431 Class 07

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Today's Agenda

- Working with `dm1000`
- Some More on Identifying Missing Data and working around it
- Summarizing Categorical Data

Today's Package Setup

```
library(Epi) ## for twoby2() function
library(gt) ## making tables
library(gtExtras) ## fancier tables
library(janitor)
library(kableExtra) ## for kbl() function
library(naniar)
library(patchwork)
library(tidyverse)

theme_set(theme_bw())
```

Loading Some New Data

```
dm1000 <- read_csv("c07/data/dm_1000.csv", show_col_types = FALSE) |>
  clean_names() |>
  mutate(across(where(is.character), as_factor)) |>
  mutate(subject = as.character(subject))
```

- 1000 (simulated) patients with diabetes between the ages of 31 and 75 who live in Cuyahoga County and are in one of four race-ethnicity categories, as well as one of four insurance categories.
- Same variables we saw in `dm431` last week, but 1000 new subjects, and one new variable (`residence`)

Listing of dm1000 tibble

```
1 dm1000
```

```
# A tibble: 1,000 × 17
   subject   age insurance  n_income    ht    wt   sbp   dbp   a1c   ldl
tobacco
   <chr>   <dbl> <fct>         <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <fct>
 1 M-0001     55 Medicaid      29853  1.63 103.    145    70   6.4   221
Current
 2 M-0002     52 Commercial    31248  1.75 112.    151    77   8.5   116 Never
 3 M-0003     69 Medicare      23362  1.65  74.9   127    73   8.9    52
Former
 4 M-0004     57 Medicaid      26033  1.63  81.4   125    74   6.8   122 Never
 5 M-0005     68 Medicare      85374  1.69  92.6   120    73  10.3    94 Never
 6 M-0006     56 Medicaid      31273  1.71  54.6   127    75  12.3    NA
Current
 7 M-0007     54 Commercial    25445  1.68  81.6   114    81   6.5   100
Current
```

`dm1000` Code Book (1 of 3)

Variable	Description
`subject`	subject code (M-0001 through M-1000)
`age`	subject's age, in years
`insurance`	primary insurance, 4 levels
`n_income`	neighborhood median income, in $
`ht`	height, in meters (2 decimal places)
`wt`	weight, in kilograms (2 decimal places)

dm1000 Code Book (2 of 3)

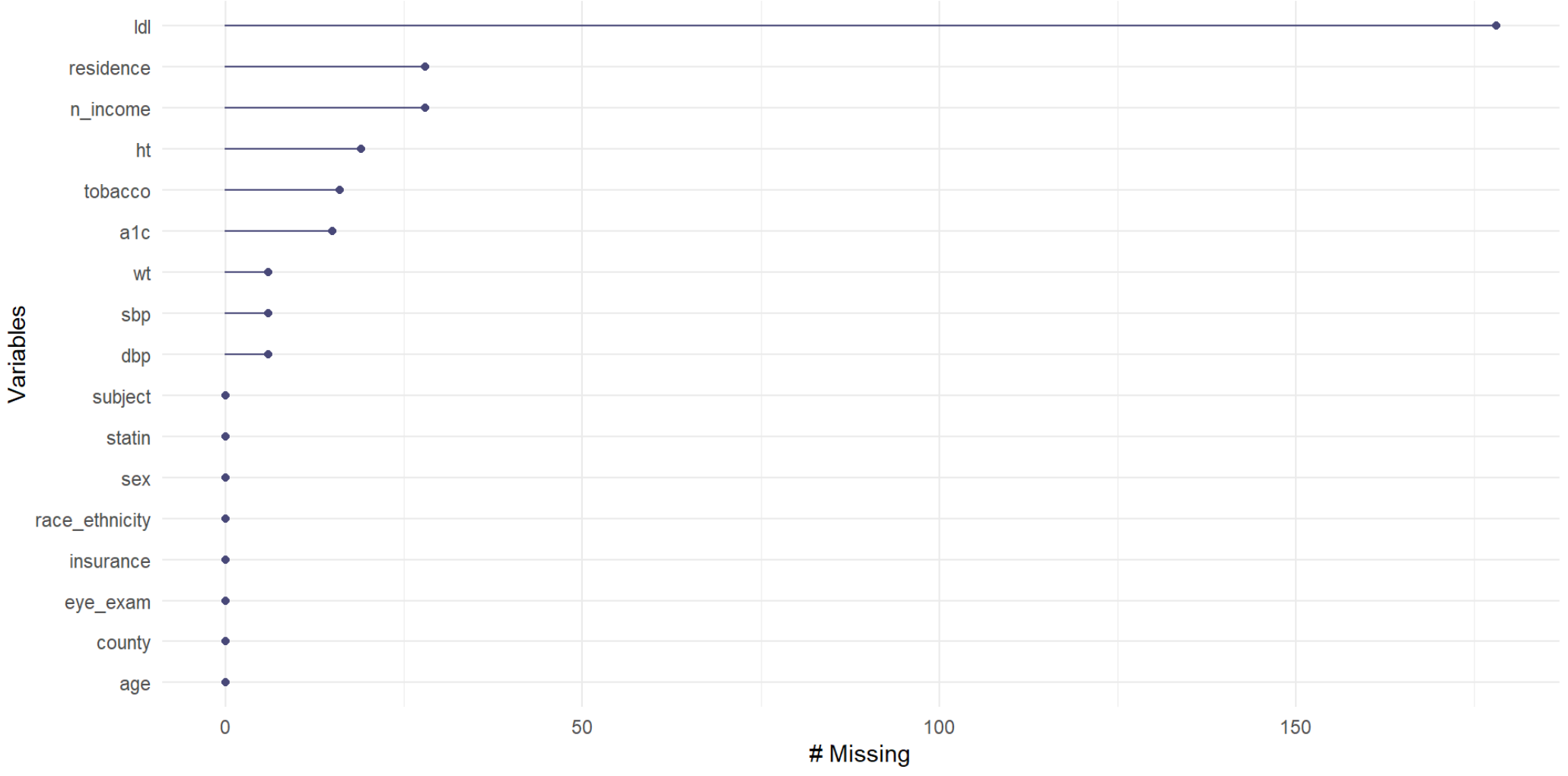
Variable	Description
sbp	most recent systolic blood pressure (mm Hg)
dbp	most recent diastolic blood pressure (mm Hg)
a1c	most recent Hemoglobin A1c (%)
ldl	most recent LDL cholesterol level (mg/dl)
tobacco	most recent tobacco status, 3 levels
statin	1 = prescribed a statin in past 12m, 0 = not

Remainder of `dm1000` codebook

Variable	Description
`eye_exam`	1 = diabetic eye exam in past 12m, 0 = no record of exam in past 12m
`race_ethnicity`	race/ethnicity category, 3 levels
`sex`	Female or Male
`county`	all subjects live in Cuyahoga County
`residence`	Cleveland or Suburbs

Any Missing Data?

```
1  gg_miss_var(dm1000)
```



Counts of missingness, by variable

```
1 miss_var_summary(dm1000)
```

```
# A tibble: 17 × 3
   variable       n_miss pct_miss
   <chr>           <int>    <dbl>
 1 ldl               178     17.8
 2 n_income           28      2.8
 3 residence          28      2.8
 4 ht                 19      1.9
 5 tobacco            16      1.6
 6 a1c                15      1.5
 7 wt                  6      0.6
 8 sbp                 6      0.6
 9 dbp                 6      0.6
10 subject             0      0
11 age                 0      0
12 insurance           0      0
13 statin              0      0
```

What does `miss_var_table()` do?

```
1 miss_var_table(dm1000)
```

```
# A tibble: 7 × 3
  n_miss_in_var n_vars pct_vars
          <int>  <int>    <dbl>
1             0      8    47.1
2             6      3    17.6
3            15      1     5.88
4            16      1     5.88
5            19      1     5.88
6            28      2    11.8
7           178      1     5.88
```

What does `miss_case_table()` do?

```
1 miss_case_table(dm1000)
```

```
# A tibble: 7 × 3
  n_miss_in_case n_cases pct_cases
           <int>   <int>     <dbl>
1              0     772      77.2
2              1     181      18.1
3              2      32       3.2
4              3       7       0.7
5              4       5       0.5
6              5       2       0.2
7              6       1       0.1
```

miss_case_summary()?

```
1 miss_case_summary(dm1000)
```

```
# A tibble: 1,000 × 3
    case n_miss pct_miss
   <int>  <int>    <dbl>
 1   230      6     35.3
 2   440      5     29.4
 3   970      5     29.4
 4   107      4     23.5
 5   284      4     23.5
 6   288      4     23.5
 7   385      4     23.5
 8   891      4     23.5
 9    91      3     17.6
10   241      3     17.6
# … with 990 more rows
```

How should we summarize data with missing values?

