IS5 in R: Sample Surveys (Chapter 10)

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Introduction and background

This document is intended to help describe how to undertake analyses introduced as examples in the Fifth Edition of *Intro Stats* (2018) by De Veaux, Velleman, and Bock. More information about the book can be found at http://wps.aw.com/aw_deveaux_stats_series. This file as well as the associated R Markdown reproducible analysis source file used to create it can be found at http://nhorton.people.amherst.edu/is5.

This work leverages initiatives undertaken by Project MOSAIC (http://www.mosaic-web.org), an NSF-funded effort to improve the teaching of statistics, calculus, science and computing in the undergraduate curriculum. In particular, we utilize the mosaic package, which was written to simplify the use of R for introductory statistics courses. A short summary of the R needed to teach introductory statistics can be found in the mosaic package vignettes (http://cran.r-project.org/web/packages/mosaic). A paper describing the mosaic approach was published in the R Journal: https://journal.r-project.org/archive/2017/RJ-2017-024.

Chapter 10: Sample Surveys

```
library(mosaic)
library(readr)
library(janitor)
```

Section 10.1: The Three Big Ideas of Sampling

Section 10.2: Populations and Parameters

Section 10.3: Simple Random Samples

Random Matters

```
Births <- read_csv("http://nhorton.people.amherst.edu/is5/data/AllBirths1998.csv")

## Warning: Missing column names filled in: 'X1' [1]

## Parsed with column specification:

## cols(

## X1 = col_integer(),

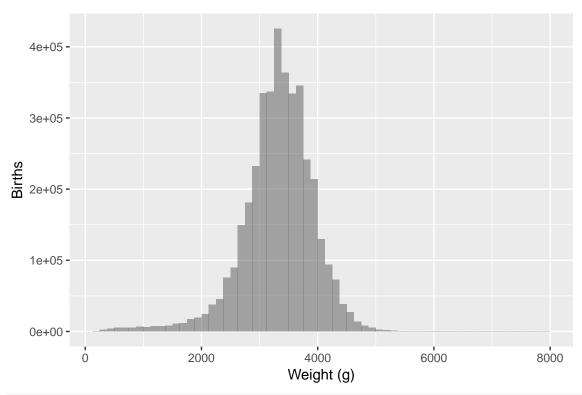
## birthweight = col_integer()

## )</pre>
```

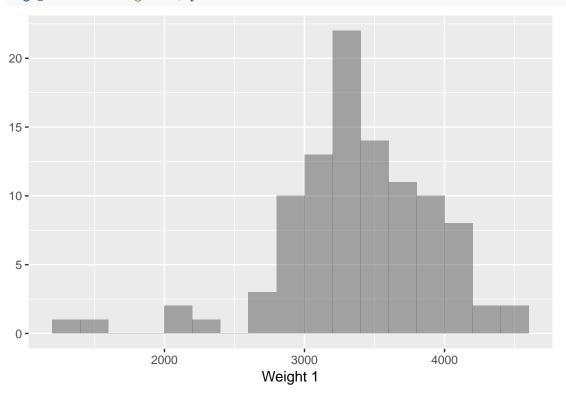
By default, read_csv() prints the variable names. These messages can be suppressed using the message = FALSE code chunk option to save space and improve readability.

```
gf_histogram(~ birthweight, data = Births, binwidth = 125, center = 62.5) %>%
gf_labs(x = "Weight (g)", y = "Births")
```

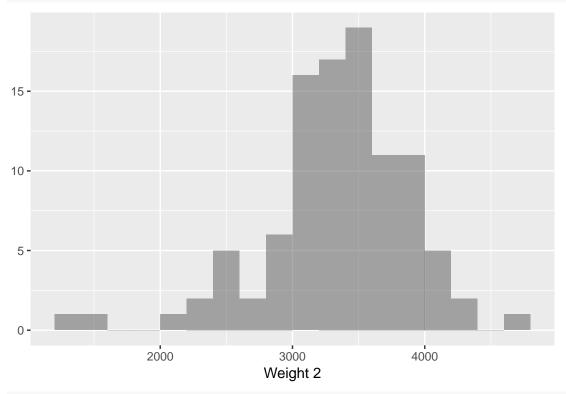
Warning: Removed 4640 rows containing non-finite values (stat_bin).



