Body Fat Regression Diagnostics Results

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Theory

Checking for the Validity of the Model Assumptions

In this document, we wish to determine the validity of the assumptions given for the least squares method. Various techniques have been proposed for verifying whether or not the assumptions are valid.

It should be noted that the diagnostic methods should only be done with a model that is reasonable for the problem or model at hand. Meaningless models produce meaningless results and we shouldn't waste our time with these results. Furthermore, we are just checking for the validity of the model under consideration, this model may or may not be the best model! That is somewhat of a separate issue.

Checks for Normality

Visual plots for the Residuals

If the proposed model assumption hold then the residuals satisfy $\hat{e}_i \sim N(0, \sigma^2(1-h_{ii}))$. A simple plots of the residuals versus the predicted values \hat{y}_i or the j^{th} independent variable x_{ji} often reveals if this assumption has been satisfied. Draper and Smith has an extensive discussion concerning plots of this type. Essentially, you should not "see" any patterns in the scatterplots. Likewise, the amount of variability should be somewhat constant across the plots.

QQ and **PP** Plots

The QQ or PP plots can be used to assess normality of the residuals. That is, let $z_{(1)} \le z_{(2)} \le \ldots \le z_{(n)}$ represent the ordered values of n independent and identically distributed N(0,1) random variables. It can be shown that the expected value of $z_{(i)}$ is

$$E(z_{(i)}) \approx \gamma_i = \Phi^{-1}[(i-3/8)/(n+1/4)]$$

where Φ is the cdf for the standard normal given by

$$\Phi(x) = (2\pi)^{-1/2} \int_{-\infty}^{x} e^{-1/2t^2} dt.$$

The QQ plot consists of a scatterplot of $(z_{(i)}, \gamma_i)$. If the data are normal then the resulting scatterplot should lie close to the line $(\gamma_i = z_{(i)})$. The PP plot is similar to the QQ plot using the ordered pairs $(\Phi(z_{(i)}), [i/n])$. If either plot differs greatly from the diagonal line, then the normality assumption likely does not hold. Note, one should only check these plots when the model is appropriate as the residuals for inappropriate models often appear to be non-normally distributed.

Residual Analysis

Standardized Residuals

From the previous chapter we have that $\hat{e}_i = y_i - \hat{y}_i \sim N(0, \sigma^2(1 - h_{ii}))$. Since σ^2 is unknown it can be estimated with either

$$\hat{\sigma}^2 = MS_E$$

or

$$\hat{\sigma}_{(i)}^2 = \frac{(n-p)\hat{\sigma}^2 - \hat{e}_i^2/(1-h_{ii})}{(n-p-1)}$$

where $\hat{\sigma}_{(i)}^2$ is the mean square for the error whenever the i^{th} observation has been omitted from the regression model. SAS provides two standardized residuals. They are:

1. Internally Studentized Residual (STUDENT) is given by

$$s_i = \frac{\hat{e}_i}{\hat{\sigma}(1 - h_{ii})^{1/2}}.$$

2. Externally Studentized Residual (RSTUDENT) is given by

$$s_{(i)} = \frac{\hat{e}_i}{\hat{\sigma}_{(i)}(1 - h_{ii})^{1/2}}.$$

- 3. Their properties are;
 - $s_i \sim t(df = n p)$.
 - $s_{(i)} \sim t(df = n p 1)$.

Leverages

The hat matrix H has the following properties;

- 1. $SS(\beta) = \hat{\beta}' X' y = y' H y = y' H^2 y = \hat{y}' \hat{y}$.
- 2. $\sum_{i=1}^{n} var(\hat{y}_i)/n = tr[\sigma^2 H]/n = \sigma^2 p/n$.
- 3. $H\mathbf{j} = \mathbf{j}$ whenever the y intercept is included in the model. In which case, the sum of every row and every column of H equals 1.
- 4. $0 \le h_{ij} \le 1$ and $\sum_{i=1}^n h_{ii} = p = rank(X)$. Since, the average of the diagonal elements for H is p/n the i^{th} observation is said to be a leverage point if $h_{ii} \ge 2p/n$.
- 5. Since $\hat{y} = Hy$ we have

$$\hat{y}_i = h_{ii} y_i + \sum_{i \neq j} h_{ij} y_j.$$

This indicates the importance that y_i has upon \hat{y}_i is given by the magnitude of h_{ii} .

Detection of Influential Observations

If one suspects that the i^{th} observation has an unusual influence upon the prediction equation \hat{y} one can recompute the regression model with the i^{th} observation omitted from the calculation. Suppose that the i^{th} observation is omitted then resultant regression estimate becomes

$$\hat{\beta}_{(i)} = (X'_{(i)}X_{(i)})^{-1}X'_{(i)}y_{(i)}$$

from which we have a new predicted value for y given by $\hat{y}_{(i)} = X\hat{\beta}_{(i)}$.