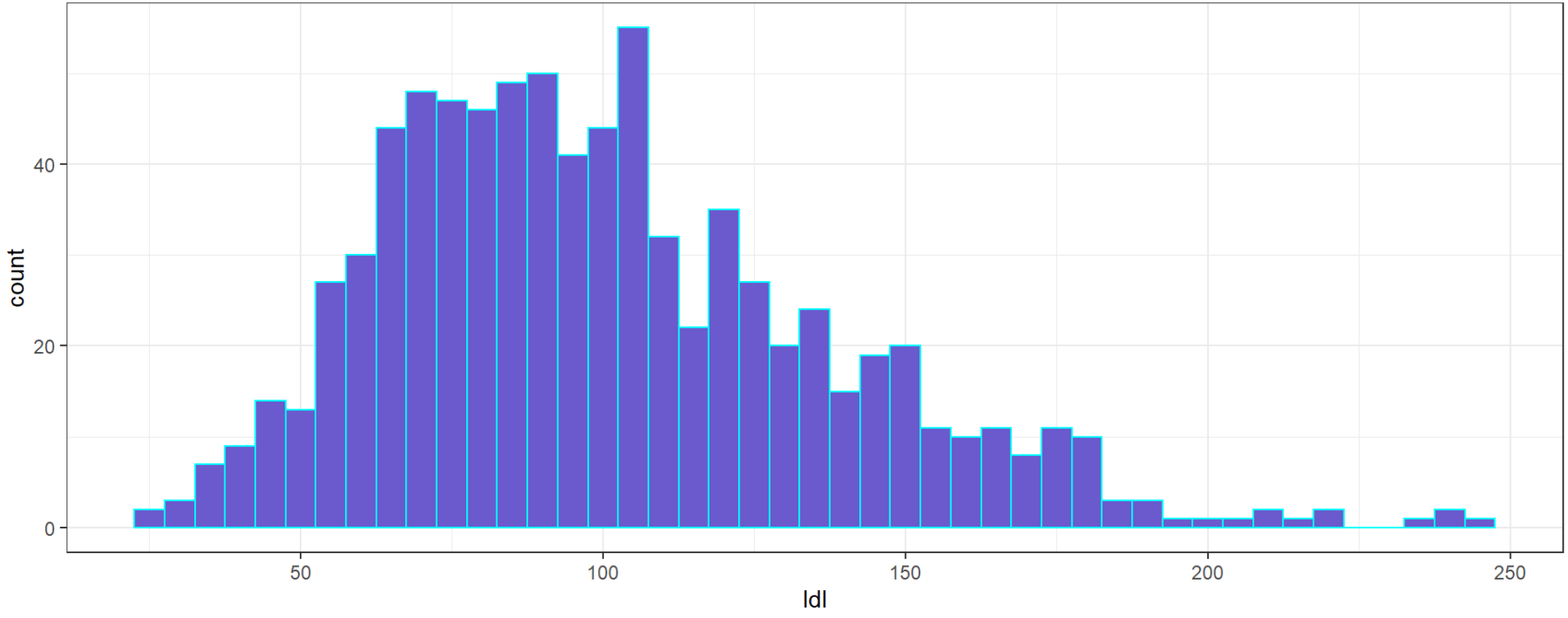
It depends on what you'll do with the data.

- If you are providing a data summary, then you should summarize the complete cases, and specify the number of missing values.
- If you are intending to use the sample you've collected to make an inference about a process or population or to build a model, then you may want to consider whether or not a complete-case analysis will introduce bias.

What do graphs do with missing data?

```
1 ggplot(data = dm1000, aes(x = ldl)) +
2   geom_histogram(binwidth = 5, fill = "slateblue", col = "cyan")
```

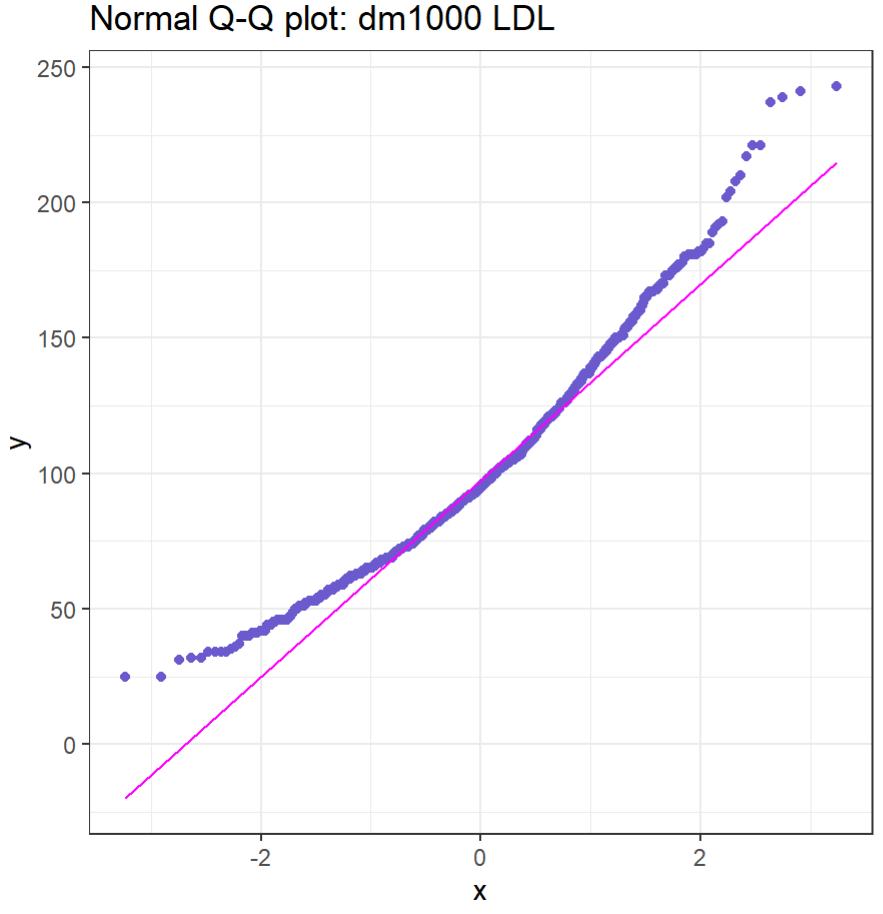
```
Warning: Removed 178 rows containing non-finite values (stat_bin).
```

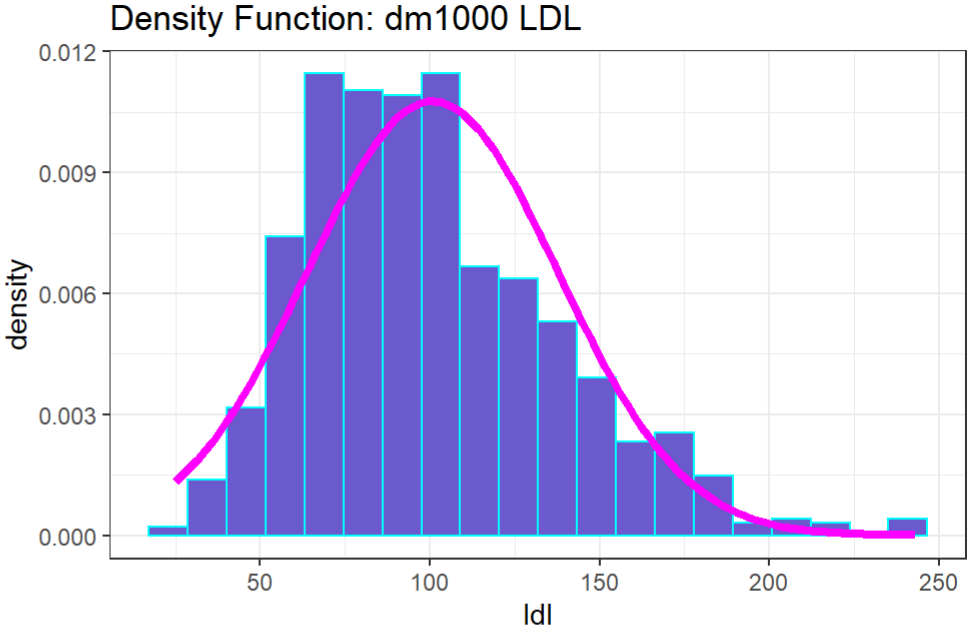


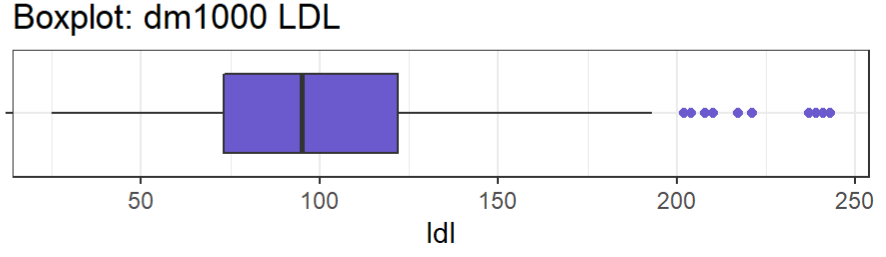
Exploring `ldl` in `dm1000`

```
p1 <- ggplot(dm1000, aes(sample = ldl)) +
  geom_qq(col = "slateblue") +
  geom_qq_line(col = "magenta") +
  theme(aspect.ratio = 1) +
  labs(title = "Normal Q-Q plot: dm1000 LDL")

p2 <- ggplot(dm1000, aes(x = ldl)) +
  geom_histogram(aes(y = stat(density)),
                 bins = 20, fill = "slateblue", col = "cyan") +
  stat_function(fun = dnorm,
                args = list(mean = mean(dm1000$ldl, na.rm = TRUE),
                            sd = sd(dm1000$ldl, na.rm = TRUE)),
                col = "magenta", lwd = 1.5) +
  labs(title = "Density Function: dm1000 LDL")

p3 <- ggplot(dm1000, aes(x = ldl, y = "")) +
  geom_boxplot(fill = "slateblue", outlier.color = "slateblue") +
  labs(title = "Boxplot: dm1000 LDL", y = "")
```

Exploring `ldl` in `dm1000`







Silenced Warnings for previous plot

```
Warning: Removed 178 rows containing non-finite values (stat_qq).
Warning: Removed 178 rows containing non-finite values (stat_qq_line).
Warning: Removed 178 rows containing non-finite values (stat_bin).
Warning: Removed 178 rows containing non-finite values (stat_boxplot).
```

Numerical Summaries and Missing Data

```
1 summary(dm1000$ldl)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
   25.0    73.0    95.0   100.7   122.0   243.0     178
```

```
1 mosaic::favstats(~ ldl, data = dm1000)
```

```
Registered S3 method overwritten by 'mosaic':
  method                           from
  fortify.SpatialPolygonsDataFrame ggplot2
```

```
 min Q1 median  Q3 max     mean       sd   n missing
  25 73     95 122 243 100.7202 37.05353 822     178
```

- There, I could/should have silenced the message with `{r, message = FALSE}` in the code chunk header.

