Gov 50: 10. Summarizing Bivariate Relationships

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Roadmap

1. Z-scores and standardization
2. Correlation
3. Writing our own functions

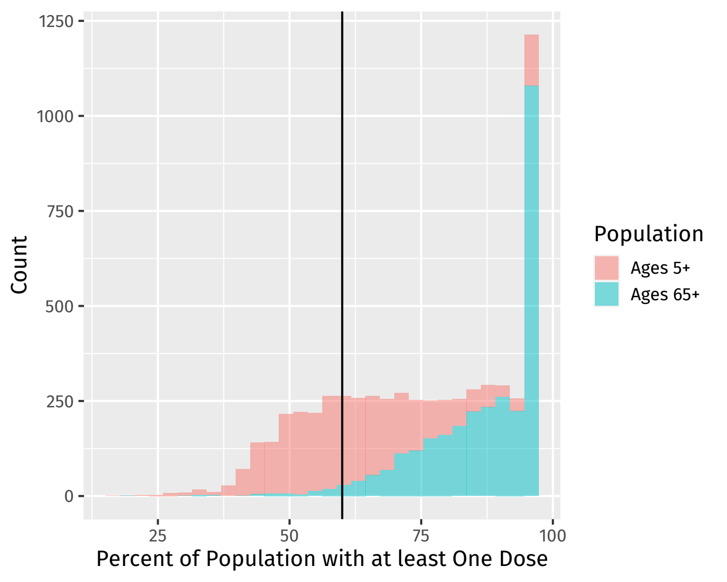
1/ Z-scores and standardization

COVID vaccination rates and votes

```r
library(tidyverse)
library(gov50data)
covid_votes
```

```
## # A tibble: 3,114 x 8
##    fips  county         state one_d~1 one_d~2 boost~3 dem_p~4
##    <chr> <chr>          <chr>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 26039 Crawford Cou~ MI       55.7    77.3   31.2      43.8
##  2 40015 Caddo County  OK       83.3    95     30.3      46.4
##  3 17007 Boone County  IL       71.1    94.5   35.1      41.8
##  4 12055 Highlands Co~ FL       68.9    93.7   24.7      40.3
##  5 34029 Ocean County  NJ       71      95     32.1      47.2
##  6 01067 Henry County  AL       58.5    85.5   18.2      40.1
##  7 27037 Dakota County MN       81      95     49.5      46.9
##  8 27115 Pine County   MN       56.5    85     31.7      47.0
##  9 51750 Radford city  VA       41.5    73.8    1.79     46.4
## 10 22009 Avoyelles Pa~ LA       59.7    80.1   21.9      45.7
## # ... with 3,104 more rows, 1 more variable:
## #   dem_pct_2020 <dbl>, and abbreviated variable names
## #   1: one_dose_5plus_pct, 2: one_dose_65plus_pct,
## #   3: booster_5plus_pct, 4: dem_pct_2000
```

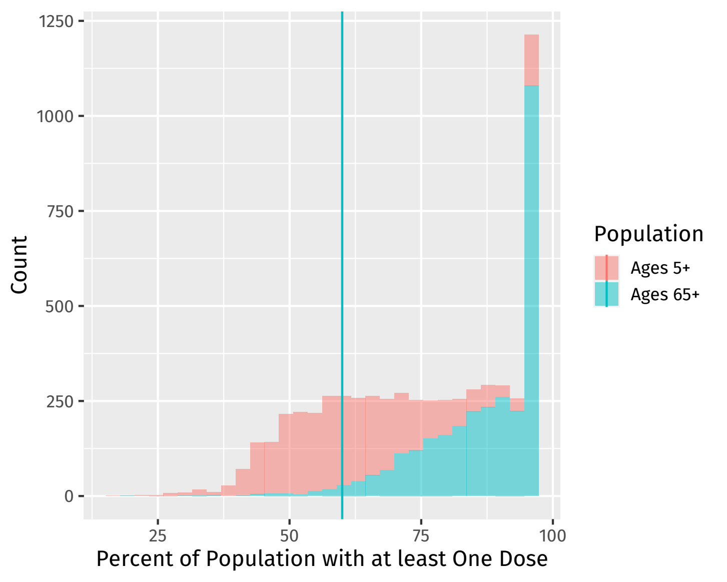
Is 60% vaccinated a lot?



