Chapter 3

Univariate Graphs

Univariate graphs plot the distribution of data from a single variable. The variable can be categorical (e.g., race, sex) or quantitative (e.g., age, weight).

3.1 Categorical

The distribution of a single categorical variable is typically plotted with a bar chart, a pie chart, or (less commonly) a tree map.

3.1.1 Bar chart

The Marriage dataset contains the marriage records of 98 individuals in Mobile County, Alabama. Below, a bar chart is used to display the distribution of wedding participants by race.

```r
library(ggplot2)
data(Marriage, package = "mosaicData")

# plot the distribution of race
ggplot(Marriage, aes(x = race)) +
  geom_bar()
```

The majority of participants are white, followed by black, with very few Hispanics or American Indians.

You can modify the bar fill and border colors, plot labels, and title by adding options to the `geom_bar` function.

```r
# plot the distribution of race with modified colors and labels
ggplot(Marriage, aes(x = race)) +
  geom_bar(fill = "cornflowerblue",
           color="black") +
  labs(x = "Race",
       y = "Frequency",
       title = "Participants by race")
```

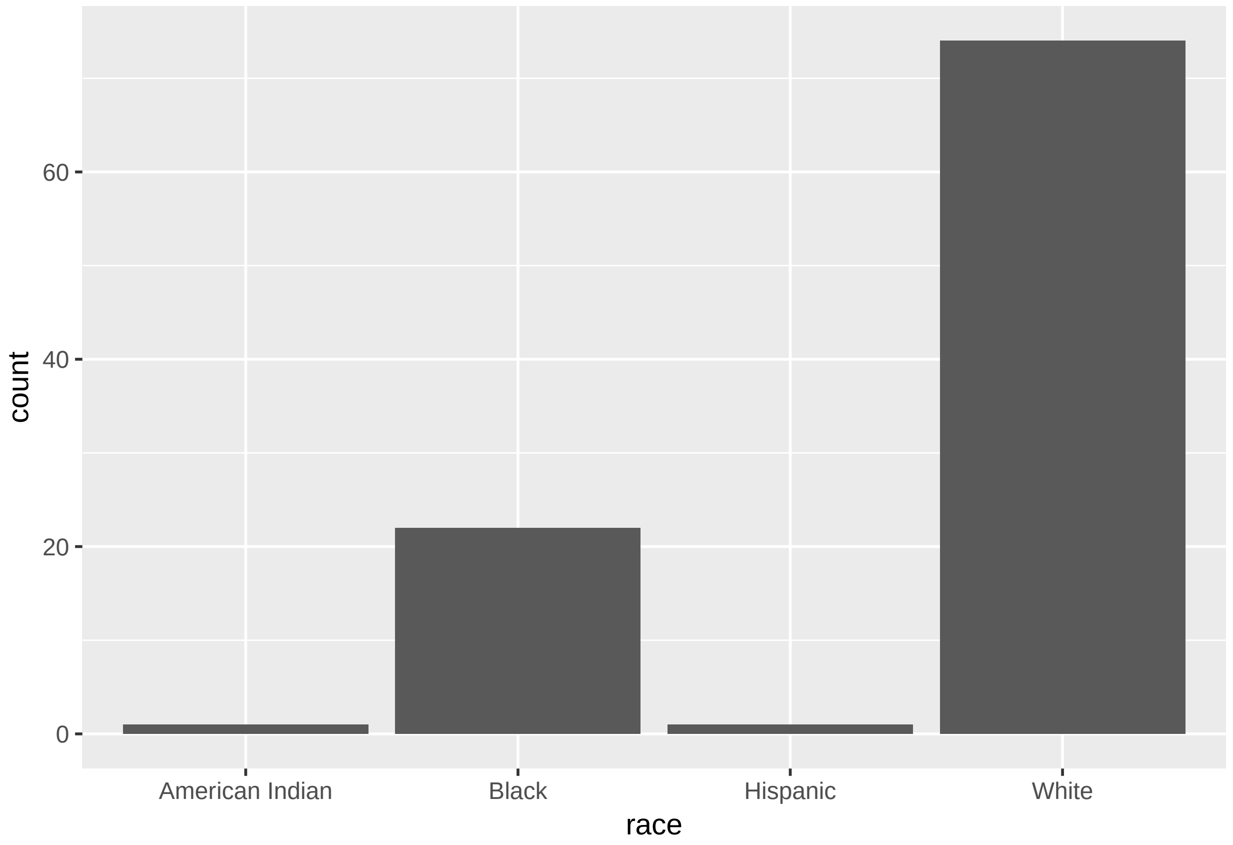


Figure 3.1: Simple barchart

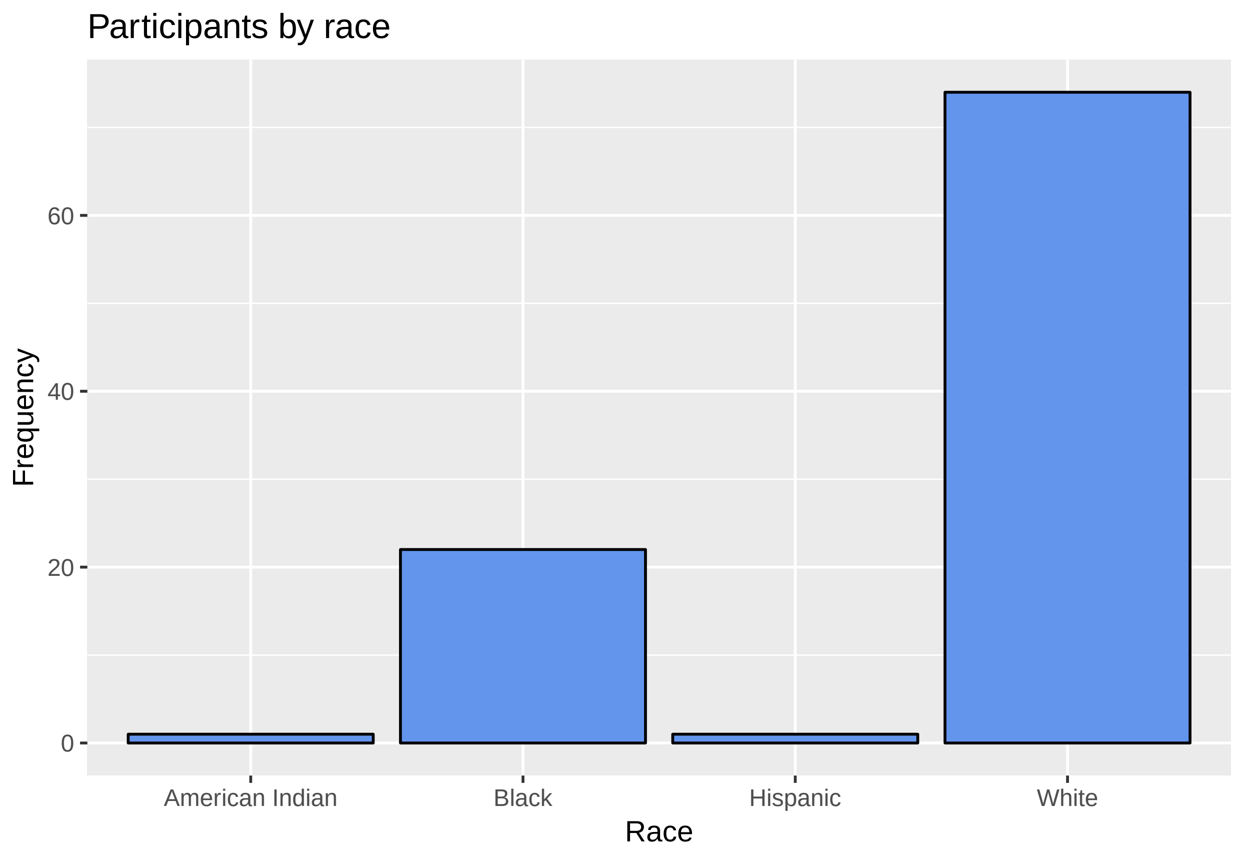


Figure 3.2: Barchart with modified colors, labels, and title

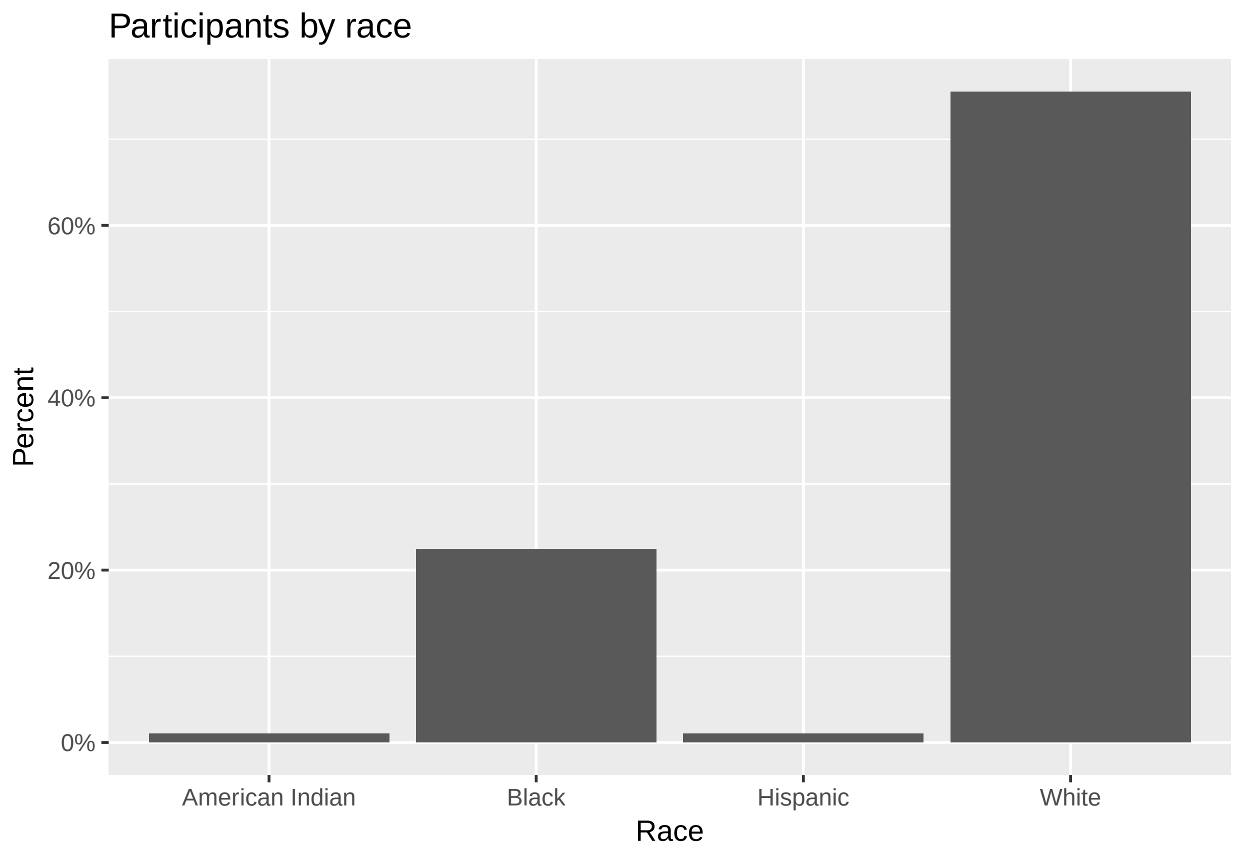


Figure 3.3: Barchart with percentages

3.1.1.1 Percents

Bars can represent percents rather than counts. For bar charts, the code `aes(x=race)` is actually a shortcut for `aes(x = race, y = ..count..)`, where `..count..` is a special variable representing the frequency within each category. You can use this to calculate percentages, by specifying the `y` variable explicitly.

```
# plot the distribution as percentages
ggplot(Marriage,
       aes(x = race,
           y = ..count.. / sum(..count..))) +
  geom_bar() +
  labs(x = "Race",
       y = "Percent",
       title  = "Participants by race") +
  scale_y_continuous(labels = scales::percent)
```

In the code above, the `scales` package is used to add % symbols to the y-axis labels.

