Uninsured	11	13	20

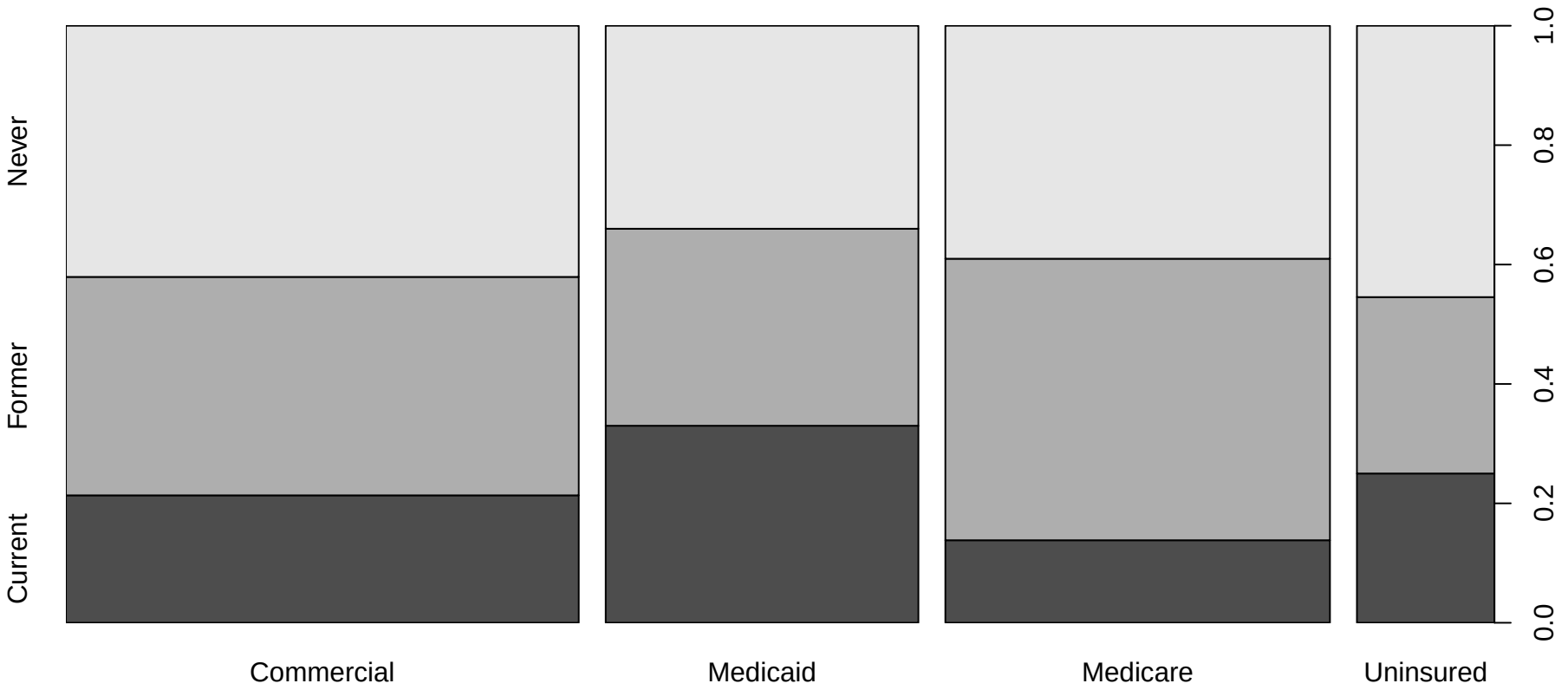
```
res$expected
```

insurance	Current	Former	Never
Commercial	36.529002	62.40371	65.06729
Medicaid	22.273782	38.05104	39.67517
Medicare	27.396752	46.80278	48.80046
Uninsured	9.800464	16.74246	17.45708