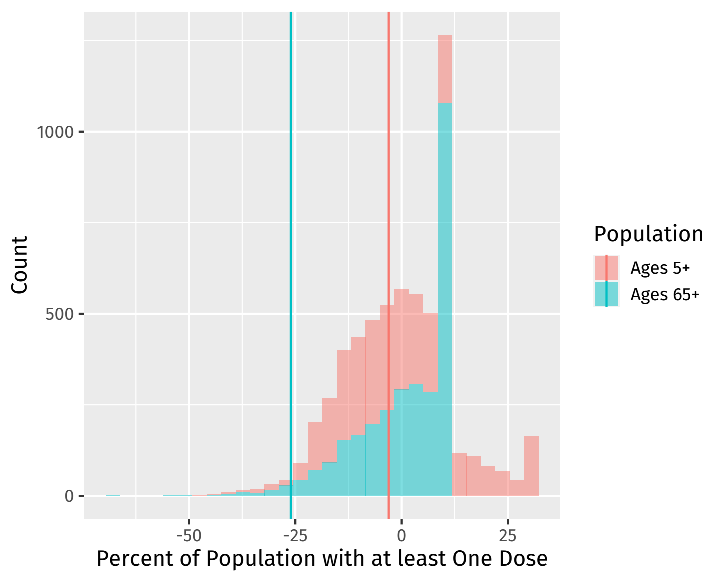
How large is large?

- How large 60% vaccinated is depends on the distribution!
    - Clear to see from the histogram
    - Middling for the 5+ group, but very low for the 65+ group.
- Can we transform the values of our variables to be **common units**?
- Yes, with two transformations:
    - **Centering**: subtract the mean of the variable from each value.
    - **Scaling**: dividing deviations from the mean by the standard deviation.

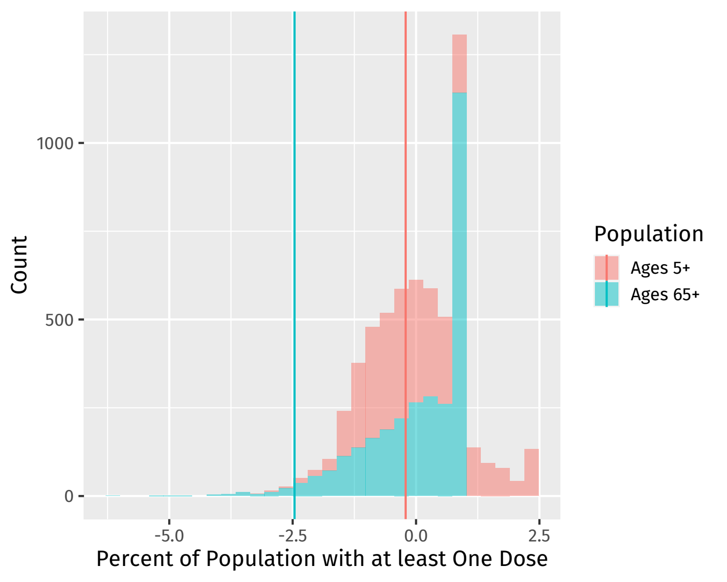
Original distributions



Centered distributions



Centered and scaled distributions



Z-scores

- Centering tells us immediately if a value is above or below the mean.
- Scaling tells us how many standard deviations away from the mean it is.
- Combine them with the **z-score** transformation:

$$\text{z-score of } x_i = \frac{x_i - \text{mean of } x}{\text{standard deviation of } x}$$

- Useful heuristic: data more than 3 SDs away from mean are rare.

