Homework 5

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A.

From the summary statistics of the full model, we can obtain that predictor “Over45” has the largest p-value = 0.88046 > alpha-to-remove = 0.15. Thus, we remove “Over45” from the full model at the first step.

Then, we check the summary statistics again and find out that “KneeC” has the largest p-value = 0.7738 > alpha-to-remove = 0.15. Thus, we remove “KneeC” from the model.

Then, we check the summary statistics again and find out that “ThighC” has the largest p-value = 0.52389 > alpha-to-remove = 0.15. Thus, we remove “ThighC” from the model.

Then, we check the summary statistics again and find out that “Weight” has the largest p-value = 0.575914 > alpha-to-remove = 0.15. Thus, we remove “Weight” from the model.

Then, we check the summary statistics again and find out that “ForearmC” has the largest p-value = 0.31165 > alpha-to-remove = 0.15. Thus, we remove “ForearmC” from the model.

Then, we check the summary statistics again and find out that “AnkleC” has the largest p-value = 0.27225 > alpha-to-remove = 0.15. Thus, we remove “AnkleC” from the model.

Then, we check the summary statistics again and find no other predictors that have p-value larger than alpha-to-remove = 0.15.

Now, we obtain the model from backward elimination:

bodyfat.percentage = 21.0251 -0.3758*Height -0.3672*NeckC -0.1856*ChestC + 0.9978*AbdomenC -0.1920*HipC + 0.3319*BicepsC -1.4628*WristC

B.

First, we set up an empty model with no predictor.

Then, we check the p-value for each predictor individually:

```
> pvalue.for1
      Over45       Weight       Height        NeckC       ChestC     AbdomenC         HipC       ThighC        KneeC
3.229072e-02 1.207304e-25 4.447621e-01 3.680961e-15 1.947170e-35 1.121969e-59 1.296390e-27 2.713443e-20 1.630623e-15
      AnkleC      BicepsC     ForearmC       WristC
1.132067e-04 2.046233e-15 9.947490e-09 3.477863e-07
```

We add “AbdomenC” into the model since it has the smallest p-value = `1.121969e-59 < alpha-to-enter = 0.15.`

```
> pvalue.for2
      Over45       Weight       Height        NeckC       ChestC         HipC       ThighC        KneeC       AnkleC
4.836650e-01 2.162394e-10 1.704152e-08 1.329576e-06 1.840764e-04 1.382336e-05 2.033388e-02 9.819230e-05 8.641085e-03
     BicepsC     ForearmC       WristC
3.766466e-02 1.370515e-02 1.643497e-09
```

We add “Weight” into the model since it has the smallest p-value = `2.162394e-10 < alpha-to-enter = 0.15.`

```
> pvalue.for3
      Over45       Height        NeckC       ChestC         HipC       ThighC        KneeC       AnkleC      BicepsC
0.0840644225 0.1115683993 0.0487609414 0.3363419540 0.7685653134 0.0288935406 0.8650559575 0.5466249851 0.0536610258
    ForearmC       WristC
0.3019235997 0.0005950752
```

We add “WristC” into the model since it has the smallest p-value = `0.0005950752 < alpha-to-enter = 0.15.`

```
> pvalue.for4
    Over45     Height      NeckC     ChestC       HipC     ThighC      KneeC     AnkleC    BicepsC   ForearmC
0.60363794 0.08931123 0.42711420 0.44242323 0.73203069 0.12522783 0.57081871 0.17464573 0.02035225 0.07923609
```

We add “BicepsC” into the model since it has the smallest p-value = `0.02035225 < alpha-to-enter = 0.15.`

```
> pvalue.for5
   Over45    Height     NeckC    ChestC      HipC    ThighC     KneeC    AnkleC  ForearmC
0.6954545 0.2729983 0.2073643 0.3112601 0.7398100 0.3270078 0.4995375 0.1292198 0.3027216
```

We add “AnkleC” into the model since it has the smallest p-value = `0.1292198 < alpha-to-enter = 0.15.`

```
> pvalue.for6
   Over45    Height     NeckC    ChestC      HipC    ThighC     KneeC  ForearmC
0.7918609 0.3002820 0.2875951 0.3555573 0.7006217 0.3853034 0.6820736 0.2924295
```

Now, no other predictor has p-vlaue < `alpha-to-enter = 0.15, so we stop.`

Thus, we obtain the model from forward selection:

bodyfat.percent = -34.9774 + 1.0133*AbdomenC -0.1490*Weight -1.8015*WristC + 0.3766*BicepsC + 0.3323*AnkleC

This model is different with the model obtained in part A.

