# STA302A2

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SETUP

```
setwd("~/Google Drive/Uni/Winter 2018/STA302/A2")
dat <- read.table("Census.txt", sep = "" ,header=T)
LIFE <- dat$LIFE
MALE <- dat$MALE
BIRTH <- dat$BIRTH
DIVO <- dat$DIVO
BEDS <- dat$BEDS
EDUC <- dat$EDUC
INCO <- dat$INCO
y <- LIFE
```

1)

```
x = as.matrix(dat)
x <-x[1:51, 2:7]
x<- cbind(1, x)
mode(x) = 'numeric'
n <- 51
p <-6
X<-x
Xt <- t(X)
XtX <- Xt %*% X
XtXinv <-solve(XtX)
Xty <- Xt %*% y
bhat <- XtXinv %*% Xty
```

1a)

```
y_hat <- X %*% bhat
y_hat
```

```
##           [,1]
##  [1,] 71.32712
##  [2,] 69.44152
##  [3,] 70.61014
##  [4,] 70.29776
##  [5,] 71.65898
##  [6,] 71.97295
##  [7,] 72.28677
##  [8,] 66.87019
##  [9,] 70.41924
## [10,] 71.38047
## [11,] 69.42376
## [12,] 71.53120
## [13,] 71.42614
## [14,] 71.04053
```

```
## [15,] 70.16589
## [16,] 70.29139
## [17,] 71.64995
## [18,] 70.78642
## [19,] 70.31884
## [20,] 70.92242
## [21,] 72.03916
## [22,] 70.25335
## [23,] 70.24288
## [24,] 71.16816
## [25,] 70.77073
## [26,] 68.72947
## [27,] 72.04422
## [28,] 70.81770
## [29,] 71.67050
## [30,] 71.22929
## [31,] 71.04496
## [32,] 72.13043
## [33,] 70.80619
## [34,] 68.76111
## [35,] 70.46957
## [36,] 70.31486
## [37,] 71.13894
## [38,] 72.51628
## [39,] 70.91515
## [40,] 71.43818
## [41,] 70.51633
## [42,] 71.11649
## [43,] 70.03452
## [44,] 70.18014
## [45,] 69.57848
## [46,] 71.56217
## [47,] 70.51127
## [48,] 72.50224
## [49,] 71.48537
## [50,] 69.92352
## [51,] 70.45665
```

```
e_hat = y - y_hat
e_hat
```

```
##              [,1]
##  [1,] -2.01712273
##  [2,] -0.39152270
##  [3,]  0.04985782
##  [4,]  0.25224335
##  [5,]  0.05102320
##  [6,]  0.08704553
##  [7,]  0.19323411
##  [8,] -1.16019333
##  [9,] -0.35923989
## [10,] -0.72046876
## [11,] -0.88376476
## [12,]  2.06880340
## [13,]  1.13386172
```

```
## [14,]  0.82946681
## [15,] -0.02589499
## [16,]  0.58861254
## [17,]  0.93004669
## [18,] -0.68642174
## [19,] -1.55884433
## [20,]  0.90758262
## [21,] -1.81915643
## [22,]  0.67665009
## [23,]  0.38711962
## [24,]  1.79184021
## [25,] -0.08073436
## [26,] -0.63947073
## [27,] -1.48421996
## [28,] -1.60770155
## [29,]  1.11949999
## [30,]  1.37071164
## [31,]  0.18503566
## [32,] -1.20043418
## [33,] -0.48618775
## [34,]  0.26888640
## [35,]  0.08043332
## [36,]  0.50514224
## [37,]  0.28105954
## [38,] -0.38627710
## [39,] -0.48514830
## [40,]  0.46181996
## [41,] -2.55632758
## [42,]  0.96350641
## [43,]  0.07548104
## [44,]  0.71986346
## [45,]  3.32151698
## [46,] -1.48217033
## [47,]  1.12872551
## [48,] -0.78223737
## [49,]  0.99463448
## [50,] -0.44351769
## [51,] -0.16664779
```

```
bhat
```

```
##                [,1]
##       70.5577812705
## MALE   0.1261018758
## BIRTH -0.5160557876
## DIVO  -0.1965375074
## BEDS  -0.0033392036
## EDUC   0.2368222541
## INCO  -0.0003612011
```

Equation: LIFE = 70.5577812705 + 0.1261018758 (MALE) - 0.5160557876 (BIRTH) - 0.1965375074 (DIVO) - 0.0033392036 (BEDS) + 0.2368222541 (EDUC) - 0.0003612011 (INCO) + e_hat

1b) - MALE

```
  bhat[2] #b_1
```

```
## [1] 0.1261019
```

b_1 (MALE) corresponds to the Expected change (+ 0.1261019) in the Averafe Lifespan with 1 unit increase in the proportion of Males to Female.

- BIRTH

```
bhat[3] #b_2
```

```
## [1] -0.5160558
```

b_2 (BIRTH) corresponds to the Expected change (-0.5160558) in the Averafe Lifespan with a unit increase in the birth rate per 1,000 people.

1c)

```
RSS <- (t(e_hat) %*% e_hat)
sigma_sq_hat = RSS / (n)
sigma_sq_hat
```

```
##          [,1]
## [1,] 1.192215
```

```
s_sq = RSS / (n-p-1)
s_sq
```

```
##          [,1]
## [1,] 1.381885
```

1d)

```
s <-c(s_sq^(1/2))
se_bs = diag(s * (XtXinv)^(1/2))
se_bs
```

```
##                      MALE        BIRTH         DIVO         BEDS
## 4.2897471299 0.0472317551 0.1172774621 0.0739532971 0.0009795303
##         EDUC         INCO
## 0.1110224835 0.0004597943
```

```
#Corresponding to B_0, B_1 ... B_6
```

1e)

```
y_bar = c(sum(y_hat)/ n)
SST <- sum((LIFE - y_bar)^(2))
R_sq <- 1 - (RSS/SST)
R_sq
```

```
##           [,1]
## [1,] 0.4684927
```

Explains the proportion of variation in the Average lifespan explained by the regression, which is 46.849%.