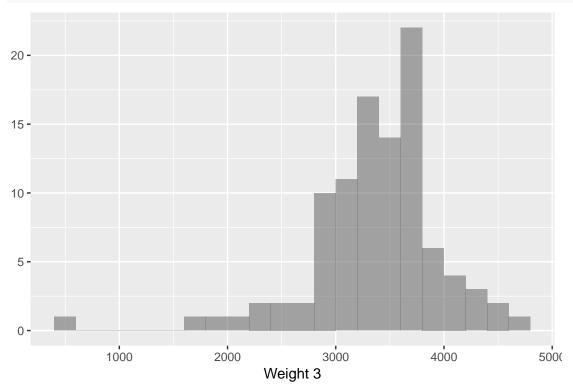
```
# Samples of 100
set.seed(12452)
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 1", y = "")
```



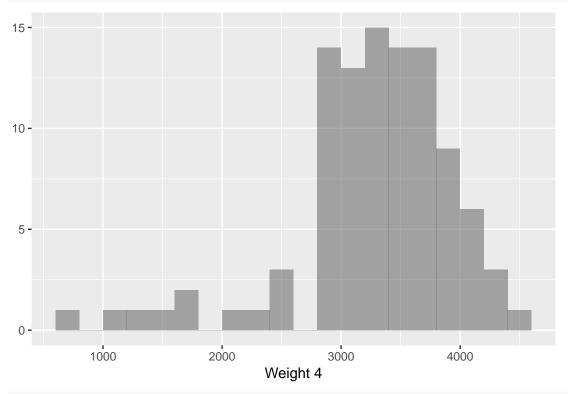
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 2", y = "")



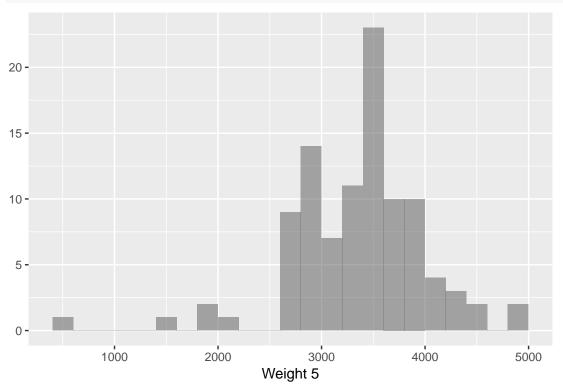
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 3", y = "")



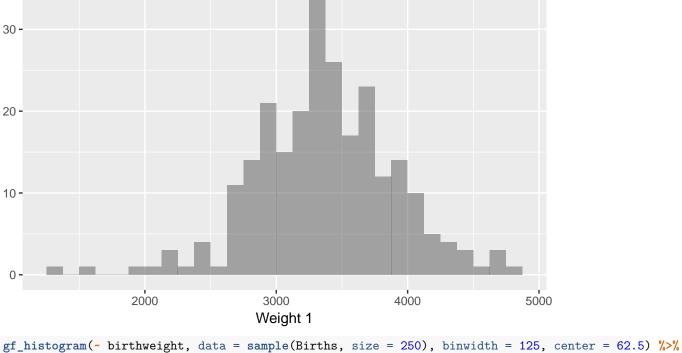
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 4", y = "")



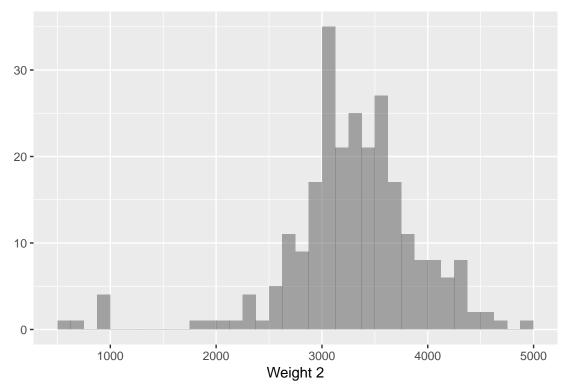
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 5", y = "")