Mosaic Plot for Cross-Tabulation

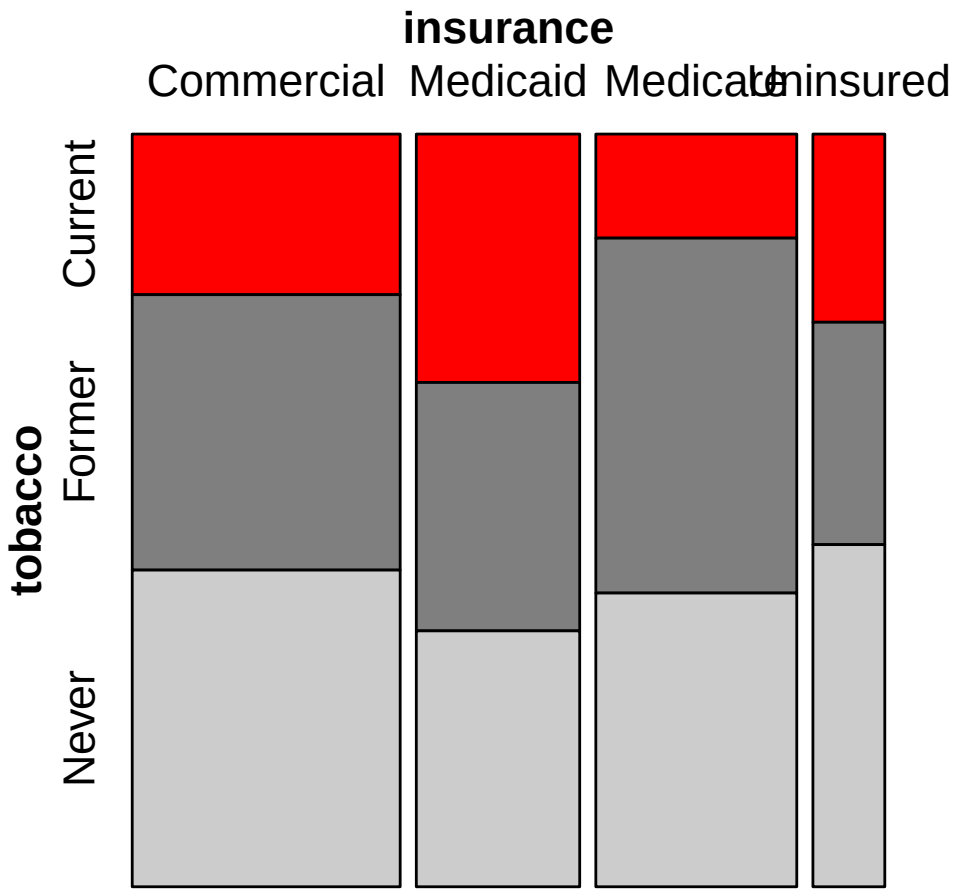
Each rectangle's area is proportional to the number of cases in that cell.

```
dm431 %$% plot(insurance, tobacco, ylab = "", xlab = "")
```



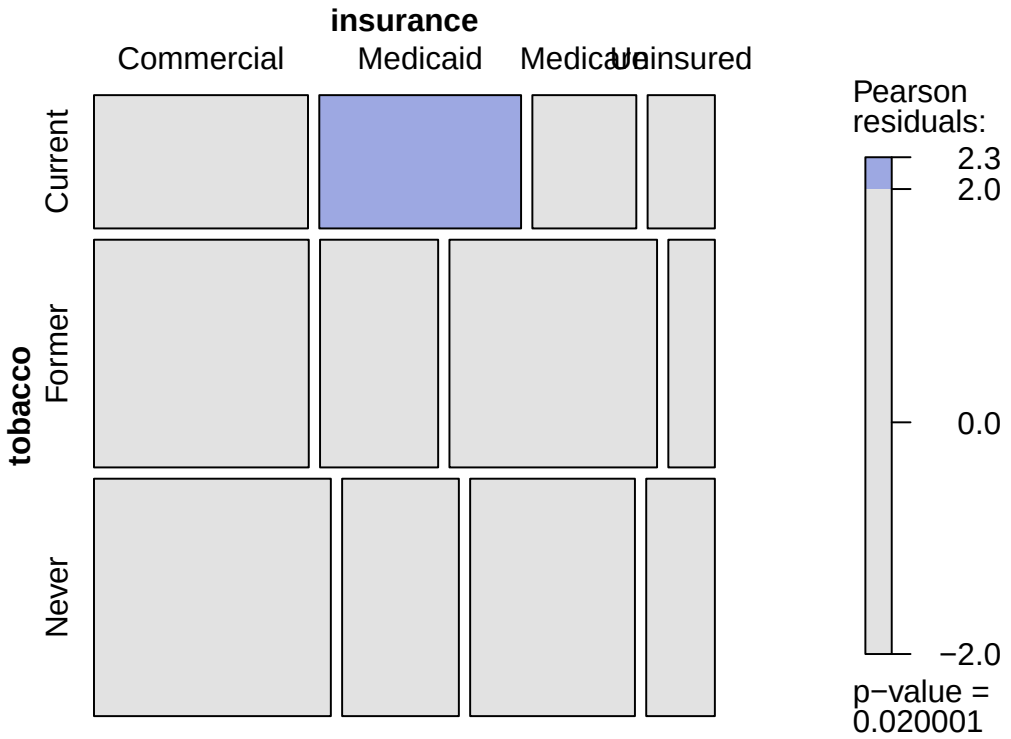
Mosaic Plot from the vcd package (highlighting)

```
mosaic(~ tobacco + insurance, data = dm431,
       highlighting = "tobacco",
       highlighting_fill = c("red", "gray50", "gray80"))
```