3.1.1.2 Sorting categories

It is often helpful to sort the bars by frequency. In the code below, the frequencies are calculated explicitly. Then the `reorder` function is used to sort the categories by the frequency. The option `stat="identity"` tells the plotting function not to calculate counts, because they are supplied directly.

Table 3.1: plotdata

race	n
American Indian	1
Black	22
Hispanic	1
White	74

```r
# calculate number of participants in
# each race category
library(dplyr)
plotdata <- Marriage %>%
 count(race)
```

The resulting dataset is give below.

This new dataset is then used to create the graph.

```r
# plot the bars in ascending order
ggplot(plotdata,
       aes(x = reorder(race, n),
           y = n)) +
  geom_bar(stat = "identity") +
  labs(x = "Race",
       y = "Frequency",
       title  = "Participants by race")
```

The graph bars are sorted in ascending order. Use `reorder(race, -n)` to sort in descending order.

3.1.1.3 Labeling bars

Finally, you may want to label each bar with its numerical value.

```r
# plot the bars with numeric labels
ggplot(plotdata,
       aes(x = race,
           y = n)) +
  geom_bar(stat = "identity") +
  geom_text(aes(label = n),
            vjust=-0.5) +
  labs(x = "Race",
       y = "Frequency",
       title  = "Participants by race")
```

Here `geom_text` adds the labels, and `vjust` controls vertical justification. See Annotations for more details.

Putting these ideas together, you can create a graph like the one below. The minus sign in `reorder(race, -pct)` is used to order the bars in descending order.

```r
library(dplyr)
library(scales)
```

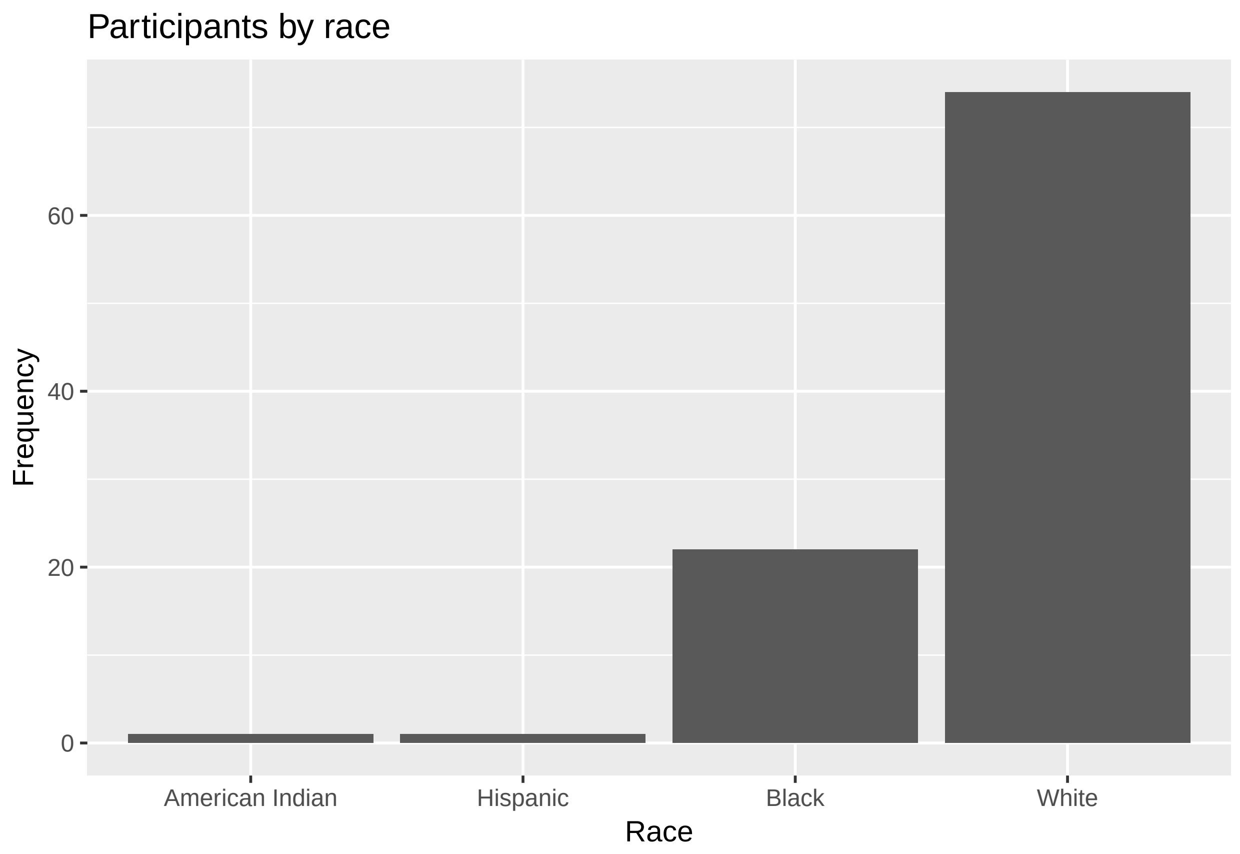


Figure 3.4: Sorted bar chart

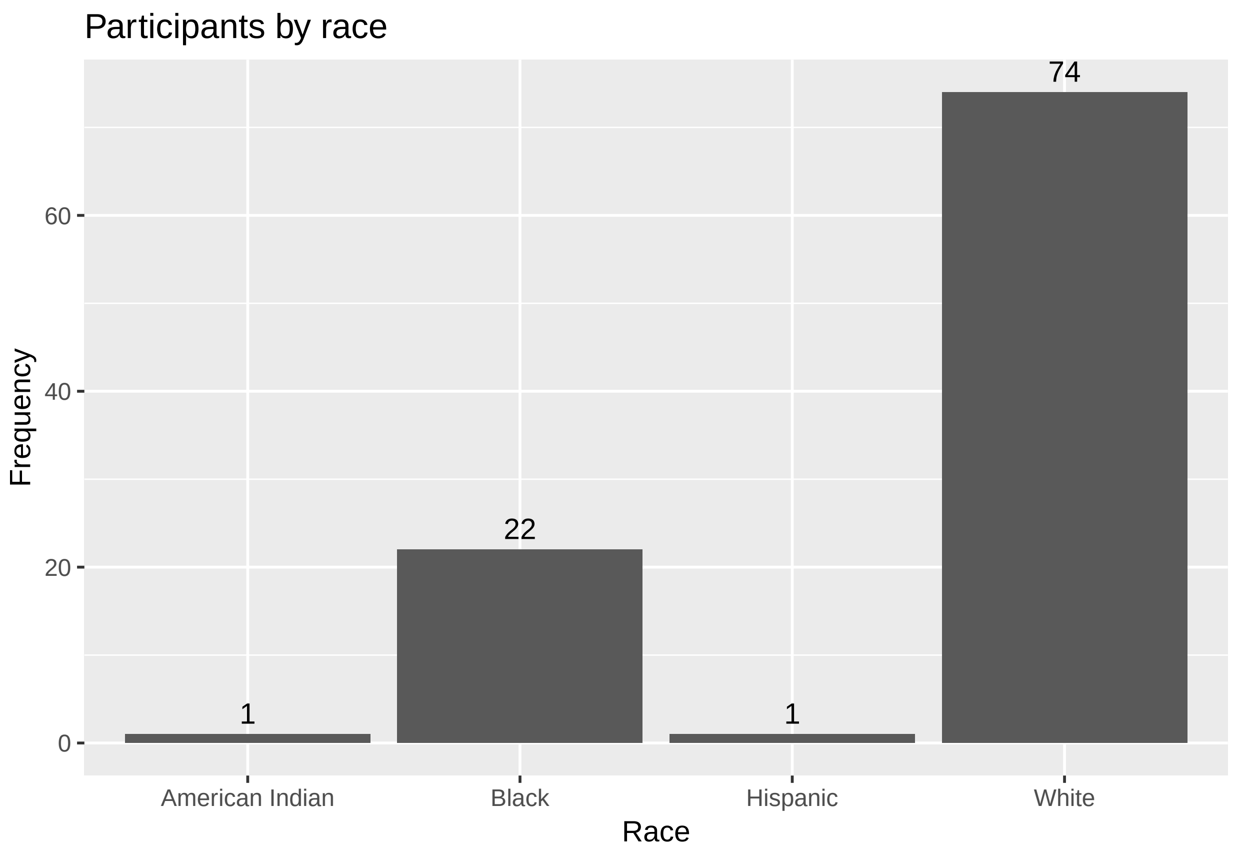


Figure 3.5: Bar chart with numeric labels

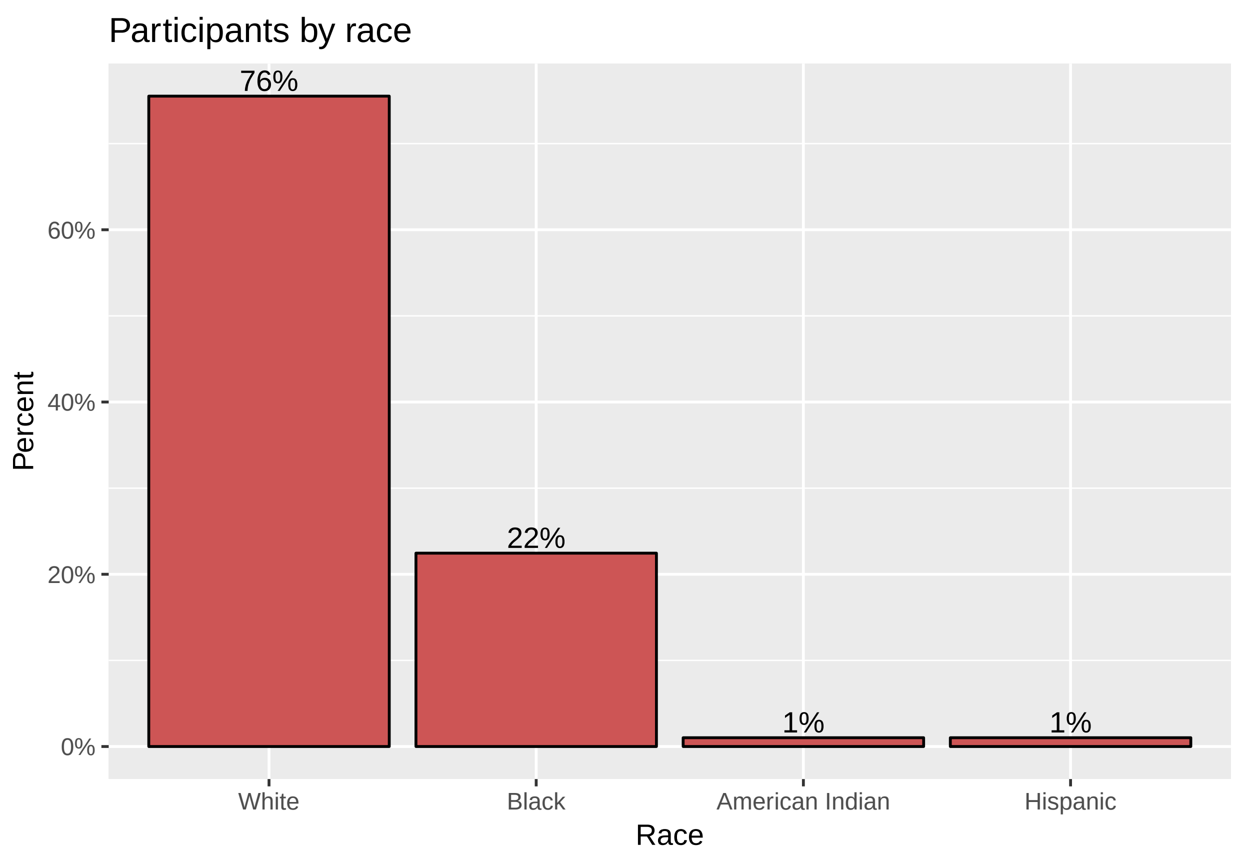


Figure 3.6: Sorted bar chart with percent labels

```
plotdata <- Marriage %>%
  count(race) %>%
  mutate(pct = n / sum(n),
         pctlabel = paste0(round(pct*100), "%"))

# plot the bars as percentages,
# in decending order with bar labels
ggplot(plotdata,
       aes(x = reorder(race, -pct),
           y = pct)) +
  geom_bar(stat = "identity",
           fill = "indianred3",
           color = "black") +
  geom_text(aes(label = pctlabel),
            vjust = -0.25) +
  scale_y_continuous(labels = percent) +
  labs(x = "Race",
       y = "Percent",
       title  = "Participants by race")
```