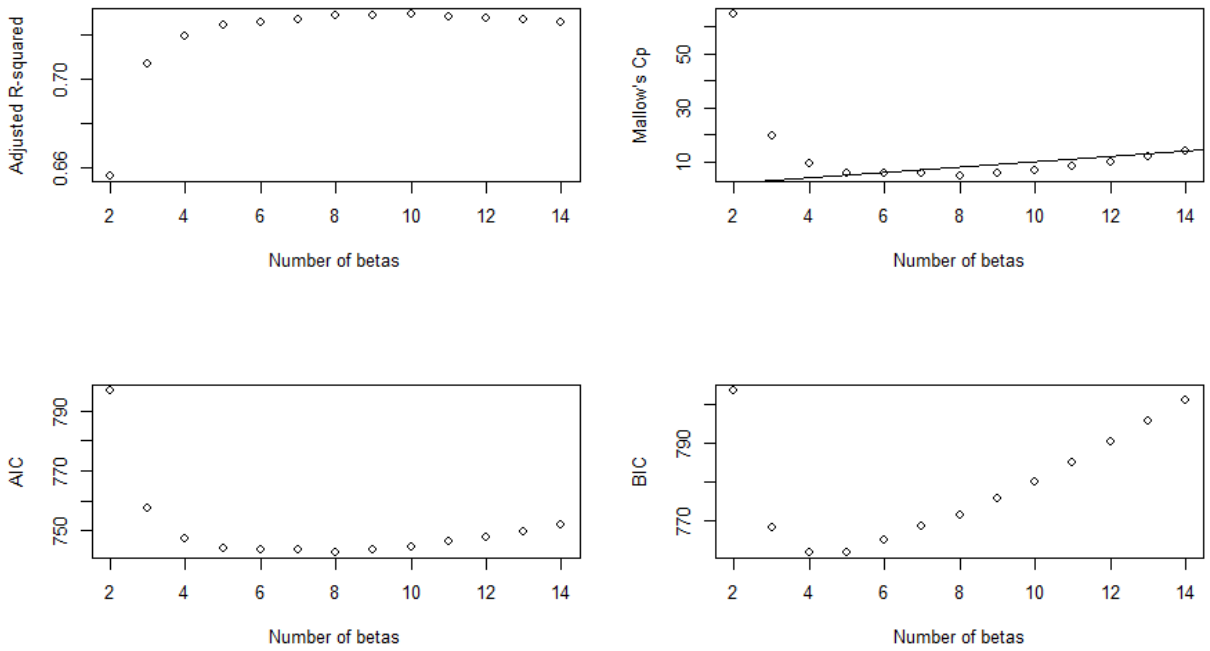
C.

The following are the best model of each size according to the RSS:

```
> sum.subset$which
   (Intercept) Over45 Weight Height NeckC ChestC AbdomenC  HipC ThighC KneeC AnkleC BicepsC ForearmC WristC
1         TRUE  FALSE  FALSE  FALSE FALSE  FALSE     TRUE FALSE  FALSE FALSE  FALSE   FALSE     FALSE  FALSE
2         TRUE  FALSE   TRUE  FALSE FALSE  FALSE     TRUE FALSE  FALSE FALSE  FALSE   FALSE     FALSE  FALSE
3         TRUE  FALSE   TRUE  FALSE FALSE  FALSE     TRUE FALSE  FALSE FALSE  FALSE   FALSE     FALSE   TRUE
4         TRUE  FALSE   TRUE  FALSE FALSE  FALSE     TRUE FALSE  FALSE FALSE  FALSE    TRUE     FALSE   TRUE
5         TRUE  FALSE   TRUE  FALSE FALSE  FALSE     TRUE FALSE  FALSE FALSE   TRUE    TRUE     FALSE   TRUE
6         TRUE  FALSE  FALSE   TRUE FALSE   TRUE     TRUE  TRUE  FALSE FALSE  FALSE    TRUE     FALSE   TRUE
7         TRUE  FALSE  FALSE   TRUE  TRUE   TRUE     TRUE  TRUE  FALSE FALSE  FALSE    TRUE     FALSE   TRUE
8         TRUE  FALSE  FALSE   TRUE  TRUE   TRUE     TRUE  TRUE  FALSE FALSE   TRUE    TRUE     FALSE   TRUE
9         TRUE  FALSE  FALSE   TRUE  TRUE   TRUE     TRUE  TRUE  FALSE FALSE   TRUE    TRUE      TRUE   TRUE
10        TRUE  FALSE   TRUE   TRUE  TRUE   TRUE     TRUE  TRUE  FALSE FALSE   TRUE    TRUE      TRUE   TRUE
11        TRUE  FALSE   TRUE   TRUE  TRUE   TRUE     TRUE  TRUE   TRUE FALSE   TRUE    TRUE      TRUE   TRUE
12        TRUE  FALSE   TRUE   TRUE  TRUE   TRUE     TRUE  TRUE   TRUE  TRUE   TRUE    TRUE      TRUE   TRUE
13        TRUE   TRUE   TRUE   TRUE  TRUE   TRUE     TRUE  TRUE   TRUE  TRUE   TRUE    TRUE      TRUE   TRUE
```