Subgroups of Interest

```
1 dm1000 |> tabyl(residence, insurance)
```

```
residence Medicaid Commercial Medicare Uninsured
  Suburbs      114         75      163         19
Cleveland      201        119      259         22
     <NA>       15          2       10          1
```

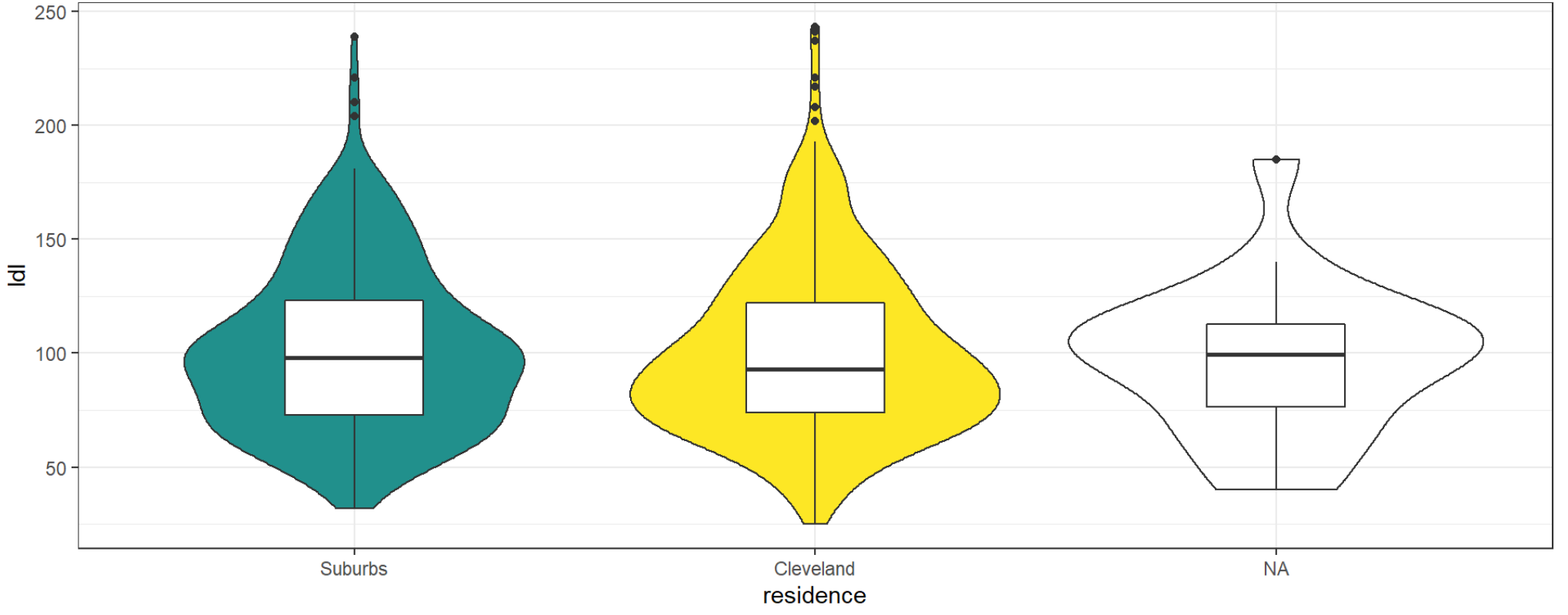
I don't like that `insurance` ordering.

```
1 dm1000 <- dm1000 |>
2   mutate(insurance = fct_relevel(insurance,
3                                  "Medicare", "Commercial", "Medicaid"))
4
5 dm1000 |> tabyl(residence, insurance)
```

```
residence Medicare Commercial Medicaid Uninsured
  Suburbs      163         75      114         19
Cleveland      259        119      201         22
     <NA>       10          2       15          1
```

LDL by Residence

```
ggplot(data = dm1000, aes(x = residence, y = ldl)) +
  geom_violin(aes(fill = residence)) +
  geom_boxplot(width = 0.3) +
  scale_fill_viridis_d(begin = 0.5, option = "D") +
  guides(fill = "none")
```



LDL by Residence, again

```
tempdat <- dm1000 |> filter(complete.cases(residence))

ggplot(data = tempdat, aes(x = residence, y = ldl)) +
  geom_violin(aes(fill = residence)) +
  geom_boxplot(width = 0.3) +
  scale_fill_viridis_d(begin = 0.5, option = "D") +
  guides(fill = "none")
```

Grouped Numerical Summaries

LDL by Residence

```
1 mosaic::favstats(ldl ~ residence, data = dm1000)
```

```
  residence min Q1 median  Q3 max     mean       sd   n missing
1   Suburbs  32 73     98 123 239 101.3814 36.51435 312      59
2 Cleveland  25 74     93 122 243 100.4347 37.57225 490     111
```

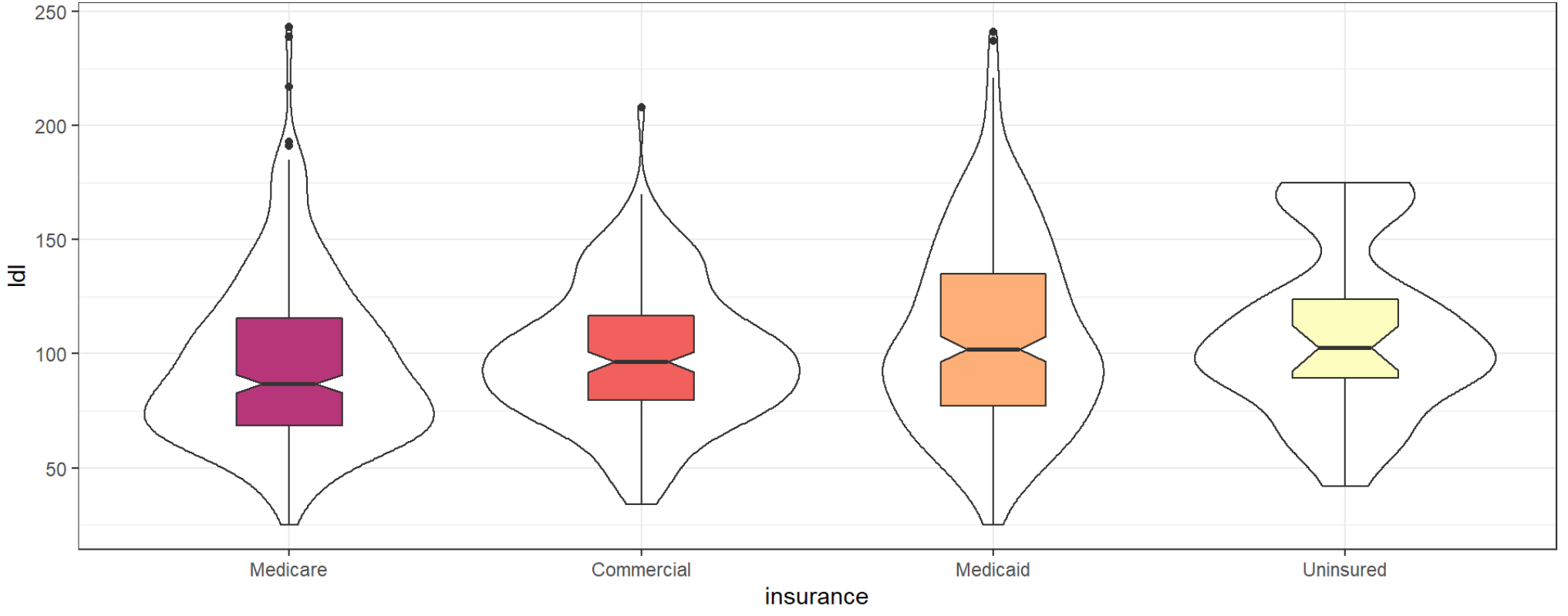
LDL by Insurance

```
1 mosaic::favstats(ldl ~ insurance, data = dm1000)
```

```
   insurance min    Q1 median    Q3 max      mean       sd   n missing
1   Medicare  25 68.50   87.0 115.5 243  95.32958 35.91871 355      77
2 Commercial  34 79.75   96.5 116.5 208  98.94643 29.67796 168      28
3   Medicaid  25 77.00  102.0 135.0 241 108.00372 41.31084 269      61
4  Uninsured  42 89.50  102.5 124.0 175 109.13333 36.57560  30      12
```

LDL by Insurance

```
ggplot(data = dm1000, aes(x = insurance, y = ldl)) +
  geom_violin() +
  geom_boxplot(aes(fill = insurance), width = 0.3, notch = TRUE) +
  scale_fill_viridis_d(begin = 0.5, option = "A") +
  guides(fill = "none")
```



Visualizing Categorical Data in `dm1000`

Categorical Variables from dm1000

```
1 dm_cat <- dm1000 |>
2   select(subject, sex, residence, insurance,
3          tobacco, race_ethnicity, statin, eye_exam)
4
5 dm_cat
```

```
# A tibble: 1,000 × 8
   subject sex    residence insurance  tobacco race_ethnicity     statin
eye_e…¹
   <chr>   <fct>  <fct>     <fct>      <fct>   <fct>                <dbl>
<dbl>
 1 M-0001  Female Suburbs   Medicaid   Current Non-Hispanic Black       1
1
 2 M-0002  Male   Cleveland Commercial Never   Non-Hispanic Black       0
1
 3 M-0003  Female Cleveland Medicare   Former  Hispanic or Latinx       1
0
 4 M-0004  Female Cleveland Medicaid   Never   Hispanic or Latinx       1
1
 5 M-0005  Female Suburbs   Medicare   Never   Non-Hispanic White       1
0
```

Codebook for `dm_cat`

- `sex` = Female or Male (no missing data)
- `insurance` = Medicare, Commercial, Medicaid, Uninsured
- `eye_exam` = 1 for eye examination in past year, else 0
- `statin` = 1 statin prescription in past year, else 0
- `race_ethnicity` = 4 levels (Hispanic or Latinx, Non-Hispanic White, Non-Hispanic Black, Non-Hispanic Asian)
- `residence` = 2 levels (Suburbs, Cleveland), some NA
- `tobacco` = 3 levels (Current, Former, Never), some NA

`summary()` check of levels

```
1 dm_cat |> select(-subject) |> summary()
```

```
    sex          residence        insurance      tobacco
Female:550   Suburbs  :371   Medicare  :432   Current:274
Male  :450   Cleveland:601   Commercial:196   Never  :343
             NA's     : 28   Medicaid  :330   Former :367
                             Uninsured : 42   NA's   : 16


          race_ethnicity     statin          eye_exam
Non-Hispanic Black:533    Min.   :0.000   Min.   :0.000
Hispanic or Latinx: 91    1st Qu.:1.000   1st Qu.:0.000
Non-Hispanic White:356    Median :1.000   Median :1.000
Non-Hispanic Asian: 20    Mean   :0.758   Mean   :0.562
                          3rd Qu.:1.000   3rd Qu.:1.000
                          Max.   :1.000   Max.   :1.000
```

- Do we need to treat `statin` and `eye_exam` differently?