z-score example

```r
covid_votes |>
  mutate(one_dose_centered = one_dose_5plus_pct -
           mean(one_dose_5plus_pct, na.rm = TRUE)) |>
  select(fips:state, one_dose_5plus_pct, one_dose_centered)
```

```
## # A tibble: 3,114 x 5
##    fips  county           state one_dose_5plus_pct one_dos~1
##    <chr> <chr>            <chr>              <dbl>     <dbl>
##  1 26039 Crawford County  MI                  55.7     -7.35
##  2 40015 Caddo County     OK                  83.3     20.2
##  3 17007 Boone County     IL                  71.1      8.05
##  4 12055 Highlands County FL                  68.9      5.85
##  5 34029 Ocean County     NJ                  71        7.95
##  6 01067 Henry County     AL                  58.5     -4.55
##  7 27037 Dakota County    MN                  81       17.9
##  8 27115 Pine County      MN                  56.5     -6.55
##  9 51750 Radford city     VA                  41.5    -21.6
## 10 22009 Avoyelles Parish LA                  59.7     -3.35
## # ... with 3,104 more rows, and abbreviated variable name
## #   1: one_dose_centered
```

z-score example

```
covid_votes |>
  mutate(
    one_dose_z =
      (one_dose_5plus_pct - mean(one_dose_5plus_pct, na.rm = TRUE)) /
      sd(one_dose_5plus_pct, na.rm = TRUE))   |>
  select(fips:state, one_dose_5plus_pct, one_dose_z)
```

```
## # A tibble: 3,114 x 5
##    fips  county           state one_dose_5plus_pct one_dos~1
##    <chr> <chr>            <chr>              <dbl>     <dbl>
##  1 26039 Crawford County  MI                  55.7    -0.508
##  2 40015 Caddo County     OK                  83.3     1.40
##  3 17007 Boone County     IL                  71.1     0.556
##  4 12055 Highlands County FL                  68.9     0.404
##  5 34029 Ocean County     NJ                  71       0.549
##  6 01067 Henry County     AL                  58.5    -0.314
##  7 27037 Dakota County    MN                  81       1.24
##  8 27115 Pine County      MN                  56.5    -0.452
##  9 51750 Radford city     VA                  41.5    -1.49
## 10 22009 Avoyelles Parish LA                  59.7    -0.231
## # ... with 3,104 more rows, and abbreviated variable name
## #   1: one_dose_z
```

2/ Correlation

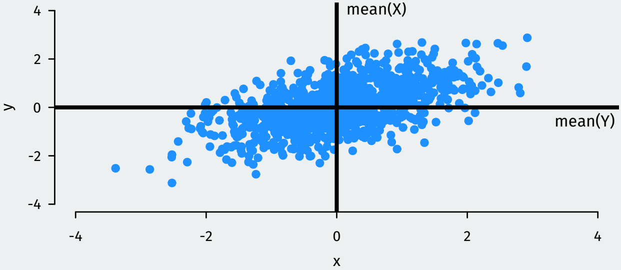
Correlation

- How do variables move together on average?
- When x_i is big, what is y_i likely to be?
  - Positive correlation: when x_i is big, y_i is also big
  - Negative correlation: when x_i is big, y_i is small
  - High magnitude of correlation: data cluster tightly around a line.
- The technical definition of the **correlation coefficient**:

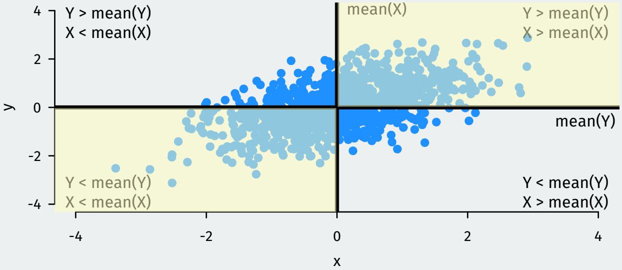
$$\frac{1}{n-1}\sum_{i=1}^{n}\left[(\text{z-score for } x_i) \times (\text{z-score for } y_i)\right]$$

- Interpretation:
  - Correlation is between -1 and 1
  - Correlation of 0 means no linear association.
  - Positive correlations $\rightsquigarrow$ positive associations.
  - Negative correlations $\rightsquigarrow$ negative associations.
  - Closer to -1 or 1 means stronger association.