2) 2a)

```
MLR <- lm(formula = LIFE~ MALE + BIRTH + DIVO + BEDS + EDUC + INCO, data=dat)
summary(MLR)
```

```
##
```

```
## Call:
## lm(formula = LIFE ~ MALE + BIRTH + DIVO + BEDS + EDUC + INCO,
##     data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.5563 -0.6629  0.0755  0.6983  3.3215
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 70.5577813  4.2897471  16.448  < 2e-16 ***
## MALE         0.1261019  0.0472318   2.670  0.01059 *
## BIRTH       -0.5160558  0.1172775  -4.400 6.78e-05 ***
## DIVO        -0.1965375  0.0739533  -2.658  0.01093 *
## BEDS        -0.0033392  0.0009795  -3.409  0.00141 **
## EDUC         0.2368223  0.1110225   2.133  0.03853 *
## INCO        -0.0003612  0.0004598  -0.786  0.43633
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.176 on 44 degrees of freedom
## Multiple R-squared:  0.4685, Adjusted R-squared:  0.396
## F-statistic: 6.464 on 6 and 44 DF,  p-value: 6.112e-05
```

2b) $H_0 : B_0 = B_1 = B_2 = B_3 = B_4 = B_5 = B_6 = 0$ $H_A : B_i \neq 0$ [any i in range 0 to 6]

```
SSReg = SST-RSS
F_val = (SSReg/(p)/(RSS/(n-p-1)))
F_val
```

```
##          [,1]
## [1,] 6.463905
```

```
F_crt = qf(.95, df1=p, df2=n-p-1)
F_crt
```

```
## [1] 2.313264
```

F_val > F_crit, hence we fail to accept $H_0$. Then atleast one of the B_i's [i = 1, ... 6] is not Zero. Our Model is significant.

2c)

# MALE

$H_0 : B_1 = 0$ $H_A : B_1 \neq 0$

```
t_value1 =2.670
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_crit| > |t_value1|, we accept $H_0$. Then $B_1 \neq 0$ and we can remove the predictor (MALE) from the model.

## BIRTH

$H_0 : B_2 = 0$ $H_A : B_2 ! = 0$

```
t_value2 = 4.400
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_value2| > |t_crit|, we fail to accept $H_0$. Then $B_2 \neq 0$ then we can't remove the predictor (BIRTH) variable from the model.

## DIVO

$H_0 : B_3 = 0$ $H_A : B_3 \neq 0$

```
t_value3 =2.658
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_crit| > |t_value3|, we accept $H_0$. Then $B_3 \neq 0$ and we can remove the predictor (DIVO) from the model.

## BEDS

$H_0 : B4 = 0$ $H_A : B4 \neq 0$

```
t_value4 =3.409
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_value4| > |t_crit|, we fail to accept $H_0$. Then $B_4 \neq 0$ then we can't remove the predictor (BEDS) variable from the model.

## EDUC

$H_0 : B5 = 0$ $H_A : B5 \neq 0$

```
t_value5 = 2.133
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_crit| > |t_value5|, we accept $H_0$. Then $B_3 \neq 0$ and we can remove the predictor (EDUC) from the model.

## INCO

$H_0 : B6 = 0$ $H_A : B6 \neq 0$

```
t_value6 =0.786
t_crit = qt(c(.005, .995), df=n-p-1)
#t_crit = [-2.692278, 2.692278]
```

Since |t_crit| > |t_value6|, we accept $H_0$. Then $B_6 \neq 0$ and we can remove the predictor (INCO) from the model.

Yes, the results indicate that variables MALE (x1), DIVO (x3), EDUC (x5) and INCO x(6) should be removed.

2d)

```
MLR_reduced <- lm(formula = LIFE~ BIRTH + BEDS, data=dat)
summary(MLR_reduced)
```

```
##
## Call:
## lm(formula = LIFE ~ BIRTH + BEDS, data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.5627 -0.8180 -0.0819  0.9261  3.6202
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 79.1473186  2.2717401  34.840  < 2e-16 ***
## BIRTH       -0.3281679  0.1026214  -3.198  0.00245 **
## BEDS        -0.0027415  0.0009388  -2.920  0.00531 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.352 on 48 degrees of freedom
## Multiple R-squared:  0.2329, Adjusted R-squared:  0.2009
## F-statistic: 7.286 on 2 and 48 DF,  p-value: 0.001725
```

LIFE = 79.1473186 - 0.3281679 (BIRTH) - 0.0027415 (BEDS)

2e) $H_0 : B_1 = B_6 = 0$ $H_A : B_1, B_6$ both not zero.