Mosaic Plot from the vcd package (with χ^2 shading)

```
mosaic(~ tobacco + insurance, data = dm431, shade = TRUE)
```



Working with Three-Way Tables (Cochran-Mantel-Haenszel Procedure) in the Treatment of Kidney Stones

Kidney Stone Treatment Example

Suppose we compare the success rates of two treatments for kidney stones.

- Treatment A (all open surgical procedures): 273/350 patients (78%) had a successful result.
- Treatment B (percutaneous nephrolithotomy - less invasive): 289/350 were successful (83%).

Kidney Stones	Successful Outcome	Bad Outcome
A (open surgery)	273 (78%)	77 (22%)
B (less invasive)	289 (83%)	61 (17%)

Which approach would you choose?

- Sources: Wikipedia and Charig CR et al. (1986) PMID 3083922.

Kidney Stones, twobytwo results

```
twobytwo(273, 77, 289, 61, "A", "B", "Success", "Bad")
```

```
2 by 2 table analysis:
------------------------------------------------------

Outcome   : Success         Comparing : A vs. B

  Success Bad    P(Success) 95% conf. interval
A     273  77        0.7800    0.7336    0.8203
B     289  61        0.8257    0.7823    0.8620

                                  95% conf. interval
         Relative Risk:  0.9446    0.8776    1.0168
     Sample Odds Ratio:  0.7483    0.5146    1.0883
Probability difference: -0.0457   -0.1045    0.0133

Exact P-value: 0.154    Asymptotic P-value: 0.1292
------------------------------------------------------
```

Kidney Stones: A Third Variable

But this comparison may be misleading.

Some kidney stones are small, and some are large.

- Open Surgery (A) used in 87 small stones, and 263 large ones.
- Less Invasive (B) used in 270 small stones, and 80 large ones.

Could that bias our results?

- Should we account for this difference in "size mix"?

Kidney Stone results stratified by stone size

- For small stones, the odds ratio for a successful outcome comparing A to B is 2.08 (95% CI 0.84, 5.11)

Small Stones	Successful Outcome	Bad Outcome
A (open surgery)	81 (93%)	6 (7%)
B (less invasive)	234 (87%)	36 (13%)

- For large stones, that odds ratio is 1.23 (95% CI 0.71, 2.12)

Large Stones	Successful Outcome	Bad Outcome
A (open surgery)	192 (73%)	71 (27%)
B (less invasive)	55 (69%)	25 (31%)

Aggregated Data: % with Successful Outcome

- 78% of Treatment A subjects, 83% of Treatment B

What We Have Here is a Three-Way Table

- rows: which treatment was received (A or B)
- columns: was the outcome Successful or Bad?
- *strata* or *layers*: was the stone Small or Large?

Size	Treatment	Good	Bad	Total	% Good
Small	A	81	6	87	93
Small	B	234	36	270	87
Large	A	192	71	263	73
Large	B	55	25	80	69

We'll talk about three-way and larger contingency tables more in 432, but in 431, we focus on the situation where a 2x2 table is repeated over multiple strata (categories in a third variable.)

Cochran-Mantel-Haenszel Test

The Cochran-Mantel-Haenszel test is designed to test whether the rate of a successful (Good) outcome is the same across the two levels of the treatment (i.e. A or B.)