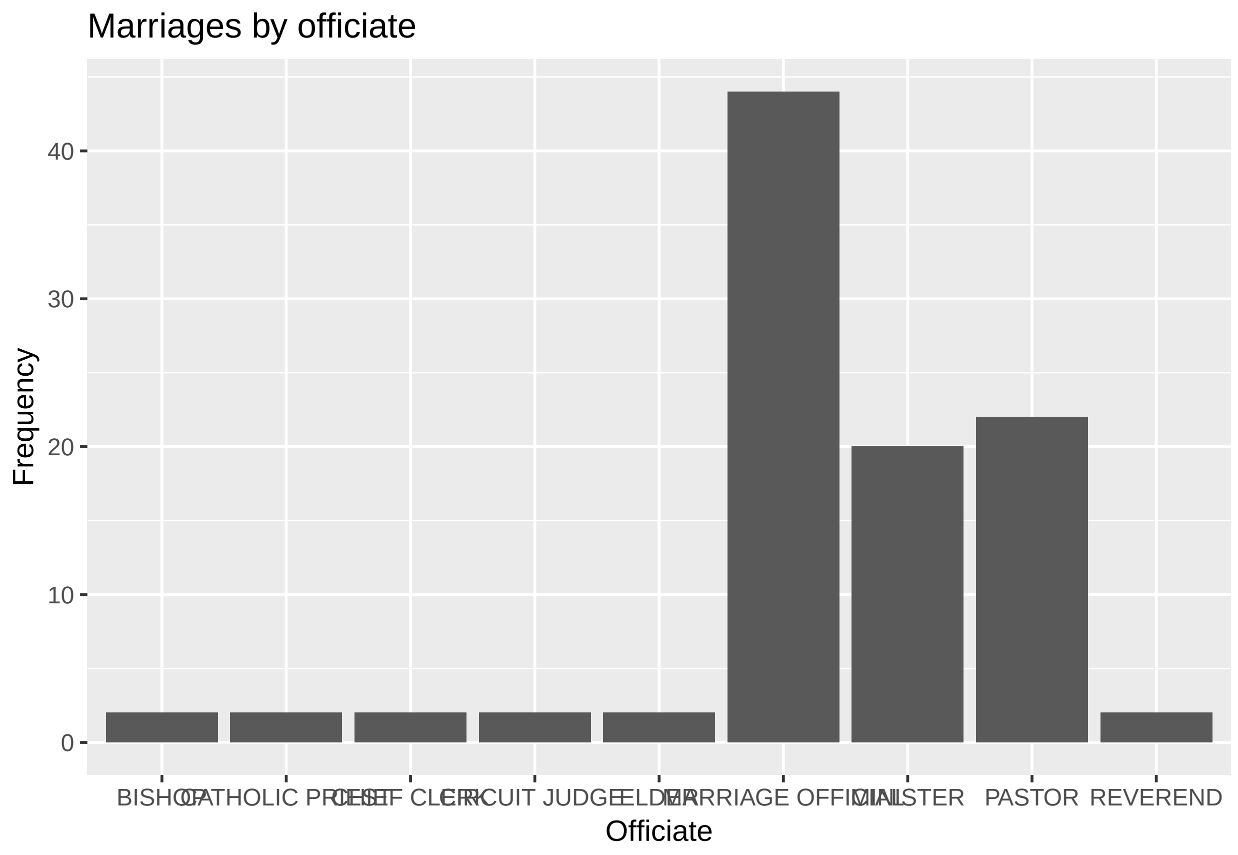


Figure 3.7: Barchart with problematic labels

3.1.1.4 Overlapping labels

Category labels may overlap if (1) there are many categories or (2) the labels are long. Consider the distribution of marriage officials.

```r
# basic bar chart with overlapping labels
ggplot(Marriage, aes(x = officialTitle)) +
  geom_bar() +
  labs(x = "Officiate",
       y = "Frequency",
       title = "Marriages by officiate")
```

In this case, you can flip the x and y axes.

```r
# horizontal bar chart
ggplot(Marriage, aes(x = officialTitle)) +
  geom_bar() +
  labs(x = "",
       y = "Frequency",
       title = "Marriages by officiate") +
  coord_flip()
```

Alternatively, you can rotate the axis labels.