Correlation intuition

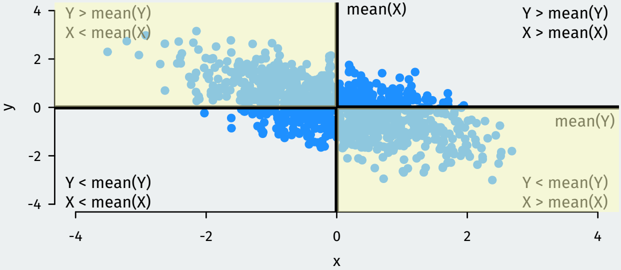


Correlation intuition



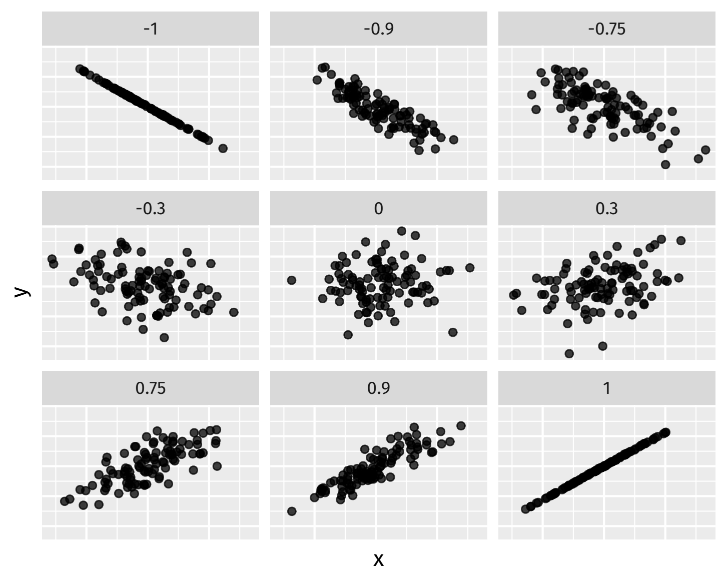
- Large values of X tend to occur with large values of Y:
  - (z-score for x_i) $\times$ (z-score for y_i) $=$ (pos. num.) $\times$ (pos. num) $= +$
- Small values of X tend to occur with small values of Y:
  - (z-score for x_i) $\times$ (z-score for y_i) $=$ (neg. num.) $\times$ (neg. num) $= +$
- If these dominate $\rightsquigarrow$ positive correlation.

Correlation intuition



- Large values of X tend to occur with small values of Y:
  - $(\text{z-score for } x_i) \times (\text{z-score for } y_i) = (\text{pos. num.}) \times (\text{neg. num}) = -$
- Small values of X tend to occur with large values of Y:
  - $(\text{z-score for } x_i) \times (\text{z-score for } y_i) = (\text{neg. num.}) \times (\text{pos. num}) = -$
- If these dominate $\rightsquigarrow$ negative correlation.