Creating a `statin_f` factor

```
1  dm_cat <- dm_cat |>
2    mutate(statin_f = fct_recode(factor(statin),
3                                 "No Statin" = "0", "Statin" = "1"))
4
5  dm_cat |> count(statin, statin_f)
```

```
# A tibble: 2 × 3
  statin statin_f      n
   <dbl> <fct>     <int>
1      0 No Statin   242
2      1 Statin      758
```

Using `count` to create a tibble of counts

```
1 dm_cat |> count(tobacco)
```

```
# A tibble: 4 × 2
  tobacco     n
  <fct>   <int>
1 Current   274
2 Never     343
3 Former    367
4 <NA>       16
```

Tabulating a categorical variable

```
1 dm_cat |> tabyl(tobacco) |>
2   adorn_pct_formatting() |>
3   adorn_totals()
```

```
tobacco    n percent valid_percent
Current  274   27.4%         27.8%
  Never  343   34.3%         34.9%
 Former  367   36.7%         37.3%
   <NA>   16    1.6%             -
  Total 1000       -             -
```

- Does this order make sense?

Changing Order of `tobacco` levels

```
1  dm_cat <- dm_cat |>
2    mutate(tobacco = fct_relevel(tobacco, "Current", "Former"))
3
4  dm_cat |> tabyl(tobacco)
```

```
tobacco   n percent valid_percent
Current 274   0.274     0.2784553
 Former 367   0.367     0.3729675
  Never 343   0.343     0.3485772
   <NA>  16   0.016            NA
```

- Does this order make more sense?
- `fct_relevel()` is one of many useful tools in `forcats`.

Using the `forcats` package

In addition to `fct_relevel()` and `fct_recode()`, ...

- `fct_reorder()`: reordering a factor by another variable
- `fct_infreq()`: reordering a factor by its frequency of values
- `fct_lump()`: collapsing least frequent values into "other"
- and several others

`forcats` references

1. I use the `forcats` tools frequently in our Course Notes
2. https://forcats.tidyverse.org/ forcats web page, especially the vignette
3. RStudio Cheat Sheet on Factors with forcats (pdf)
4. R for Data Science on Factors

Using gt to make a table prettier

```
dm_cat |>
  tabyl(tobacco) |>
  adorn_pct_formatting() |>
  adorn_totals() |>
  gt() |>
  tab_header(title = "Tobacco Status from dm1000")
```

Tobacco Status from dm1000

tobacco	n	percent	valid_percent
Current	274	27.4%	27.8%
Former	367	36.7%	37.3%
Never	343	34.3%	34.9%
NA	16	1.6%	-
Total	1000	-	-

- https://gt.rstudio.com/ provides an amazing array of options.

gtExtras lets us build 538-style tables

```
dm_cat |>
  tabyl(tobacco) |>
  adorn_pct_formatting() |>
  adorn_totals() |>
  gt() |>
  gt_theme_538() |>
  tab_header(title = "Table styled like 538")
```

Table styled like 538

TOBACCO	N	PERCENT	VALID_PERCENT
Current	274	27.4%	27.8%
Former	367	36.7%	37.3%
Never	343	34.3%	34.9%
NA	16	1.6%	-
Total	1000	-	-

`gtExtras` lets us build NYT-style tables

```
dm_cat |> tabyl(tobacco) |> adorn_pct_formatting() |> adorn_totals() |>
  gt() |>
  gt_theme_nytimes() |>
  tab_header(title = "Table styled like the New York Times")
```

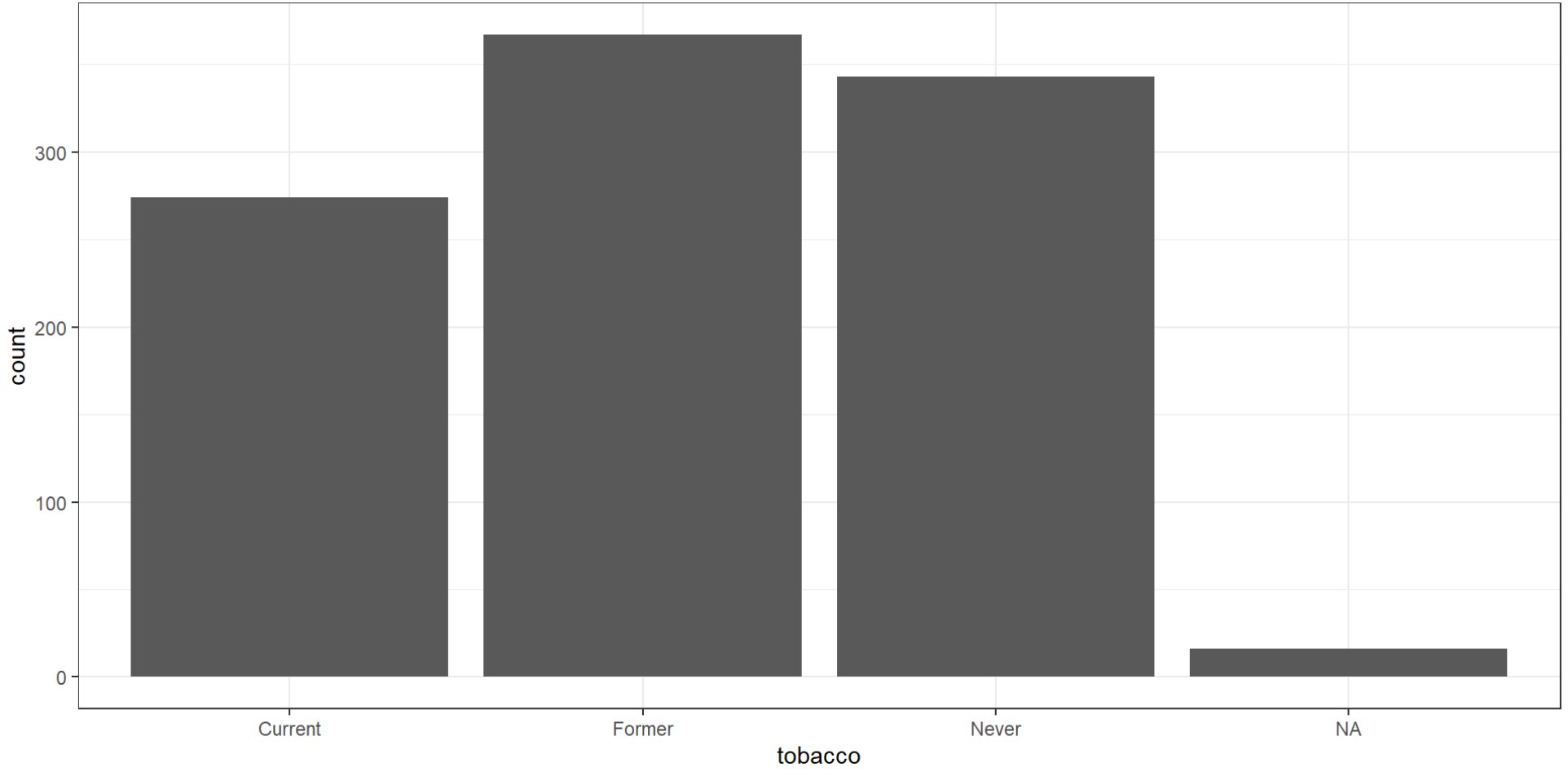
Table styled like the New York Times

TOBACCO	N	PERCENT	VALID_PERCENT
Current	274	27.4%	27.8%
Former	367	36.7%	37.3%
Never	343	34.3%	34.9%
NA	16	1.6%	-
Total	1000	-	-

- There's also a `gt_theme_espn()` and several others.

Using `geom_bar` to show a distribution

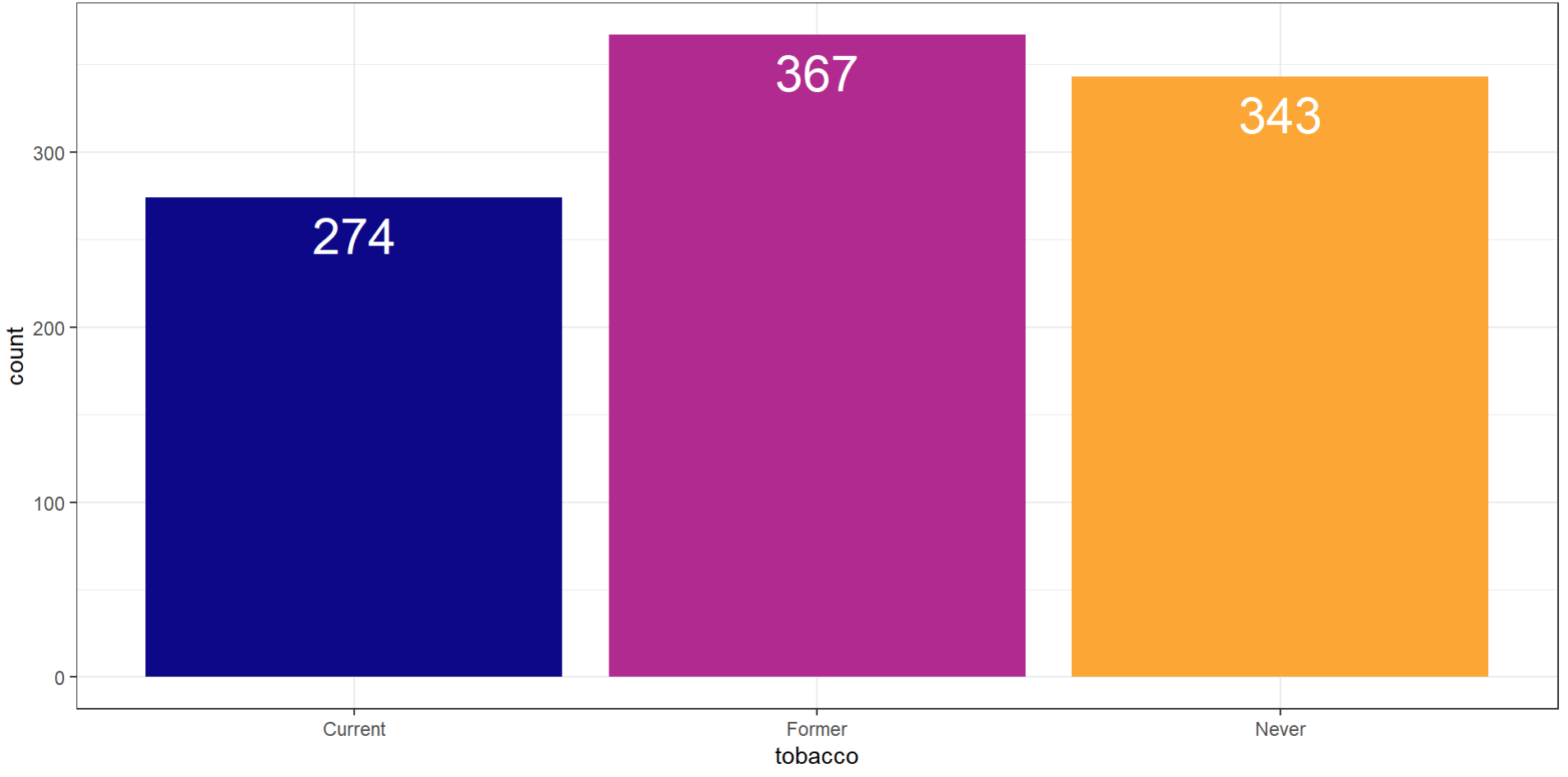
```
1 ggplot(dm_cat, aes(x = tobacco)) +
2   geom_bar()
```