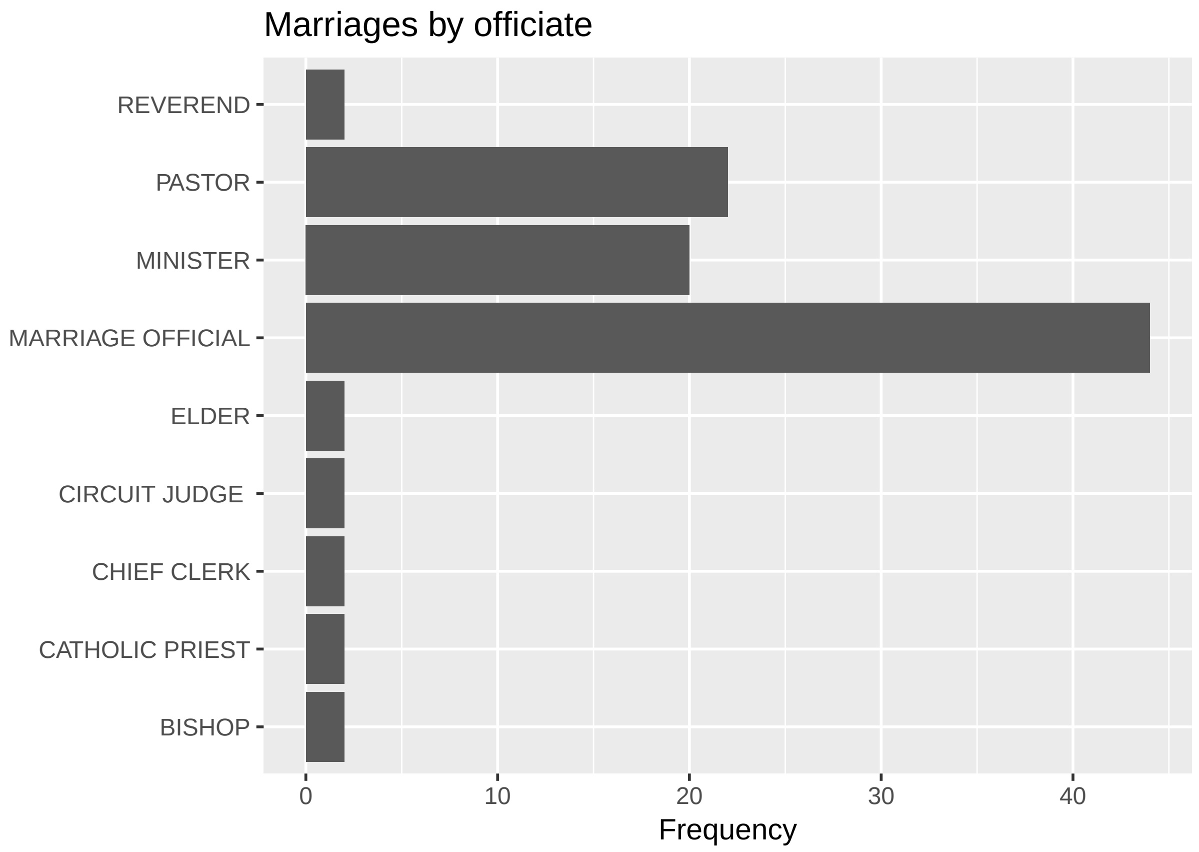


Figure 3.8: Horizontal barchart

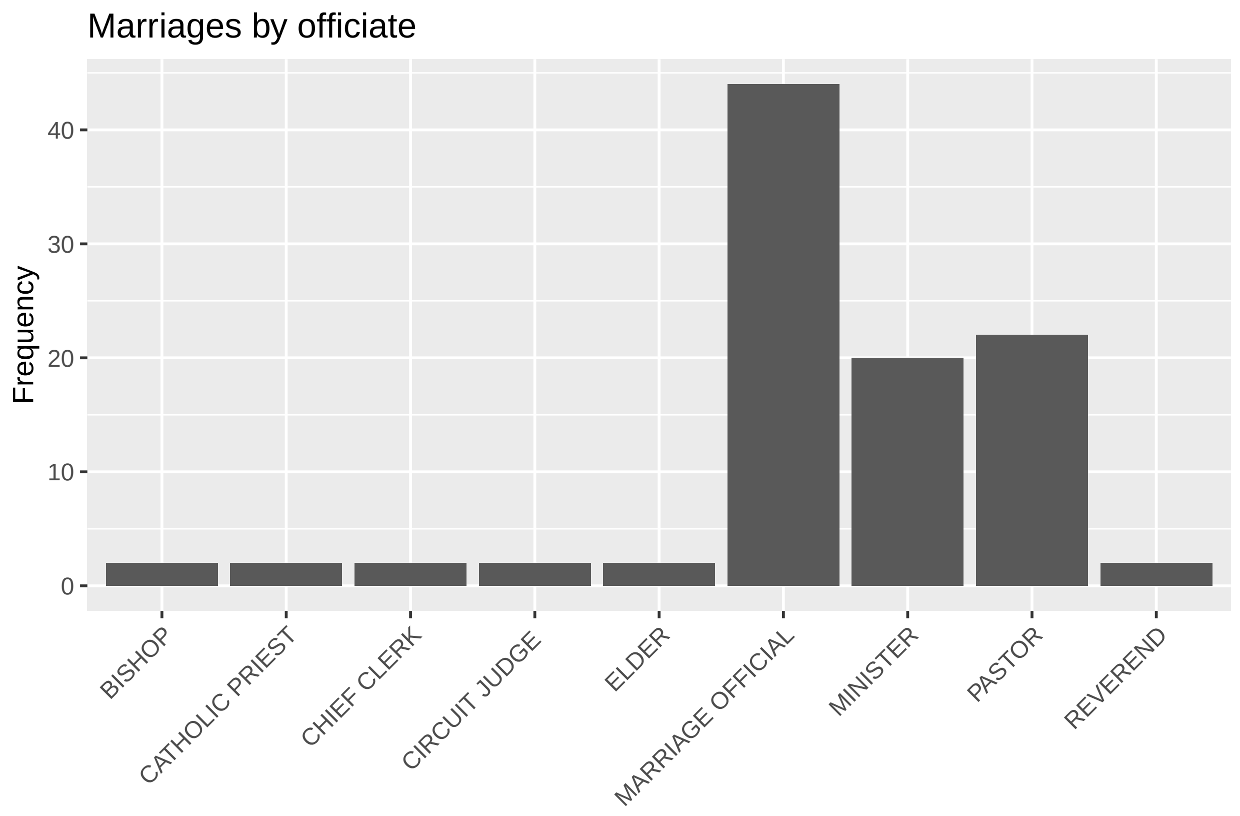
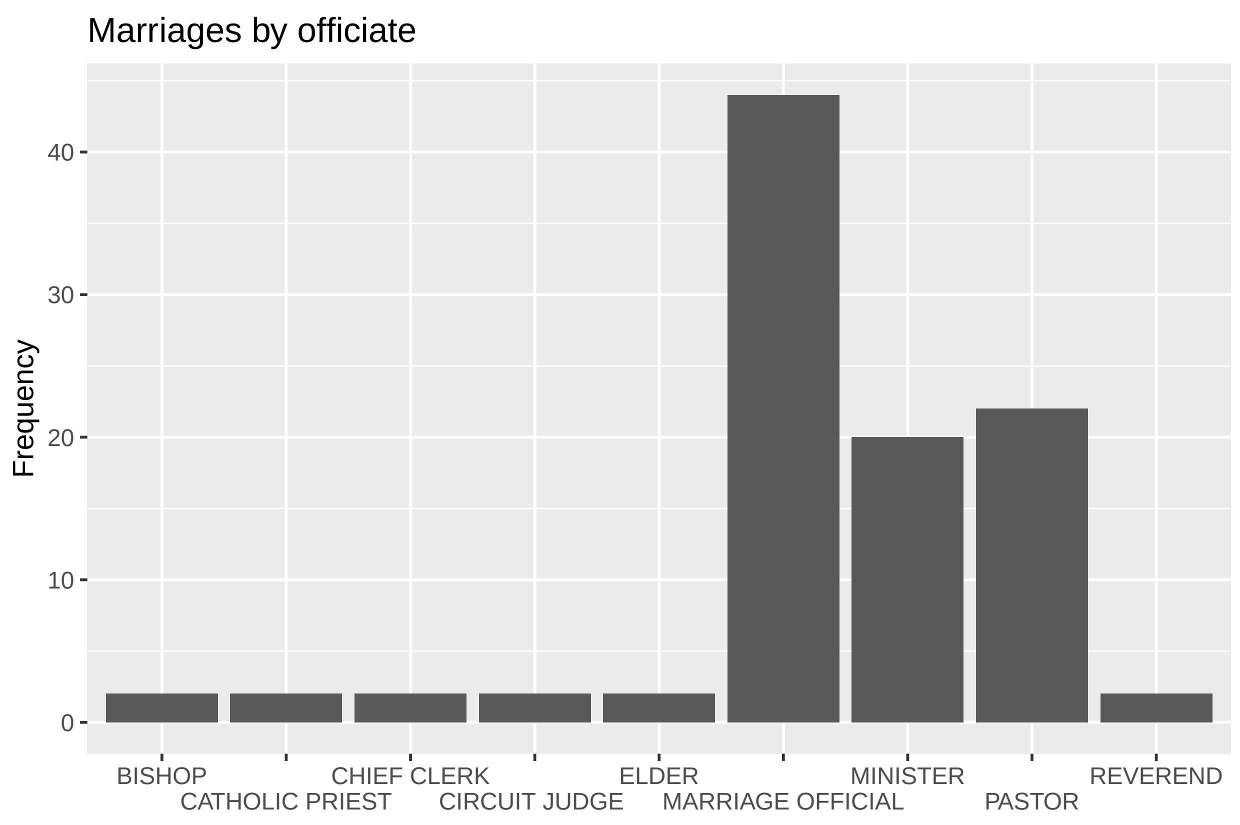


Figure 3.9: Barchart with rotated labels

```r
# bar chart with rotated labels
ggplot(Marriage, aes(x = officialTitle)) +
  geom_bar() +
  labs(x = "",
       y = "Frequency",
       title = "Marriages by officiate") +
  theme(axis.text.x = element_text(angle = 45,
                                   hjust = 1))
```

Finally, you can try staggering the labels. The trick is to add a newline `\n` to every other label.

```r
# bar chart with staggered labels
lbls <- paste0(c("", "\n"),
               levels(Marriage$officialTitle))
ggplot(Marriage,
       aes(x=factor(officialTitle,
                    labels = lbls))) +
  geom_bar() +
  labs(x = "",
       y = "Frequency",
       title = "Marriages by officiate")
```



### Pie chart

Pie charts are controversial in statistics. If your goal is to compare the frequency of categories, you are better off with bar charts (humans are better at judging the length of bars than the volume of pie slices). If your goal is compare each category with the the whole (e.g., what portion of participants are Hispanic compared to all participants), and the number of categories is small, then pie charts may work for you. It takes a bit more code to make an attractive pie chart in R.

```
# create a basic ggplot2 pie chart
 plotdata <- Marriage %>%
    count(race) %>%
    arrange(desc(race)) %>%
    mutate(prop = round(n * 100 / sum(n), 1),
           lab.ypos = cumsum(prop) - 0.5  *prop)

  ggplot(plotdata,
         aes(x = "",
             y = prop,
             fill = race)) +
    geom_bar(width = 1,
             stat = "identity",
             color = "black") +
    coord_polar("y",
                start = 0,
                direction = -1) +
    theme_void()
```

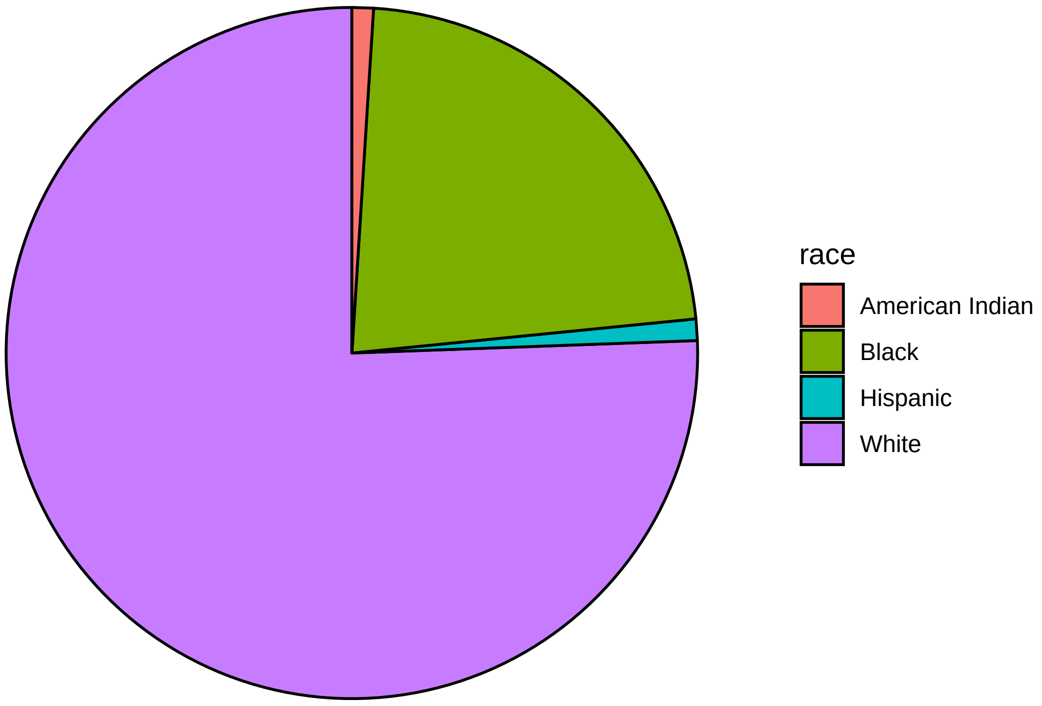


Figure 3.10: Basic pie chart

Now let's get fancy and add labels, while removing the legend.

```r
# create a pie chart with slice labels
plotdata <- Marriage %>%
  count(race) %>%
  arrange(desc(race)) %>%
  mutate(prop = round(n*100/sum(n), 1),
         lab.ypos = cumsum(prop) - 0.5*prop)

plotdata$label <- paste0(plotdata$race, "\n",
                         round(plotdata$prop), "%")

ggplot(plotdata,
       aes(x = "",
           y = prop,
           fill = race)) +
  geom_bar(width = 1,
           stat = "identity",
           color = "black") +
  geom_text(aes(y = lab.ypos, label = label),
            color = "black") +
  coord_polar("y",
              start = 0,
              direction = -1) +
  theme_void() +
  theme(legend.position = "FALSE") +
  labs(title = "Participants by race")
```

The pie chart makes it easy to compare each slice with the whole. For example, Back is seen to roughly a quarter of the total participants.

3.1.2 Tree map

An alternative to a pie chart is a tree map. Unlike pie charts, it can handle categorical variables that have *many* levels.

```r
library(treemapify)

# create a treemap of marriage officials
plotdata <- Marriage %>%
  count(officialTitle)

ggplot(plotdata,
       aes(fill = officialTitle,
           area = n)) +
  geom_treemap() +
  labs(title = "Marriages by officiate")
```

Here is a more useful version with labels.

```r
# create a treemap with tile labels
ggplot(plotdata,
```