- We *could* do this by simply adding up the results across the stone sizes, but that wouldn't be wise, because the stone size is likely to be related to the outcome and the choice of procedure.
- But we can account for the differences between stone sizes to some extent by adjusting for stone size as a stratifying variable in a CMH test.
- The big assumption we'll have to make, though, is that the odds ratio for a good outcome for treatment A versus treatment B is the same for small stones and large stones. Is this reasonable here? We'll use a Woolf test to decide.

But first, let's get the data into a useful form.

Building the Three-Way Table

```
stone <- c(rep("Small", 4), rep("Large", 4))
treat <- c(rep(c("A", "A", "B", "B"), 2))
result <- c(rep(c("Good", "Bad"), 4))
counts <- c(81, 6, 234, 36, 192, 71, 55, 25)

kidney_dat <- tibble(stone, treat, result, counts)
```

What do we have so far?

```
kidney_dat
```

```
# A tibble: 8 x 4
  stone treat result counts
  <chr> <chr> <chr>   <dbl>
1 Small A     Good       81
2 Small A     Bad         6
3 Small B     Good      234
4 Small B     Bad        36
5 Large A     Good      192
6 Large A     Bad        71
7 Large B     Good       55
8 Large B     Bad        25
```

The Three-Way Table

```
big.tab <- xtabs(counts ~ treat + result + stone,
                 data = kidney_dat)
big.tab
```

```
, , stone = Large

     result
treat Bad Good
    A  71  192
    B  25   55

, , stone = Small

     result
treat Bad Good
    A   6   81
    B  36  234
```

Three-Way Table as a "Flat" Table

```
ftable(big.tab)
```

```
                stone Large Small
treat result
A     Bad               71     6
      Good             192    81
B     Bad               25    36
      Good              55   234
```

Can we assume a Common Odds Ratio?

- Recall the sample odds ratio in small stones was 2.08 and in large stones was 1.23

The Woolf test checks a key assumption for the Cochran-Mantel-Haenszel test. The Woolf test assesses the null hypothesis of a common odds ratio across the two stone sizes.

```
woolf_test(big.tab)
```

```
    Woolf-test on Homogeneity of Odds Ratios (no
    3-Way assoc.)

data:  big.tab
X-squared = 0.95353, df = 1, p-value = 0.3288
```

Our conclusion from the Woolf test is that we are able to retain the null hypothesis of homogeneous odds ratios. So it's not crazy to fit a test that requires that all of the odds ratios be the same in the population.

Running the Cochran-Mantel-Haenszel test

So, we can use the Cochran-Mantel-Haenszel test to make inferences about the population odds ratio (for revascularization given niacin rather than placebo) accounting for the five studies. We'll use a 90% confidence interval, and the results appear on the next slide.

```
mantelhaen.test(big.tab, conf.level = .90)
```

Complete CMH output (Edited to fit on the screen)

```
mantelhaen.test(big.tab, conf.level = .90)
```

```
Mantel-Haenszel chi-squared test with continuity correction

data:  big.tab
Mantel-Haenszel X-squared = 2.0913, df = 1, p-value = 0.1481

alt. hypothesis: true common odds ratio is not equal to 1

90 percent confidence interval: 0.4708539 1.0145392
sample estimates: common odds ratio 0.6911583
```

What can we conclude in this case?

OK. That's everything for Part B of the course, and that's everything that you need to complete Project Study A.

Bonus: The Niacin and Heart Disease Meta-Analysis

Duggal et al (2010) did a meta-analysis[1] of 5 placebo-controlled studies (AFREGS, ARBITER2, CLAS1, FATS and HATS) of niacin and heart disease, where the primary outcome was the need to do a coronary artery revascularization procedure.

For example, the FATS study had these results:

FATS	Revascularization	No Revasc.
Niacin	2	46
Placebo	11	41

FATS is just one of the five studies, and this table exists in each!

[1] Duggal JK et al. 2010. Effect of niacin therapy on cardiovascular outcomes in patients with coronary artery disease. J Cardiovasc Pharmacology & Therapeutics 15: 158-166. My Source: http://www.biostathandbook.com/cmh.html

Exploring the FATS study

FATS	Revascularization	No Revasc.
Niacin	2	46
Placebo	11	41

- Pr(revascularization | Niacin) $= \frac{2}{2+46} = 0.042$
- Odds(revascularization | Niacin) $= \frac{2}{46} = 0.043$
- Pr(revascularization | Placebo) $= \frac{11}{11+41} = 0.212$
- Odds(revascularization | Placebo) $= \frac{11}{41} = 0.268$

and so the Odds Ratio $= \frac{2*41}{11*46} = 0.16$.

