**Probability mass functions** 

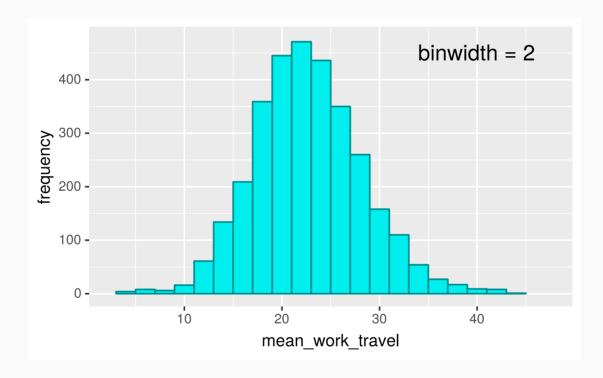


We've already learned that histograms (geom\_histogram()) are a convenient way to represent numerical data in a single column (variable)

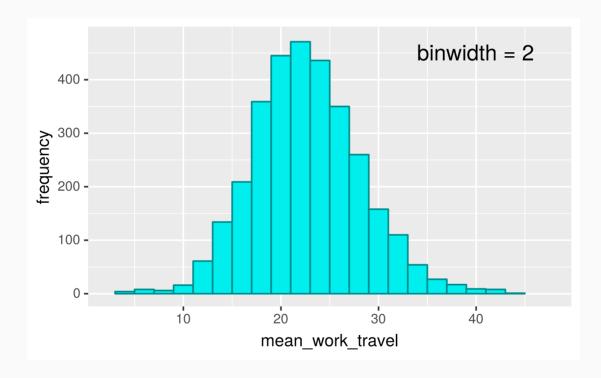
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mean_work_travel
25.1
25.8
23.8
28.3
33.2
28.1
25.1
•••

We've already learned that histograms (geom\_histogram()) are a convenient way to represent numerical data in a single column (variable)

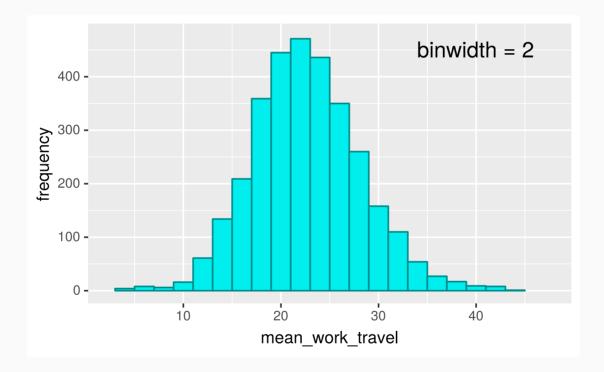


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A histogram represents the **frequency** that values show up for a given variable

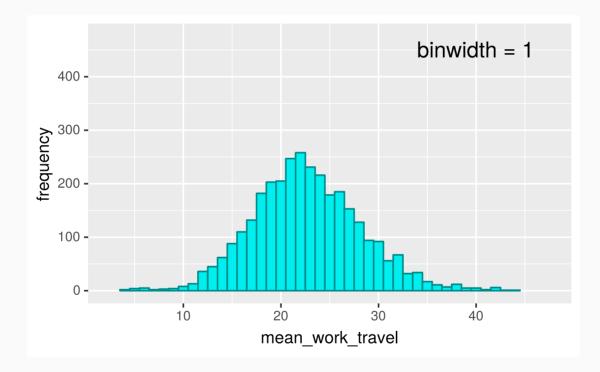
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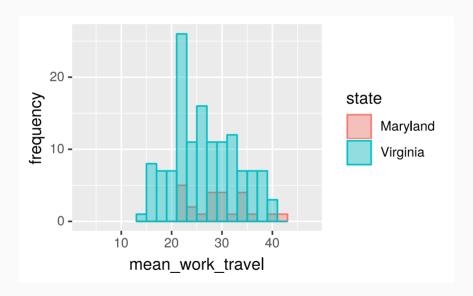
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In our current example of average times to travel to work, we can group the data by state and compare Virginia to Maryland.

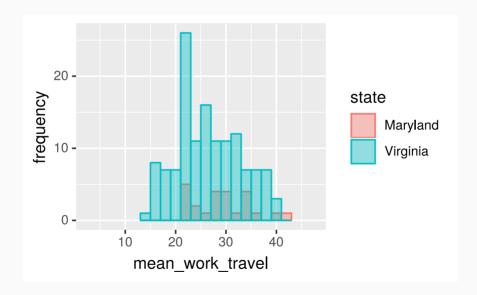
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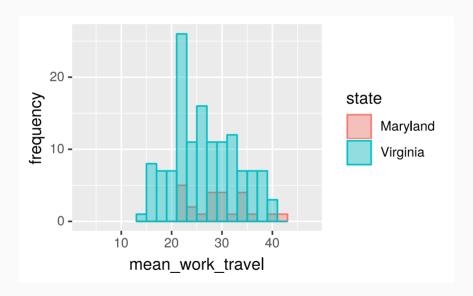
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In which state am I more likely to have a 30 minute commute?