```
MLR_red_MALE_INCO <- lm(formula = LIFE~ BIRTH + BEDS + DIVO + EDUC, data=dat)
anova(MLR, MLR_red_MALE_INCO)
```

```
## Analysis of Variance Table
##
## Model 1: LIFE ~ MALE + BIRTH + DIVO + BEDS + EDUC + INCO
## Model 2: LIFE ~ BIRTH + BEDS + DIVO + EDUC
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1     44 60.803
## 2     46 70.654 -2   -9.8507 3.5642 0.03676 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
F_val = 3.5642
F_Crit =  qf(.99, df1=2, df2=n-p-1)
#F_Crit = 5.122628
```

|F_val| > |F_crit| we fail to reject $H_0$, hence the predictors MALE and INCO can be removed from the model.

2f)

```
MLR_MALE <- lm(LIFE ~ MALE, data=dat)
anova(MLR, MLR_MALE)
```

```
## Analysis of Variance Table
##
## Model 1: LIFE ~ MALE + BIRTH + DIVO + BEDS + EDUC + INCO
## Model 2: LIFE ~ MALE
##   Res.Df     RSS Df Sum of Sq      F    Pr(>F)
## 1     44  60.803
## 2     49 109.834 -5   -49.031 7.0963 6.099e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
F_val = 7.0963
```

As per ANOVA Output, our F test Statistic is 7.0963.

2g) $H_0 : B_i = 0$ [i = 1, 2] $H_A : B_1, B_2$ , both not zero.

```
MLR_B0 = lm(LIFE ~ 1, data=dat)
MLR_MALE_BIRTH <- lm(LIFE ~ MALE + BIRTH, data=dat)
anova(MLR_B0, MLR_MALE_BIRTH)
```

```
## Analysis of Variance Table
##
## Model 1: LIFE ~ 1
## Model 2: LIFE ~ MALE + BIRTH
##   Res.Df     RSS Df Sum of Sq    F    Pr(>F)
## 1     50 114.397
## 2     48  85.424  2    28.973 8.14 0.0009036 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
F_val = 8.14
```

We fail to accept the $H_0$, we infer that (MALE) x1 and(BIRTH) x2 are significant/useful in predicting the response.

2h)

```
MLR_B0 = lm(LIFE ~ 1, data=dat)
MLR_B0B3 = lm(LIFE ~ DIVO)
MLR_B0B2B3 = lm(LIFE ~ BIRTH + DIVO)
MLR_MALE_BIRTH_DIVO <- lm(LIFE~ MALE + BIRTH + DIVO, data=dat)
MLR_BIRTH_DIVO <- lm(LIFE ~ BIRTH + DIVO, data=dat)
```

```
SSRegB3B0 <- anova(MLR_B0)["Residuals", "Sum Sq"] - anova(MLR_B0B3)["Residuals", "Sum Sq"]
SSRegB3B0
```

```
## [1] 3.307311
```

```
SSRegB2_B0B3 <- anova(MLR_B0B3)["Residuals", "Sum Sq"] - anova(MLR_B0B2B3)["Residuals", "Sum Sq"]
SSRegB2_B0B3
```

```
## [1] 8.914548
```

```
RSSB0B1B2B3 <- anova(MLR_MALE_BIRTH_DIVO)["Residuals", "Sum Sq"]

RSS_B0B2B3 <- anova(MLR_BIRTH_DIVO)["Residuals", "Sum Sq"]

SSRegB1_B0B2B3 <- RSS_B0B2B3 - RSSB0B1B2B3
SSRegB1_B0B2B3
```

```
## [1] 21.42422
```

```
SSRegB1B2B3_B0 =  SSRegB3B0 + SSRegB2_B0B3 + SSRegB1_B0B2B3
SSRegB1B2B3_B0
```

```
## [1] 33.64607
```

2i) - 2i) (1)

```
#MLR_B0
#MLR_MALE
MLR_BIRTH <- lm(LIFE ~ BIRTH, data=dat)
MLR_DIVO <- lm(LIFE ~ DIVO, data=dat)
MLR_INCO <- lm(LIFE ~ INCO, data=dat)
#MLR_MALE_BIRTH
MLR_MALE_DIVO <- lm(LIFE~ MALE + DIVO, data=dat)
MLR_MALE_INCO <- lm(LIFE~ MALE + INCO, data=dat)
#MLR_BIRTH_DIVO
MLR_BIRTH_INCO <- lm(LIFE ~ BIRTH + INCO, data=dat)
MLR_DIVO_INCO <- lm(LIFE ~ DIVO + INCO, data=dat)
MLR_MALE_BIRTH_DIVO
```

```
##
## Call:
## lm(formula = LIFE ~ MALE + BIRTH + DIVO, data = dat)
##
## Coefficients:
## (Intercept)         MALE        BIRTH         DIVO
##     62.3656       0.1689      -0.3912      -0.1272
```

```
MLR_MALE_BIRTH_INCO <- lm(LIFE~ MALE + BIRTH + INCO, data=dat)
MLR_BIRTH_DIVO_INCO <- lm(LIFE ~ BIRTH + DIVO + INCO, data=dat)
MLR_MALE_DIVO_INCO <- lm(LIFE ~ MALE + DIVO + INCO, data=dat)
MLR_mbdi <- lm(LIFE ~ MALE + BIRTH + DIVO + INCO, data=dat)

