PCR: Seat position

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Seat Position

We reconsider the **seat position** data set. Recall that it is from the `faraway` library.

```
#install.packages("faraway")
library(faraway)
```

The data set `seatpos` is used to predict the carseat position (`hipcenter`) based on biometric data of the driver.

```
data(seatpos)
```

This is what we got when we tried multiple linear regression.

```
lm.fit=lm(hipcenter~.,data=seatpos)
summary(lm.fit)
```

```
##
## Call:
## lm(formula = hipcenter ~ ., data = seatpos)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -73.827 -22.833  -3.678  25.017  62.337
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 436.43213  166.57162   2.620   0.0138 *
## Age           0.77572    0.57033   1.360   0.1843
## Weight        0.02631    0.33097   0.080   0.9372
## HtShoes      -2.69241    9.75304  -0.276   0.7845
## Ht            0.60134   10.12987   0.059   0.9531
## Seated        0.53375    3.76189   0.142   0.8882
## Arm          -1.32807    3.90020  -0.341   0.7359
## Thigh        -1.14312    2.66002  -0.430   0.6706
## Leg          -6.43905    4.71386  -1.366   0.1824
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 37.72 on 29 degrees of freedom
## Multiple R-squared:  0.6866, Adjusted R-squared:  0.6001
## F-statistic:  7.94 on 8 and 29 DF,  p-value: 0.00001306
```

Does PCA help? Let's import the requisite library.

```
library(stats)
```

I will reimagine my predictor variables to be the ones with the biometric data (so, we exclude `Age` and the

response).

```
data=seatpos[,2:8]
attach(data)
```

Let's look at the principal components analysis.

```
pr.out=prcomp(data,scale=TRUE)
pr.out$center
```

```
##    Weight   HtShoes        Ht    Seated       Arm     Thigh       Leg
## 155.63158 171.38947 169.08421  88.95263  32.21579  38.65526  36.26316
```

```
pr.out$scale
```

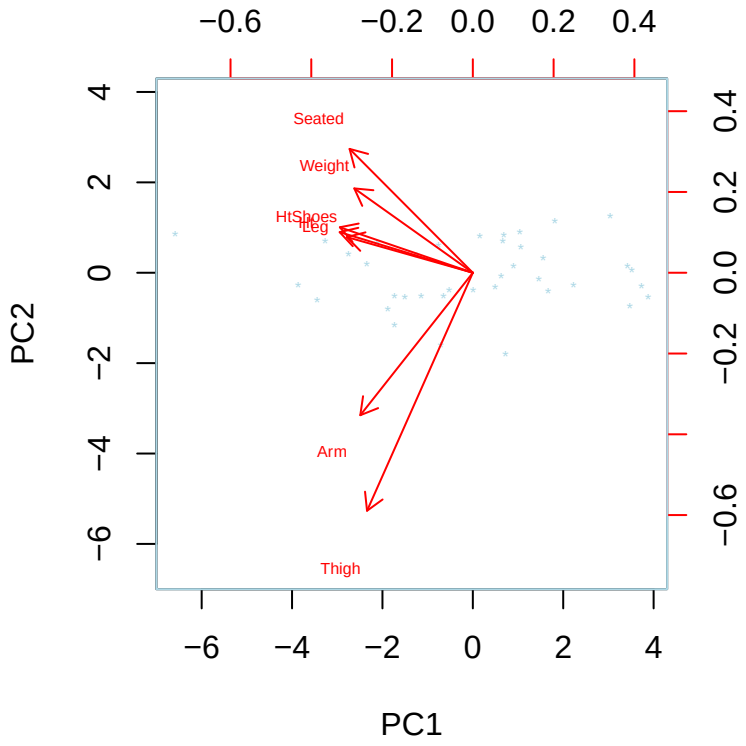
```
##    Weight   HtShoes        Ht    Seated       Arm     Thigh       Leg
## 35.781183 11.148259 11.173316  4.931791  3.371464  3.874985  3.403688
```

```
pr.out$rotation
```

```
##                PC1        PC2        PC3        PC4         PC5         PC6
## Weight  -0.3669000  0.2609907  0.3583572  0.8108919 -0.09990080  0.03621216
## HtShoes -0.4115997  0.1407447 -0.1565664 -0.1352201  0.05194816 -0.52851487
## Ht      -0.4122101  0.1256624 -0.1677289 -0.1229614  0.03494283 -0.50618661
## Seated  -0.3815355  0.3833142 -0.3163432 -0.1186066  0.51335147  0.57430863
## Arm     -0.3483026 -0.4409166  0.6837027 -0.2740335  0.37316939  0.04934303
## Thigh   -0.3274140 -0.7367171 -0.4882332  0.2871929 -0.08944022  0.14451162
## Leg     -0.3898319  0.1104287  0.1141931 -0.3706867 -0.75849557  0.33164299
##                 PC7
## Weight  -0.003349489
## HtShoes -0.697102953
## Ht       0.716654290
## Seated  -0.000440318
## Arm      0.006629621
## Thigh   -0.017704188
## Leg     -0.009235742
```