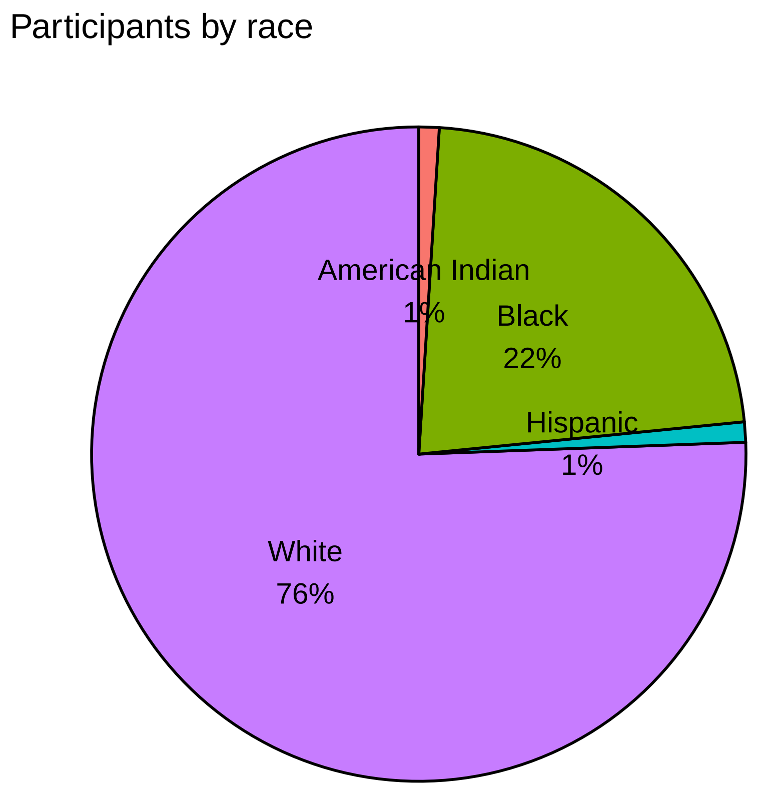


Figure 3.11: Pie chart with percent labels

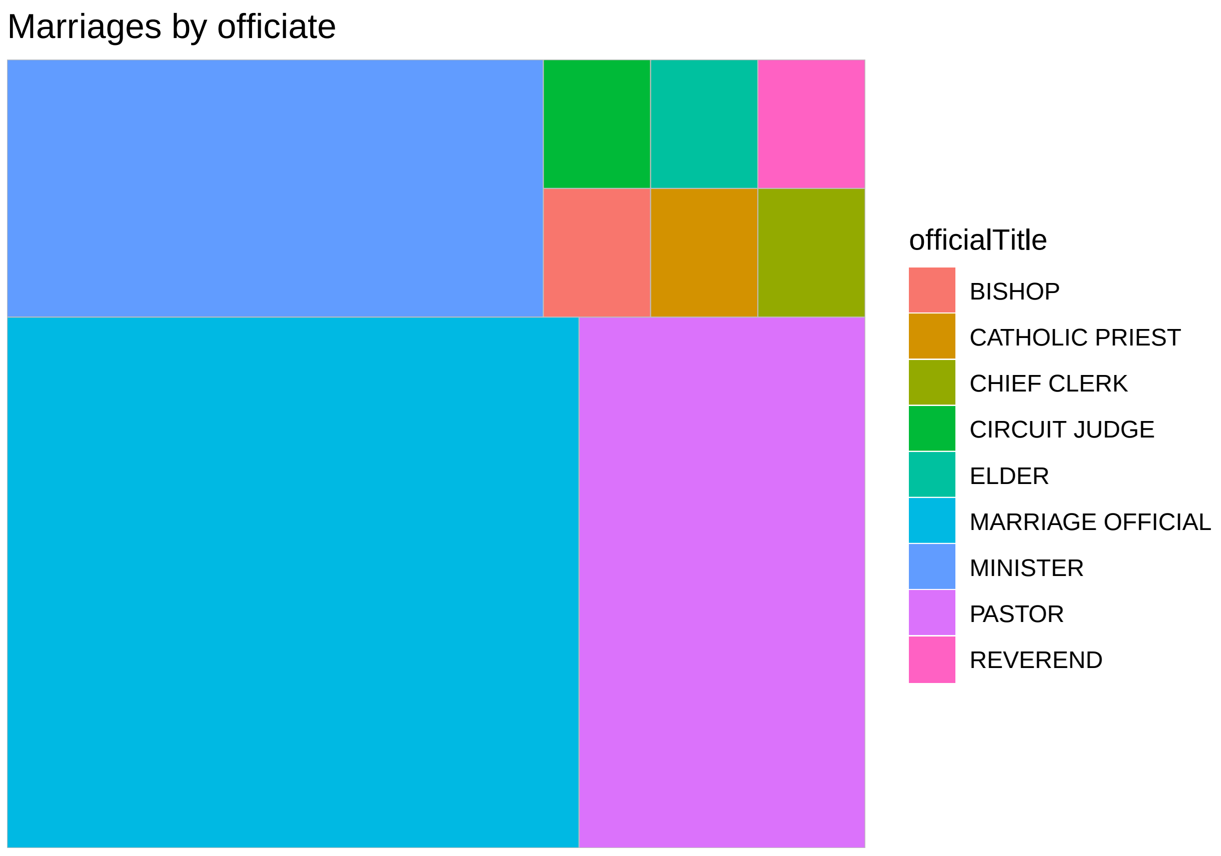


Figure 3.12: Basic treemap

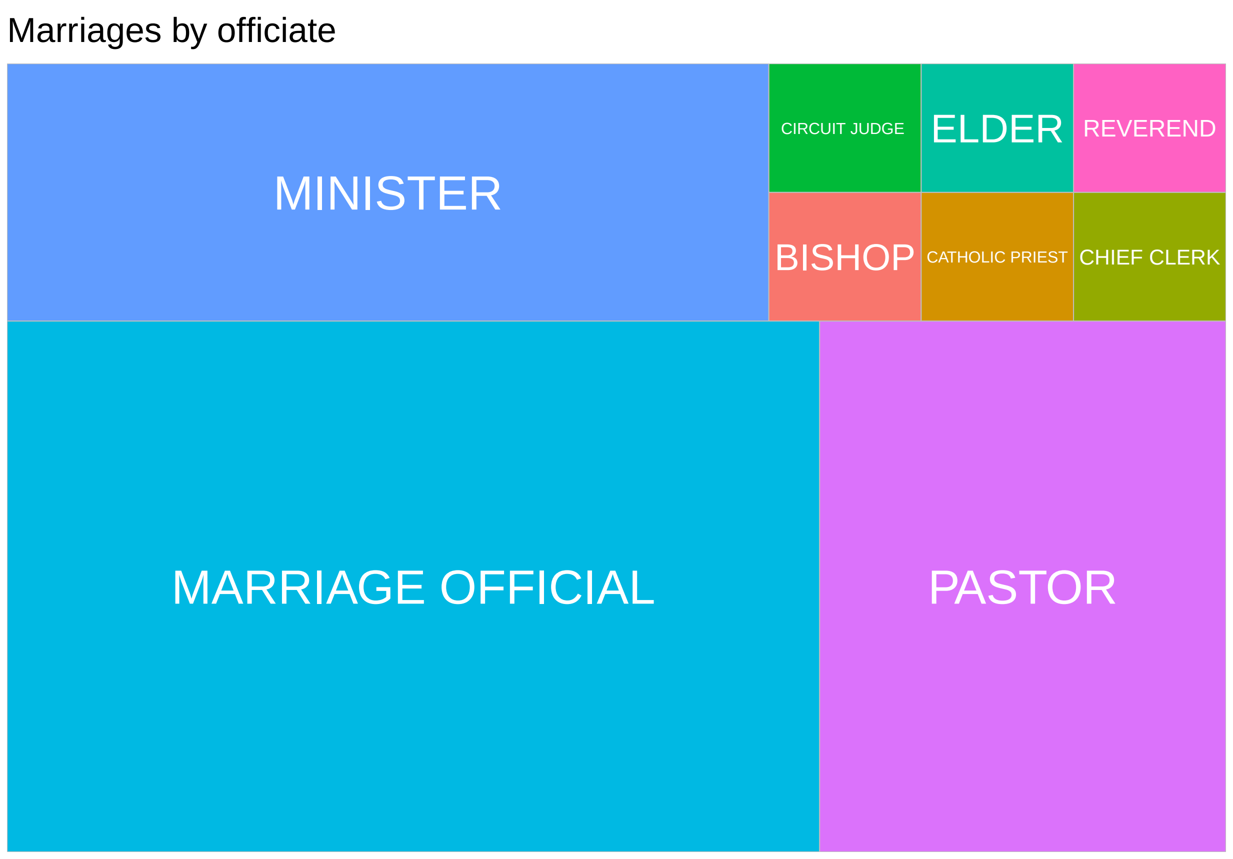


Figure 3.13: Treemap with labels

```
       aes(fill = officialTitle,
           area = n,
           label = officialTitle)) +
  geom_treemap() +
  geom_treemap_text(colour = "white",
                    place = "centre") +
  labs(title = "Marriages by officiate") +
  theme(legend.position = "none")
```

3.2 Quantitative

The distribution of a single quantitative variable is typically plotted with a histogram, kernel density plot, or dot plot.

3.2.1 Histogram

Using the Marriage dataset, let's plot the ages of the wedding participants.

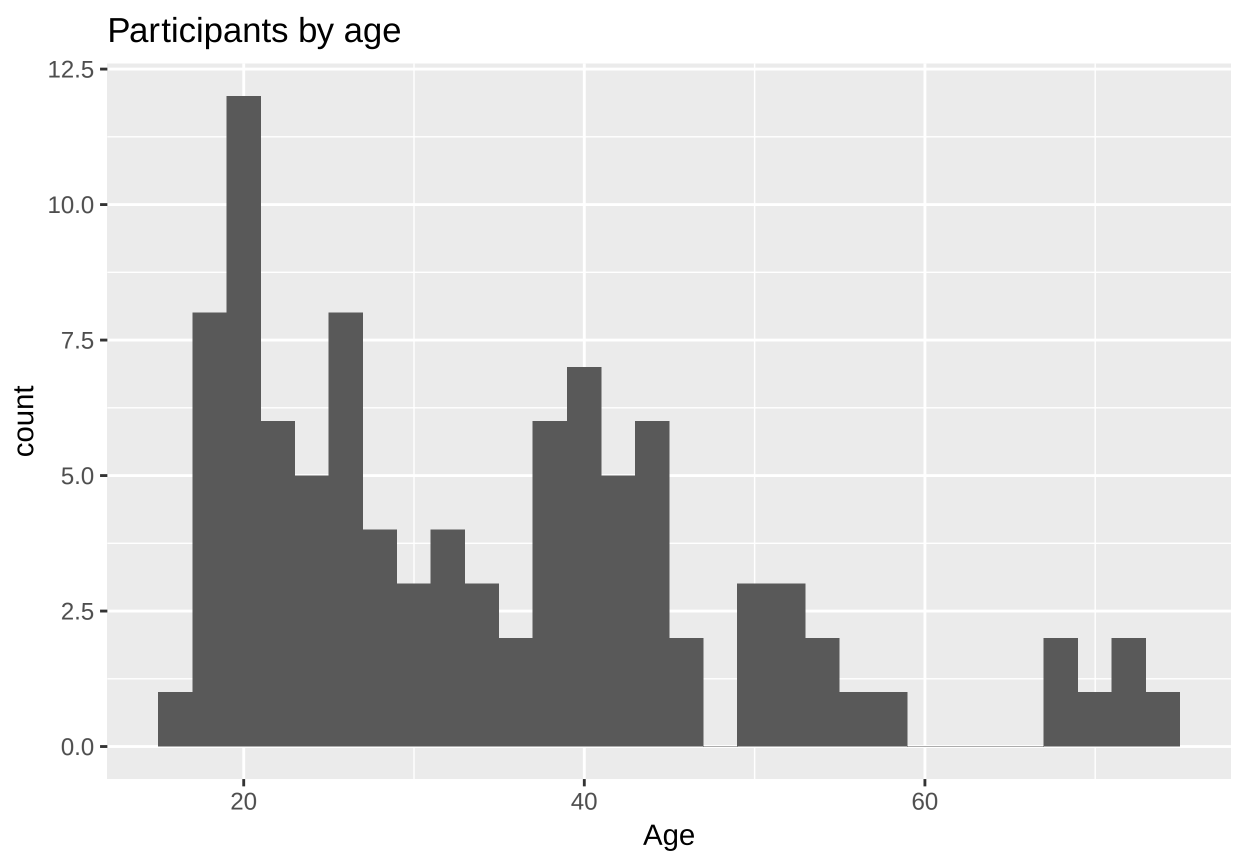


Figure 3.14: Basic histogram

```r
library(ggplot2)

# plot the age distribution using a histogram
ggplot(Marriage, aes(x = age)) +
  geom_histogram() +
  labs(title = "Participants by age",
       x = "Age")
```

Most participants appear to be in their early 20's with another group in their 40's, and a much smaller group in their later sixties and early seventies. This would be a *multimodal* distribution.