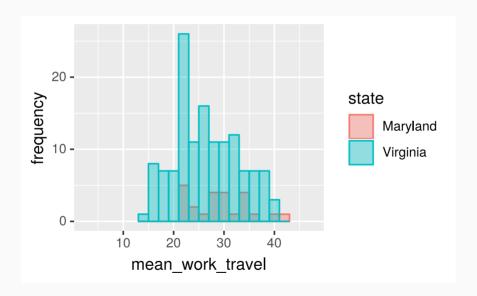
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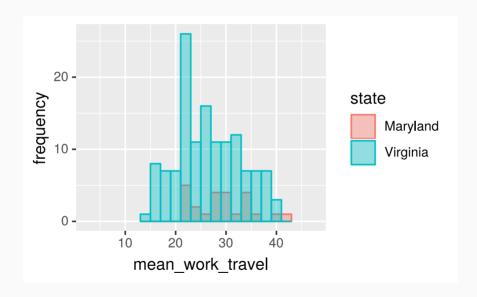
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We need to **normalize** the frequency counts.

Normalization is straightforward, just divide the frequency count in each "bucket" by the total number of observations in the histogram.

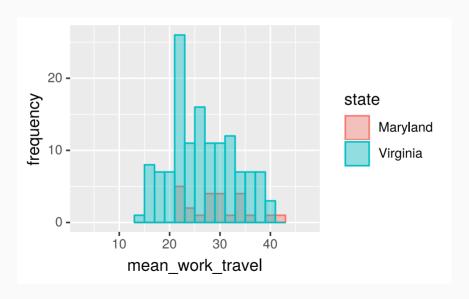
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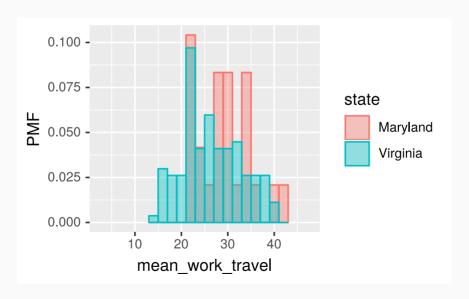
To normalize the histograms from the prior example, we need to divide the Virginia frequencies by 134 and the Maryland frequencies by 24.

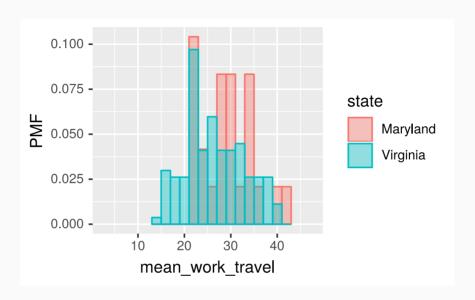


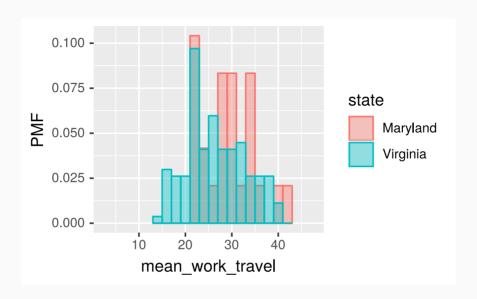
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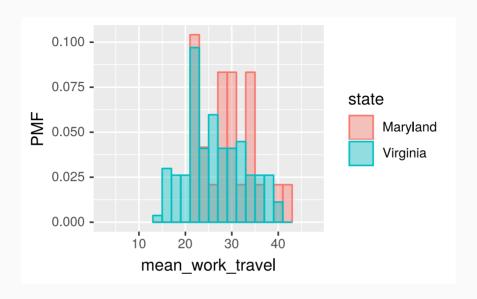
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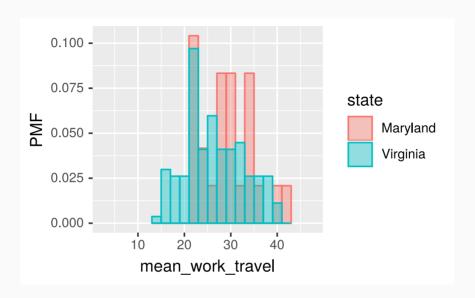


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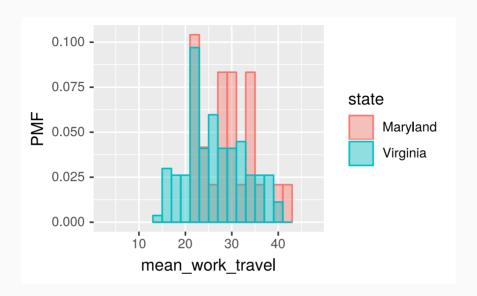
Allows for a meaningful comparison of distributions with different numbers of observations.