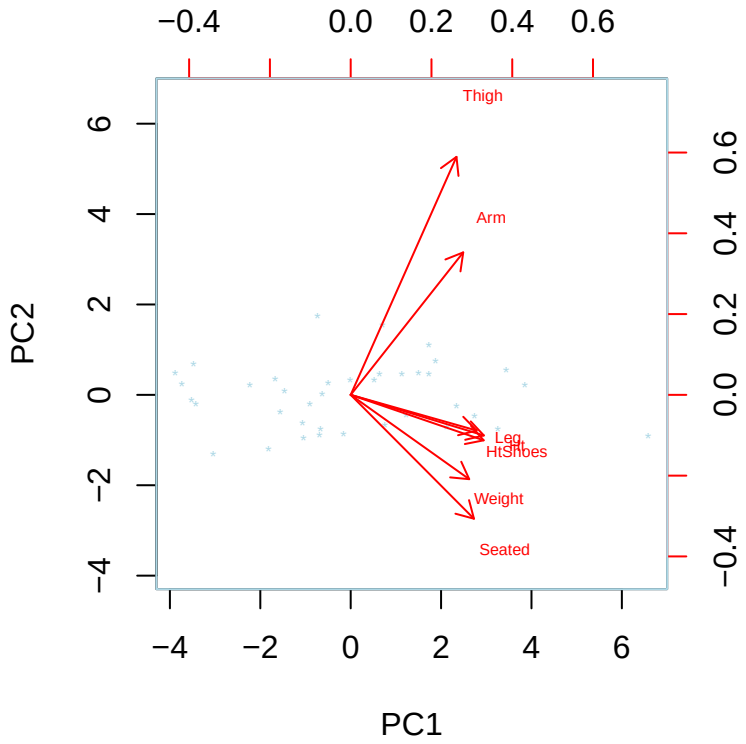
What does the biplot tell us?

```
biplot(pr.out,scale=0, cex=0.5, xlabs=rep("*", length(Ht)),
       col=c("lightblue", "red"))
```



I am not happy with all the negative loadings, so let's take the negatives.

```
pr.out$rotation=-pr.out$rotation
#pr.out$rotation
pr.out$x=-pr.out$x
biplot(pr.out,scale=0, cex=0.5, xlabs=rep("*", length(Ht)),
       col=c("lightblue", "red"))
```