Histogram colors can be modified using two options

- `fill` - fill color for the bars
- `color` - border color around the bars

```r
# plot the histogram with blue bars and white borders
ggplot(Marriage, aes(x = age)) +
  geom_histogram(fill = "cornflowerblue",
                 color = "white") +
  labs(title="Participants by age",
       x = "Age")
```

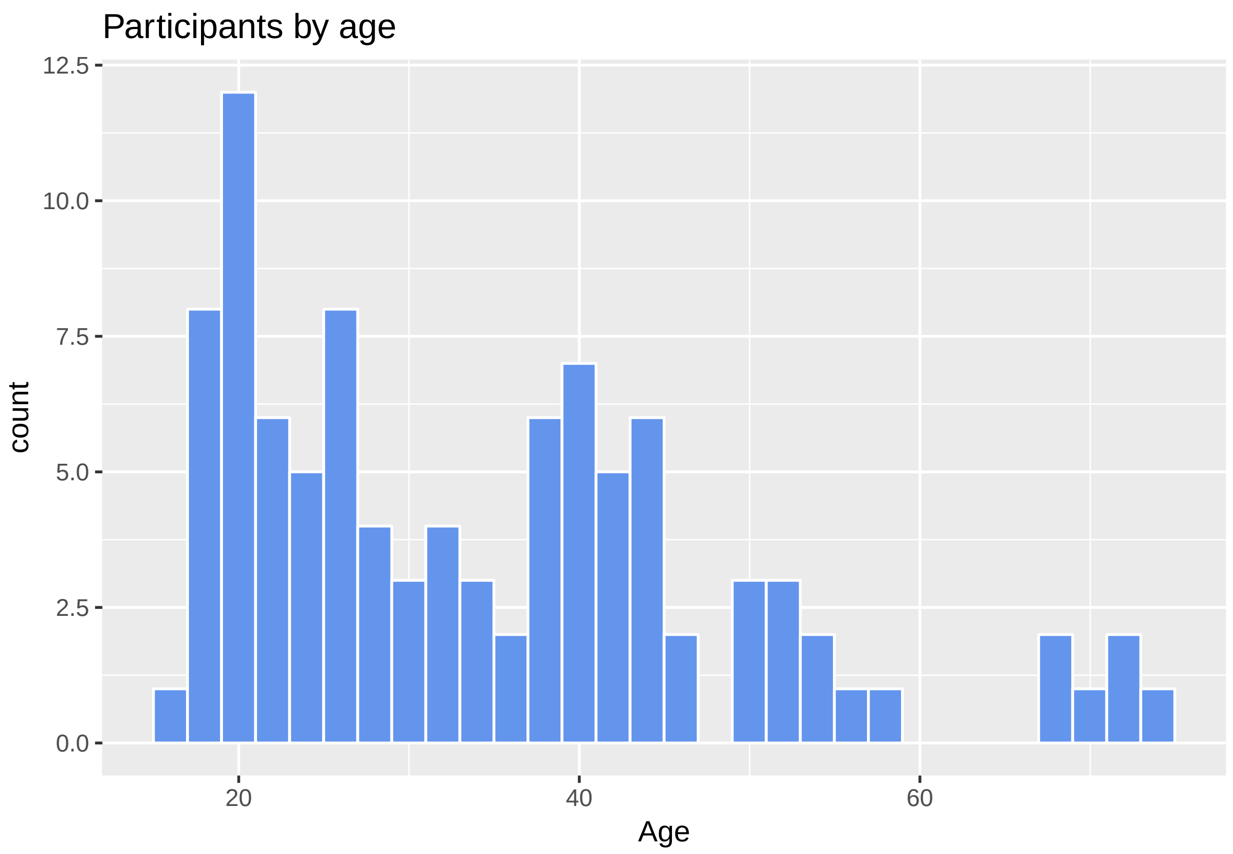


Figure 3.15: Histogram with specified fill and border colors

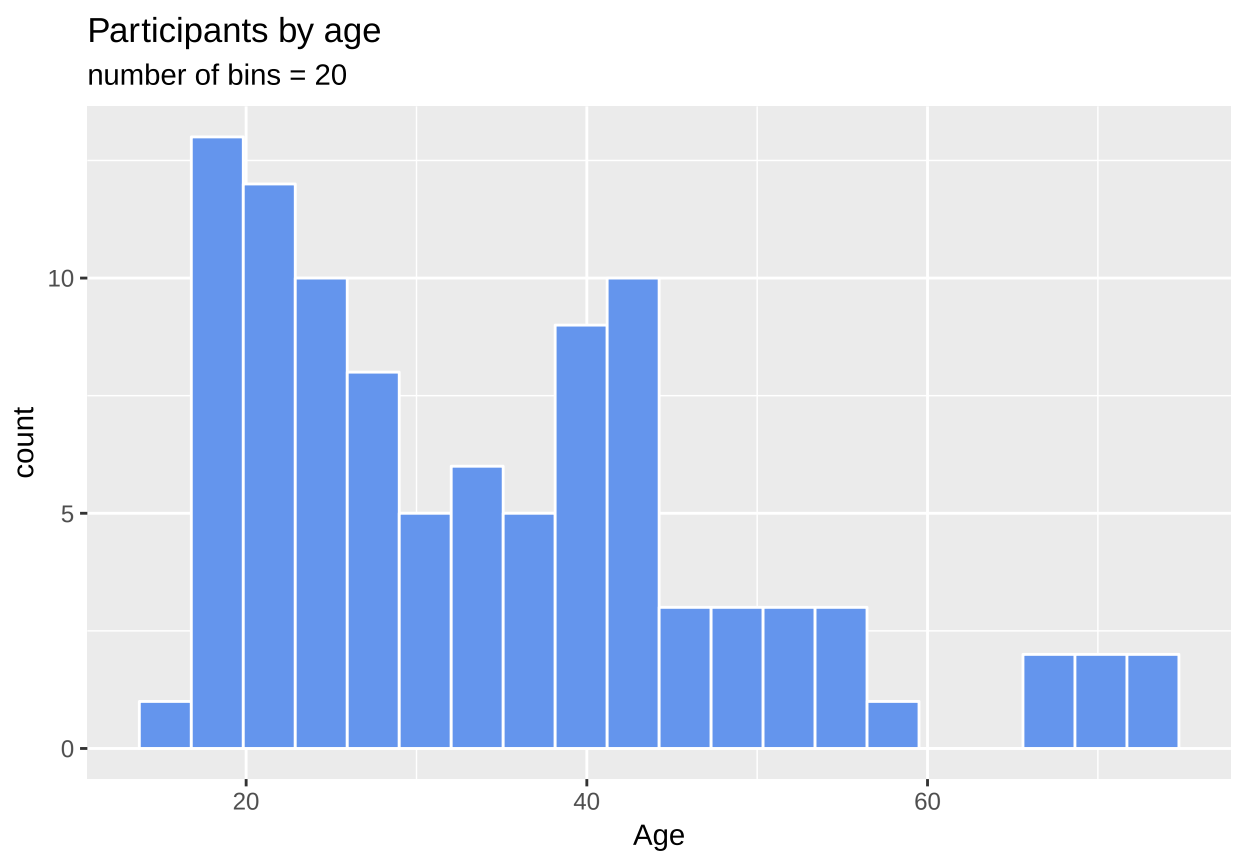


Figure 3.16: Histogram with a specified number of bins

3.2.1.1 Bins and bandwidths

One of the most important histogram options is `bins`, which controls the number of bins into which the numeric variable is divided (i.e., the number of bars in the plot). The default is 30, but it is helpful to try smaller and larger numbers to get a better impression of the shape of the distribution.

```r
# plot the histogram with 20 bins
ggplot(Marriage, aes(x = age)) +
  geom_histogram(fill = "cornflowerblue",
                 color = "white",
                 bins = 20) +
  labs(title="Participants by age",
       subtitle = "number of bins = 20",
       x = "Age")
```

Alternatively, you can specify the `binwidth`, the width of the bins represented by the bars.

```r
# plot the histogram with a binwidth of 5
ggplot(Marriage, aes(x = age)) +
  geom_histogram(fill = "cornflowerblue",
                 color = "white",
                 binwidth = 5) +
  labs(title="Participants by age",
```

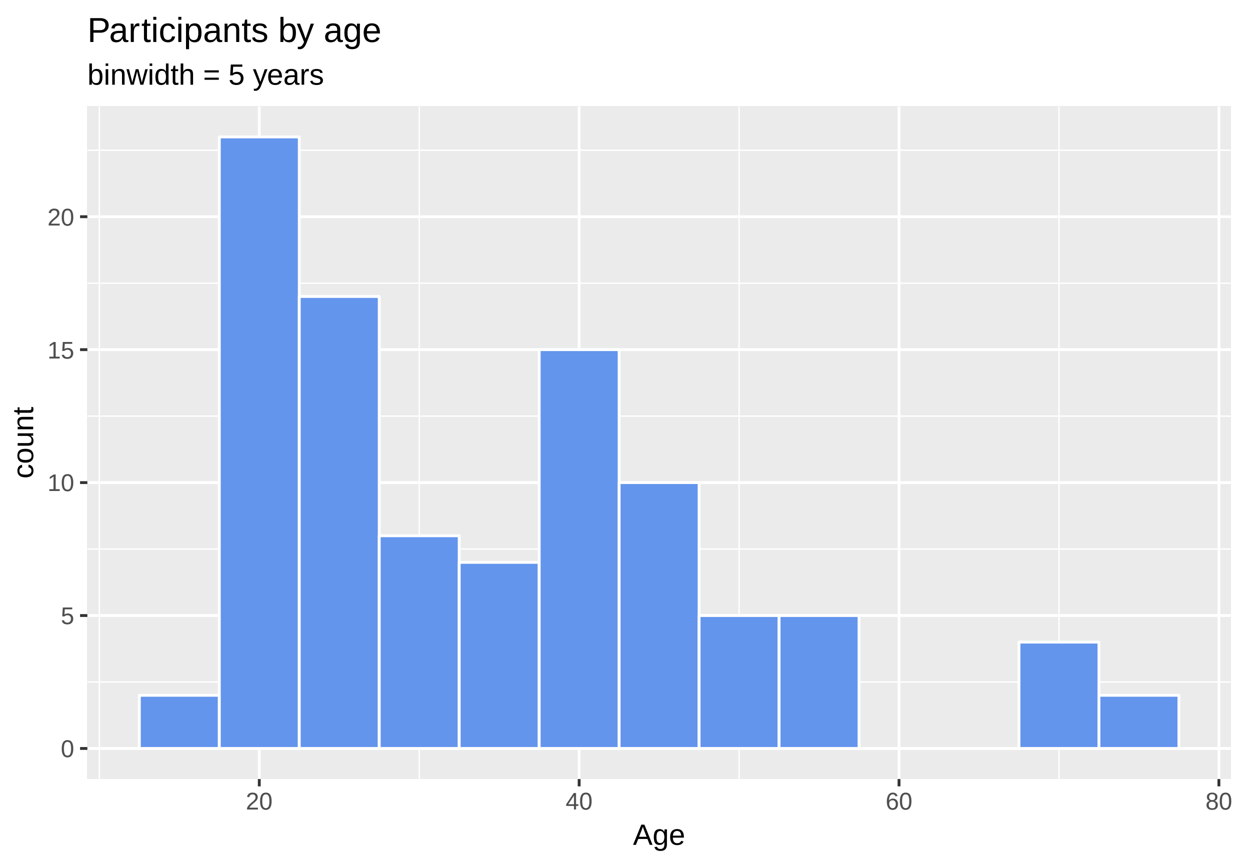
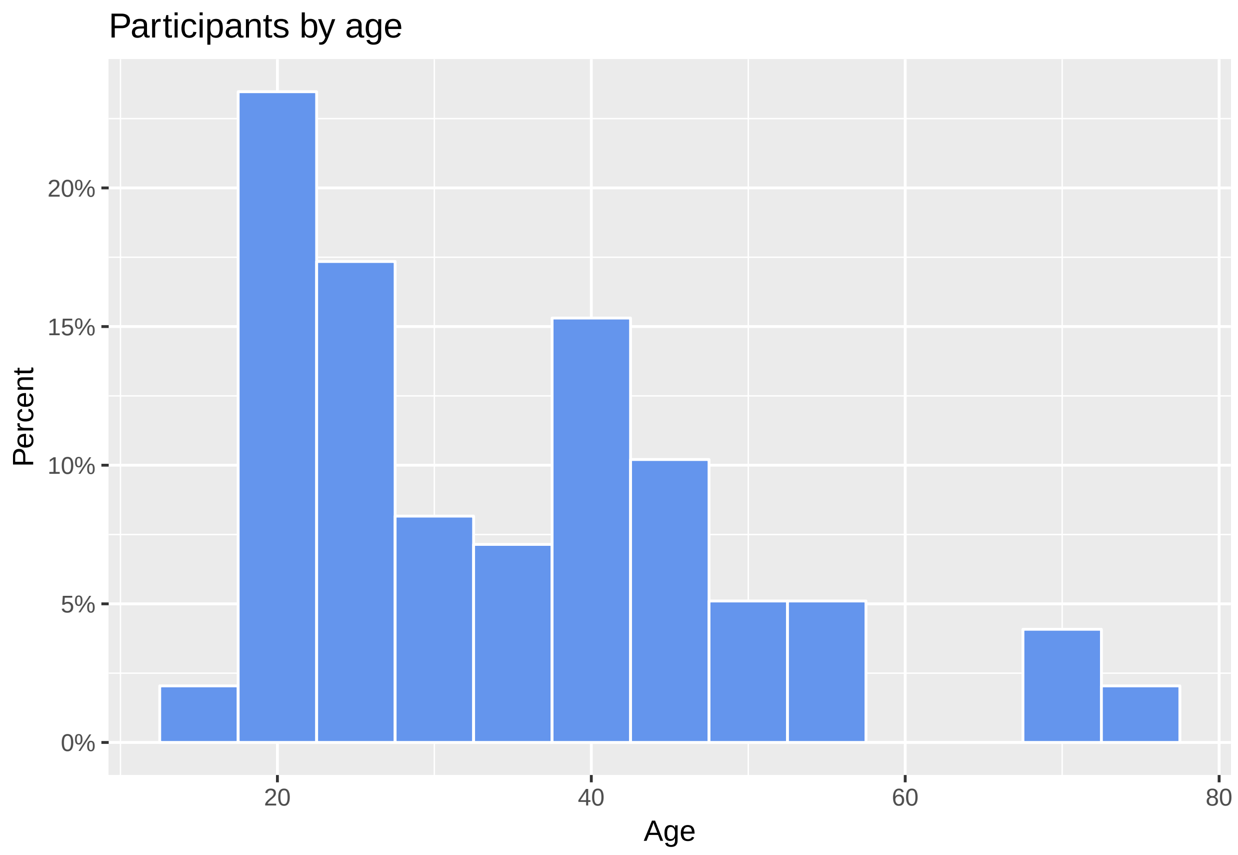