The following are the values of RSS of the model for each size:

```
> RSS.p
 [1] 5952.557 5054.503 4817.476 4712.603 4668.264 4631.512 4580.936 4558.034 4538.593 4532.643 4524.897 4523.317
[13] 4522.882
```



The following are adjusted R squares:

```
> R2.adj
 [1] 0.6563888 0.7070477 0.7196504 0.7246340 0.7261069 0.7271450 0.7290094 0.7292453 0.7292768 0.7285005 0.7278256
[12] 0.7267727 0.7256413
```

We choose the model with 10 betas based on the adjusted R square and the predictors are Height, NeckC, ChestC, AbdomenC, HipC, AnkleC, BicepsC, ForearmC, WristC.

The following are values of Mallow's C_p:

```
> C.p
 [1] 64.599152 19.739499  9.371655  5.899460  5.585886  5.668192  5.029166  5.834179  6.819792  8.509313 10.105127
[12] 12.022667 14.000000
```

We choose the model with 5 betas based on the Mallow's C_p and the predictors are Weight, AbdomenC, BicepsC, WristC.

The following are values of AIC:

```
> aic.p
 [1] 796.5288 757.6435 747.6361 744.1337 743.7704 743.7944 743.0494 743.7964 744.7279 746.3999 747.9723 749.8850 751.8610
```

We choose the model with 8 betas based on the Mallow's C_p and the predictors are Height, NeckC, ChestC, AbdomenC, HipC, BicepsC, WristC.

The following are values of BIC:

```
> bic.p
 [1] 803.5717 768.2079 761.7220 761.7410 764.8992 768.4447 771.2211 775.4896 779.9425 785.1360 790.2298 795.6640 801.1614
```

We choose the model with 4 betas based on the Mallow's C_p and the predictors are Weight, AbdomenC, WristC.

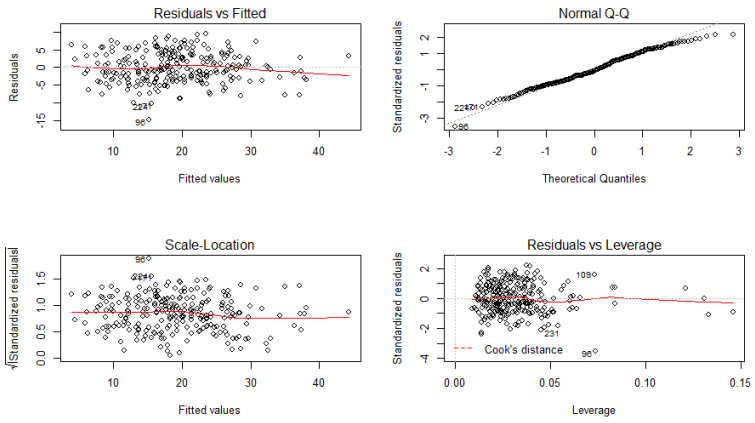
The model obtained based on the adjusted R square is most complicated model and the model obtained based on the BIC is the simplest model. All 4 models are different with each other.