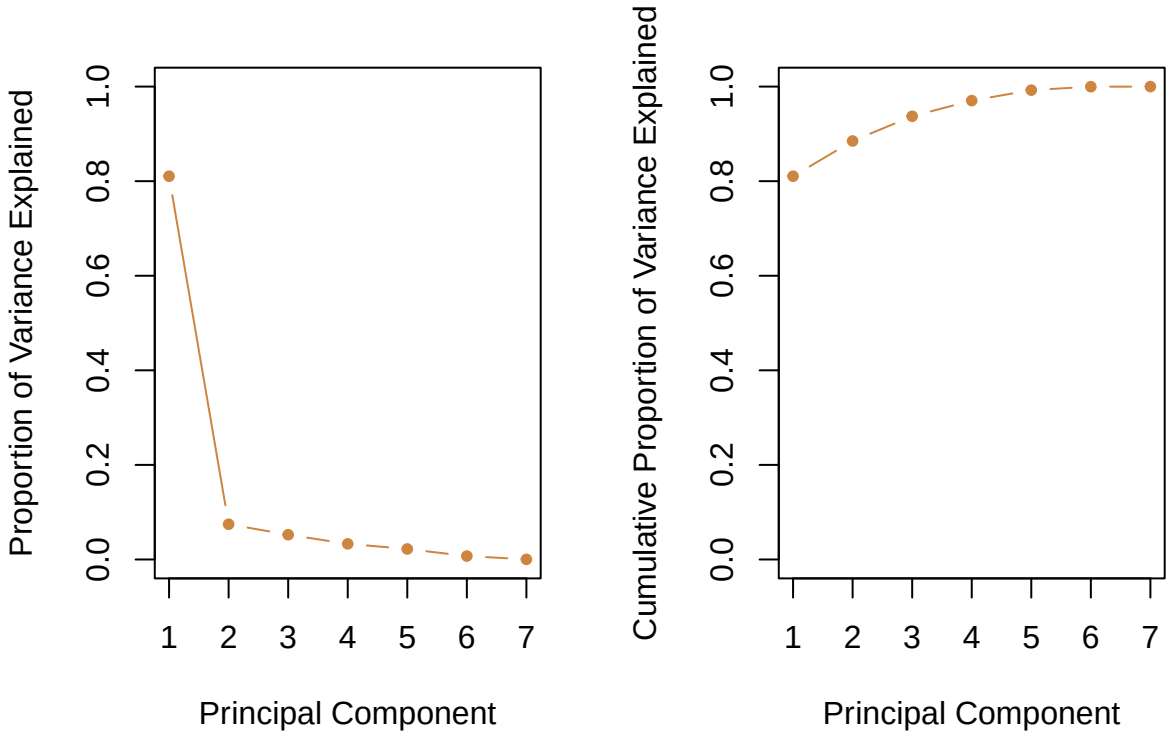


Let's look at the variance explained.

```
pr.var=pr.out$sdev^2
pve=pr.var/sum(pr.var)
pve
```

```
## [1] 0.8104205665 0.0745307740 0.0523285870 0.0330533459 0.0221980944
## [6] 0.0072232129 0.0002454193
```

```
par(mfrow = c(1, 2))
plot(pve,xlab="Principal Component",
     ylab="Proportion of Variance Explained", col="peru",
     pch=20, ylim=c(0,1),type='b')
plot(cumsum(pve),xlab="Principal Component",
     ylab="Cumulative Proportion of Variance Explained",
     col="peru", pch=20, ylim=c(0,1),type='b')
```



What would principal component regression give us?

```
library(pls)
```

```
##
## Attaching package: 'pls'
```

```
## The following object is masked from 'package:stats':
##
##     loadings
```

```
set.seed(1)
data=seatpos[,-1]
attach(data)
```