Figure 3.17: Histogram with specified a bin width

```
       subtitle = "binwidth = 5 years",
       x = "Age")
```

As with bar charts, the y-axis can represent counts or percent of the total.

```
# plot the histogram with percentages on the y-axis
library(scales)
ggplot(Marriage,
       aes(x = age,
           y= ..count.. / sum(..count..))) +
  geom_histogram(fill = "cornflowerblue",
                 color = "white",
                 binwidth = 5) +
  labs(title="Participants by age",
       y = "Percent",
       x = "Age") +
  scale_y_continuous(labels = percent)
```



### Kernel Density plot {#Kernel}

An alternative to a histogram is the kernel density plot. Technically, kernel density estimation is a nonparametric method for estimating the probability density function of a continuous random variable. (What??) Basically, we are trying to draw a smoothed histogram, where the area under the curve equals one.

```r
# Create a kernel density plot of age
ggplot(Marriage, aes(x = age)) +
  geom_density() +
  labs(title = "Participants by age")
```

The graph shows the distribution of scores. For example, the proportion of cases between 20 and 40 years old would be represented by the area under the curve between 20 and 40 on the x-axis.

As with previous charts, we can use `fill` and `color` to specify the fill and border colors.

```r
# Create a kernel density plot of age
ggplot(Marriage, aes(x = age)) +
  geom_density(fill = "indianred3") +
  labs(title = "Participants by age")
```

3.2.1.2 Smoothing parameter

The degree of smoothness is controlled by the bandwidth parameter `bw`. To find the default value for a particular variable, use the `bw.nrd0` function. Values that are larger will result in more smoothing, while values that are smaller will produce less smoothing.