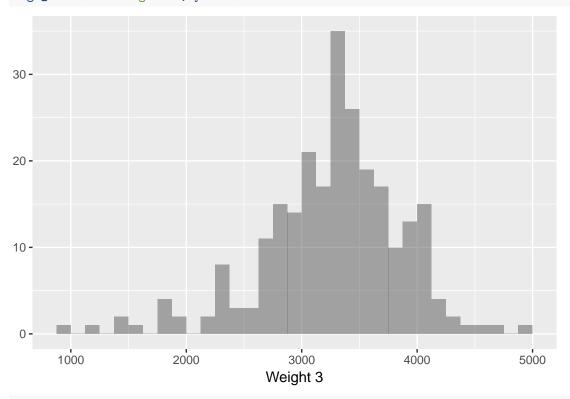
```
# Samples of 250
set.seed(12452)
gf_histogram(~ birthweight, data = sample(Births, size = 250), binwidth = 125, center = 62.5) %>%
gf_labs(x = "Weight 1", y = "")
```



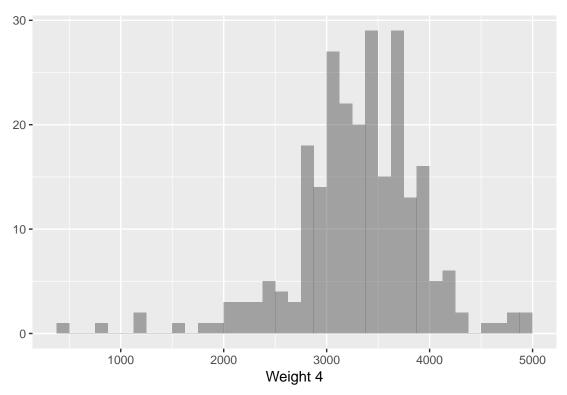
gf_histogram(~ birthweight, data = sample(Births, size = 250), binwidth = 125, center = 62.5) %>7
gf_labs(x = "Weight 2", y = "")



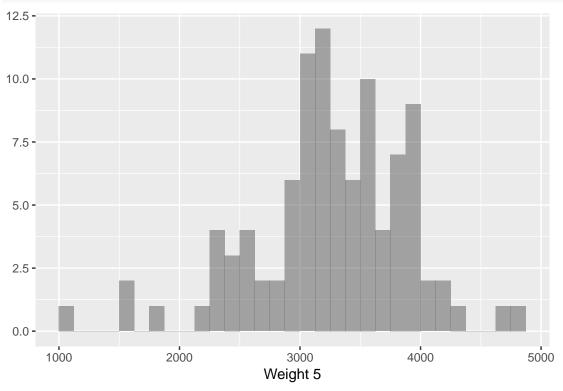
gf_histogram(~ birthweight, data = sample(Births, size = 250), binwidth = 125, center = 62.5) %>%
gf_labs(x = "Weight 3", y = "")



gf_histogram(~ birthweight, data = sample(Births, size = 250), binwidth = 125, center = 62.5) %>%
gf_labs(x = "Weight 4", y = "")



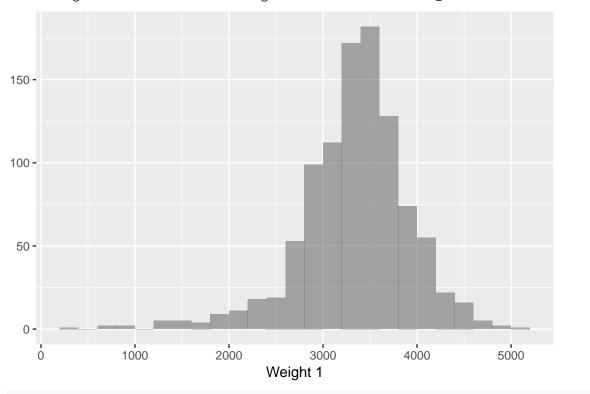
gf_histogram(~ birthweight, data = sample(Births, size = 100), binwidth = 125, center = 62.5) %>%
gf_labs(x = "Weight 5", y = "")



```
# Samples of 1000
set.seed(12452)
gf_histogram(~ birthweight, data = sample(Births, size = 1000), binwidth = 200, center = 100) %>%
```