Augmenting the `geom_bar` result

```
tempdat <- dm_cat |> filter(complete.cases(tobacco))

ggplot(data = tempdat, aes(x = tobacco, fill = tobacco)) +
  geom_bar() +
  geom_text(aes(label = ..count..), stat = "count",
            vjust = 1.5, col = "white", size = 8) +
  scale_fill_viridis_d(option = "C", end = 0.8) +
  guides(fill = "none")
```

Augmenting the `geom_bar` result



Using `count` to create a tibble of counts

```
1 dm_cat |>
2   count(statin, tobacco)
```

```
# A tibble: 8 × 3
  statin tobacco     n
   <dbl> <fct>   <int>
1      0 Current    67
2      0 Former     80
3      0 Never      92
4      0 <NA>        3
5      1 Current   207
6      1 Former    287
7      1 Never     251
8      1 <NA>       13
```

```
1 dm_cat |>
2   count(insurance, residence)
```

```
# A tibble: 12 × 3
   insurance  residence     n
   <fct>      <fct>     <int>
 1 Medicare   Suburbs     163
 2 Medicare   Cleveland   259
 3 Medicare   <NA>         10
 4 Commercial Suburbs      75
 5 Commercial Cleveland   119
 6 Commercial <NA>          2
 7 Medicaid   Suburbs     114
 8 Medicaid   Cleveland   201
 9 Medicaid   <NA>         15
10 Uninsured  Suburbs      19
11 Uninsured  Cleveland    22
12 Uninsured  <NA>          1
```

Cross-Tabulations

```
1 dm_cat |> tabyl(insurance, residence)
```

```
  insurance Suburbs Cleveland NA_
   Medicare     163       259  10
 Commercial      75       119   2
   Medicaid     114       201  15
 Uninsured       19        22   1
```

```
1 dm_cat |>
2   filter(complete.cases(insurance, residence)) |>
3   tabyl(insurance, residence) |>
4   adorn_totals(where = c("row", "col")) |>
5   gt()
```

insurance	Suburbs	Cleveland	Total
Medicare	163	259	422
Commercial	75	119	194
Medicaid	114	201	315
Uninsured	19	22	41
Total	371	601	972

Were suburban residents more likely to have a statin prescription?

```
1 dm_cat |>
2   filter(complete.cases(statin, residence)) |>
3   tabyl(residence, statin)
```

```
residence   0   1
  Suburbs  77 294
Cleveland 157 444
```

Revise statin order, add percentages

```
dm_cat |> filter(complete.cases(statin, residence)) |>
  mutate(statin = fct_relevel(factor(statin), "1", "0")) |>
  tabyl(residence, statin)
```

```
residence   1   0
  Suburbs 294  77
Cleveland 444 157
```

```
dm_cat |> filter(complete.cases(statin, residence)) |>
  mutate(statin = fct_relevel(factor(statin), "1", "0")) |>
  tabyl(residence, statin) |>
  adorn_percentages(denom = "row") |>
  adorn_pct_formatting()
```

```
residence     1     0
  Suburbs 79.2% 20.8%
Cleveland 73.9% 26.1%
```

Create using `table` instead

```
tempdat1 <- dm_cat |>
  filter(complete.cases(statin, residence)) |>
  mutate(statin = fct_relevel(factor(statin), "1", "0"))

tab1 <- table(tempdat1$residence, tempdat1$statin)

tab1
```

```
           1   0
Suburbs   294  77
Cleveland 444 157
```

Assess 2x2 table

```
1 twoby2(tab1)  # twoby2() is part of the Epi package
```

```
2 by 2 table analysis:
------------------------------------------------------
Outcome   : 1
Comparing : Suburbs vs. Cleveland

            1   0    P(1) 95% conf. interval
Suburbs   294  77  0.7925    0.7482   0.8307
Cleveland 444 157  0.7388    0.7022   0.7723

                                  95% conf. interval
            Relative Risk: 1.0727    0.9996   1.1510
        Sample Odds Ratio: 1.3501    0.9903   1.8407
Conditional MLE Odds Ratio: 1.3497    0.9805   1.8679
    Probability difference: 0.0537   -0.0018   0.1065

                Exact P-value: 0.0628
```

A three-by-four two-way table

```
1 dm_cat |> filter(complete.cases(tobacco, insurance)) |>
2   tabyl(tobacco, insurance) |>
3   adorn_totals(where = c("row", "col"))
```

```
tobacco Medicare Commercial Medicaid Uninsured Total
Current       99          44      118         13   274
 Former      183          70      103         11   367
  Never      140          80      105         18   343
  Total      422         194      326         42   984
```

- 3 rows, 4 columns: hence, this is a 3 x 4 table
- It's a two-way table, because we are studying the association of two variables (`tobacco` and `insurance`)
- Compare insurance percentages by tobacco group?

Insurance rates by tobacco group

```
dm_cat |> filter(complete.cases(tobacco, insurance)) |>
  tabyl(tobacco, insurance) |>
  adorn_percentages(denominator = "row") |>
  adorn_totals(where = "col") |> kbl(digits = 3)
```

tobacco	Medicare	Commercial	Medicaid	Uninsured	Total
Current	0.361	0.161	0.431	0.047	1
Former	0.499	0.191	0.281	0.030	1
Never	0.408	0.233	0.306	0.052	1

- These are **proportions** and not percentages.
- Proportions fall between 0 and 1: multiply by 100 for percentages.

Insurance rates by tobacco group?

```
tempdat2 <- dm_cat |>
  filter(complete.cases(tobacco, insurance))

tab2 <- table(tempdat2$tobacco, tempdat2$insurance)

tab2
```

```
         Medicare Commercial Medicaid Uninsured
Current        99         44      118        13
Former        183         70      103        11
Never         140         80      105        18
```

```
chisq.test(tab2)
```

```
    Pearson's Chi-squared test

data:  tab2
X-squared = 25.592, df = 6, p-value = 0.0002651
```

Using `count` for three variables

```
1 dm_cat |> count(sex, statin, residence)
```

```
# A tibble: 12 × 4
   sex    statin residence     n
   <fct>   <dbl> <fct>     <int>
 1 Female      0 Suburbs      42
 2 Female      0 Cleveland    87
 3 Female      0 <NA>          4
 4 Female      1 Suburbs     160
 5 Female      1 Cleveland   245
 6 Female      1 <NA>         12
 7 Male        0 Suburbs      35
 8 Male        0 Cleveland    70
 9 Male        0 <NA>          4
10 Male        1 Suburbs     134
11 Male        1 Cleveland   199
12 Male        1 <NA>          8
```

A three-way table via `tabyl`

```
dm_cat |>
  filter(complete.cases(statin, residence, sex)) |>
  tabyl(statin, residence, sex) |>
  adorn_totals(where = c("row", "col")) |>
  adorn_title()
```

```
$Female
        residence
 statin   Suburbs Cleveland Total
      0        42        87   129
      1       160       245   405
  Total       202       332   534

$Male
        residence
 statin   Suburbs Cleveland Total
      0        35        70   105
      1       134       199   333
  Total       169       269   438
```