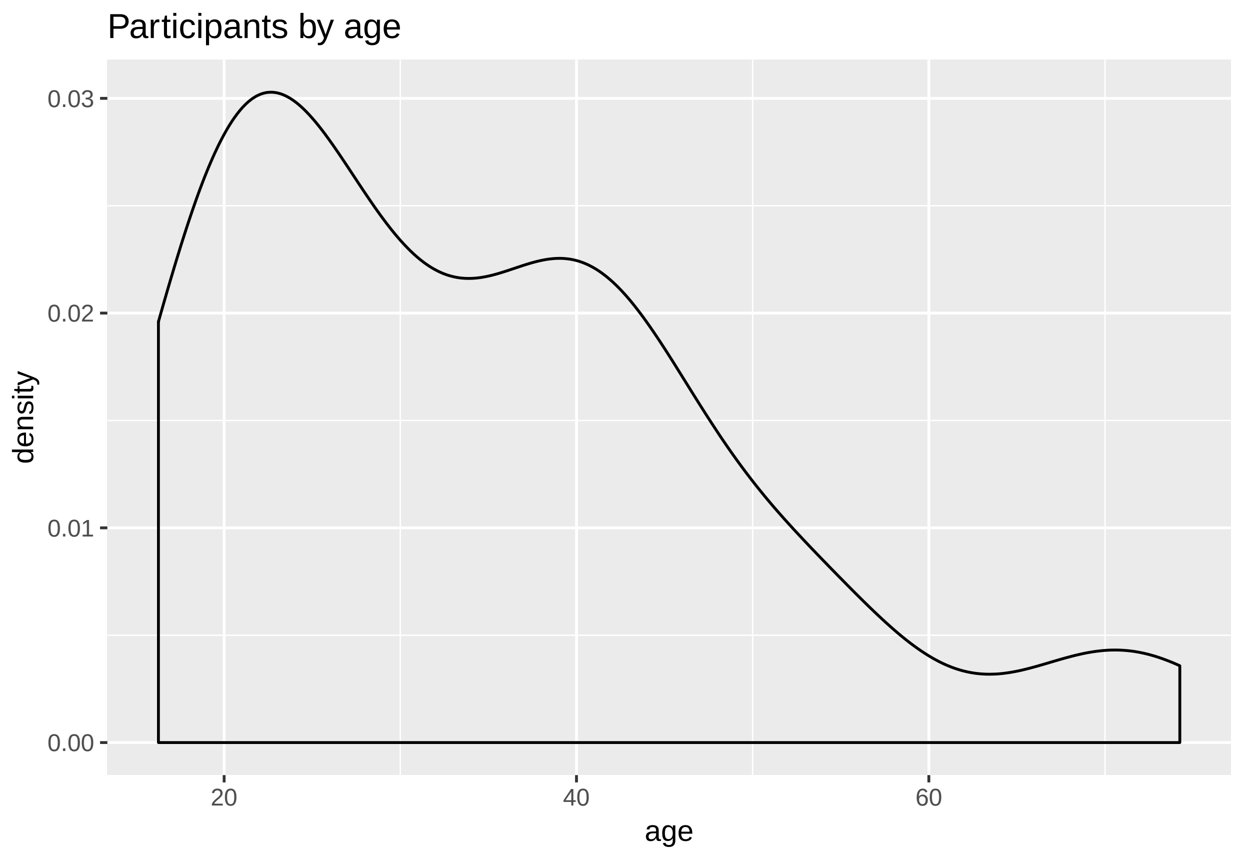


Figure 3.18: Basic kernel density plot

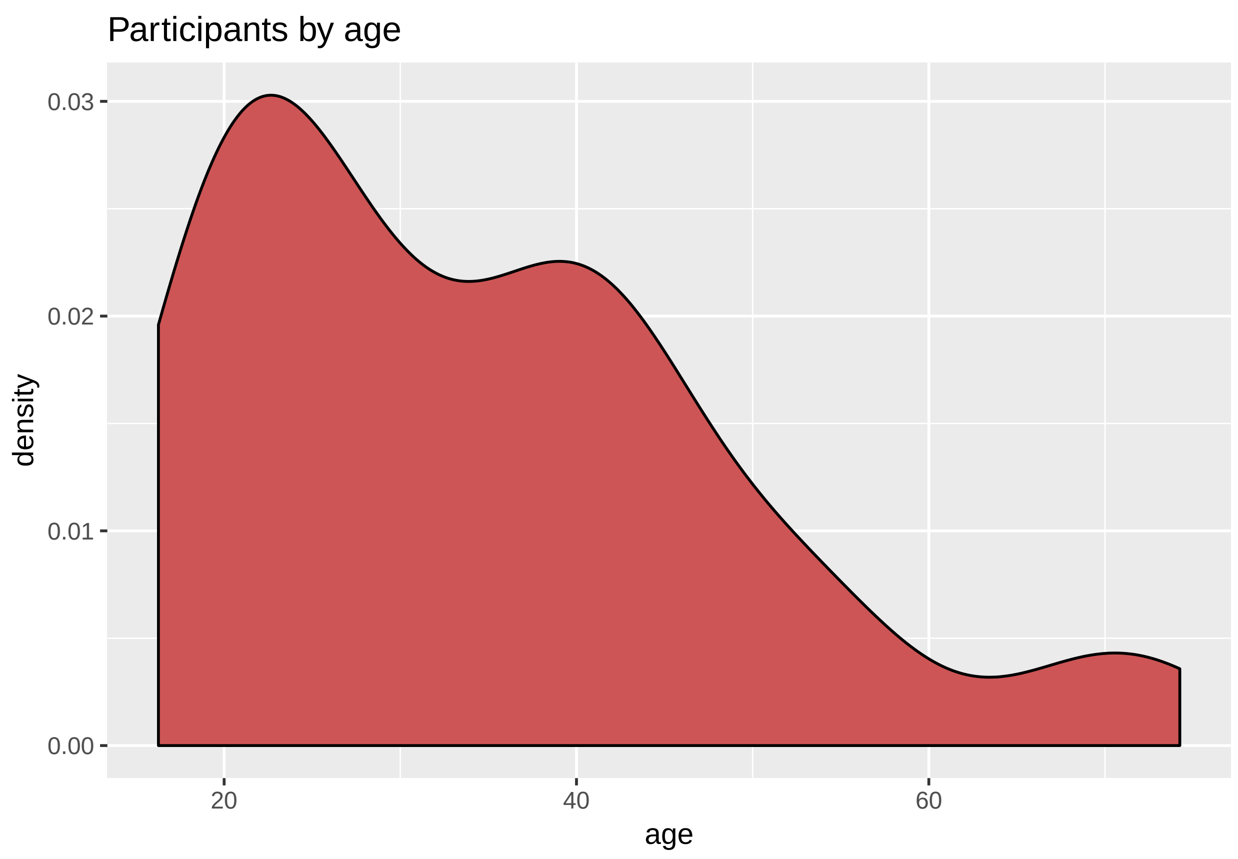


Figure 3.19: Kernel density plot with fill

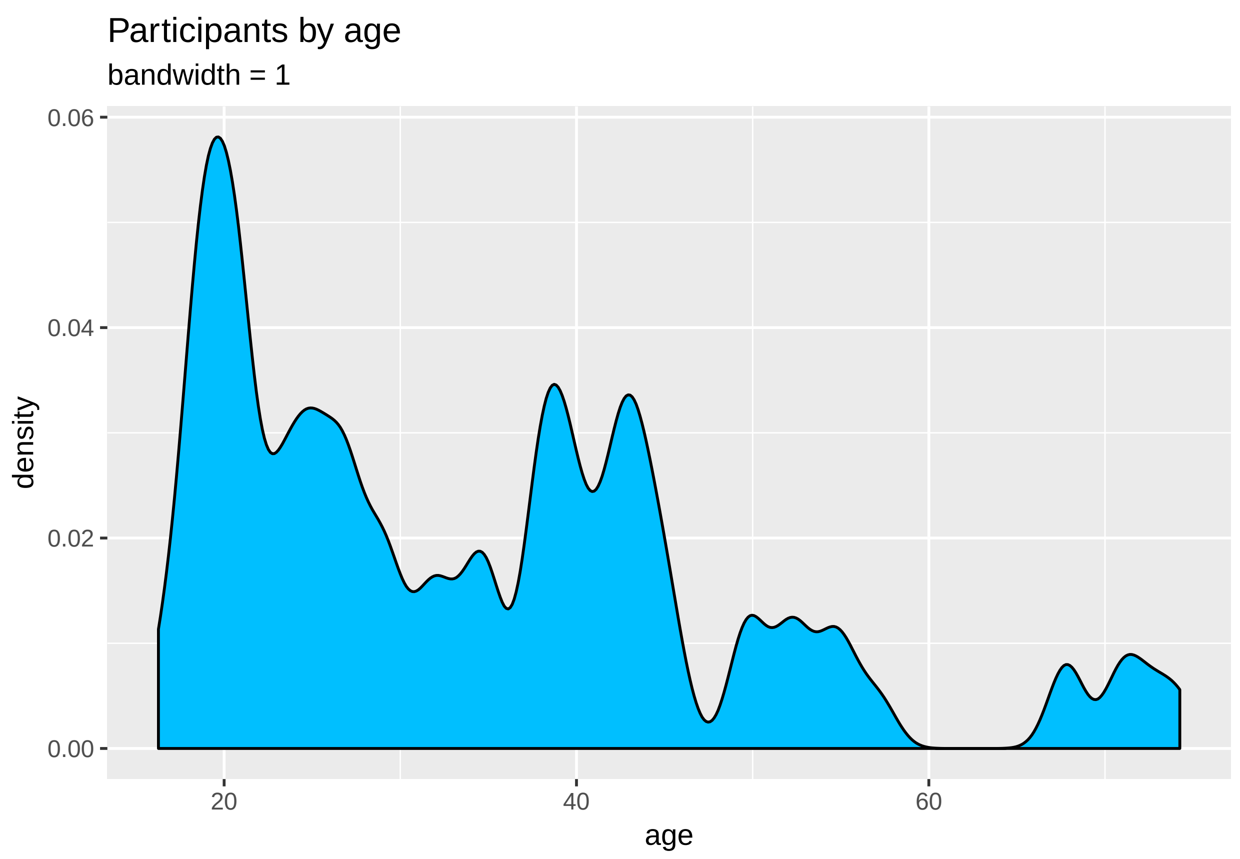


Figure 3.20: Kernel density plot with a specified bandwidth

```r
# default bandwidth for the age variable
bw.nrd0(Marriage$age)
```

```
## [1] 5.181946
```

```r
# Create a kernel density plot of age
ggplot(Marriage, aes(x = age)) +
  geom_density(fill = "deepskyblue",
               bw = 1) +
  labs(title = "Participants by age",
       subtitle = "bandwidth = 1")
```

In this example, the default bandwidth for age is 5.18. Choosing a value of 1 resulted in less smoothing and more detail.

Kernel density plots allow you to easily see which scores are most frequent and which are relatively rare. However it can be difficult to explain the meaning of the y-axis to a non-statistician. (But it will make you look really smart at parties!)

3.2.2 Dot Chart

Another alternative to the histogram is the dot chart. Again, the quantitative variable is divided into bins, but rather than summary bars, each observation is represented by a dot. By default, the width of a dot

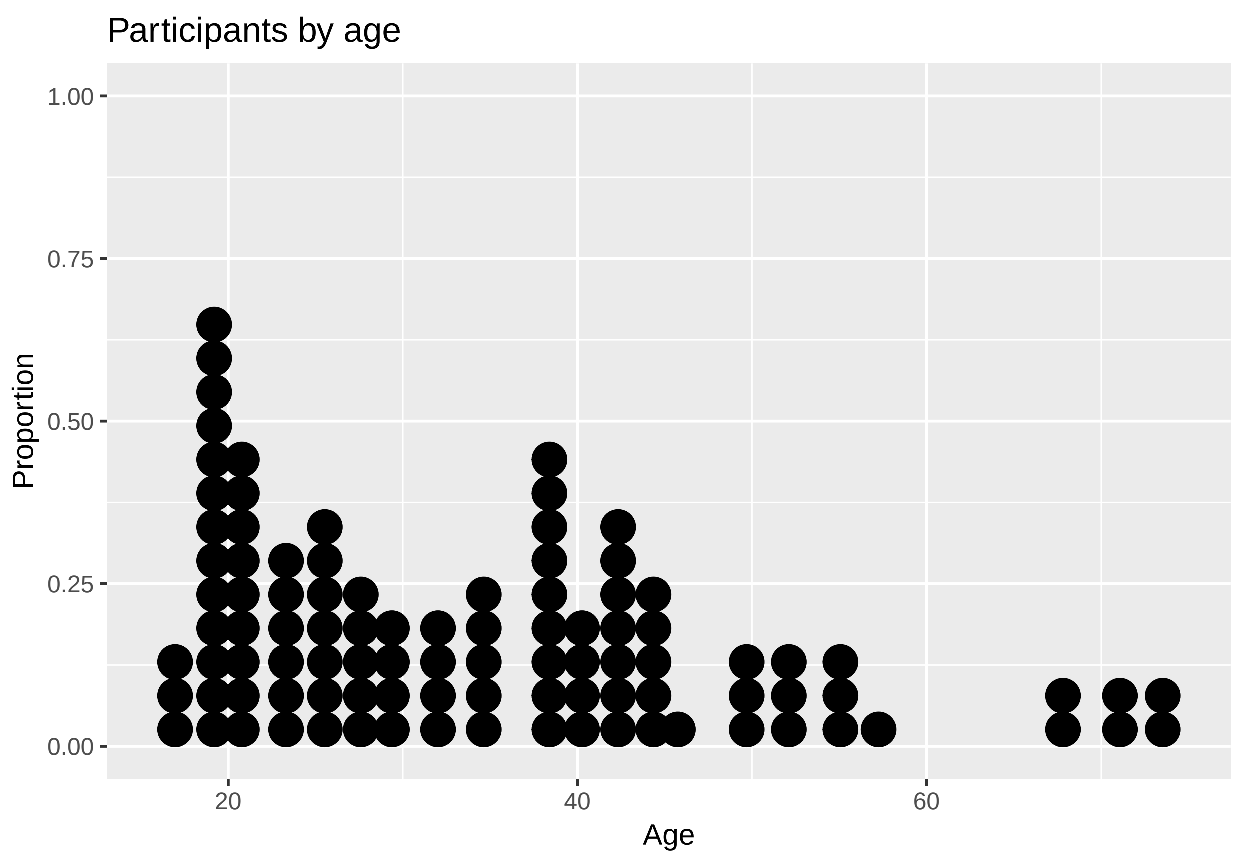


Figure 3.21: Basic dotplot

corresponds to the bin width, and dots are stacked, with each dot representing one observation. This works best when the number of observations is small (say, less than 150).

```r
# plot the age distribution using a dotplot
ggplot(Marriage, aes(x = age)) +
  geom_dotplot() +
  labs(title = "Participants by age",
       y = "Proportion",
       x = "Age")
```

The `fill` and `color` options can be used to specify the fill and border color of each dot respectively.

```r
# Plot ages as a dot plot using
# gold dots with black borders
ggplot(Marriage, aes(x = age)) +
  geom_dotplot(fill = "gold",
               color = "black") +
  labs(title = "Participants by age",
       y = "Proportion",
       x = "Age")
```

There are many more options available. See the help for details and examples.

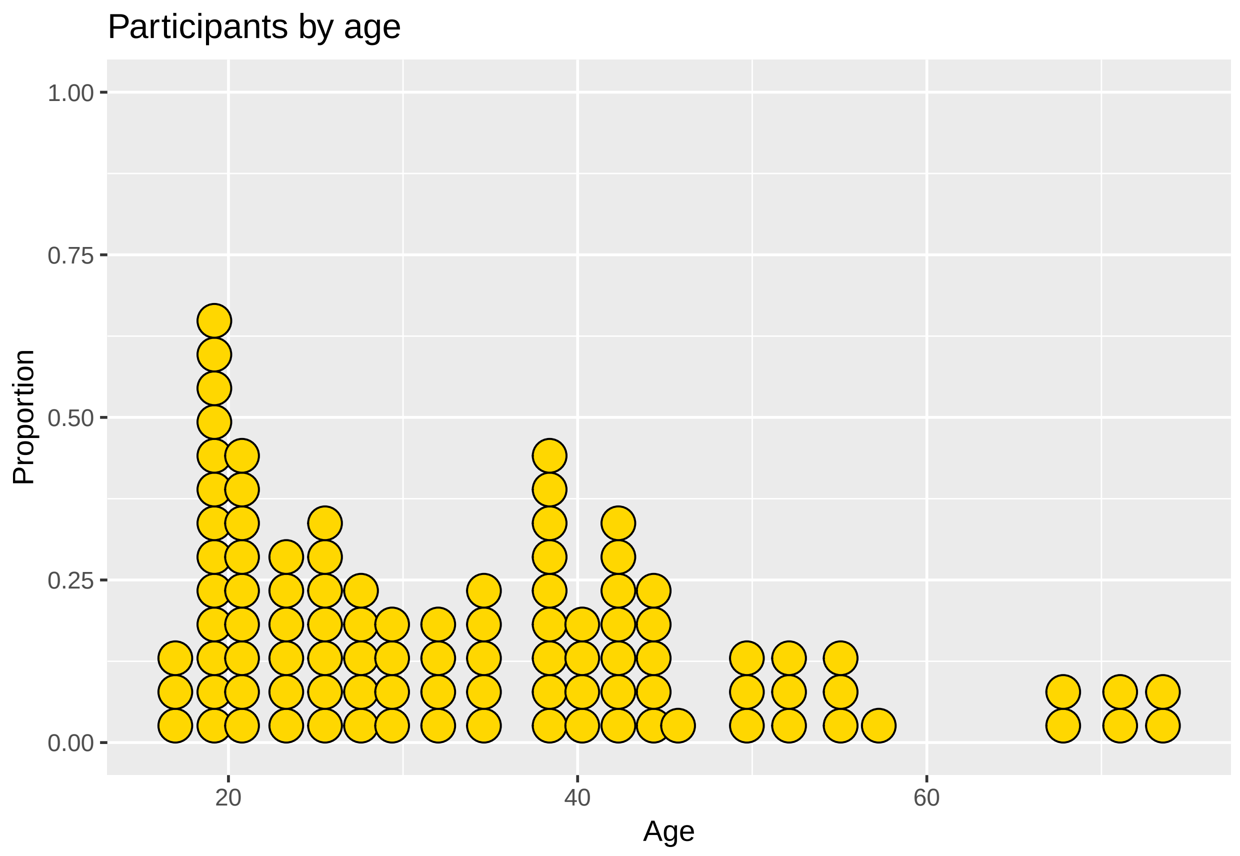


Figure 3.22: Dotplot with a specified color scheme