IS5 in R: More About Tests and Intervals (Chapter 16)

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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 16: More About Tests and Intervals

Section 16.1: Interpreting P-Values

What to Do with a Low P-Value

What to Do with a High P-Value

No need for tables: we can calculate everything in R!

curve on page 511
xqnorm(p = .467, mean = 0, sd = 1, verbose = FALSE)



[1] -0.08281329

Section 16.2: Alpha Levels and Critical Values

Figure 16.1, page 513
xpnorm(q = c(-1.96, 1.96), mean = 0, sd = 1, verbose = FALSE)



[1] 0.0249979 0.9750021

Section 16.3: Practical vs. Statistical Significance

Section 16.4: Errors

Power

Effect Size

A Picture Worth $\frac{1}{P(z > 3.09)}$ Words

When in doubt, draw a picture!

```
# Figure 16.2, page 520
gf_dist("norm",
    mean = 0, sd = 1, fill = ~ cut(x, c(-Inf, 2, 100, Inf)), geom = "area",
    alpha = .5
) |>
    gf_dist("norm",
        mean = 4, sd = 1, fill = ~ cut(x, c(-Inf, -100, 2, Inf)), geom = "area",
        alpha = .5
    ) |>
    gf_labs(x = "p", y = "") |>
```

```
gf_vline(xintercept = 2) |>
gf_refine(annotate(geom = "text", x = .75, y = .42, label = "Fail to Reject HO")) |>
gf_refine(annotate(geom = "text", x = 2.95, y = .42, label = "Reject HO")) |>
gf_refine(annotate(geom = "text", x = 0, y = .15, size = 3, label = "Suppose HO is true"))
gf_refine(annotate(geom = "text", x = 1.35, y = .01, size = 2.5, label = "Type 2 Error"))
gf_refine(annotate(geom = "text", x = 2.6, y = .01, size = 2.5, label = "Type 1 Error")) |1
gf_refine(annotate(geom = "text", x = 4, y = .15, size = 3, label = "Suppose HO is not true"))
```

