

# IS5 in R: Linear Regression (Chapter 7)

Nicholas Horton (nhorton@amherst.edu)

December 19, 2020

## 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 R Markdown reproducible analysis source file used to create it can be found at <http://nhorton.people.amherst.edu/is5>.

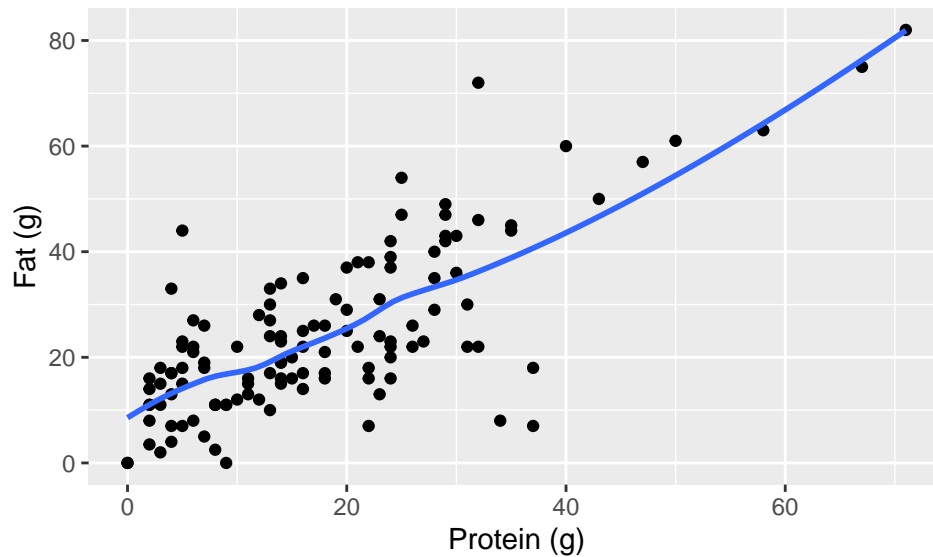
This work leverages initiatives undertaken by Project MOSAIC (<http://www.mosaic-web.org>), an NSF-funded effort to improve the teaching of statistics, calculus, science and computing in the undergraduate curriculum. In particular, we utilize the `mosaic` package, which was written to simplify the use 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 (<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>.

## Chapter 7: Linear Regression

```
library(mosaic)
library(readr)
library(janitor)
# Figure 7.1
BurgerKing <- read_csv("http://nhorton.people.amherst.edu/is5/data/Burger_King_items.csv") %>%
  janitor::clean_names()
```

By default, `read_csv()` prints the variable names. These messages have been suppressed using the `message=FALSE` code chunk option to save space and improve readability. Here we use the `clean_names()` function from the `janitor` package to sanitize the names of the columns (which would otherwise contain special characters or whitespace).

```
gf_point(fat_g ~ protein_g, data = BurgerKing) %>%
  gf_smooth() %>%
  gf_labs(x = "Protein (g)", y = "Fat (g)")
```



Here we add a smoother to show a clearer picture of the relationship.

### Section 7.1: Least Squares: The Line of “Best Fit”

See display on page 197.

We can calculate the residual for a particular value with 31 grams of protein by creating an function called `burgerfun` using the `mosaic::makeFun()` function.

```
burgerlm <- lm(fat_g ~ protein_g, data = BurgerKing)
burgerfun <- makeFun(burgerlm)
burgerfun(protein_g = 31)
```

```
##          1
## 36.70931
```

### Section 7.2: The Linear Model

```
coef(burgerlm)
```

```
## (Intercept)  protein_g
##   8.4021494    0.9131343
```

```
burgerfun(protein_g = 0)
```

```
##          1
## 8.402149
```

```
burgerfun(32) - burgerfun(31)
```

```
##          1
## 0.9131343
```

```
msummary(burgerlm)
```

```
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.40215    1.60400   5.238 7.02e-07 ***
## protein_g    0.91313    0.07177  12.723 < 2e-16 ***
##
## Residual standard error: 10.57 on 120 degrees of freedom
```