#AIC
aic_b0 <- AIC(MLR_B0)
aic_b0
```

```
## [1] 189.9321
```

```
aic_m <- AIC(MLR_MALE)
aic_m
```

```
## [1] 189.8561
```

```
aic_d <- AIC(MLR_DIVO)
aic_d
```

```
## [1] 190.4359
```

```
aic_i <- AIC(MLR_INCO)
aic_i
```

```
## [1] 191.2477
```

```
aic_b <- AIC(MLR_BIRTH)
aic_b
```

```
## [1] 186.7525
```

```
aic_mb <- AIC(MLR_MALE_BIRTH)
aic_mb
```

```
## [1] 179.0377
```

```
aic_md <- AIC(MLR_MALE_DIVO)
aic_md
```

```
## [1] 188.5535
```

```
aic_mi <- AIC(MLR_MALE_INCO)
aic_mi
```

```
## [1] 191.4429
```

```
aic_bd <- AIC(MLR_BIRTH_DIVO)
aic_bd
```

```
## [1] 188.1698
```

```
aic_bi <- AIC(MLR_BIRTH_INCO)
aic_bi
```

```
## [1] 188.5226
```

```
aic_di <- AIC(MLR_DIVO_INCO)
aic_di
```

```
## [1] 191.4755
```

```
aic_mbd <- AIC(MLR_MALE_BIRTH_DIVO)
aic_mbd
```

```
## [1] 178.1686
```

```
aic_mbi <- AIC(MLR_MALE_BIRTH_INCO)
aic_mbi
```

```
## [1] 180.932
```

```
aic_bdi <- AIC(MLR_BIRTH_DIVO_INCO)
aic_bdi
```

```
## [1] 189.8012
```

```
aic_mdi <- AIC(MLR_MALE_DIVO_INCO)
aic_mdi
```

```
## [1] 189.9273
```

```
aic_mbdi <- AIC(MLR_mbdi)
aic_mbdi
```

```
## [1] 180.1406
```

Lowest AIC is with model LIFE ~ BIRTH + MALE + DIVO

- 2i) (2)

```
null<- MLR_B0
full<- MLR_mbdi
forwdAIC=step(null, scope=list(lower=null, upper=full), direction="forward")
```

```
## Start:  AIC=43.2
## LIFE ~ 1
##
##         Df Sum of Sq    RSS    AIC
## + BIRTH  1   11.0479 103.35 40.021
## + MALE   1    4.5632 109.83 43.124
## <none>               114.40 43.200
## + DIVO   1    3.3073 111.09 43.704
## + INCO   1    1.5249 112.87 44.516
##
## Step:  AIC=40.02
## LIFE ~ BIRTH
##
##        Df Sum of Sq     RSS    AIC
## + MALE  1   17.9252  85.424 32.306
## <none>              103.349 40.021
## + DIVO  1    1.1739 102.175 41.438
## + INCO  1    0.4647 102.885 41.791
##
## Step:  AIC=32.31
## LIFE ~ BIRTH + MALE
##
##        Df Sum of Sq    RSS    AIC
## + DIVO  1    4.6730 80.751 31.437
## <none>              85.424 32.306
## + INCO  1    0.1768 85.247 34.200
##
## Step:  AIC=31.44
## LIFE ~ BIRTH + MALE + DIVO
##
##        Df Sum of Sq    RSS    AIC
## <none>              80.751 31.437
## + INCO  1  0.044334 80.707 33.409
```

```
forwdAIC
```

```
##
## Call:
## lm(formula = LIFE ~ BIRTH + MALE + DIVO, data = dat)
##
## Coefficients:
## (Intercept)        BIRTH         MALE         DIVO
##     62.3656      -0.3912       0.1689      -0.1272
```

Best Model according to forwardAIC is LIFE ~ BIRTH + MALE + DIVO

- 2i) (3)

```
backAIC=step(full, direction="backward", data=dat)
```

```
## Start:  AIC=33.41
## LIFE ~ MALE + BIRTH + DIVO + INCO
##
##         Df Sum of Sq     RSS    AIC
## - INCO   1    0.0443  80.751 31.437
## <none>                80.707 33.409
## - DIVO   1    4.5405  85.247 34.200
```

```
## - MALE   1   20.7328 101.440 43.070
## - BIRTH  1   20.9838 101.691 43.196
##
## Step:  AIC=31.44
## LIFE ~ MALE + BIRTH + DIVO
##
##         Df Sum of Sq     RSS    AIC
## <none>                 80.751 31.437
## - DIVO   1     4.673  85.424 32.306
## - MALE   1    21.424 102.175 41.438
## - BIRTH  1    22.196 102.947 41.822
```