Cook's Distance

Cook's distance is a measure of how far the original "line" (\hat{y}) is from the "new line" $(\hat{y}_{(i)})$ when the i^{th} observation is omitted from the calculation. Cook's distance is

$$D_{i} = (\hat{y} - \hat{y}_{(i)})'(\hat{y} - \hat{y}_{(i)})/(p\hat{\sigma}^{2})$$

$$= (\hat{\beta} - \hat{\beta}_{(i)})'X'X(\hat{\beta} - \hat{\beta}_{(i)})/(p\hat{\sigma}^{2})$$

$$= \left[\frac{\hat{e}_{i}}{\hat{\sigma}(1 - h_{ii})^{1/2}}\right]^{2} \left[\frac{h_{ii}}{p(1 - h_{ii})}\right].$$

DFFITS

A related measure to Cook's distance is the DFFITS statistic given by

$$DFFITS_i^2 = (\hat{\beta} - \hat{\beta}_{(i)})'X'X(\hat{\beta} - \hat{\beta}_{(i)})/(\hat{\sigma}_{(i)}^2).$$

COVRATIO

Another measure of influence is the COVRATIO which is the ratio of the determinant of the covariance matrix for the estimate $\hat{\beta}$, given by $det[\hat{\sigma}^2(X'X)^{-1}]$ when the i^{th} observation has been removed for the computation of the estimate $\hat{\beta}_{(i)}$. That is,

$$COVRATIO = det[\hat{\sigma}_{(i)}^2(X'_{(i)}X_{(i)})^{-1}]/det[\hat{\sigma}^2(X'X)^{-1}].$$

This statistic should be close to one whenever the observation has little influence upon the estimation of β . If the statistics is much different from one then the observation is said to be influential.

Belsley, Kuh, and Welsch suggest that observations with

$$|COVRATIO - 1| \ge \frac{3p}{n}$$

where p is the number of parameters in the model and n is the number of observations used to fit the model, are worth investigation.

DFBETAS

The DFBETAS statistics are the scaled measures of the change in each parameter estimate and are calculated by deleting the i^{th} observation:

$$DFBETAS_{j} = \frac{\hat{\beta}_{j} - \hat{\beta}_{(i)j}}{\hat{\sigma}_{(i)} \sqrt{(X'X)_{jj}^{-1}}}$$

where $(X'X)_{jj}$ is the $(j,j)^{th}$ element of $(X'X)^{-1}$.

In general, large values of DFBETAS indicate observations that are influential in estimating a given parameter. Belsley, Kuh, and Welsch recommend 2 as a general cutoff value to indicate influential observations and as a size-adjusted cutoff.

R

```
# clear the environment and set seed
rm(list = 1s())
set.seed(123)
```

Read Body Fat Data

```
library(foreign)
bf = read.dbf("new_bfat.dbf") #define bf as the bodyfat data
```

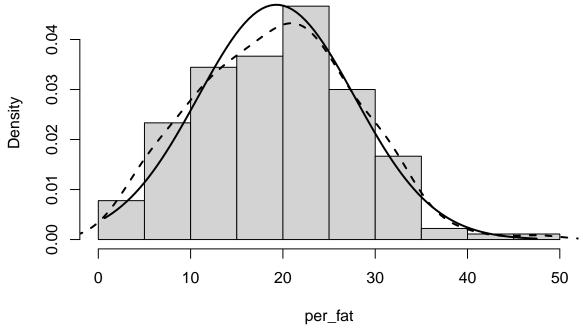
Define a few variables

```
abdomen=bf$abdomen
thigh = bf$thigh
neck = bf$neck
```

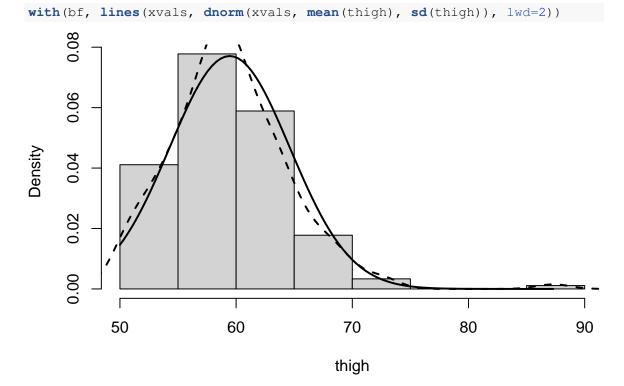
```
per_fat = bf$per_fat
density = bf$density
age=bf$age
wt = bf$wt
ht = bf$ht
chest = bf$chest
hip = bf$hip
thigh = bf$thigh
knee = bf$knee
ankle = bf$ankle
biceps = bf$forearm
wrist = bf$wrist
```

Plots of Percent Fat and Thigh Circumference

```
with(bf, hist(per_fat, main="", freq=FALSE))
with(bf, lines(density(per_fat), main="PERCENT FAT", lty=2, lwd=2))
xvals = with(bf, seq(from=min(per_fat), to=max(per_fat), length=100))
with(bf, lines(xvals, dnorm(xvals, mean(per_fat), sd(per_fat)), lwd=2))
```



```
with(bf, hist(thigh, main="", freq=FALSE))
with(bf, lines(density(thigh), main="Thigh", lty=2, lwd=2))
xvals = with(bf, seq(from=min(thigh), to=max(thigh), length=100))
```



Checking Regression Assumptions

Linear regression makes several assumptions about the data, such as:

- 1) Linearity of the data: The relationship between the predictor (x) and the outcome (y) is assumed to be linear.
- 2) Normality of residuals: The residual errors are assumed to be normally distributed.
- 3) Homogeneity of residuals variance: The residuals are assumed to have a constant variance (homoscedasticity).
- 4) Independence of residuals error terms.

You should check whether or not these assumptions hold true.

Potential Problems

- 1) Non-linearity of the outcome predictor relationships
- 2) Heteroscedasticity: Non-constant variance of error terms.
- 3) Presence of influential values in the data that can be:
 - -Outliers: extreme values in the outcome (y) variable
 - -High-leverage points: extreme values in the predictors (x) variable
 - All these assumptions and potential problems can be checked by producing some diagnostic plots visualizing the residual errors.