D.

```
> vif(lm.backward)
  Height    NeckC   ChestC AbdomenC     HipC  BicepsC   WristC
1.456085 3.482255 7.188742 8.272218 5.599539 2.618959 2.419499
> vif(lm.forward)
AbdomenC   Weight   WristC  BicepsC   AnkleC
4.570160 8.655984 2.245620 2.668126 1.689372
> vif(lm.R2.adj)
  Height    NeckC   ChestC AbdomenC     HipC   AnkleC  BicepsC ForearmC   WristC
1.487721 3.634850 7.282090 8.518866 5.860135 1.627480 2.974710 2.322658 2.658725
> vif(lm.C.p)
  Weight AbdomenC  BicepsC   WristC
7.529088 4.298628 2.657965 2.146810
> vif(lm.aic.p)
  Height    NeckC   ChestC AbdomenC     HipC  BicepsC   WristC
1.456085 3.482255 7.188742 8.272218 5.599539 2.618959 2.419499
> vif(lm.bic.p)
  Weight AbdomenC   WristC
5.729221 4.263829 2.127194
```

By checking the VIF, there is no significant collinearity between predictors in each model. Thus, we do will not remove any predictors from each model. Only further investigation is needed for predictors that has VIF $\geqslant$ 4. In addition, we observe that model obtained from AIC is the same as the model obtained from backward elimination.

The following is the model obtained from backward elimination:



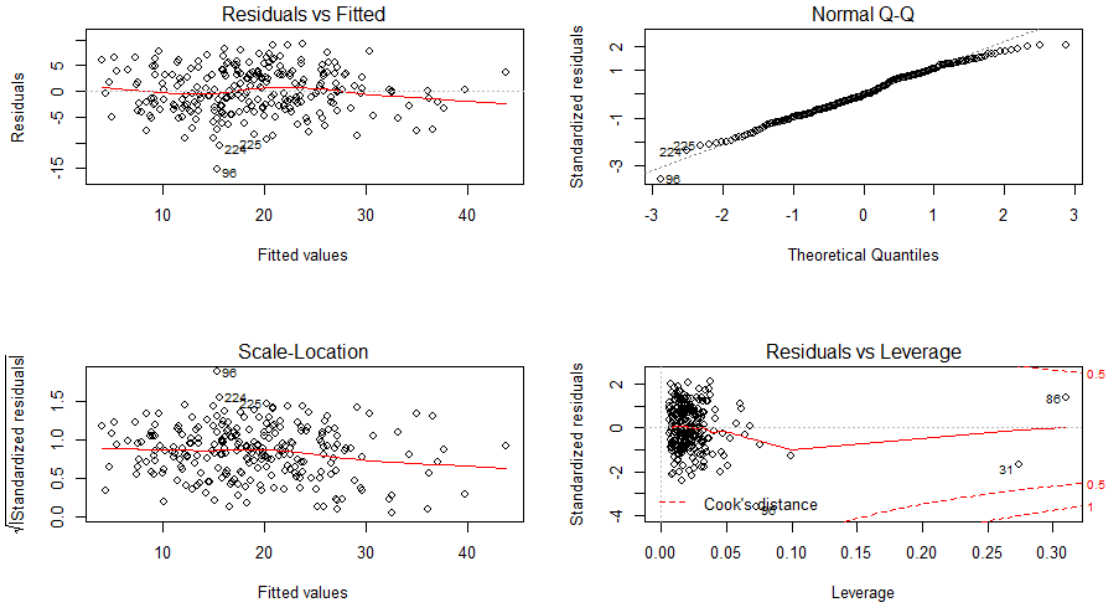
```
> shapiro.test(lm.backward$residuals)

        Shapiro-Wilk normality test

data:  lm.backward$residuals
W = 0.98949, p-value = 0.06669
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test indicates normality. Thus, all assumptions are satisfied. This model has R-square=0.7366.

The following is the model obtained from forward selection:



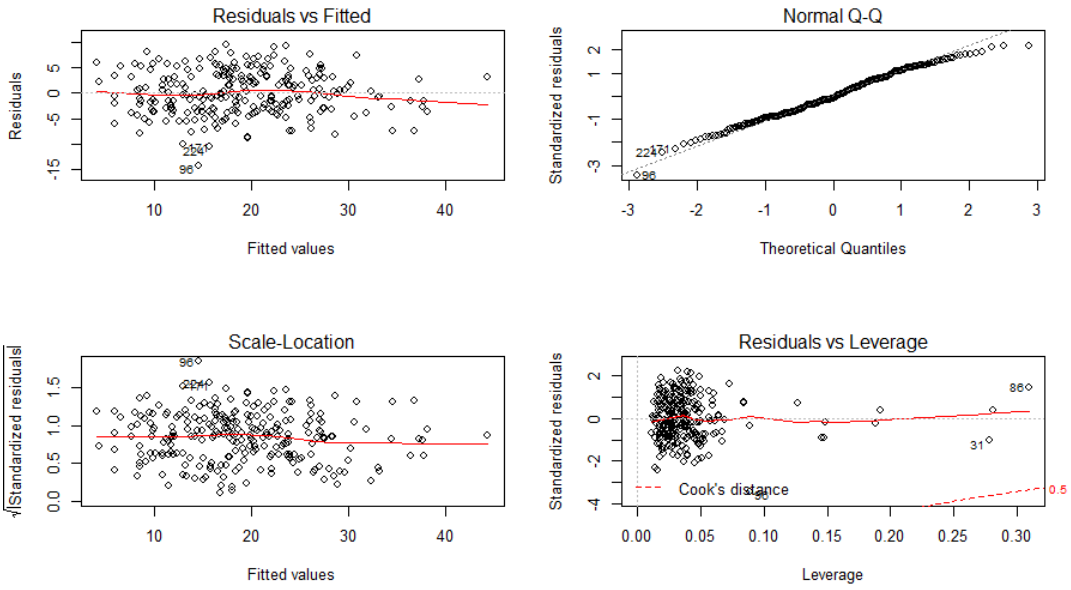