Flattening a three-way table

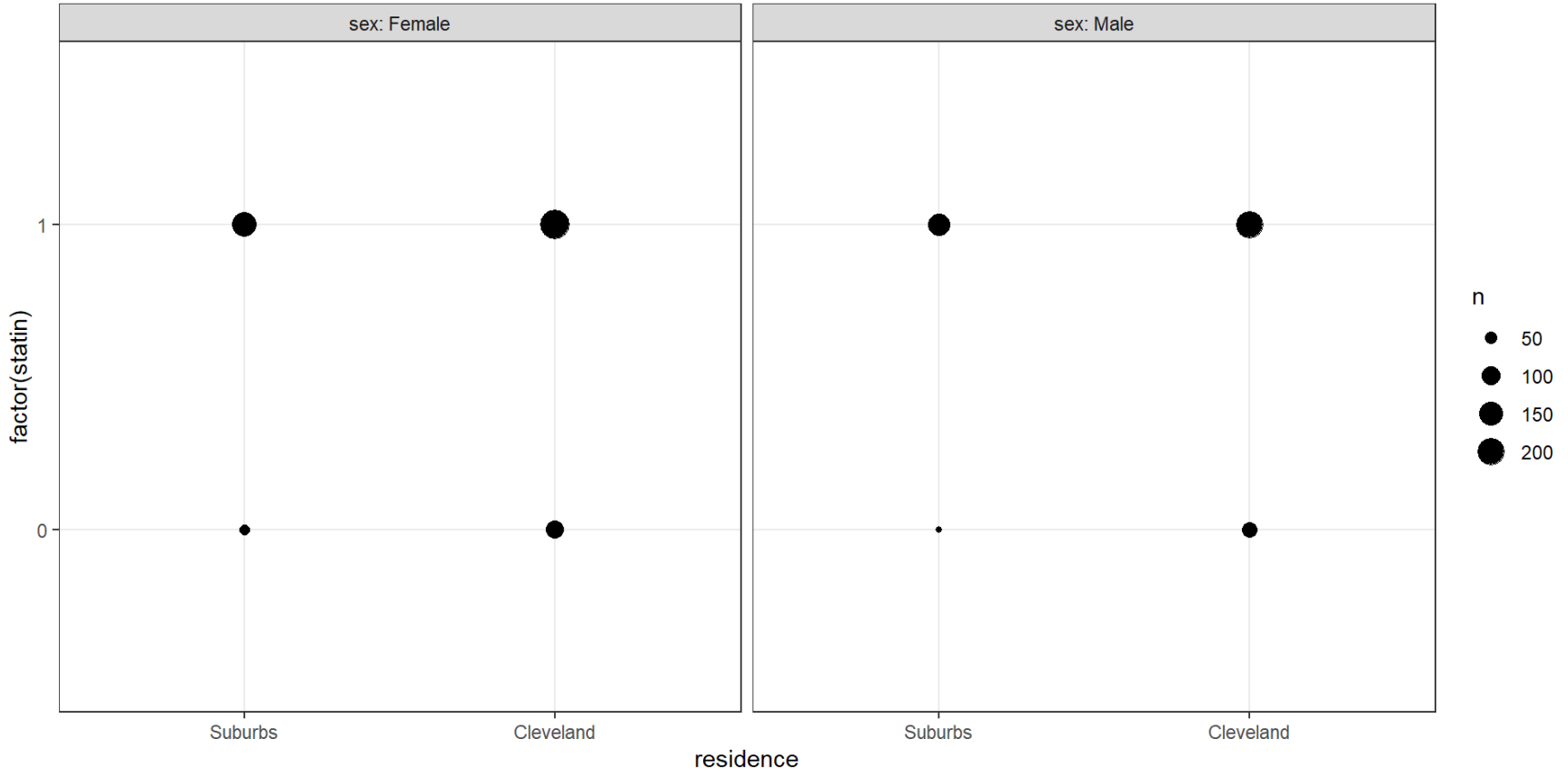
```
1 ftable(dm_cat$sex, dm_cat$residence, dm_cat$statin)
```

```
                    0   1
Female Suburbs     42 160
       Cleveland   87 245
Male   Suburbs     35 134
       Cleveland   70 199
```

- Note that `ftable()` excludes the missing `residence` values by default.

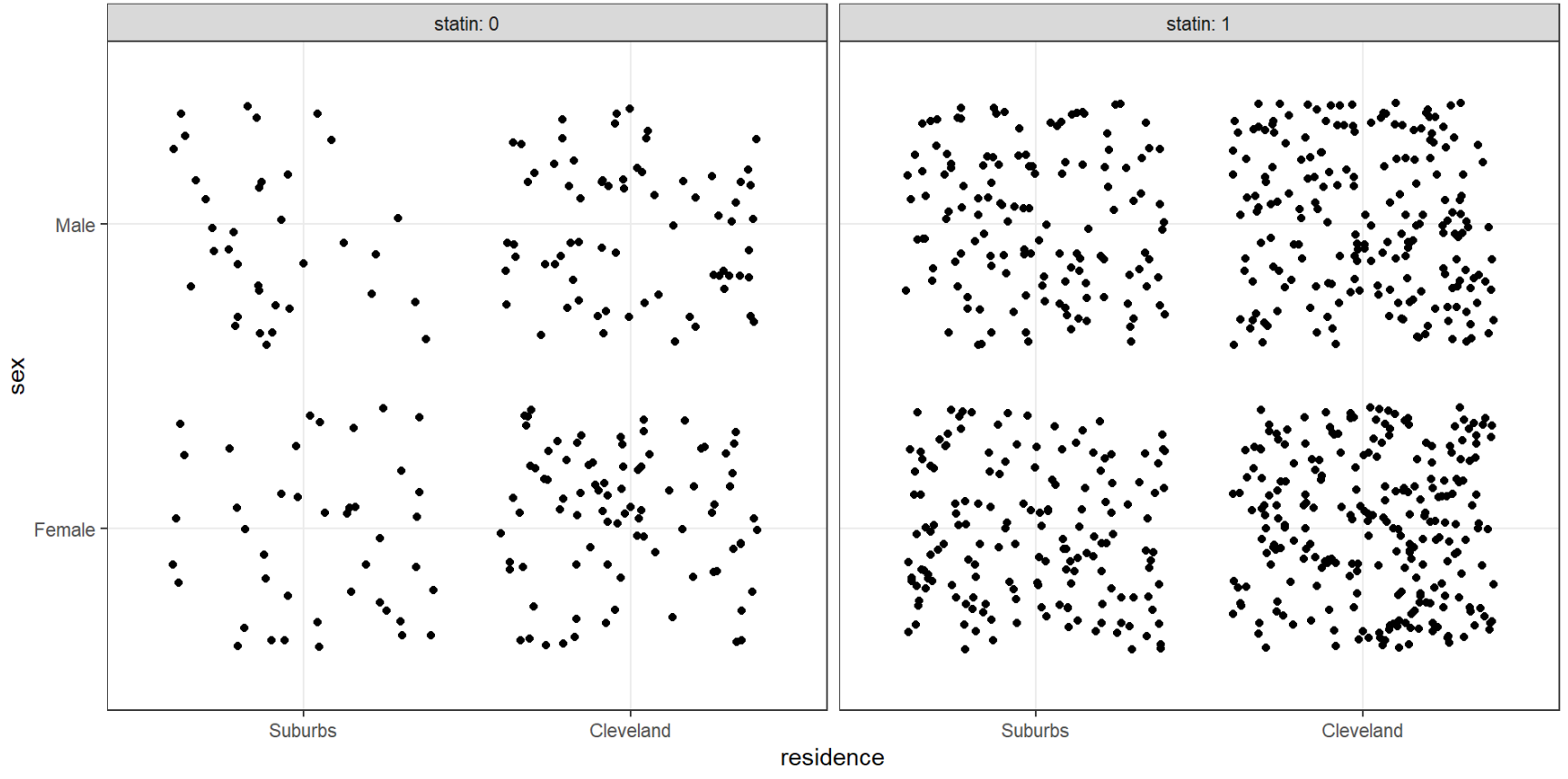
Plotting a 3-Way Table (Counts)

```
ggplot(data = filter(dm_cat, complete.cases(residence)),
       aes(x = residence, y = factor(statin))) +
   geom_count() +
   facet_wrap(~ sex, labeller = "label_both")
```



Plotting a 3-Way Table (Jitter)

```
ggplot(data = filter(dm_cat, complete.cases(residence)),
       aes(x = residence, y = sex)) +
   geom_jitter() +
   facet_wrap(~ statin, labeller = "label_both")
```



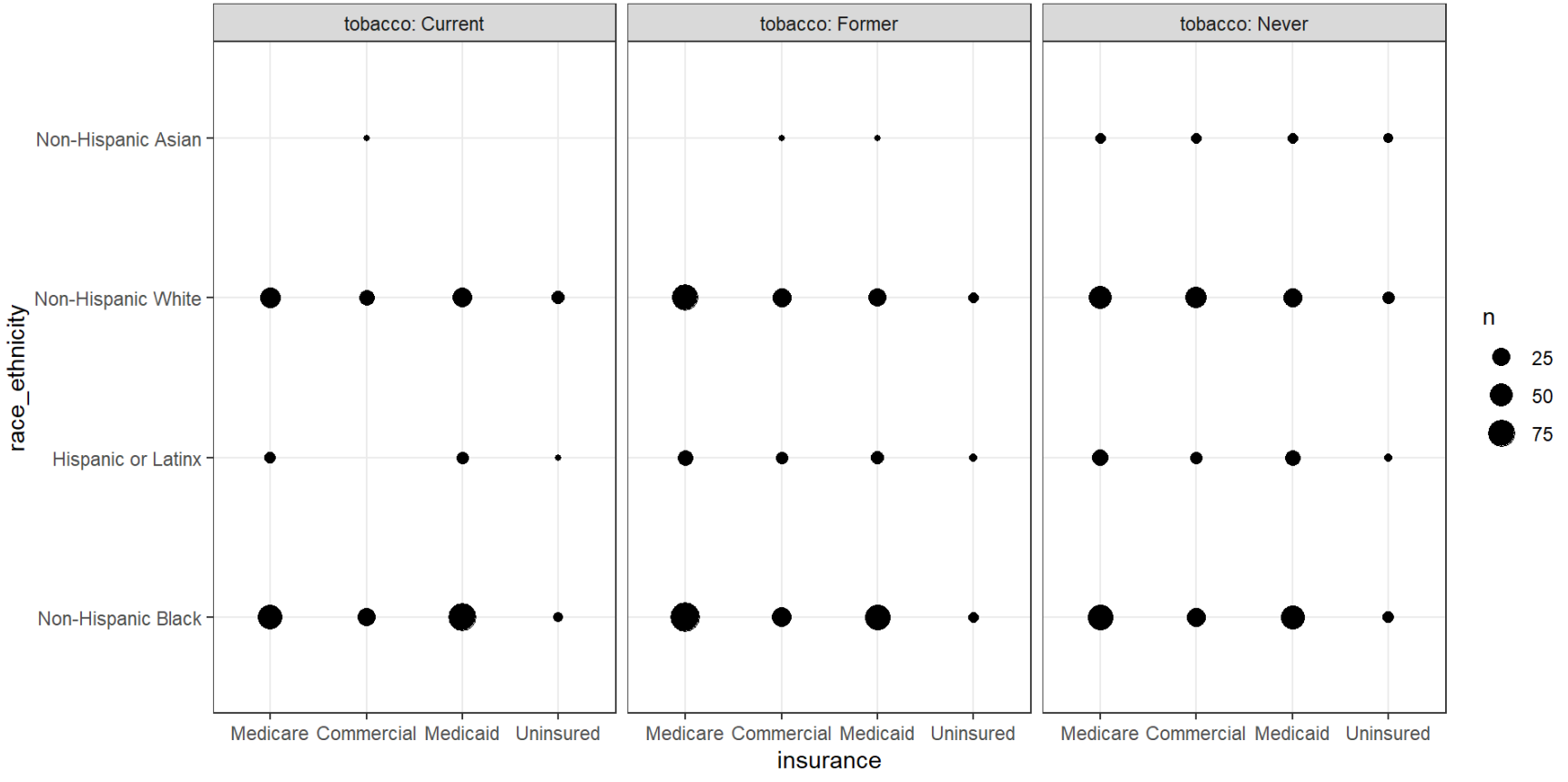
Multi-categorical 3-Way Table

```
1 dm_cat |>
2   filter(complete.cases(insurance, race_ethnicity, tobacco)) |>
3   tabyl(race_ethnicity, insurance, tobacco) |>
4   adorn_totals(where = c("row", "col")) |>
5   adorn_title()
```

```
$Current
                   insurance
     race_ethnicity  Medicare Commercial Medicaid Uninsured Total
 Non-Hispanic Black        58         26        80         3   167
 Hispanic or Latinx         6          0         7         1    14
 Non-Hispanic White        35         17        31         9    92
 Non-Hispanic Asian         0          1         0         0     1
              Total        99         44       118        13   274

$Former
                   insurance
     race_ethnicity  Medicare Commercial Medicaid Uninsured Total
 Non-Hispanic Black        96         34        66         5   201
 Hispanic or Latinx        15          7         9         2    33
 Non-Hispanic White        72         28        27         4   131
```