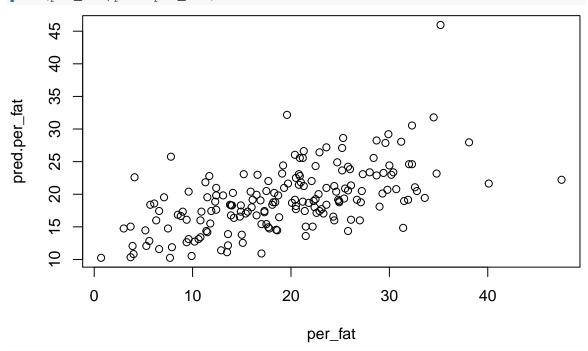
Linear Regression

```
mod1 = lm(per_fat ~ thigh, data=bf)
summary (mod1)
##
## Call:
## lm(formula = per_fat ~ thigh, data = bf)
##
## Residuals:
## Min
                10
                    Median
                                  3Q
                                          Max
## -18.4979 -4.4168 -0.2866
                             4.6279 25.2850
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) -37.61195
                          5.96533 -6.305 2.21e-09 ***
                          0.09997 9.575 < 2e-16 ***
## thigh
                0.95723
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 6.923 on 178 degrees of freedom
## Multiple R-squared: 0.34, Adjusted R-squared: 0.3363
## F-statistic: 91.68 on 1 and 178 DF, p-value: < 2.2e-16
covb = vcov (mod1)
coeff.mod1 = coef(mod1)
covb = vcov (mod1)
covb
              (Intercept)
## (Intercept) 35.5851820 -0.594122135
               -0.5941221 0.009994111
## thigh
library (broom)
diagnostics <- augment (mod1)</pre>
diagnostics
## # A tibble: 180 x 8
##
     per_fat thigh .fitted .resid .std.resid
                                              .hat .sigma .cooksd
##
       <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
                                                             <dbl>
                     18.9 -6.56
## 1
        12.3 59
                                     -0.951 0.00560
                                                    6.92 0.00254
## 2
         6.1 58.7
                     18.6 -12.5
                                     -1.81 0.00567
                                                    6.88 0.00932
##
   3
        28.7 63.2
                      22.9
                           5.81
                                     0.844 0.00849
                                                    6.93 0.00305
## 4
        20.9 66
                      25.6 - 4.67
                                     -0.679 0.0145
                                                    6.93 0.00339
## 5
       12.4 60
                     19.8 -7.42
                                     -1.08 0.00562 6.92 0.00327
## 6
        4.1 62.9
                     22.6 -18.5
                                     -2.68 0.00804
                                                    6.80 0.0292
## 7
        11.7 63.1
                                                    6.89 0.0109
                      22.8 -11.1
                                     -1.61 0.00834
```

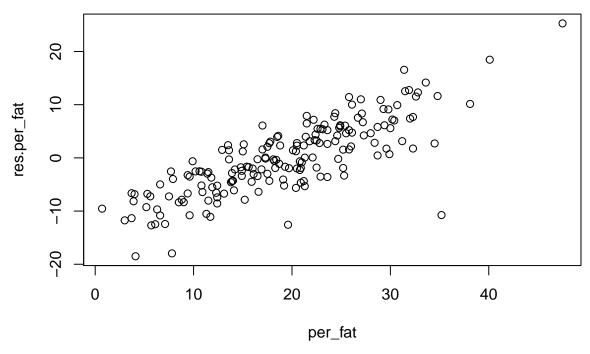
```
##
         7.1 59.7
                       19.5 -12.4
                                       -1.80 0.00557
                                                        6.88 0.00908
         7.8
               66.2
                       25.8 -18.0
                                       -2.61 0.0151
                                                        6.81 0.0522
         20.8 63.4
                       23.1 -2.28
                                       -0.330 0.00881
                                                        6.94 0.000485
  # ... with 170 more rows
pred.per_fat = predict(mod1)
res.per_fat = residuals(mod1)
```

Predicted Plots

plot (per_fat, pred.per_fat)

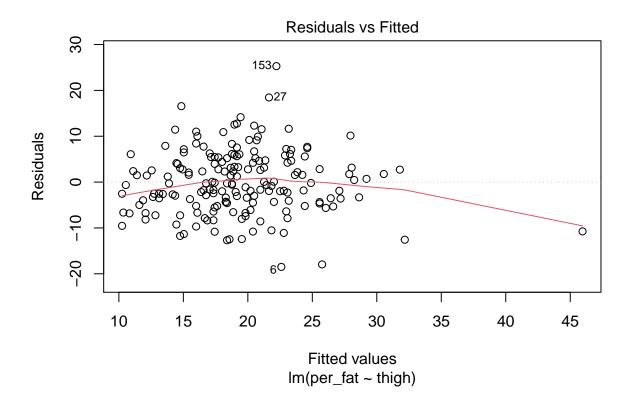


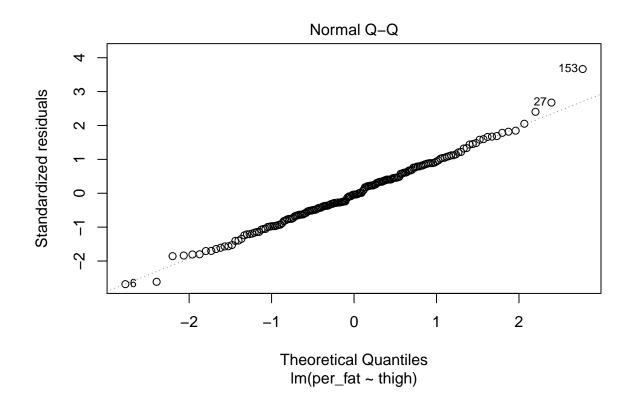
plot (per_fat, res.per_fat)