```
backAIC
```

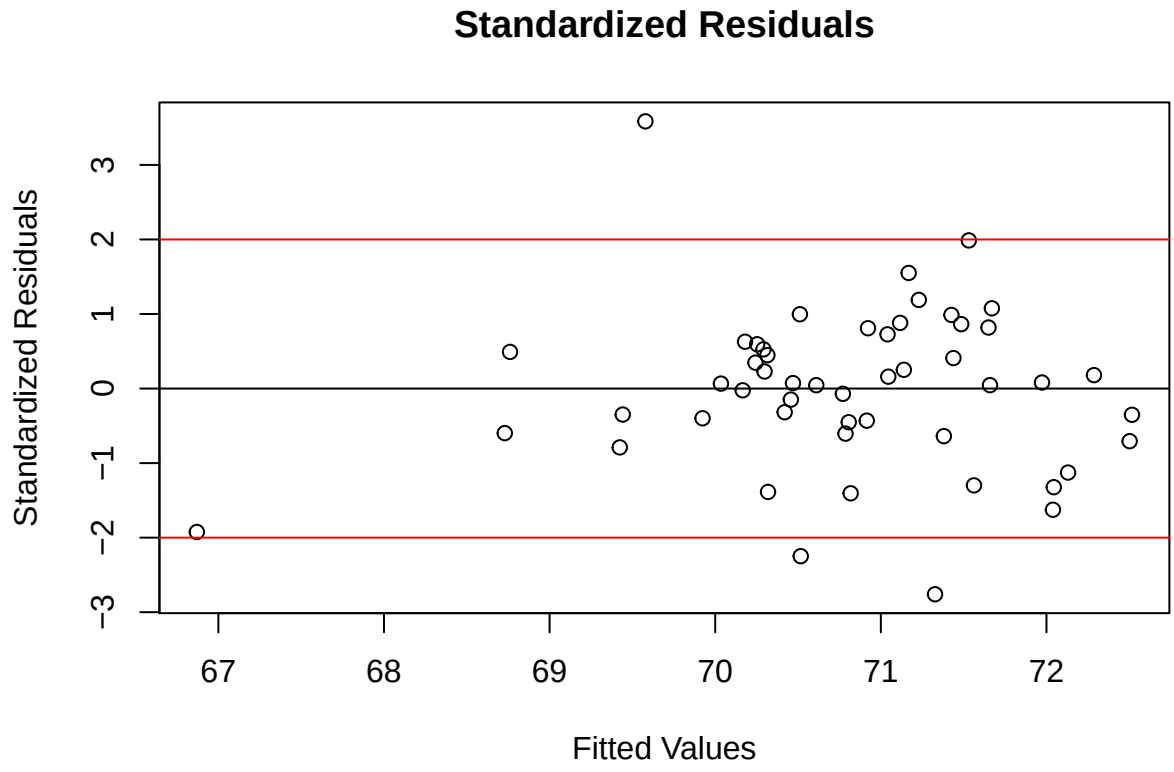
```
##
## Call:
## lm(formula = LIFE ~ MALE + BIRTH + DIVO, data = dat)
##
## Coefficients:
## (Intercept)         MALE        BIRTH         DIVO
##     62.3656       0.1689      -0.3912      -0.1272
```

Best Model according to backwardAIC is LIFE ~ BIRTH + MALE + DIVO

3)

3a)

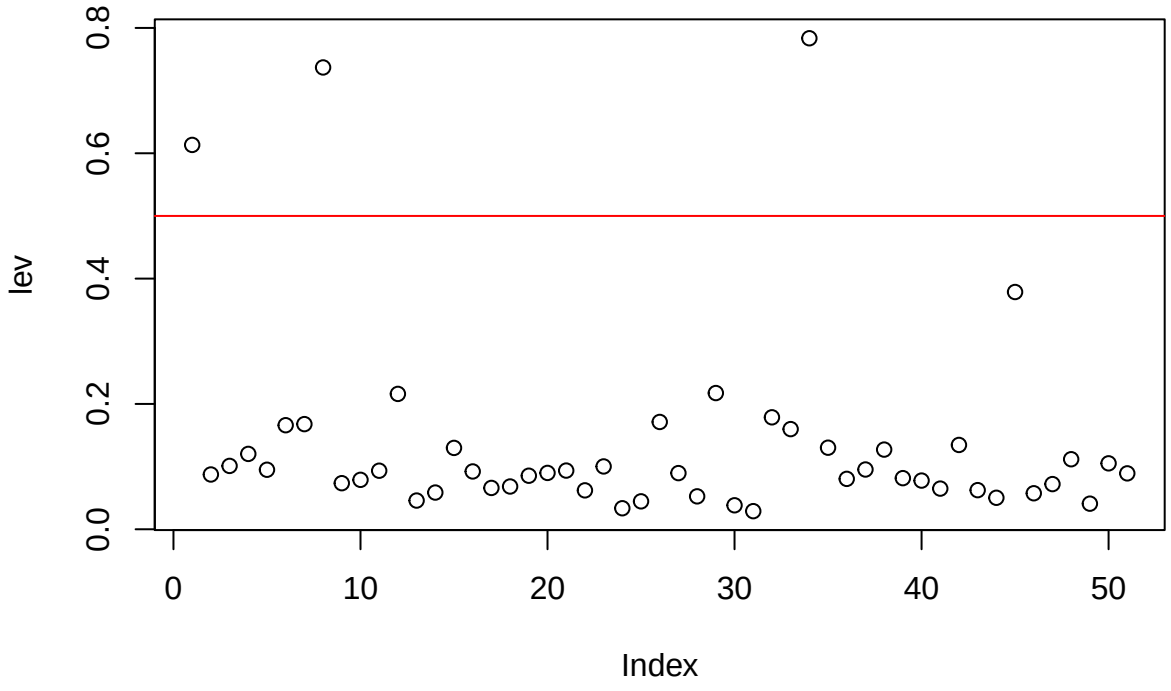
```
std_res <- rstandard(MLR)
plot(MLR$fitted.values, std_res, ylab="Standardized Residuals", xlab="Fitted Values", main="Standardize
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
```




Yes, there are 3 points with residuals greater than |2| and an outlier that may be influential with the lowest fitted value (~67).

3b)

```
lev = hat(model.matrix(MLR))
plot(lev)
abline(0.5, 0, col=c("red"))
```



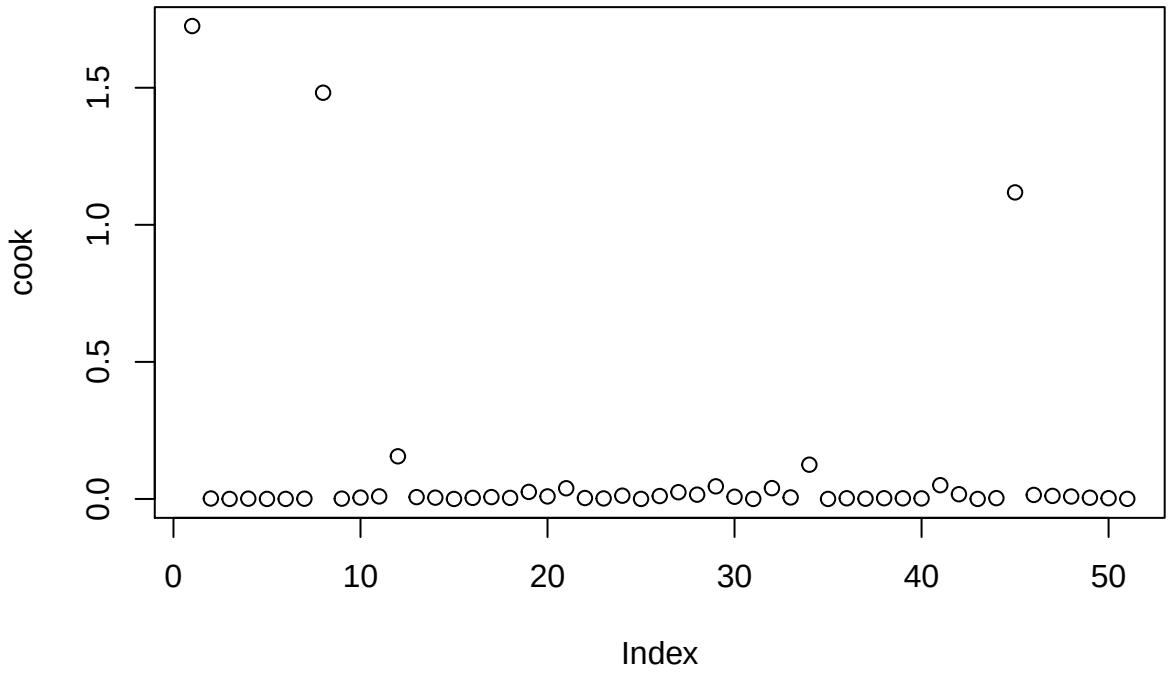
```
dat[lev >0.5,]
```