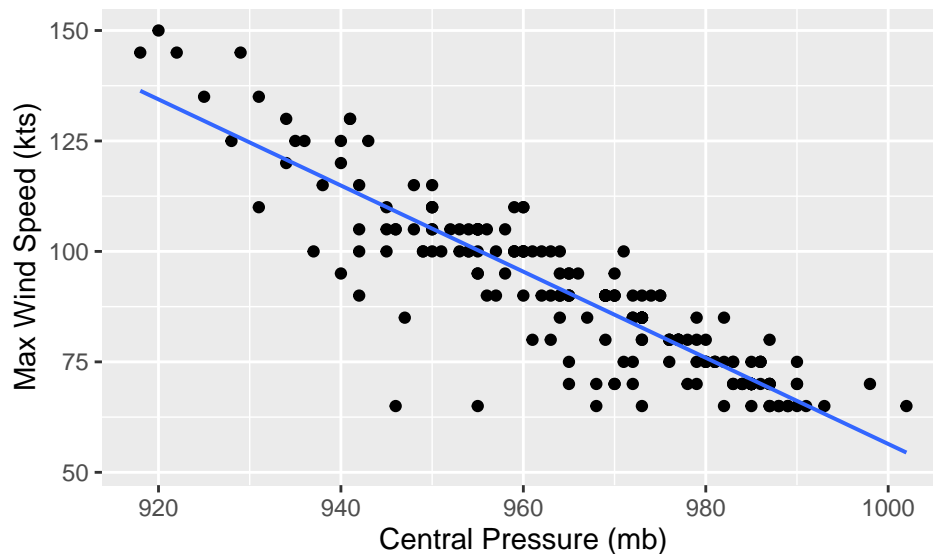
```
## Multiple R-squared:  0.5743, Adjusted R-squared:  0.5707
## F-statistic: 161.9 on 1 and 120 DF,  p-value: < 2.2e-16
```

**Example 7.1: A Linear Model for Hurricanes** We begin by reading in the data.

```
Hurricanes <- read_csv("http://nhorton.people.amherst.edu/is5/data/Hurricanes_2015.csv") %>%
  janitor::clean_names()
gf_point(max_wind_speed_kts ~ central_pressure_mb, data = Hurricanes) %>%
  gf_lm() %>%
  gf_labs(x = "Central Pressure (mb)", y = "Max Wind Speed (kts)")
```

```
## Warning: Removed 7 rows containing non-finite values (stat_lm).
```

```
## Warning: Removed 7 rows containing missing values (geom_point).
```



The function generates a warning because some of the data are missing: this output can (and should!) be suppressed by adding `warning=FALSE` as an option in this code chunk. Later examples will suppress this extraneous output.

### Section 7.3: Finding the Least Squares Line

```
df_stats(~protein_g, data = BurgerKing)
```

**Example 7.2: Finding the Regression Equation**

```
##      response min Q1 median   Q3 max      mean      sd  n missing
## 1 protein_g   0  7  15.5 24.75  71 17.93443 13.38911 122      0
```

```
df_stats(~fat_g, data = BurgerKing)
```

```
##      response min   Q1 median Q3 max      mean      sd  n missing
## 1   fat_g   0 14.25   22  33  82 24.77869 16.13362 122      0
```

```
sx <- sd(~protein_g, data = BurgerKing)
sx
```

```
## [1] 13.38911
```

```
sy <- sd(~fat_g, data = BurgerKing)
sy
```

```
## [1] 16.13362
r <- cor(protein_g ~ fat_g, data = BurgerKing)
r # same as cor(fat_g ~ protein_g)!

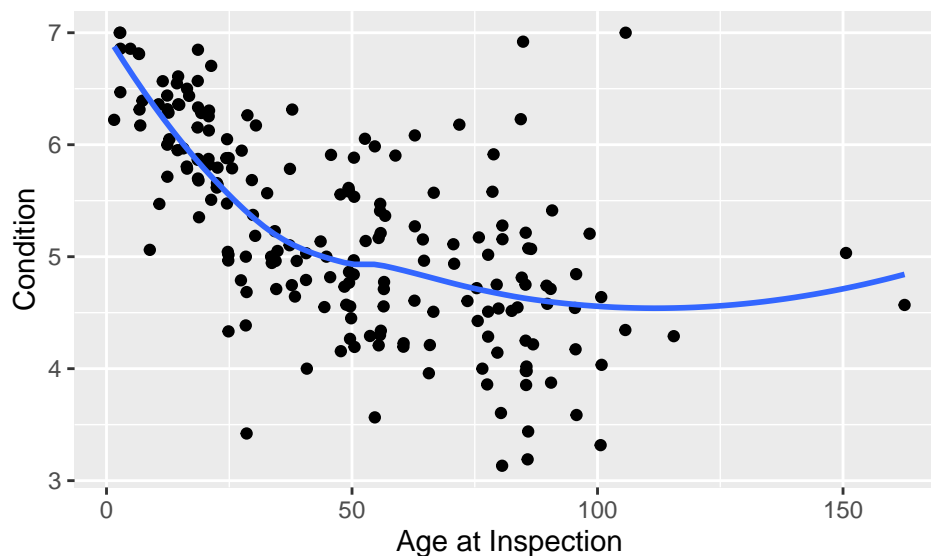
## [1] 0.7578003
r * sy / sx

## [1] 0.9131343
coef(burgerlm)[2]

## protein_g
## 0.9131343
```

**Step-by-Step Example: Calculating a Regression Equation** We begin by loading the bridge dataset.

```
TompkinsBridges <-
  read_csv("http://nhorton.people.amherst.edu/is5/data/Tompkins_county_bridges_2016.csv") %>%
  janitor::clean_names()
gf_point(condition ~ age_at_inspection, data = TompkinsBridges) %>%
  gf_smooth() %>% # To show relationship
  gf_labs(x = "Age at Inspection", y = "Condition")
```



See calculations on page 203.