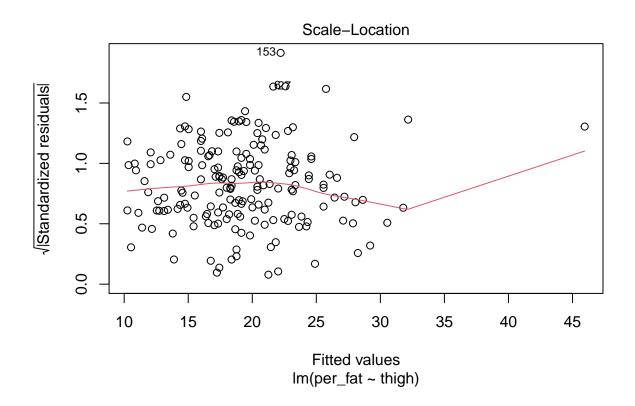


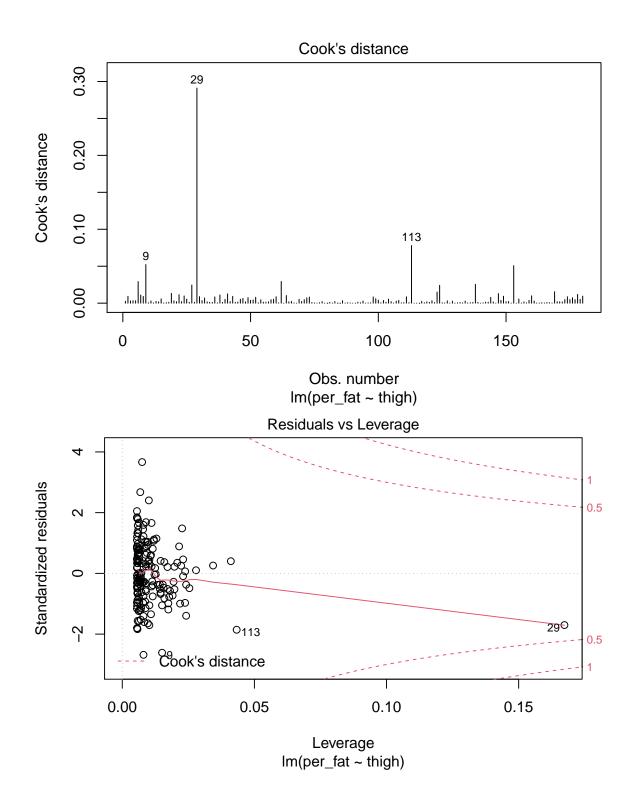
Residual Plots

```
#par (mfrow=c(1,1))
plot (mod1, which = c(1, 2,3,4,5))
```









Residual by Thigh for Percent Fat

```
library(GGally)
## Loading required package: ggplot2
## Registered S3 method overwritten by 'GGally':
     method from
##
     +.gg
           ggplot2
ggplot (diagnostics) +
  geom_point(aes(x = thigh, y = .resid)) +
  geom_hline(yintercept = 0) +
  ylab("Residual") +
  theme_minimal()
   20
   10
Residual
  -10
```

Multiple Regression

50

-20

```
mod2 = lm(per_fat ~ wrist + thigh + neck, data=bf)
summary(mod2)
##
## Call:
```