```
##    STATE  MALE BIRTH DIVO   BEDS EDUC INCO  LIFE
## 1     AK 119.1  24.8  5.6  603.3 14.1 4638 69.31
## 8     DC  86.8  20.1  3.0 1859.4 17.8 4644 65.71
## 34    NV 102.8  19.6 18.7  560.7 10.8 4583 69.03
```

3 points have lev $> 0.5$. Indices 1, 8 and 34. Corresponding to States: AK, DC and NV.

3c)

```
cook = cooks.distance(MLR)
plot(cook)
```



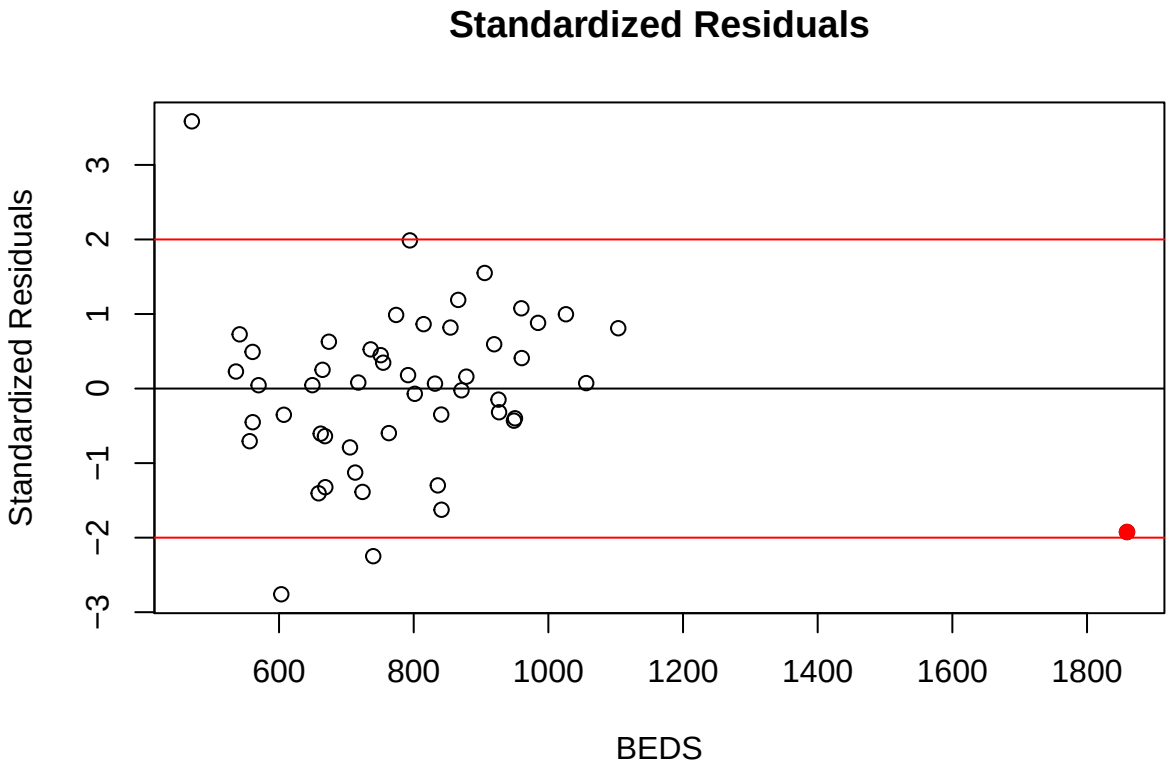

```
dat[cook > 1,]
```

```
##    STATE  MALE BIRTH DIVO   BEDS EDUC INCO  LIFE
## 1     AK 119.1  24.8  5.6  603.3 14.1 4638 69.31
## 8     DC  86.8  20.1  3.0 1859.4 17.8 4644 65.71
## 45    UT  97.6  25.5  3.7  470.5 14.0 3169 72.90
```

No, not all Observations are the same. We now see data corresponding to UT instead of NV.

3d)