#### Section 7.4: Regression to the Mean

See Figure 7.4 on page 205 to visualize standard deviations.

#### Section 7.5: Examining the Residuals

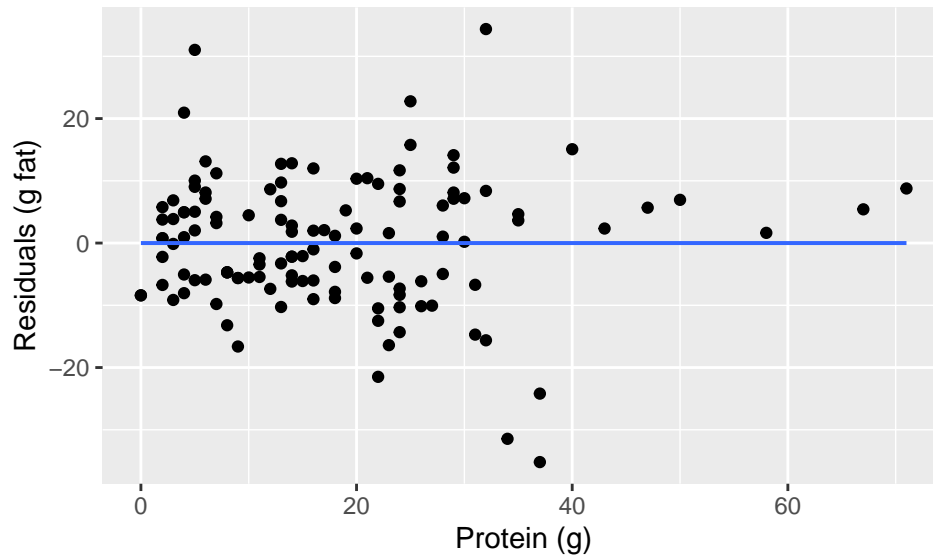
```
msummary(burgerlm)

##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  8.40215    1.60400   5.238 7.02e-07 ***
## protein_g    0.91313    0.07177  12.723 < 2e-16 ***
```

```
##
## Residual standard error: 10.57 on 120 degrees of freedom
## Multiple R-squared:  0.5743, Adjusted R-squared:  0.5707
## F-statistic: 161.9 on 1 and 120 DF,  p-value: < 2.2e-16
```

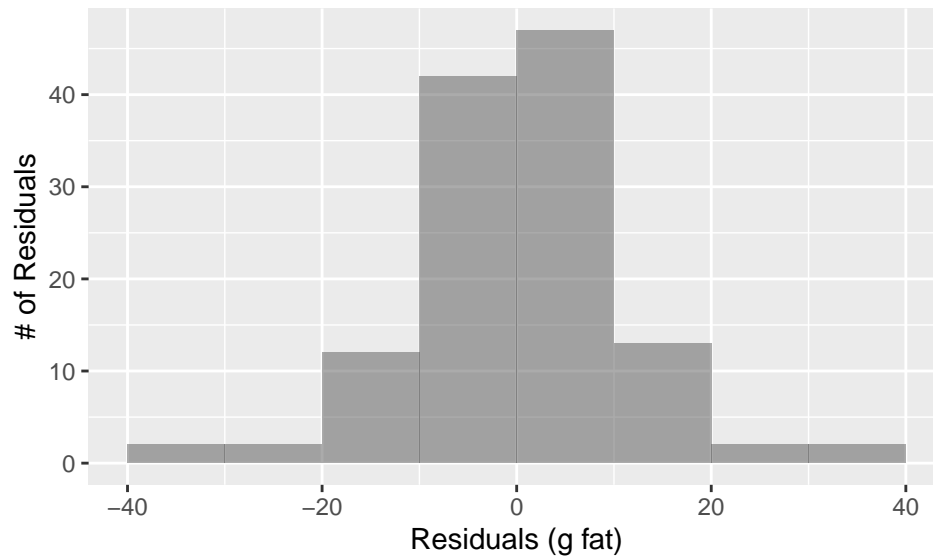
*# Figure 7.5 , page 207*

```
gf_point(resid(burgerlm) ~ protein_g, data = BurgerKing) %>%
  gf_lm() %>%
  gf_labs(x = "Protein (g)", y = "Residuals (g fat)")
```



*# Figure 7.6*

```
gf_histogram(~ resid(burgerlm), binwidth = 10, center = 5) %>%
  gf_labs(x = "Residuals (g fat)", y = "# of Residuals")
```



## Section 7.6: $R^2$ —The Proportion of Variation Accounted for by the Model

```
rsquared(burgerlm)
```

```
## [1] 0.5742613
```

## Section 7.7: Regression Assumptions and Conditions