60

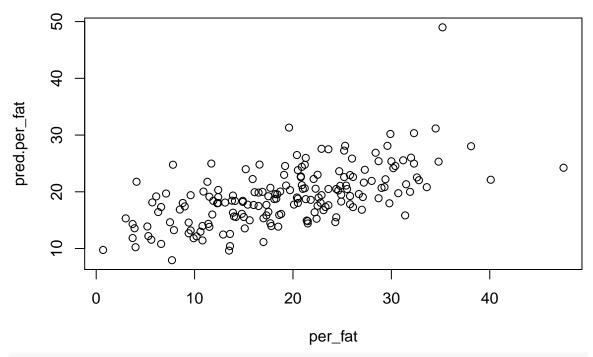
70

thigh

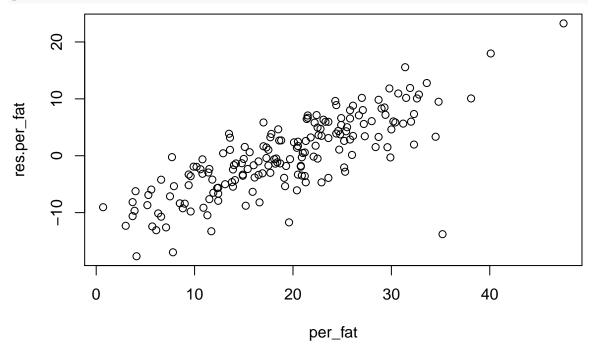
80

```
## lm(formula = per_fat ~ wrist + thigh + neck, data = bf)
## Residuals:
     Min
              1Q Median
                               3Q
                                      Max
## -17.667 -4.232 -0.285 4.665 23.263
##
## Coefficients:
##
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -45.9472
                           9.7726 -4.702 5.19e-06 ***
## wrist
               -0.6507
                           0.8395 - 0.775
                                           0.4393
## thigh
                0.7019
                           0.1466
                                   4.787 3.57e-06 ***
## neck
                0.9293
                           0.3830
                                  2.426
                                          0.0163 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.835 on 176 degrees of freedom
## Multiple R-squared: 0.3639, Adjusted R-squared: 0.3531
## F-statistic: 33.57 on 3 and 176 DF, p-value: < 2.2e-16
diagnostics <- augment (mod2)</pre>
diagnostics
## # A tibble: 180 x 10
     per_fat wrist thigh neck .fitted .resid .std.resid
                                                           .hat .sigma .cooksd
       <dbl> <dbl> <dbl> <dbl> <dbl>
                                 <dbl> <dbl>
                                                 <dbl>
                                                          <dbl> <dbl>
##
                                                                         <dbl>
        12.3 17.1 59
##
                          36.2
                                  18.0 -5.68
                                                 -0.838 0.0166
                                                                  6.84 0.00297
   1
         6.1 18.2 58.7 38.5
                                                 -1.92 0.00691
##
   2
                                  19.2 -13.1
                                                                  6.78 0.00642
##
        28.7 17.7 63.2 34.4
                                 18.9 9.84
                                                 1.49 0.0609
                                                                  6.81 0.0358
   3
##
   4
        20.9 18.8 66
                          39
                                  24.4 - 3.49
                                                 -0.515 0.0191
                                                                  6.85 0.00129
##
   5
        12.4 18.8 60
                          37.8
                                 19.1 -6.66
                                                 -0.981 0.0125
                                                                  6.84 0.00303
##
         4.1 18.2 62.9 38.1
                                 21.8 -17.7
                                                 -2.60 0.0109
                                                                  6.72 0.0185
##
   7
        11.7 19.2 63.1 42.1
                                  25.0 -13.3
                                                 -1.97 0.0240
                                                                  6.78 0.0238
         7.1 18.5 59.7 38.5
## 8
                                  19.7 -12.6
                                                 -1.85 0.00624
                                                                  6.79 0.00536
         7.8 19
##
   9
                    66.2 39.4
                                 24.8 -17.0
                                                 -2.51 0.0188
                                                                  6.73 0.0301
## 10
        20.8 17.7 63.4 38.4
                                 22.7 -1.92
                                                 -0.284 \ 0.0176
                                                                  6.85 0.000360
## # ... with 170 more rows
pred.per_fat = predict (mod2)
res.per_fat = residuals(mod2)
Predicted Plots
```

plot (per_fat, pred.per_fat)

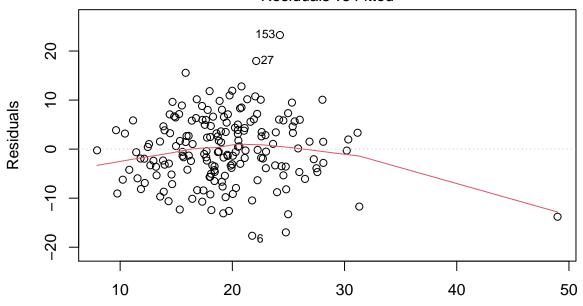


plot (per_fat, res.per_fat)