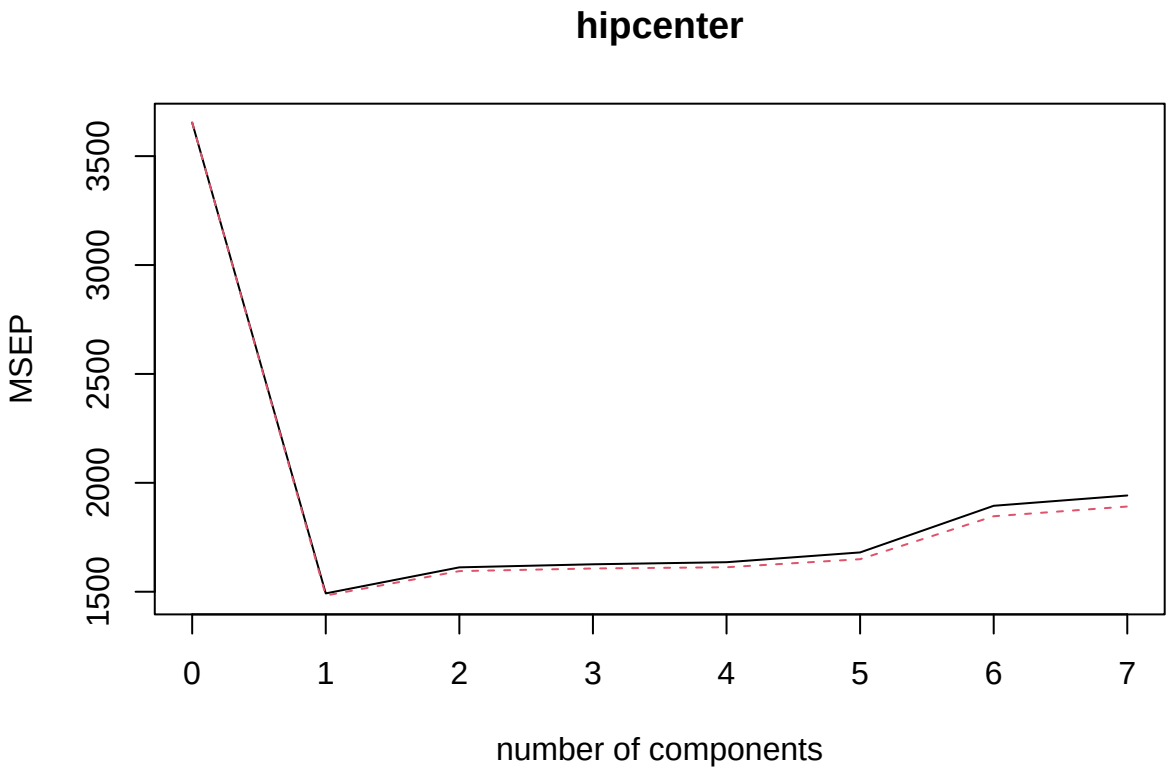
```
## The following objects are masked from data (pos = 4):
##
##     Arm, Ht, HtShoes, Leg, Seated, Thigh, Weight
```

```
pcr.fit=pcr(hipcenter~.,data=data,scale=TRUE,validation="CV")
summary(pcr.fit)
```

```
## Data:    X dimension: 38 7
##  Y dimension: 38 1
## Fit method: svdpc
## Number of components considered: 7
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           60.45    38.63    40.15    40.32    40.44    40.99    43.53
## adjCV        60.45    38.51    39.93    40.08    40.16    40.61    42.97
##        7 comps
## CV       44.07
## adjCV    43.49
##
## TRAINING: % variance explained
##            1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X            81.04    88.50    93.73    97.03    99.25    99.98   100.00
## hipcenter    62.00    62.54    63.50    64.85    66.51    66.61    66.66
```

Exactly **one** component works wonderfully. Let's confirm with the validation plot.

```
validationplot(pcr.fit,val.type="MSEP")
```



What if we did the training and testing instead?

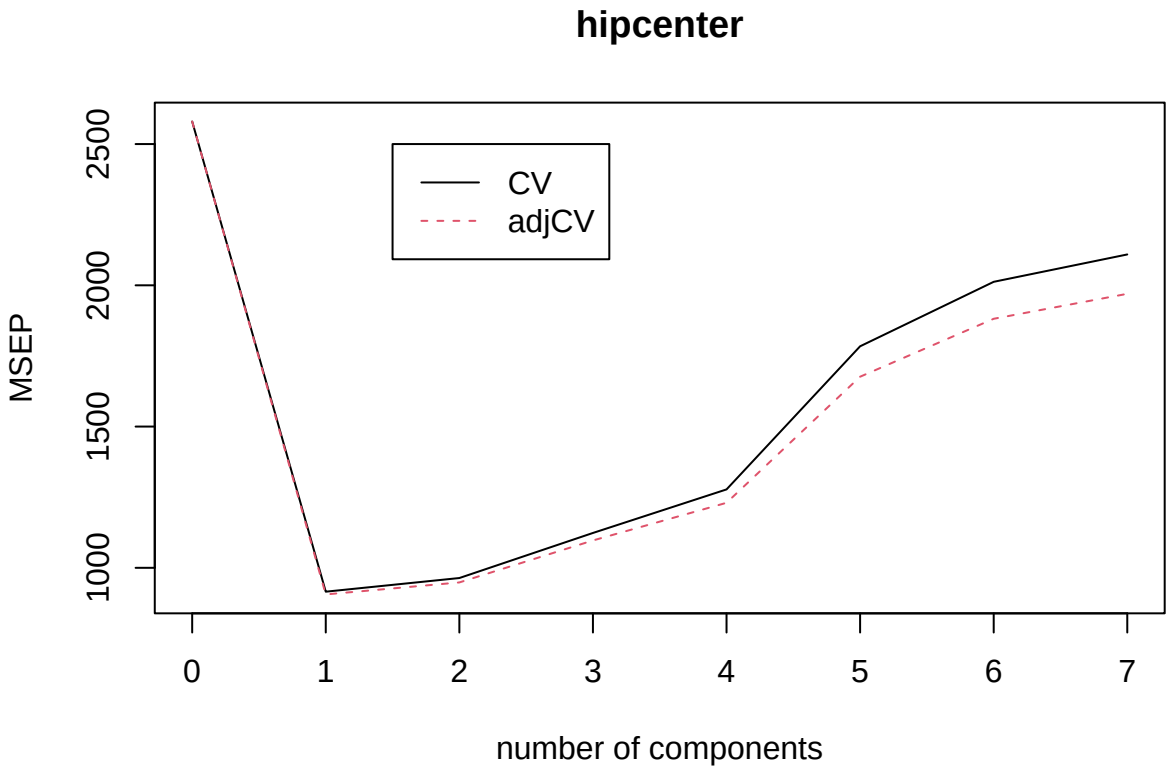
```
set.seed(1)
train.ind <- sample(nrow(data), floor(nrow(data)*0.6))
training <- data[train.ind,]
```

```r
test <- data[-train.ind,]

pcr.fit=pcr(hipcenter~.,data=training,scale=TRUE, validation="CV")
summary(pcr.fit)
```

```
## Data:    X dimension: 22 7
##  Y dimension: 22 1
## Fit method: svdpc
## Number of components considered: 7
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           50.79    30.26    31.05    33.52    35.74    42.24    44.86
## adjCV        50.79    30.10    30.79    33.12    35.07    40.94    43.38
##        7 comps
## CV       45.93
## adjCV    44.38
##
## TRAINING: % variance explained
##            1 comps  2 comps  3 comps  4 comps  5 comps  6 comps  7 comps
## X            84.77    92.09    96.00    98.58    99.62    99.97   100.00
## hipcenter    69.45    70.44    70.48    72.27    72.31    72.54    73.88
```

```r
validationplot(pcr.fit,val.type="MSEP", legendpos = t(c(1.5,2500)))
```