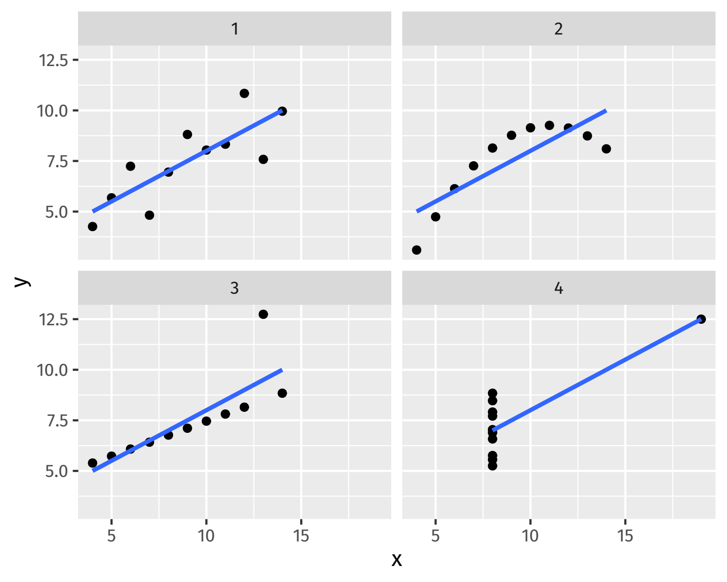
Correlation examples



Properties of correlation coefficient

- Correlation measures **linear** association.
- Order doesn't matter: `cor(x,y) = cor(y,x)`
- Not affected by changes of scale:
    - `cor(x,y) = cor(ax+b, cy+d)`
    - Celsius vs. Fahreneheit; dollars vs. pesos; cm vs. in.

All 4 relationships have 0.816 correlation



Correlation in R

Use the `cor()` function:

```
cor(covid_votes$one_dose_5plus_pct, covid_votes$dem_pct_2020)
```

```
## [1] NA
```

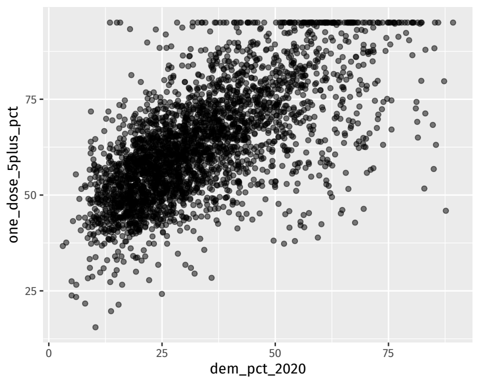
Missing values: set the `use = ”pairwise”` → available case analysis

```
cor(covid_votes$one_dose_5plus_pct, covid_votes$dem_pct_2020,
    use = ”pairwise”)
```

```
## [1] 0.666
```

Comparing correlations

```
covid_votes |>
  ggplot(aes(x = dem_pct_2020, y = one_dose_5plus_pct)) +
  geom_point(alpha = 0.5)
```

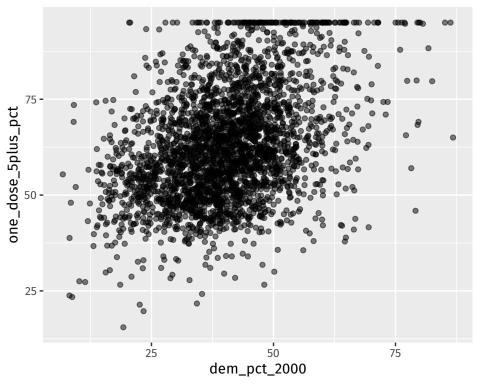


```
cor(covid_votes$one_dose_5plus_pct, covid_votes$dem_pct_2020,
    use = "pairwise")
```

```
## [1] 0.666
```

Comparing correlations

```r
covid_votes |>
  ggplot(aes(x = dem_pct_2000, y = one_dose_5plus_pct)) +
  geom_point(alpha = 0.5)
```

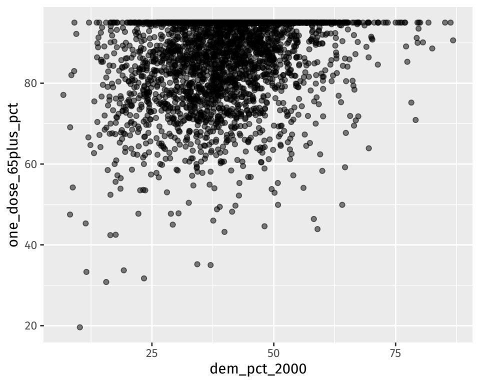


```r
cor(covid_votes$one_dose_5plus_pct, covid_votes$dem_pct_2000,
    use = "pairwise")
```

```
## [1] 0.394
```

Comparing correlations

```
covid_votes |>
  ggplot(aes(x = dem_pct_2000, y = one_dose_65plus_pct)) +
  geom_point(alpha = 0.5)
```



```
cor(covid_votes$one_dose_65plus_pct, covid_votes$dem_pct_2000,
    use = "pairwise")
```

```
## [1] 0.263
```

3/ Writing our own functions

Why write functions?