```
plot(BEDS, std_res, ylab="Standardized Residuals",
     xlab="BEDS", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(BEDS[8], std_res[8] , col='red', pch = 19)
```




There are 3 points that are outliers based on std_res (>2) and the outlier red point corresponding to DC (RED)

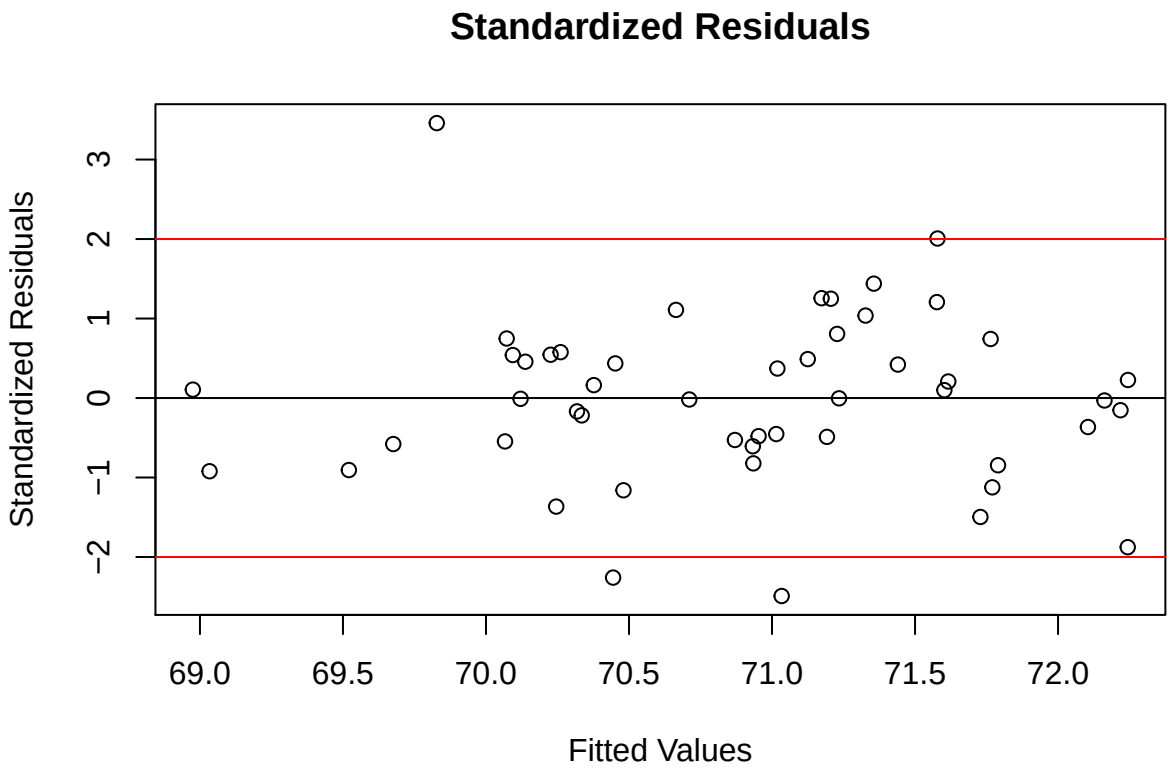
3e)

```
dat2 <- subset(dat, STATE != 'DC')
LIFE2 <- dat2$LIFE
MALE2 <- dat2$MALE
BIRTH2 <- dat2$BIRTH
DIVO2 <- dat2$DIVO
BEDS2 <- dat2$BEDS
EDUC2 <- dat2$EDUC
INCO2 <- dat2$INCO
MLR_NoDC <- lm(formula = LIFE2 ~ MALE2 + BIRTH2 + DIVO2 + BEDS2 + EDUC2 + INCO2, data=dat2)
summary(MLR_NoDC)
```

```
##
## Call:
## lm(formula = LIFE2 ~ MALE2 + BIRTH2 + DIVO2 + BEDS2 + EDUC2 +
##     INCO2, data = dat2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.48448 -0.61603 -0.00768  0.58701  3.07199
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 69.8207566  4.1692564  16.747  < 2e-16 ***
## MALE2        0.0922054  0.0487996   1.889  0.06558 .
## BIRTH2      -0.4261398  0.1222113  -3.487  0.00114 **
## DIVO2       -0.1377833  0.0774530  -1.779  0.08232 .
```

```
## BEDS2       -0.0011637  0.0014481  -0.804  0.42604
## EDUC2        0.3157699  0.1145801   2.756  0.00855 **
## INCO2       -0.0004698  0.0004485  -1.048  0.30064
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.138 on 43 degrees of freedom
## Multiple R-squared:  0.3679, Adjusted R-squared:  0.2797
## F-statistic: 4.171 on 6 and 43 DF,  p-value: 0.002171
```