Note that the RMSE for 1 principal component is 30.26. This implies that the MSE is $30.26^2 = 915.6676$. Now, we look at the performance on the testing set with 1 principal component.

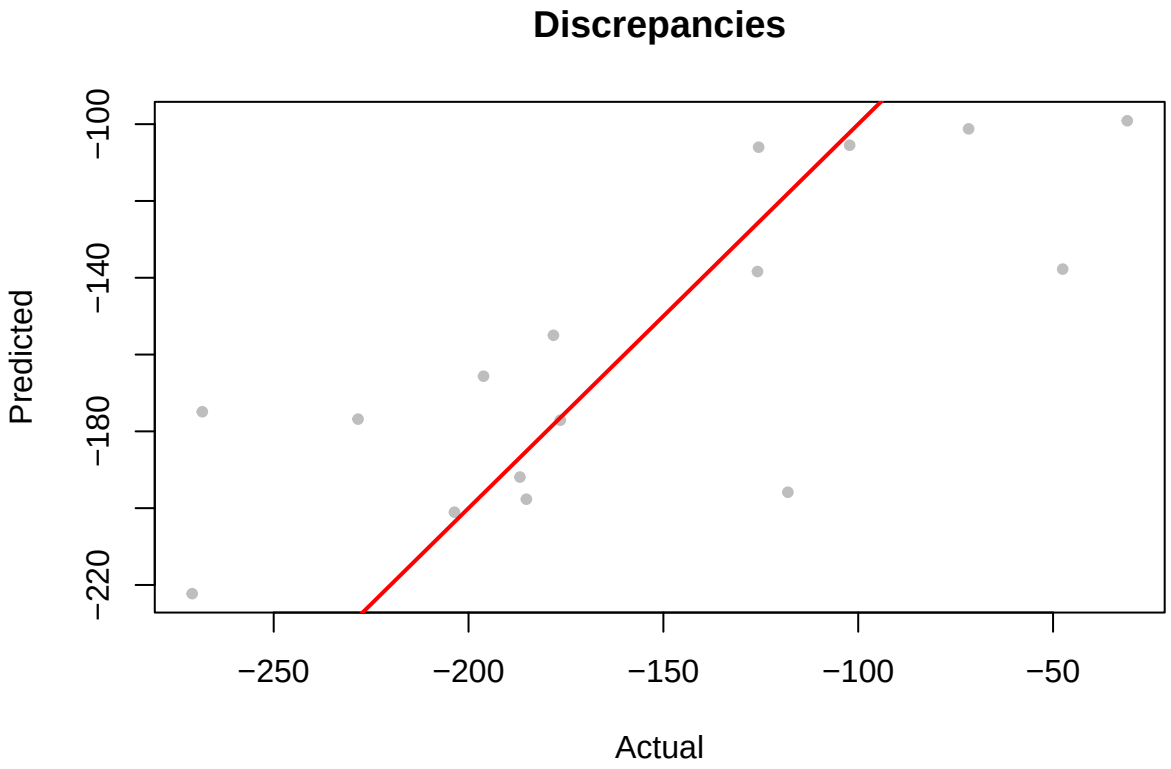
```
pcr.pred=predict(pcr.fit,newdata=test,ncomp=1)
#pcr.pred
mean((pcr.pred-test$hipcenter)^2)
```

```
## [1] 2229.636
```