```
> shapiro.test(lm.forward$residuals)

        Shapiro-Wilk normality test

data:  lm.forward$residuals
W = 0.9887, p-value = 0.04754
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test (p-value=0.04754, reject null hypothesis) does not indicate normality. Thus, one assumption (normality) is not satisfied. If we use this model, we need to be careful with the result since the result may be inaccurate. This model has R-square = 0.7316.

The following is the model obtained from adjusted R-square:



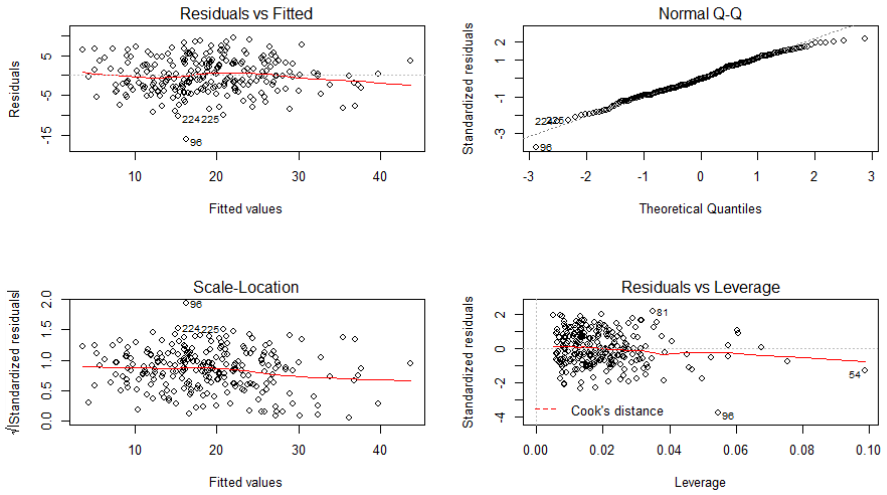

```
> shapiro.test(lm.R2.adj$residuals)

        Shapiro-Wilk normality test

data:  lm.R2.adj$residuals
W = 0.99067, p-value = 0.1105
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test indicates normality. Thus, all assumptions are satisfied. This model has R-square = 0.7391.

The following is the model obtained from Mallow's C_p:



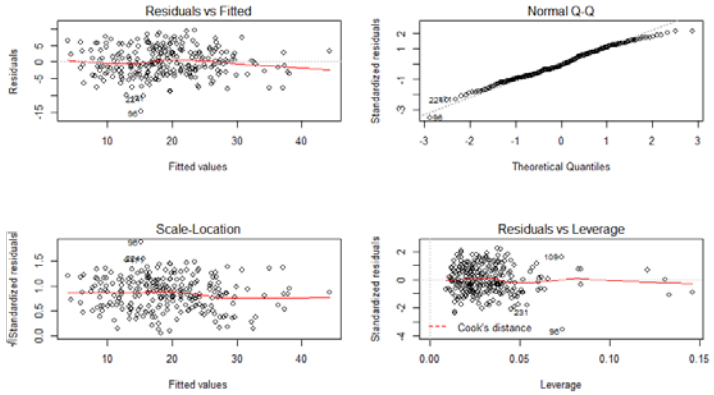
```
> shapiro.test(lm.C.p$residuals)

