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. This file as well as the associated Quarto 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 (https://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.

We begin by loading packages that will be required for our analyses.

```
library(mosaic)
library(tidyverse)
```

Chapter 10: Sample Surveys

Section 10.1: The Three Big Ideas of Sampling

Section 10.2: Populations and Parameters

Section 10.3: Simple Random Samples

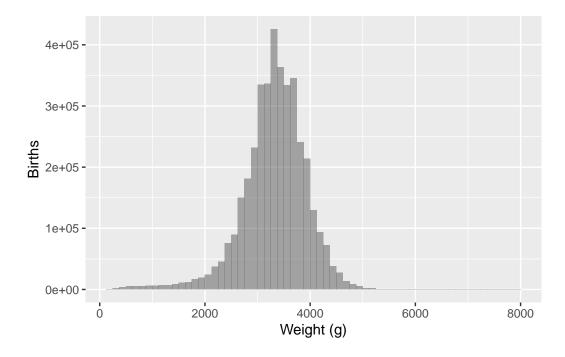
Random Matters

We begin by loading in the data on birthweights.

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

By default, read_csv() prints the variable names. These messages were suppressed using the message: false code chunk option to save space and improve readability.

```
# Histogram of known population
gf_histogram(~ birthweight, data = Births, binwidth = 125, center = 62.5) |>
gf_labs(x = "Weight (g)", y = "Births")
```

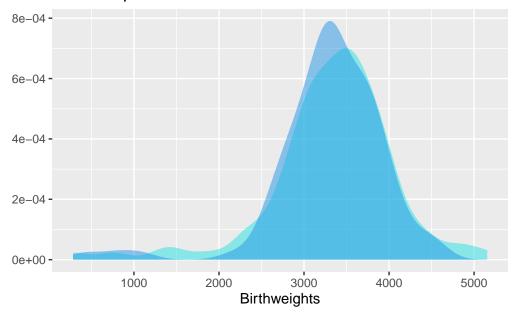


The histogram shows the distribution of the population of nearly four million births. Warning messages about missing values were suppressed using the warnings: false code chunk option.

Figure 10.2 (page 326):

```
# Samples of 100
set.seed(12452)
gf_density(~ birthweight, data = sample(Births, size = 100), fill = 5) |>
    gf_density(~ birthweight, data = sample(Births, size = 100), fill = 4) |>
    gf_labs(x = "Birthweights", y = "", title = "Two Samples of Size 100")
```

Two Samples of Size 100

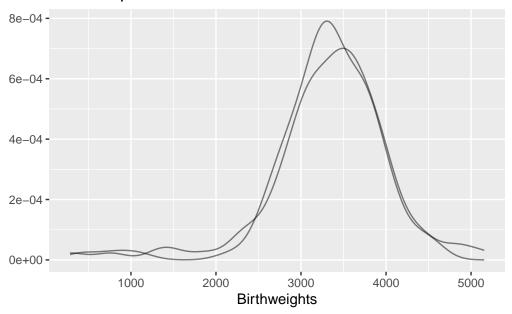


Here we set an (arbitrary) random number seed (12452). This sets our location in a long list of pseudo-random numbers. Use of a seed in this manner allows us to rerun the code and get the same answer.

It's not necessarily a best practice to display overlapping densities (or histograms). Perhaps a better approach would be to use gf_dens() to only display the line.

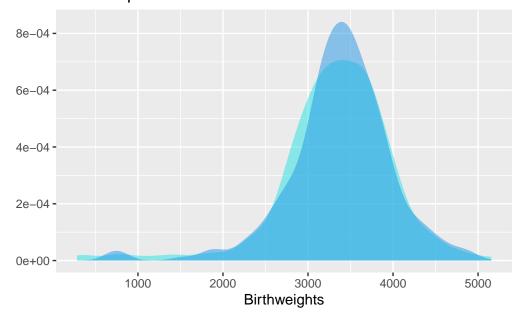
```
set.seed(12452)
gf_dens(~ birthweight, data = sample(Births, size = 100)) |>
    gf_dens(~ birthweight, data = sample(Births, size = 100)) |>
    gf_labs(x = "Birthweights", y = "", title = "Two Samples of Size 100")
```

Two Samples of Size 100



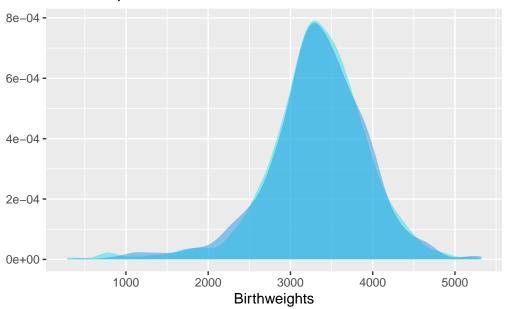
```
# Samples of 250
set.seed(12452)
gf_density(~ birthweight, data = sample(Births, size = 250), fill = 5) |>
    gf_density(~ birthweight, data = sample(Births, size = 250), fill = 4) |>
    gf_labs(x = "Birthweights", y = "", title = "Two Samples of Size 250")
```

Two Samples of Size 250



```
# Samples of 1000
set.seed(12452)
gf_density(~ birthweight, data = sample(Births, size = 1000), fill = 5) |>
    gf_density(~ birthweight, data = sample(Births, size = 1000), fill = 4) |>
    gf_labs(x = "Birthweights", y = "", title = "Two Samples of Size 1000")
```

Two Samples of Size 1000



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