The MSE is much higher than on the training set.

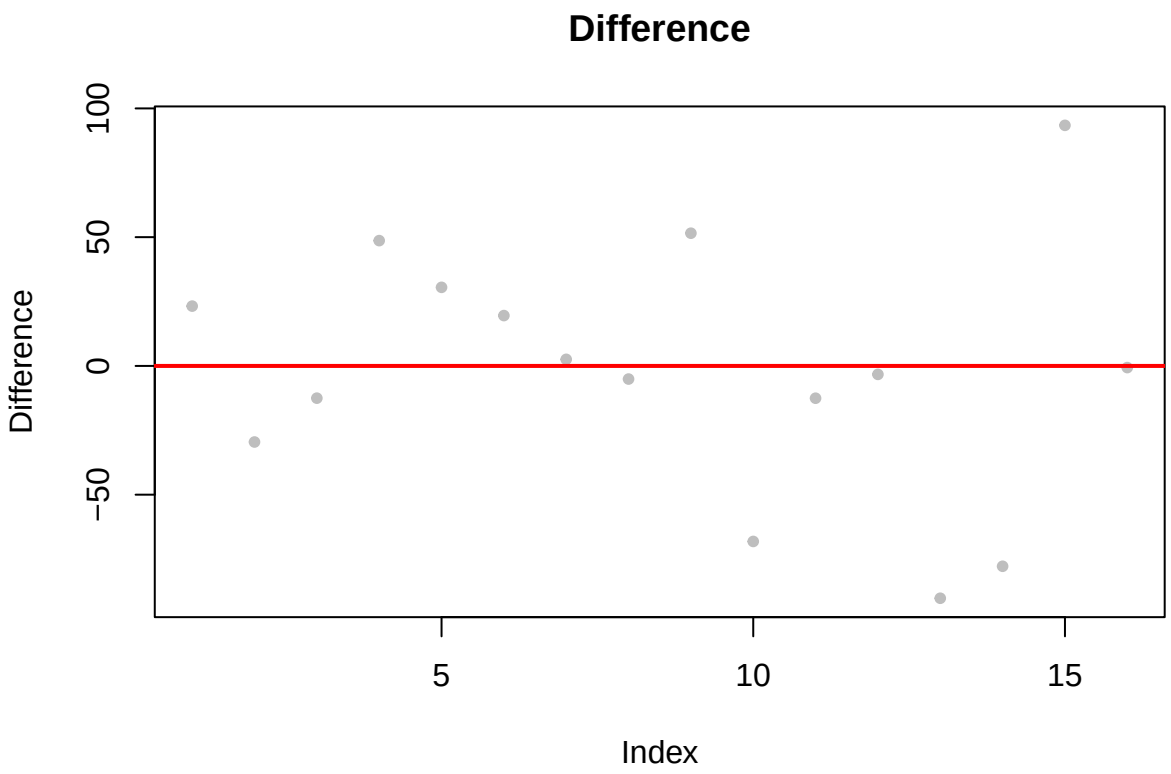
It is interesting to consider the scatterplot of the predicted and actual values in the testing set.

```
plot(pcr.pred~test$hipcenter, pch=20, col="grey",
     main="Discrepancies",
     xlab="Actual", ylab="Predicted")
abline(0,1, col="red", lwd=2)
```



What about the difference?

```
plot(pcr.pred-test$hipcenter, pch=20, col="grey",
     main="Difference",
     xlab="Index", ylab="Difference")
abline(0,0, col="red", lwd=2)
```


Difference
Difference
100
50
0
−50
5
10
15
Index