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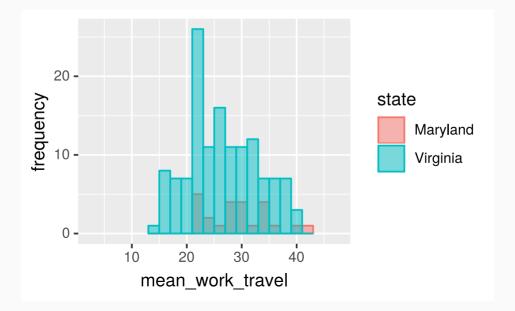
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Maryland

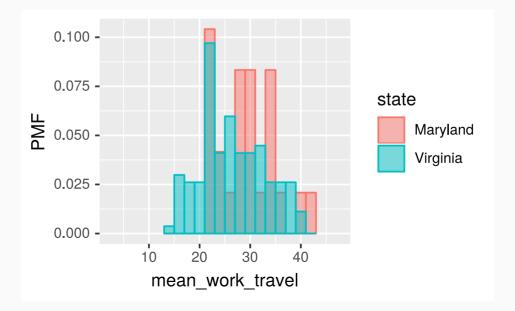
```
county %>%
  filter(state == "Virginia" | state == "Maryland") %>%
  ggplot() +
  geom_histogram(
    mapping = aes(x = mean_work_travel, fill = state),
    position = "identity",
    alpha = 0.5
)
```

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county %>%
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```
county %>%
  filter(state == "Virginia" | state == "Maryland") %>%
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  geom_histogram(
    mapping = aes(x = mean_work_travel, y = ..density.., fill = state),
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    alpha = 0.5
)
```



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- 2. Extract them from your ggplot2 visualization

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#### Assign the figure to a variable

```
va_md_pmf_figure <- county %>%
  filter(state == "Virginia" | state == "Maryland") %>%
  ggplot() +
  geom_histogram(
    mapping = aes(x = mean_work_travel, y = ..density.., fill = state),
    binwidth = 2,
    center = 0
)
```

- 1. Compute them manually
- 2. Extract them from your ggplot2 visualization

Assign the figure to a variable

```
va_md_pmf_figure <- county %>%
  filter(state == "Virginia" | state == "Maryland") %>%
  ggplot() +
  geom_histogram(
    mapping = aes(x = mean_work_travel, y = ..density.., fill = state),
    binwidth = 2,
    center = 0
)
```

Use ggplot\_build() with purrr::pluck() and as\_data\_frame() as follows:

```
va_md_pmf_data <- va_md_pmf_figure %>%
  ggplot_build() %>%
  purrr::pluck("data", 1) %>%
  as_data_frame()
```

```
va_md_pmf_data %>%
  glimpse()
```

```
## Observations: 30
## Variables: 17
## $ fill
          <chr> "#00BFC4", "#F8766D", "#00BFC4", "#F8766D", "#00BFC4"...
## $ v
          <dbl> 0.003731343, 0.003731343, 0.029850746, 0.029850746, 0...
## $ count
          <dbl> 1, 0, 8, 0, 7, 0, 7, 0, 26, 5, 11, 2, 16, 1, 11, 4, 1...
## $ x
          <dbl> 14, 14, 16, 16, 18, 18, 20, 20, 22, 22, 24, 24, 26, 2...
## $ xmin
          <dbl> 13, 13, 15, 15, 17, 17, 19, 19, 21, 21, 23, 23, 25, 2...
## $ xmax
          <dbl> 15, 15, 17, 17, 19, 19, 21, 21, 23, 23, 25, 25, 27, 2...
## $ density
          <dbl> 0.003731343, 0.0000000000, 0.029850746, 0.000000000, 0...
## $ ncount
          <dbl> 0.03846154, 0.000000000, 0.30769231, 0.00000000, 0.269...
## $ ndensity <dbl> 0.03846154, 0.00000000, 0.30769231, 0.00000000, 0.269...
## $ PANEL
          ## $ group
          <int> 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, 2, 1, ...
## $ ymin
          <dbl> 0.000000000, 0.003731343, 0.000000000, 0.029850746, 0...
## $ vmax
          <dbl> 0.003731343, 0.003731343, 0.029850746, 0.029850746, 0...
## $ colour
          ## $ size
          ## $ alpha
```

#### To get the Maryland PMF data:

```
md_pmf_data <- va_md_pmf_data %>%
  filter(group == 1) %>%
  select(x, density)
```

X	density
14	0
16	0
18	0
20	0
22	0.104166666666667
24	0.0416666666666667
26	0.0208333333333333
•••	•••

#### To get the Virginia PMF data:

```
va_pmf_data <- va_md_pmf_data %>%
  filter(group == 2) %>%
  select(x, density)
```

x	density
14	0.00373134328358209
16	0.0298507462686567
18	0.0261194029850746
20	0.0261194029850746
22	0.0970149253731343
24	0.041044776119403
26	0.0597014925373134
•••	•••

## **Credits**

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