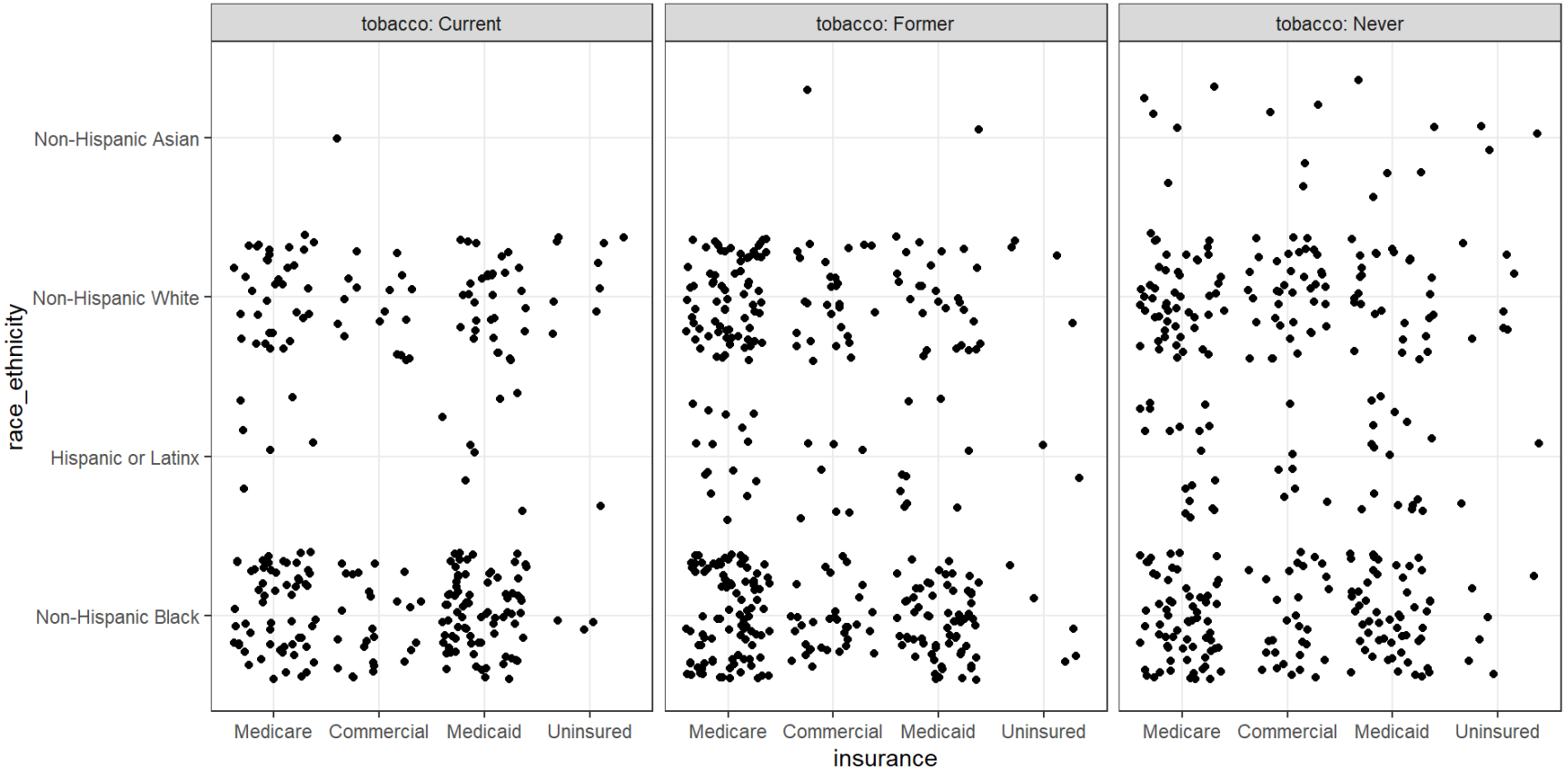
Multi-categorical 3-Way Counts

```
ggplot(data = filter(dm_cat, complete.cases(tobacco)),
       aes(x = insurance, y = race_ethnicity)) +
   geom_count() +
   facet_wrap(~ tobacco, labeller = "label_both")
```



Multi-categorical 3-Way Jitter Plot

```
ggplot(data = filter(dm_cat, complete.cases(tobacco)),
       aes(x = insurance, y = race_ethnicity)) +
   geom_jitter() +
   facet_wrap(~ tobacco, labeller = "label_both")
```



RStudio Cheat Sheets

https://www.rstudio.com/resources/cheatsheets/

- Data visualization with ggplot2 Cheatsheet shown on next two slides…

Other cheatsheets I use a lot include:

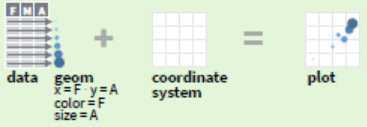
- Data transformation with dplyr
- Data import with readr, readxl, and googlesheets4
- Factors with forcats
- Dynamic documents with rmarkdown

Data visualization with ggplot2 : : CHEAT SHEET

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and **geoms**—visual marks that represent data points.

To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

required

```
ggplot (data = <DATA>) +
<GEOM_FUNCTION>(mapping = aes(<MAPPINGS>),
 stat = <STAT>, position = <POSITION>) +
<COORDINATE_FUNCTION> +
<FACET_FUNCTION> +
<SCALE_FUNCTION> +
<THEME_FUNCTION>
```

Not required, sensible defaults supplied

ggplot(data = mpg, **aes**(x = cty, y = hwy)) Begins a plot that you finish by adding layers to. Add one geom function per layer.

last_plot() Returns the last plot.

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

Aes

Common aesthetic values.

color and **fill** - string ("red", "#RRGGBB")

linetype - integer or string (0 = "blank", 1 = "solid", 2 = "dashed", 3 = "dotted", 4 = "dotdash", 5 = "longdash", 6 = "twodash")

lineend - string ("round", "butt", or "square")

linejoin - string ("round", "mitre", or "bevel")

size - integer (line width in mm)

shape - integer/shape name or a single character ("a")

RStudio

Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

GRAPHICAL PRIMITIVES

```
a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))
```

a + geom_blank() and **a + expand_limits()**
Ensure limits include values across all plots.

b + geom_curve(aes(yend = lat + 1, xend = long + 1), curvature = 1) - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend = "butt", linejoin = "round", linemitre = 1)
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(alpha = 50)) - x, y, alpha, color, fill, group, subgroup, linetype, size

b + geom_rect(aes(xmin = long, ymin = lat, xmax = long + 1, ymax = lat + 1)) - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin = unemploy - 900, ymax = unemploy + 900)) - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept = 0, slope = 1))
b + geom_hline(aes(yintercept = lat))
b + geom_vline(aes(xintercept = long))

b + geom_segment(aes(yend = lat + 1, xend = long + 1))
b + geom_spoke(aes(angle = 1:1155, radius = 1))

ONE VARIABLE continuous

```
c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)
```

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian")
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly()
x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5)
x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy))
x, y, alpha, color, fill, linetype, size, weight

discrete

```
d <- ggplot(mpg, aes(fl))
```

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

both continuous

```
e <- ggplot(mpg, aes(cty, hwy))
```

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1) - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_point()
x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile()
x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl")
x, y, alpha, color, linetype, size

e + geom_smooth(method = lm)
x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1) - x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

one discrete, one continuous

```
f <- ggplot(mpg, aes(class, hwy))
```

f + geom_col()
x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot()
x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center")
x, y, alpha, color, fill, group

f + geom_violin(scale = "area")
x, y, alpha, color, fill, group, linetype, size, weight

both discrete

```
g <- ggplot(diamonds, aes(cut, color))
```

g + geom_count()
x, y, alpha, color, fill, shape, size, stroke

e + geom_jitter(height = 2, width = 2)
x, y, alpha, color, fill, shape, size

continuous bivariate distribution

```
h <- ggplot(diamonds, aes(carat, price))
```

h + geom_bin2d(binwidth = c(0.25, 500))
x, y, alpha, color, fill, linetype, size, weight

h + geom_density_2d()
x, y, alpha, color, group, linetype, size

h + geom_hex()
x, y, alpha, color, fill, size

continuous function

```
i <- ggplot(economics, aes(date, unemploy))
```

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error

```
df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit - se, ymax = fit + se))
```

j + geom_crossbar(fatten = 2) - x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar() - x, ymax, ymin, alpha, color, group, linetype, size, width
Also **geom_errorbarh**().