Copy-pasting code tedious and prone to failure:

```
covid_votes |>
  mutate(
    one_dose_5p_z =
      (one_dose_5plus_pct - mean(one_dose_5plus_pct, na.rm = TRUE)) /
      sd(one_dose_5plus_pct, na.rm = TRUE),
    one_dose_65p_z =
      (one_dose_65plus_pct - mean(one_dose_65plus_pct, na.rm = TRUE)) /
      sd(one_dose_65plus_pct, na.rm = TRUE),
    booster_z =
      (booster_5plus_pct - mean(booster_5plus_pct, na.rm = TRUE)) /
      sd(booster_5plus_pct, na.rm = TRUE),
    dem_pct_2000_z =
      (dem_pct_2000 - mean(dem_pct_2000, na.rm = TRUE)) /
      sd(dem_pct_2000, na.rm = TRUE),
    dem_pct_2020_z =
      (dem_pct_2020 - mean(dem_pct_2020, na.rm = TRUE)) /
      sd(dem_pct_2020, na.rm = TRUE)
  )
```

Writing a new function

Notice that all of the mutations follow the same template:

```
(█ - mean(█, na.rm = TRUE)) / sd(█, na.rm = TRUE)
```

Only one thing varies: the column of data, represented with █

Components of a function

We create functions like so:

```r
name <- function(arguments) {
  body
}
```

Three components:

1. **Name**: the name of the function that we'll use to call it. Maybe `z_score`?
2. **Arguments**: things that we want to vary across calls of our function. We'll use x.
3. **Body**: the code that the function performs.

Our first function

Convert our template to a function:

```r
z_score <- function(x) {
  (x - mean(x, na.rm = TRUE)) / sd(x, na.rm = TRUE)
}
```

Check that it seems to work:

```r
z_score(c(1,2, 3, 4, 5))
```

```
## [1] -1.265 -0.632  0.000  0.632  1.265
```

Cleaning up our code

```r
covid_votes |>
  mutate(
    one_dose_5p_z = z_score(one_dose_5plus_pct),
    one_dose_65p_z = z_score(one_dose_65plus_pct),
    booster_z = z_score(booster_5plus_pct),
    dem_pct_2000_z = z_score(dem_pct_2000),
    dem_pct_2020_z = z_score(dem_pct_2020)
  )
```

across() function

If we want to replace our variables with z-scores, we can use the across() function to perform many mutations at once:

```
covid_votes |>
  mutate(across(one_dose_5plus_pct:dem_pct_2020, z_score))
```

```
## # A tibble: 3,114 x 8
##    fips  county        state one_d~1 one_d~2 boost~3 dem_p~4
##    <chr> <chr>         <chr>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 26039 Crawford Cou~ MI     -0.508 -0.829    0.531  0.340
##  2 40015 Caddo County  OK      1.40   0.843    0.439  0.556
##  3 17007 Boone County  IL      0.556  0.795    0.927  0.163
##  4 12055 Highlands Co~ FL      0.404  0.720   -0.135  0.0402
##  5 34029 Ocean County  NJ      0.549  0.843    0.623  0.624
##  6 01067 Henry County  AL     -0.314 -0.0545  -0.799  0.0255
##  7 27037 Dakota County MN      1.24   0.843    2.40   0.598
##  8 27115 Pine County   MN     -0.452 -0.102    0.577  0.612
##  9 51750 Radford city  VA     -1.49  -1.16    -2.47   0.556
## 10 22009 Avoyelles Pa~ LA     -0.231 -0.564   -0.424  0.501
## # ... with 3,104 more rows, 1 more variable:
## #   dem_pct_2020 <dbl>, and abbreviated variable names
## #   1: one_dose_5plus_pct, 2: one_dose_65plus_pct,
```