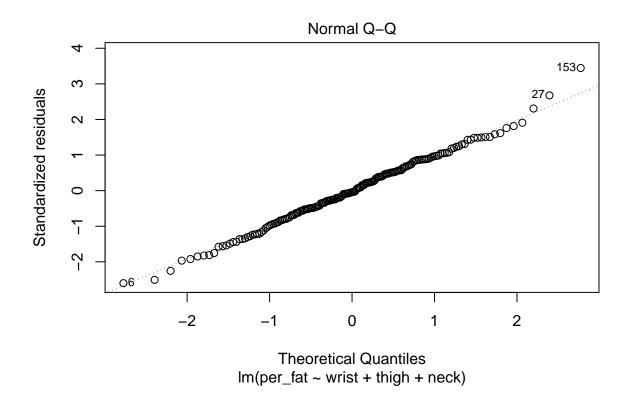


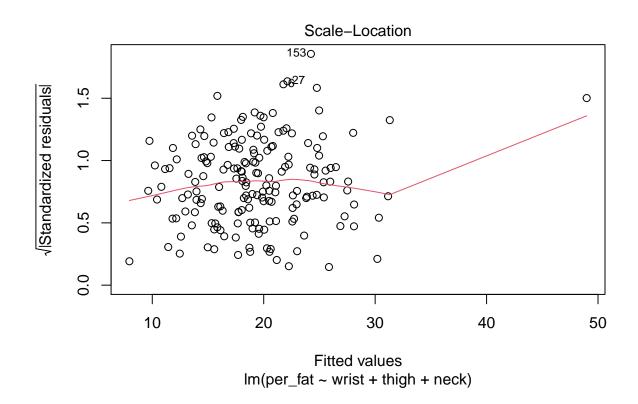
Residual Plots

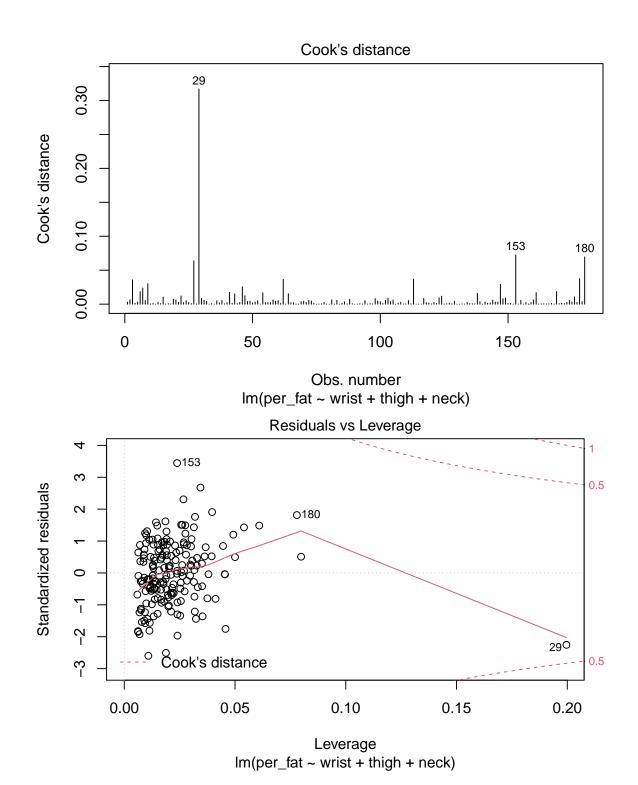
Residuals vs Fitted

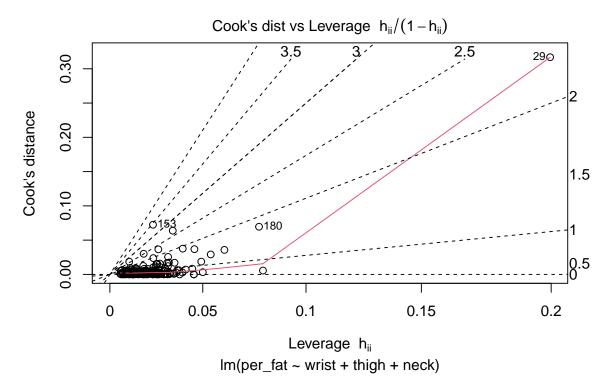


Fitted values Im(per_fat ~ wrist + thigh + neck)



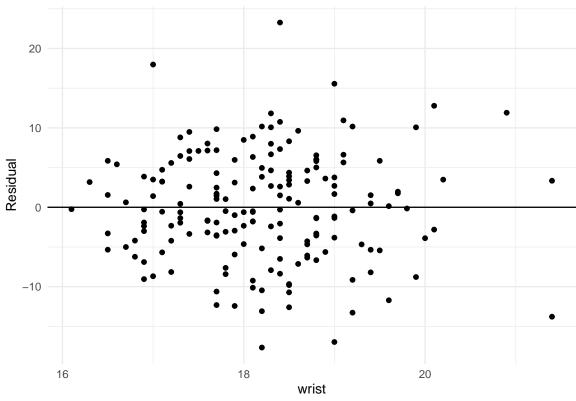






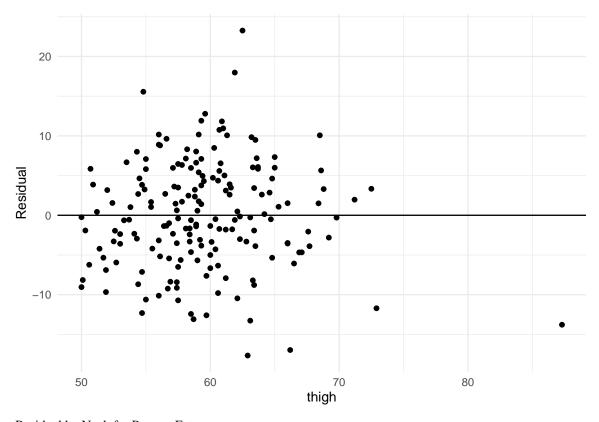
Residual by Wrist for Percent Fat

```
#library(GGally)
ggplot(diagnostics) +
  geom_point(aes(x = wrist, y = .resid)) +
  geom_hline(yintercept = 0) +
  ylab("Residual") +
  theme_minimal()
```



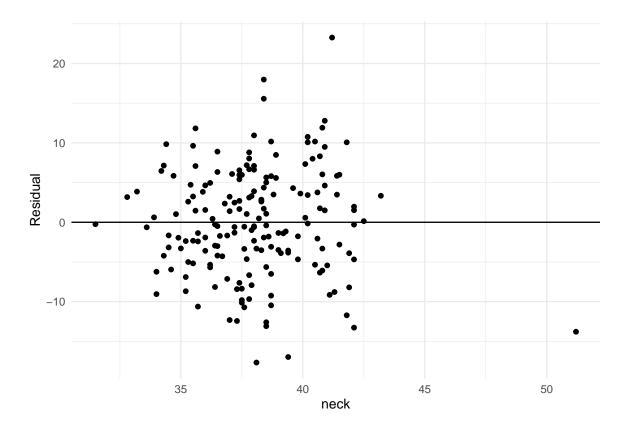
Residual by Thigh for Percent Fat

```
#library(GGally)
ggplot(diagnostics) +
  geom_point(aes(x = thigh, y = .resid)) +
  geom_hline(yintercept = 0) +
  ylab("Residual") +
  theme_minimal()
```



Residual by Neck for Percent Fat

```
#library(GGally)
ggplot(diagnostics) +
  geom_point(aes(x = neck, y = .resid)) +
  geom_hline(yintercept = 0) +
  ylab("Residual") +
  theme_minimal()
```



SAS

Code

```
title1 'Body Fat Data';
Density determined from underwater weighing
Percent body fat from Siri's (1956) equation
Age (years)
Weight (lbs)
Height (inches)
Neck circumference (cm)
Chest circumference (cm)
Abdomen 2 circumference (cm)
Hip circumference (cm)
Thigh circumference (cm)
Knee circumference (cm)
Ankle circumference (cm)
Biceps (extended) circumference (cm)
Forearm circumference (cm)
Wrist circumference (cm)
```