        Shapiro-Wilk normality test

data:  lm.C.p$residuals
W = 0.98836, p-value = 0.04113
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test (p-value=0.04113, reject null hypothesis) does not indicate normality. Thus, one assumption (normality) is not satisfied. If we use this model, we need to be careful with the result since the result may be inaccurate. This model has R-square = 0.7291.

The following is the model obtained from AIC:



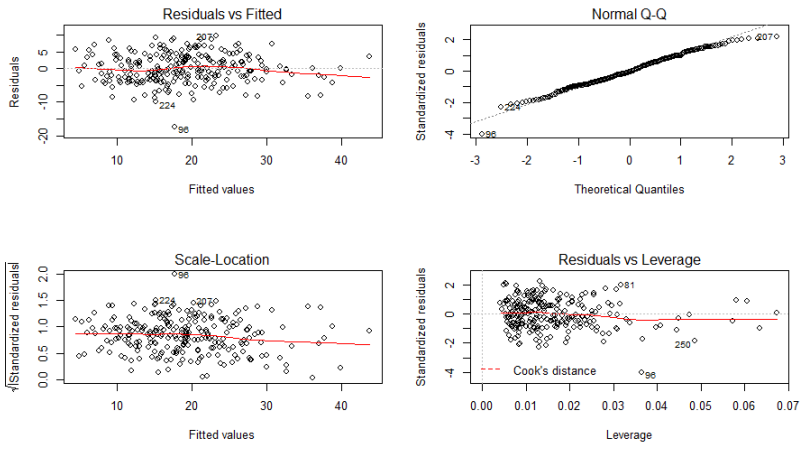

```
> shapiro.test(lm.aic.p$residuals)

        Shapiro-Wilk normality test

data:  lm.aic.p$residuals
W = 0.98949, p-value = 0.06669
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test indicates normality. Thus, all assumptions are satisfied. This model has R-square = 0.7366.

The following is the model obtained from BIC:



```
> shapiro.test(lm.bic.p$residuals)

        Shapiro-Wilk normality test

data:  lm.bic.p$residuals
W = 0.9889, p-value = 0.0517
```

The model obtained from backward elimination satisfies the linearity and constant variance. The Q-Q plot and the Shapiro-Wilk test indicates normality. Thus, all assumptions are satisfied. This model has R-square = 0.723.

Based on the information above, we can tell that each model has similar R-square and variability and only models obtained from forward election and Mallow's C_p do not satisfy normality. **Thus, we choose the model obtained from BIC**, which is simpler than other models and is useful just like other models, because all models are similar by looking at the diagnostic graphs and we want to choose the model that is both simple and useful.

Interpretation:

Holding other variables constant, the body fat percentage decrease 0.09985 when weight increase 1 unit.
Holding other variables constant, the body fat percentage increase 0.97919 when AbdomenC increase 1 unit.
Holding other variables constant, the body fat percentage decrease 1.55701 when WristC increase 1 unit.
The intercept of the model has no real meaning in the real life, because the body fat percentage cannot be negative, and the weight cannot be 0.

For 95% prediction interval:

```
> x0=data.frame(Weight=mean(bodyfat$Weight),AbdomenC=mean(bodyfat$AbdomenC),W
ristC=mean(bodyfat$WristC))
> PI=predict(lm.bic.p,new=x0,interval='prediction',level=0.95)
> PI
      fit      lwr      upr
1 18.9852 10.25148 27.71892
```

The prediction interval for the average men is **[10.25148, 27.71892].**