Alternative approach

We could also target all the numeric variables:

```r
covid_votes |>
  mutate(across(where(is.numeric), z_score))
```

```
## # A tibble: 3,114 x 8
##    fips  county        state one_d~1 one_d~2 boost~3 dem_p~4
##    <chr> <chr>         <chr>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 26039 Crawford Cou~ MI     -0.508 -0.829    0.531  0.340
##  2 40015 Caddo County  OK      1.40    0.843    0.439  0.556
##  3 17007 Boone County  IL      0.556   0.795    0.927  0.163
##  4 12055 Highlands Co~ FL      0.404   0.720   -0.135  0.0402
##  5 34029 Ocean County  NJ      0.549   0.843    0.623  0.624
##  6 01067 Henry County  AL     -0.314 -0.0545  -0.799  0.0255
##  7 27037 Dakota County MN      1.24    0.843    2.40   0.598
##  8 27115 Pine County   MN     -0.452 -0.102    0.577  0.612
##  9 51750 Radford city  VA     -1.49  -1.16    -2.47   0.556
## 10 22009 Avoyelles Pa~ LA     -0.231 -0.564   -0.424  0.501
## # ... with 3,104 more rows, 1 more variable:
## #   dem_pct_2020 <dbl>, and abbreviated variable names
## #   1: one_dose_5plus_pct, 2: one_dose_65plus_pct,
## #   3: booster_5plus_pct, 4: dem_pct_2000
```

Alternative approach

We could also target only the first dose variables:

```
covid_votes |>
  mutate(across(starts_with("one_dose"), z_score))
```

```
## # A tibble: 3,114 x 8
##    fips  county        state one_d~1 one_d~2 boost~3 dem_p~4
##    <chr> <chr>         <chr>   <dbl>   <dbl>   <dbl>   <dbl>
##  1 26039 Crawford Cou~ MI     -0.508 -0.829     31.2    43.8
##  2 40015 Caddo County  OK      1.40   0.843     30.3    46.4
##  3 17007 Boone County  IL      0.556  0.795     35.1    41.8
##  4 12055 Highlands Co~ FL      0.404  0.720     24.7    40.3
##  5 34029 Ocean County  NJ      0.549  0.843     32.1    47.2
##  6 01067 Henry County  AL     -0.314 -0.0545    18.2    40.1
##  7 27037 Dakota County MN      1.24   0.843     49.5    46.9
##  8 27115 Pine County   MN     -0.452 -0.102     31.7    47.0
##  9 51750 Radford city  VA     -1.49  -1.16       1.79   46.4
## 10 22009 Avoyelles Pa~ LA     -0.231 -0.564     21.9    45.7
## # ... with 3,104 more rows, 1 more variable:
## #   dem_pct_2020 <dbl>, and abbreviated variable names
## #   1: one_dose_5plus_pct, 2: one_dose_65plus_pct,
## #   3: booster_5plus_pct, 4: dem_pct_2000
```

Adding arguments to our function

What if we want to be able to control `na.rm` in the calls to `mean()` and `sd()` in our `z_score` function? Add an argument!

```
z_score2 <- function(x, na.rm = FALSE) {
  (x - mean(x, na.rm = na.rm)) / sd(x, na.rm = na.rm)
}
```

```
head(z_score2(covid_votes$one_dose_5plus_pct))
```

```
## [1] NA NA NA NA NA NA
```

```
head(z_score2(covid_votes$one_dose_5plus_pct, na.rm = TRUE))
```

```
## [1] -0.508  1.398  0.556  0.404  0.549 -0.314
```