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange() - x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

```
data <- data.frame(murder = USArrests$Murder,
                   state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))
```

k + geom_map(aes(map_id = state), map = map) + **expand_limits**(x = map$long, y = map$lat)
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

```
seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2)); l <- ggplot(seals, aes(long, lat))
```

l + geom_contour(aes(z = z))
x, y, z, alpha, color, group, linetype, size, weight

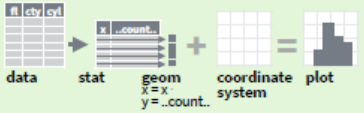
l + geom_contour_filled(aes(fill = z))
x, y, alpha, color, fill, group, linetype, size, subgroup

l + geom_raster(aes(fill = z), hjust = 0.5, vjust = 0.5, interpolate = FALSE)
x, y, alpha, fill

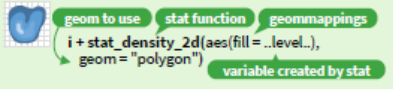
l + geom_tile(aes(fill = z))
x, y, alpha, color, fill, linetype, size, width

Stats An alternative way to build a layer.

A stat builds new variables to plot (e.g., count, prop).



Visualize a stat by changing the default stat of a geom function, **geom_bar(stat="count")** or by using a stat function, **stat_count(geom="bar")**, which calls a default geom to make a layer (equivalent to a geom function). Use **..name..** syntax to map stat variables to aesthetics.



c + stat_bin(binwidth = 1, boundary = 10)
x, y | ..count.., ..ncount.., ..density.., ..ndensity..

c + stat_count(width = 1) x, y | ..count.., ..prop..

c + stat_density(adjust = 1, kernel = "gaussian")
x, y | ..count.., ..density.., ..scaled..

e + stat_bin_2d(bins = 30, drop = T)
x, y, fill | ..count.., ..density..

e + stat_bin_hex(bins = 30) x, y, fill | ..count.., ..density..

e + stat_density_2d(contour = TRUE, n = 100)
x, y, color, size | ..level..

e + stat_ellipse(level = 0.95, segments = 51, type = "t")

l + stat_contour(aes(z = z)) x, y, z, order | ..level..

l + stat_summary_hex(aes(z = z), bins = 30, fun = max)
x, y, z, fill | ..value..

l + stat_summary_2d(aes(z = z), bins = 30, fun = mean)
x, y, z, fill | ..value..

f + stat_boxplot(coef = 1.5)
x, y | ..lower.., ..middle.., ..upper.., ..width.. , ..ymin.., ..ymax..

f + stat_ydensity(kernel = "gaussian", scale = "area") x, y
| ..density.., ..scaled.., ..count.., ..n.., ..violinwidth.., ..width..

e + stat_ecdf(n = 40) x, y | ..x.., ..y..

e + stat_quantile(quantiles = c(0.1, 0.9),
formula = y ~ log(x), method = "rq") x, y | ..quantile..

e + stat_smooth(method = "lm", formula = y ~ x, se = T,
level = 0.95) x, y | ..se.., ..x.., ..y.., ..ymin.., ..ymax..

ggplot() + xlim(-5, 5) + **stat_function**(fun = dnorm,
n = 20, geom = "point") x | ..x.., ..y..

ggplot() + stat_qq(aes(sample = 1:100))
x, y, **sample** | ..sample.., ..theoretical..

e + stat_sum() x, y, **size** | ..n.., ..prop..

e + stat_summary(fun.data = "mean_cl_boot")

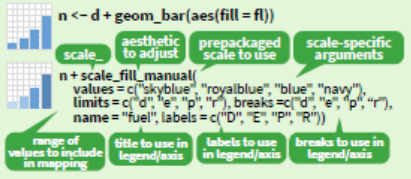
h + stat_summary_bin(fun = "mean", geom = "bar")

e + stat_identity()

e + stat_unique()

Scales Override defaults with scales package.

Scales map data values to the visual values of an aesthetic. To change a mapping, add a new scale.



GENERAL PURPOSE SCALES

Use with most aesthetics

scale_*_continuous() - Map cont' values to visual ones.
scale_*_discrete() - Map discrete values to visual ones.
scale_*_binned() - Map continuous values to discrete bins.
scale_*_identity() - Use data values as visual ones.
scale_*_manual(values = c()) - Map discrete values to manually chosen visual ones.
scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - Treat data values as dates.
scale_*_datetime() - Treat data values as date times. Same as scale_*_date(). See ?strptime for label formats.

X & Y LOCATION SCALES

Use with x or y aesthetics (x shown here)

scale_x_log10() - Plot x on log10 scale.
scale_x_reverse() - Reverse the direction of the x axis.
scale_x_sqrt() - Plot x on square root scale.

COLOR AND FILL SCALES (DISCRETE)

n + scale_fill_brewer(palette = "Blues")
For palette choices:
RColorBrewer::display.brewer.all()

n + scale_fill_grey(start = 0.2,
end = 0.8, na.value = "red")

COLOR AND FILL SCALES (CONTINUOUS)

o <- c + geom_dotplot(aes(fill = ..x..))

o + scale_fill_distiller(palette = "Blues")

o + scale_fill_gradient(low="red", high="yellow")

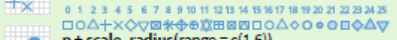
o + scale_fill_gradient2(low = "red", high = "blue",
mid = "white", midpoint = 25)

o + scale_fill_gradientn(colors = topo.colors(6))
Also: rainbow(), heat.colors(), terrain.colors(),
cm.colors(), RColorBrewer::brewer.pal()

SHAPE AND SIZE SCALES

p <- e + geom_point(aes(shape = fl, size = cyl))

p + scale_shape() + **scale_size()**
p + scale_shape_manual(values = c(3:7))



p + scale_radius(range = c(1,6))
p + scale_size_area(max_size = 6)

Coordinate Systems

r <- d + geom_bar()

r + coord_cartesian(xlim = c(0, 5)) - xlim, ylim
The default cartesian coordinate system.

r + coord_fixed(ratio = 1/2)
ratio, xlim, ylim - Cartesian coordinates with fixed aspect ratio between x and y units.

ggplot(mpg, aes(y = fl)) + **geom_bar()**
Flip cartesian coordinates by switching x and y aesthetic mappings.

r + coord_polar(theta = "x", direction=1)
theta, start, direction - Polar coordinates.

r + coord_trans(y = "sqrt") - x, y, xlim, ylim
Transformed cartesian coordinates. Set xtrans and ytrans to the name of a window function.

π + coord_quickmap()
π + coord_map(projection = "ortho", orientation = c(41, -74, 0)) - projection, xlim, ylim
Map projections from the mapproj package (mercator (default), azequalarea, lagrange, etc.).

Position Adjustments

Position adjustments determine how to arrange geoms that would otherwise occupy the same space.

s <- ggplot(mpg, aes(fl, fill = drv))

s + geom_bar(position = "dodge")
Arrange elements side by side.

s + geom_bar(position = "fill")
Stack elements on top of one another, normalize height.

e + geom_point(position = "jitter")
Add random noise to X and Y position of each element to avoid overplotting.

e + geom_label(position = "nudge")
Nudge labels away from points.

s + geom_bar(position = "stack")
Stack elements on top of one another.

Each position adjustment can be recast as a function with manual **width** and **height** arguments:
s + geom_bar(position = position_dodge(width = 1))

Themes

r + theme_bw()
White background with grid lines.

r + theme_gray()
Grey background (default theme).

r + theme_dark()
Dark for contrast.

r + theme_classic()

r + theme_light()

r + theme_linedraw()

r + theme_minimal()
Minimal theme.

r + theme_void()
Empty theme.

r + theme() Customize aspects of the theme such as axis, legend, panel, and facet properties.
r + ggtitle("Title") + theme(plot.title.position = "plot")
r + theme(panel.background = element_rect(fill = "blue"))

Faceting

Facets divide a plot into subplots based on the values of one or more discrete variables.

t <- ggplot(mpg, aes(cty, hwy)) + geom_point()

t + facet_grid(**cols** = vars(fl))
Facet into columns based on fl.

t + facet_grid(**rows** = vars(year))
Facet into rows based on year.

t + facet_grid(**rows** = vars(year), **cols** = vars(fl))
Facet into both rows and columns.

t + facet_wrap(vars(fl))
Wrap facets into a rectangular layout.

Set **scales** to let axis limits vary across facets.

t + facet_grid(**rows** = vars(drv), **cols** = vars(fl),
scales = "free")
x and y axis limits adjust to individual facets:
"free_x" - x axis limits adjust
"free_y" - y axis limits adjust

Set **labeller** to adjust facet label:

t + facet_grid(**cols** = vars(fl), **labeller** = **label_both**)

fl: c	fl: d	fl: e	fl: p	fl: r

t + facet_grid(**rows** = vars(fl),
labeller = **label_bquote**(alpha ^ .(fl)))

α^c	α^d	α^e	α^p	α^r

Labels and Legends

Use **labs()** to label the elements of your plot.

t + labs(x = "New x axis label", y = "New y axis label",
title = "Add a title above the plot",
subtitle = "Add a subtitle below title",
caption = "Add a caption below plot",
alt = "Add alt text to the plot",
<AES> = "New <AES> legend title")

t + annotate(geom = "text", x = 8, y = 9, label = "A")
Places a geom with manually selected aesthetics.

p + guides(x = guide_axis(n.dodge = 2)) Avoid crowded or overlapping labels with guide_axis(n.dodge or angle).

n + guides(fill = "none") Set legend type for each aesthetic: colorbar, legend, or none (no legend).

n + theme(legend.position = "bottom")
Place legend at "bottom", "top", "left", or "right".

n + scale_fill_discrete(name = "Title",
labels = c("A", "B", "C", "D", "E"))
Set legend title and labels with a scale function.

Zooming

Without clipping (preferred):
t + coord_cartesian(xlim = c(0, 100), ylim = c(10, 20))

With clipping (removes unseen data points):
t + xlim(0, 100) + **ylim**(10, 20)

t + scale_x_continuous(limits = c(0, 100)) +
scale_y_continuous(limits = c(0, 100))

Session Information

```
1 sessionInfo()
```

```
R version 4.2.1 (2022-06-23 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 22000)

Matrix products: default

locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base
```