But that is just the result for the FATS study.

Building the Meta-Analysis Table

```
study <- c(rep("FATS", 4), rep("AFREGS", 4),
           rep("ARBITER2", 4), rep("HATS", 4),
           rep("CLAS1", 4))
treat <- c(rep(c("Niacin", "Niacin",
                 "Placebo", "Placebo"),5))
outcome <- c(rep(c("Revasc.", "No Rev."), 10))
counts <- c(2, 46, 11, 41, 4, 67, 12, 60, 1, 86,
            4, 76, 1, 37, 6, 32, 2, 92, 1, 93)
meta <- data.frame(study, treat, outcome, counts) %>% tbl_df
meta$treat <- fct_relevel(meta$treat, "Niacin")
meta$outcome <- fct_relevel(meta$outcome, "Revasc.")
meta.tab <- xtabs(counts ~ treat + outcome + study,
                  data = meta)
```

Five Studies in the Meta-Analysis

```
ftable(meta.tab)
```

```
                study AFREGS ARBITER2 CLAS1 FATS HATS
treat   outcome
Niacin  Revasc.           4        1     2    2    1
        No Rev.          67       86    92   46   37
Placebo Revasc.          12        4     1   11    6
        No Rev.          60       76    93   41   32
```

The three variables we are studying are:

- `treat` (2 levels: Niacin/Placebo),
- `outcome` (2 levels: Revascularization or No Revascularization) across
- `study` (5 levels: AFREGS, ARBITER2, CLAS1, FATS, HATS)

Cochran-Mantel-Haenszel Test

The Cochran-Mantel-Haenszel test is designed to test whether the rate of revascularization is the same across the two levels of the treatment (i.e. Niacin or Placebo).

- We *could* do this by simply adding up the results across the five studies, but that wouldn't be wise, because the studies used different populations and looked for revascularization after different lengths of time.
- But we can account for the differences between studies to some extent by adjusting for study as a stratifying variable in a CMH test.
- The big assumption we'll have to make, though, is that the odds ratio for revascularization given Niacin instead of Placebo does not change across the studies. Is this reasonable in our case?

Looking at the Study-Specific Odds Ratios

We'll calculate the odds ratios, comparing revascularization odds with niacin vs. placebo, within each separate study.

Study	Rev N	Rev P	NoRev N	NoRev P	Odds Ratio
AFREGS	4	67	12	60	$\frac{4*60}{67*12} = 0.3$
ARBITER2	1	86	4	76	0.22
CLAS1	2	92	1	93	2.02
FATS	2	46	11	41	0.16
HATS	1	37	6	32	0.14

The table shows patient counts for the categories in each of the respective two-by-two tables (Rev N = Revascularization and Niacin, NoRev P = No Revascularization and Placebo, etc.)

Can we assume a Common Odds Ratio?

The Woolf test checks a key assumption for the Cochran-Mantel-Haenszel test. The Woolf test assesses the null hypothesis of a common odds ratio across the five studies.

```
woolf_test(meta.tab)
```

```
    Woolf-test on Homogeneity of Odds Ratios (no
    3-Way assoc.)

data:  meta.tab
X-squared = 3.4512, df = 4, p-value = 0.4853
```

Our conclusion from the Woolf test is that we are able to retain the null hypothesis of homogeneous odds ratios. So it's not crazy to fit a test that requires that all of the odds ratios be the same in the population.

Running the Cochran-Mantel-Haenszel test

So, we can use the Cochran-Mantel-Haenszel test to make inferences about the population odds ratio (for revascularization given niacin rather than placebo) accounting for the five studies. We'll use a 90% confidence interval, and the results appear on the next slide.

```
mantelhaen.test(meta.tab, conf.level = .90)
```

Complete CMH output

```
mantelhaen.test(meta.tab, conf.level = .90)
```

```
Mantel-Haenszel chi-squared test with continuity correction

data:  meta.tab
Mantel-Haenszel
X-squared = 12.746, df = 1, p-value = 0.0003568

alt. hypothesis: true common odds ratio is not equal to 1

90 percent confidence interval: 0.1468942 0.4968686
sample estimates: common odds ratio 0.2701612
```

What can we conclude in this case?