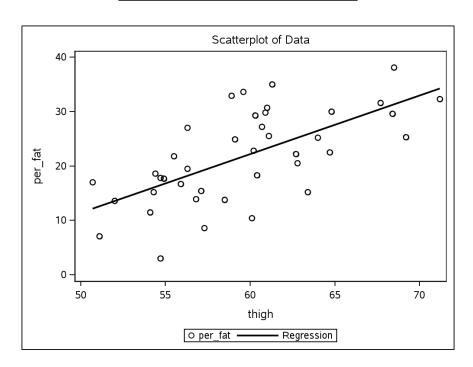
```
*/
data bodyfat; set ldata.bodyfat; run;
/*
Use per_fat or density as the dependent variable with a subset of the data
title2 'Simple Random Sampling of size = 40';
proc surveyselect data=bodyfat
  method=srs n=40 out=new_bfat seed = 12345;
run;
proc sgplot data=new_bfat;
 scatter y=per_fat x=abdomen ;
 reg y=per_fat x=abdomen;
 loess y=per_fat x=abdomen;
run;
proc sgplot data=new_bfat;
histogram per_fat;
density per_fat;
density per_fat/ type=kernel;
run;
/*
proc sgscatter data=new_bfat;
 matrix per_fat density thigh knee ankle biceps forearm
 wrist/diagonal=(histogram normal);run;
title2 'Simple Linear Model - Neck';
 proc reg data=new_bfat    plots = diagnostics;
model per_fat=thigh;
run;
title2 'Multiple Regression';
proc reg data=new_bfat plots = diagnostics;
model per_fat=neck thigh wrist/press influence ss2;
run;
```

Output

Simple Random Sampling of size = 40 The SURVEYSELECT Procedure

Selection Method | Simple Random Sampling

Input Data Set	BODYFAT
Random Number Seed	12345
Sample Size	40
Selection Probability	0.15873
Sampling Weight	6.3
Output Data Set	NEW_BFAT



Simple Linear Model - Neck

The REG Procedure

Model: MODEL1

Number of Observations Read	
Number of Observations Used	40

Analysis of Variance									
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F				
Model	1	1164.86111	1164.86111	27.85	<.0001				
Error	38	1589.16864	41.82023						
Corrected Total	39	2754.02975							

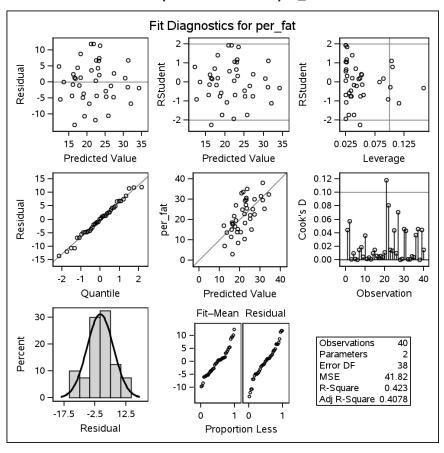
Root MSE	6.46686	R-Square	0.4230
Dependent Mean	21.77750	Adj R-Sq	0.4078
Coeff Var	29.69513		

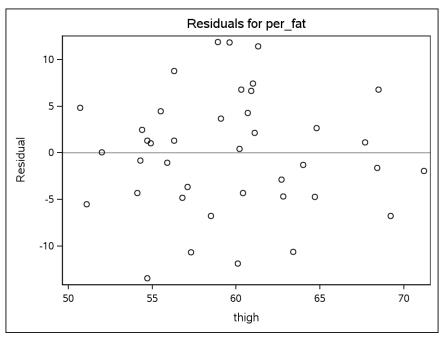
Parameter Estimates										
Variable DF Parameter Estimate Standard Error t Value										
Intercept	1	-42.40929	12.20482	-3.47	0.0013					
thigh	1	1.07624	0.20392	5.28	<.0001					

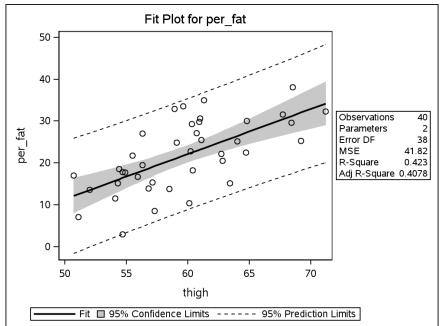
Simple Linear Model - Neck

The REG Procedure

Model: MODEL1







Multiple Regression

The REG Procedure

Model: MODEL1

Number of Observations Read	
Number of Observations Used	40

Analysis of Variance									
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F				
Model	3	1165.08957	388.36319	8.80	0.0002				
Error	36	1588.94018	44.13723						
Corrected Total	39	2754.02975							

Root MSE	6.64359	R-Square	0.4230
Dependent Mean	21.77750	Adj R-Sq	0.3750
Coeff Var	30.50665		

	Parameter Estimates										
Variable	DF	Parameter Estimate	Standard Error	t Value	Pr > t	Type II SS					
Intercept	1	-42.40999	20.56651	-2.06	0.0465	187.68106					
neck	1	0.05879	0.86103	0.07	0.9459	0.20578					
thigh	1	1.07114	0.29479	3.63	0.0009	582.74287					
wrist	1	-0.10649	1.76638	-0.06	0.9523	0.16043					