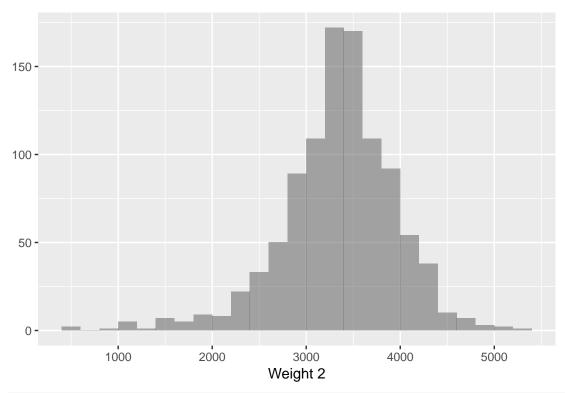
```
gf_labs(x = "Weight 1", y = "")
```

Warning: Removed 3 rows containing non-finite values (stat_bin).

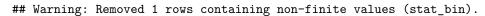


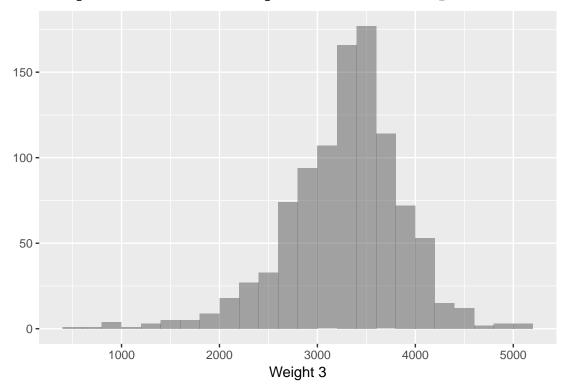
```
gf_histogram(~ birthweight, data = sample(Births, size = 1000), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 2", y = "")
```

Warning: Removed 1 rows containing non-finite values (stat_bin).



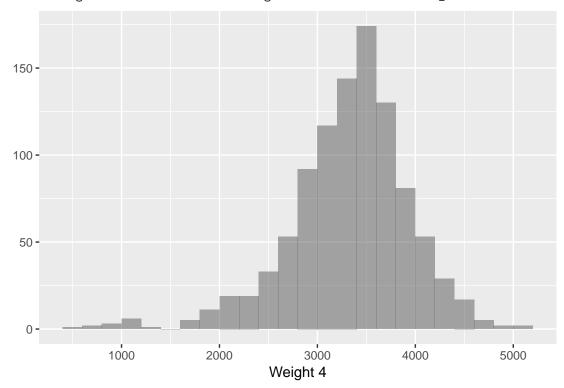
gf_histogram(~ birthweight, data = sample(Births, size = 1000), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 3", y = "")



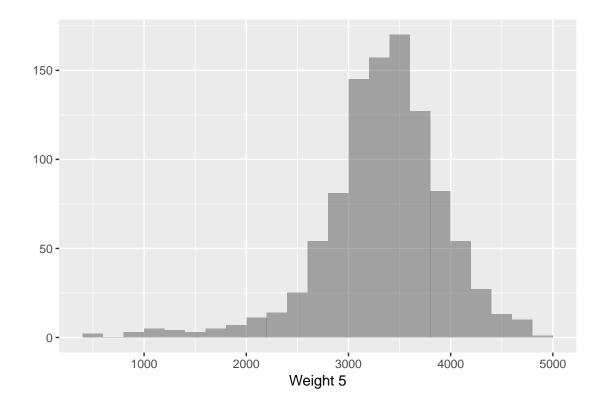


```
gf_histogram(~ birthweight, data = sample(Births, size = 1000), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 4", y = "")
```

Warning: Removed 1 rows containing non-finite values (stat_bin).



```
gf_histogram(~ birthweight, data = sample(Births, size = 1000), binwidth = 200, center = 100) %>%
gf_labs(x = "Weight 5", y = "")
```



Section 10.4: Other Sampling Designs

Section 10.5: From the Population to the Sample: You Can't Always Get What You Want

Section 10.6: The Valid Survey

Section 10.7: Common Sampling Mistakes, or How to Sample Badly