SDM4 in R: Linear Regression (Chapter 7)

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Introduction and background

This document is intended to help describe how to undertake analyses introduced as examples in the Fourth Edition of *Stats: Data and Models* (2014) 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/sdm4.

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 7: Linear Regression

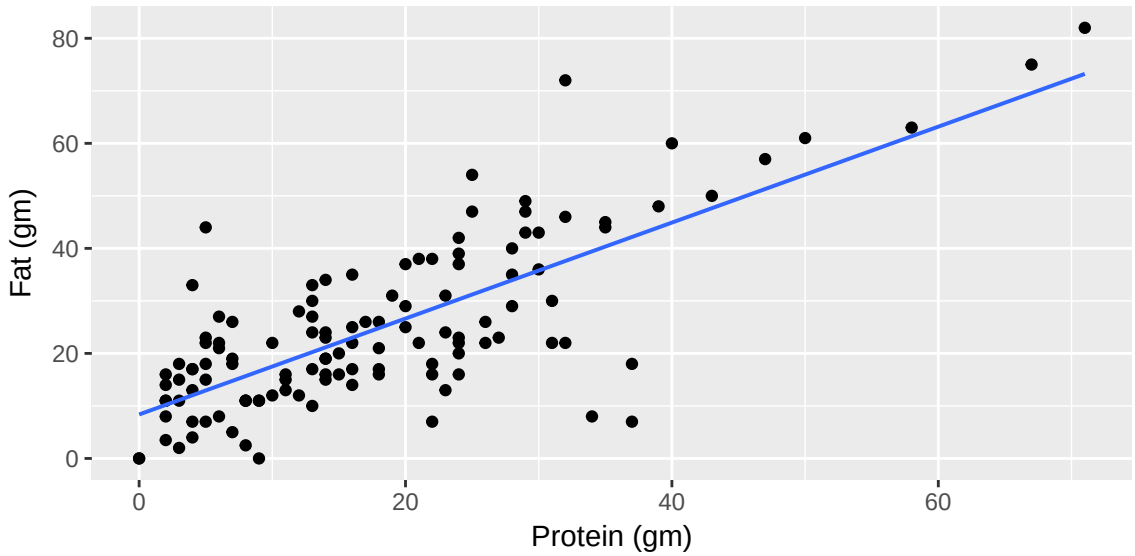
Section 7.1: Least squares: the line of best fit

Figure 7.2 (page 183) displays a scatterplot of the Burger King data with a superimposed regression line.

```
library(mosaic)
library(readr)
options(digits = 3)
BK <- read_csv("http://nhorton.people.amherst.edu/sdm4/data/Burger_King_Items.csv")
names(BK)
```

```
##  [1] "Item"        "Servingsize" "Calories"    "Fatcal"      "Fat"
##  [6] "Sat"         "Transfat(g)" "Chol(mg)"    "Sodium(mg)"  "Carb(g)"
## [11] "Fiber(g)"    "Sugar(g)"    "Protein"
```

```
gf_point(Fat ~ Protein, ylab = "Fat (gm)", xlab = "Protein (gm)", data = BK) %>%
  gf_lm()
```



We can calculate the residual for a particular value with 31 grams of protein.

```
BKmod <- lm(Fat ~ Protein, data = BK)
BKfun <- makeFun(BKmod)
BKfun(31)    # predicted value for a item with 31 grams of protein
```

```
##    1
## 36.7
```

Section 7.2 The linear model

```
coef(BKmod)
```

```
## (Intercept)     Protein
##       8.372       0.913
```

```
BKfun(0)
```

```
##    1
## 8.37
```

```
BKfun(32) - BKfun(31)
```

```
##     1
## 0.913
```

Section 7.3 Finding the least squares line

```
sx <- sd(~ Protein, data = BK)
sx
```

```
## [1] 13.5
```

```
sy <- sd(~ Fat, data = BK)
sy
```

```
## [1] 16.2
```

```
r <- cor(Protein ~ Fat, data = BK)
r   # same as cor(Fat ~ Protein)!
```

```
## [1] 0.761
```

```
r*sy/sx
```

```
## [1] 0.913
```

```
coef(BKmod)[2]
```

```
## Protein
##   0.913
```

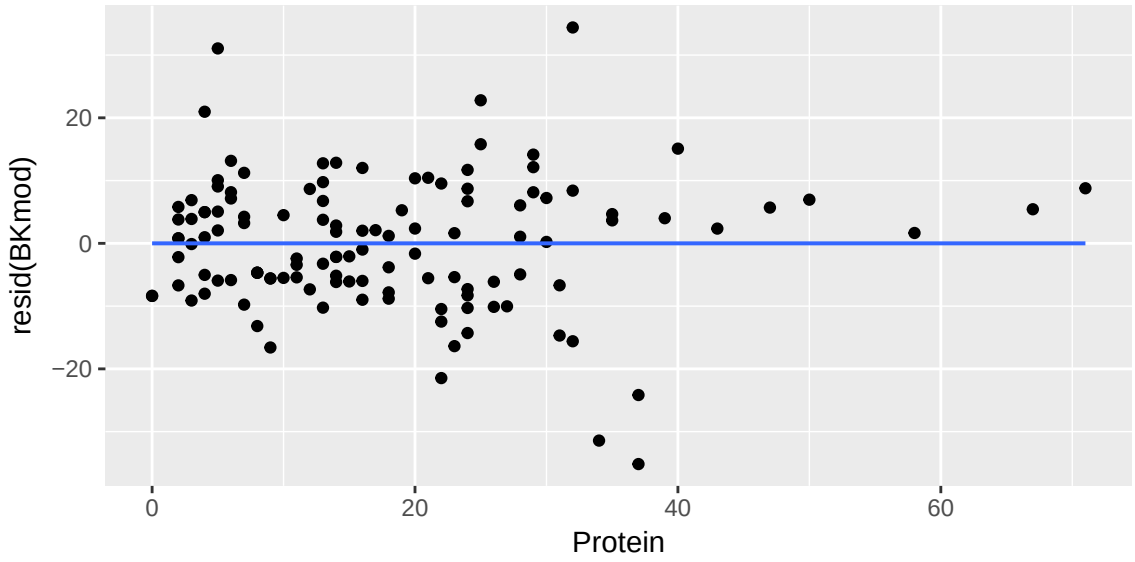
Section 7.4 Regression to the mean

Section 7.5 Examining the residuals

Figure 7.5 (page 193) displays the scatterplot of residuals as a function of the amount of protein.

The `msummary()` function generates a lot of output (much of which won't be familiar).

```
gf_point(resid(BKmod) ~ Protein, type = c("p", "r"), data = BK) %>%
  gf_lm()
```



```
msummary(BKmod)
```

```
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   8.3720     1.5991    5.24  7.1e-07 ***
## Protein       0.9134     0.0712   12.84  < 2e-16 ***
##
## Residual standard error: 10.6 on 120 degrees of freedom
## Multiple R-squared:  0.579,  Adjusted R-squared:  0.575
## F-statistic:  165 on 1 and 120 DF,  p-value: <2e-16
```

The residual standard error of 10.6 grams matches the value reported on page 194.

Section 7.6 R-squared: variation accounted for by the model

```
rsquared(BKmod)
```

```
## [1] 0.579
```

Section 7.7 Regression assumptions and conditions