Multiple Regression

The REG Procedure

Model: MODEL1

Output Statistics									
Obs	Residual	RStudent	Hat Diag H	Cov Ratio	DFFITS		DFBE	TAS	
						Intercept	neck	thigh	wrist
1	-11.8264	-1.8765	0.0370	0.7921	-0.3680	-0.0744	0.2053	-0.1272	-0.1026
2	-10.6094	-1.7367	0.1071	0.9006	-0.6016	0.4950	-0.0963	0.1465	-0.3072
3	1.0381	0.1595	0.0663	1.1953	0.0425	0.0339	-0.0117	-0.0017	-0.0080
4	-1.9327	-0.3134	0.1599	1.3174	-0.1367	0.0821	-0.0131	-0.0785	0.0020
5	1.2601	0.2100	0.2061	1.4027	0.1070	0.0119	-0.0709	0.0945	0.0144
6	0.1180	0.0194	0.1824	1.3689	0.0091	0.0080	-0.0050	0.0010	-0.0005
7	6.8331	1.1304	0.1658	1.1624	0.5039	0.1102	-0.4613	0.2470	0.2723
8	7.5701	1.2000	0.0873	1.0437	0.3710	-0.1008	-0.2465	0.0431	0.2991
9	2.5867	0.4016	0.0820	1.1970	0.1200	-0.0472	0.0723	0.0235	-0.0543
10	8.7580	1.3745	0.0574	0.9623	0.3392	0.0150	0.2009	-0.2206	-0.0870
11	1.4460	0.2266	0.1015	1.2384	0.0761	0.0156	-0.0471	-0.0211	0.0509
12	-2.9536	-0.4545	0.0644	1.1684	-0.1192	0.0217	-0.0764	-0.0144	0.0697
13	-1.0588	-0.1612	0.0495	1.1741	-0.0368	-0.0266	0.0032	0.0032	0.0111
14	-4.8648	-0.8086	0.1877	1.2796	-0.3887	0.2160	-0.1862	0.3038	-0.1182
15	-6.7515	-1.0310	0.0267	1.0203	-0.1707	-0.0476	0.0046	0.0135	0.0130
16	4.1362	0.6668	0.1417	1.2398	0.2709	0.0775	0.1736	0.0365	-0.2430
17	3.5743	0.5824	0.1624	1.2857	0.2564	0.1391	0.1128	0.0573	-0.2321
18	-4.2374	-0.6540	0.0639	1.1389	-0.1708	-0.0779	0.1105	-0.0998	-0.0121
19	-1.7014	-0.2752	0.1565	1.3155	-0.1185	0.0190	-0.0457	-0.0685	0.0703
20	4.3829	0.6846	0.0850	1.1599	0.2087	0.0299	0.1482	-0.1278	-0.0970
21	-13.4720	-2.1873	0.0502	0.7059	-0.5028	-0.1956	-0.0633	0.2901	0.0195
22	-6.7125	-1.0954	0.1444	1.1432	-0.4501	0.3256	0.0795	-0.1870	-0.1932
23	-4.6996	-0.7342	0.0835	1.1488	-0.2216	-0.0382	0.0783	-0.1848	0.0414
24	-4.2943	-0.6639	0.0667	1.1408	-0.1775	-0.1311	0.0493	0.0343	0.0111
25	-10.7448	-1.7279	0.0756	0.8727	-0.4940	0.0673	-0.3702	0.3069	0.1583
26	-4.7545	-0.7372	0.0696	1.1311	-0.2017	0.0987	-0.1388	0.0240	0.0616
27	6.7983	1.0941	0.1205	1.1124	0.4049	-0.3087	0.0216	0.1381	0.1058
28	0.4669	0.0739	0.1215	1.2733	0.0275	0.0182	-0.0147	0.0182	-0.0061

Output Statistics										
Obs	Residual	RStudent	Hat Diag H	Cov Ratio	DFFITS	DFBETAS				
						Intercept	neck	thigh	wrist	
29	2.2017	0.3342	0.0410	1.1524	0.0691	-0.0210	-0.0285	0.0079	0.0400	
30	11.7632	1.9826	0.1375	0.8478	0.7916	0.1756	0.6092	-0.0953	-0.6714	
31	-5.4772	-0.8655	0.0990	1.1413	-0.2868	-0.1329	0.0072	0.1900	-0.0310	
32	1.3336	0.2045	0.0617	1.1872	0.0524	-0.0109	0.0035	-0.0359	0.0241	
33	-1.2355	-0.1891	0.0588	1.1844	-0.0473	-0.0005	0.0194	-0.0351	-0.0013	
34	-3.6696	-0.5570	0.0354	1.1201	-0.1068	-0.0171	-0.0349	0.0522	0.0152	
35	2.4368	0.3786	0.0835	1.2014	0.1142	-0.0100	0.0407	-0.0955	0.0189	
36	4.8200	0.7709	0.1242	1.1947	0.2902	0.2332	0.0053	-0.1036	-0.0936	
37	11.5337	1.8842	0.0909	0.8366	0.5958	-0.2755	-0.2926	-0.0204	0.4962	
38	-0.7172	-0.1137	0.1236	1.2753	-0.0427	-0.0020	0.0228	0.0172	-0.0320	
39	11.9057	2.0655	0.1790	0.8605	0.9644	-0.6723	0.0934	-0.5338	0.6373	
40	6.7499	1.0397	0.0430	1.0356	0.2204	0.0150	0.1236	-0.0010	-0.1298	

Sum of Residuals	0
Sum of Squared Residuals	1588.94018
Predicted Residual SS (PRESS)	1954.84380