```
std_res_NoDC <- rstandard(MLR_NoDC)
plot(MLR_NoDC$fitted.values, std_res_NoDC, ylab="Standardized Residuals", xlab="Fitted Values", main="S
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
```

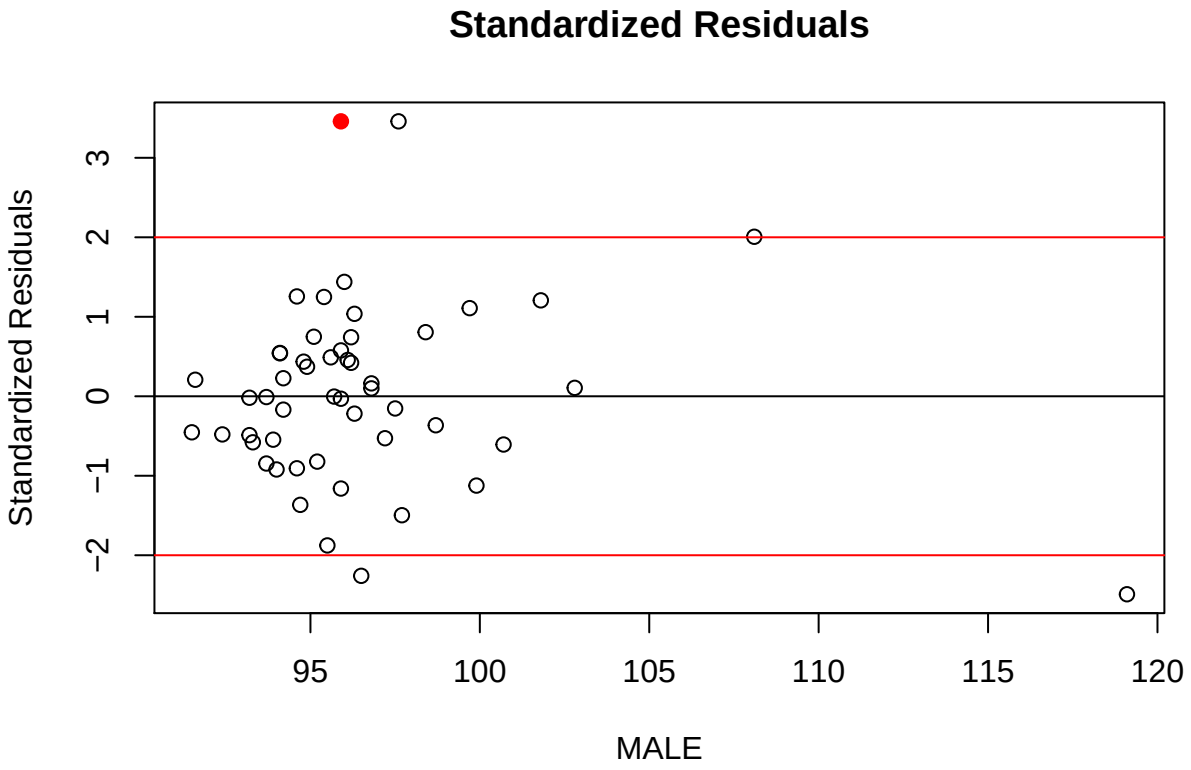



Yes there is a noticeable change in the Standardised residuals. The fitted line has changed. NEW: - LIFE = 69.8207566 + 0.0922054 (MALE2) - 0.4261398 (BIRTH2) - 0.1377833 (DIVO2) - 0.0011637 (BEDS2) + 0.3157699 (EDUC2) - 0.0004698 (INCO2) OLD: - LIFE = 70.5577813 + 0.1261019 (MALE2) - 0.5160558 (BIRTH2) - 0.1965375 (DIVO2) - 0.0033392 (BEDS2) + 0.2368223 (EDUC2) - 0.0003612 (INCO2)

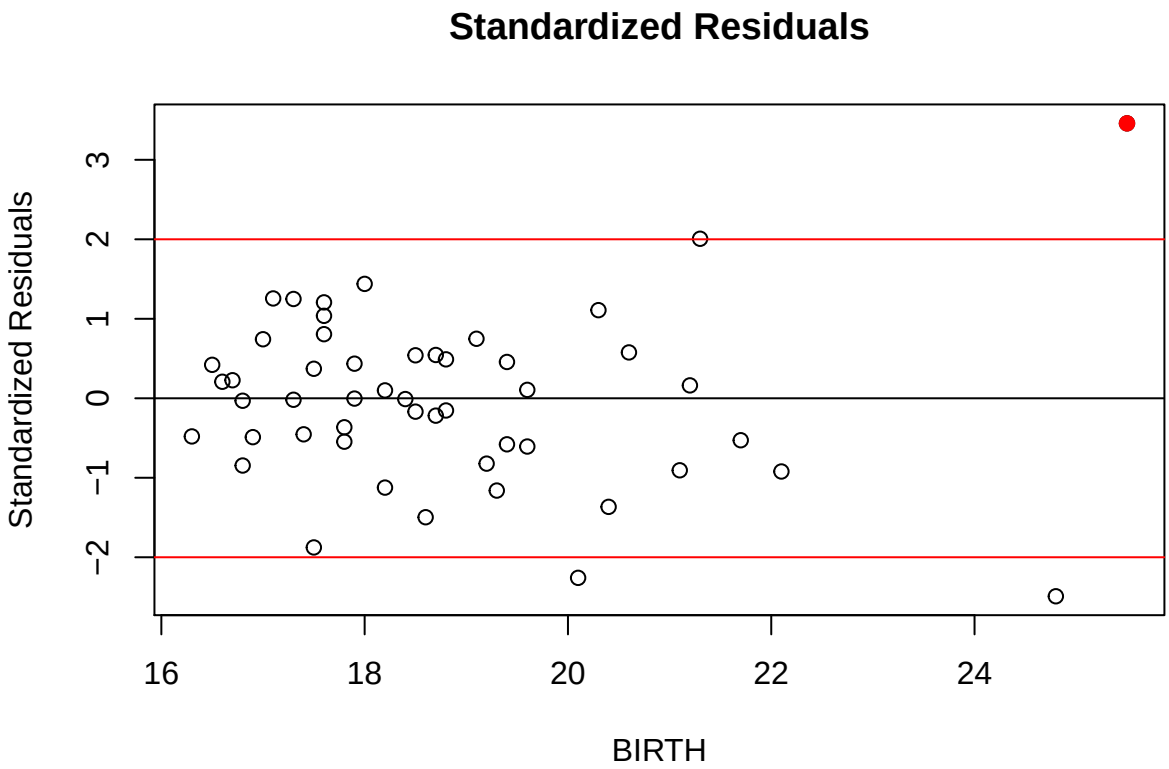
Also, $R^2$s changed: New: Multiple R-squared: 0.3679 Old: Multiple R-squared: 0.4685

f)

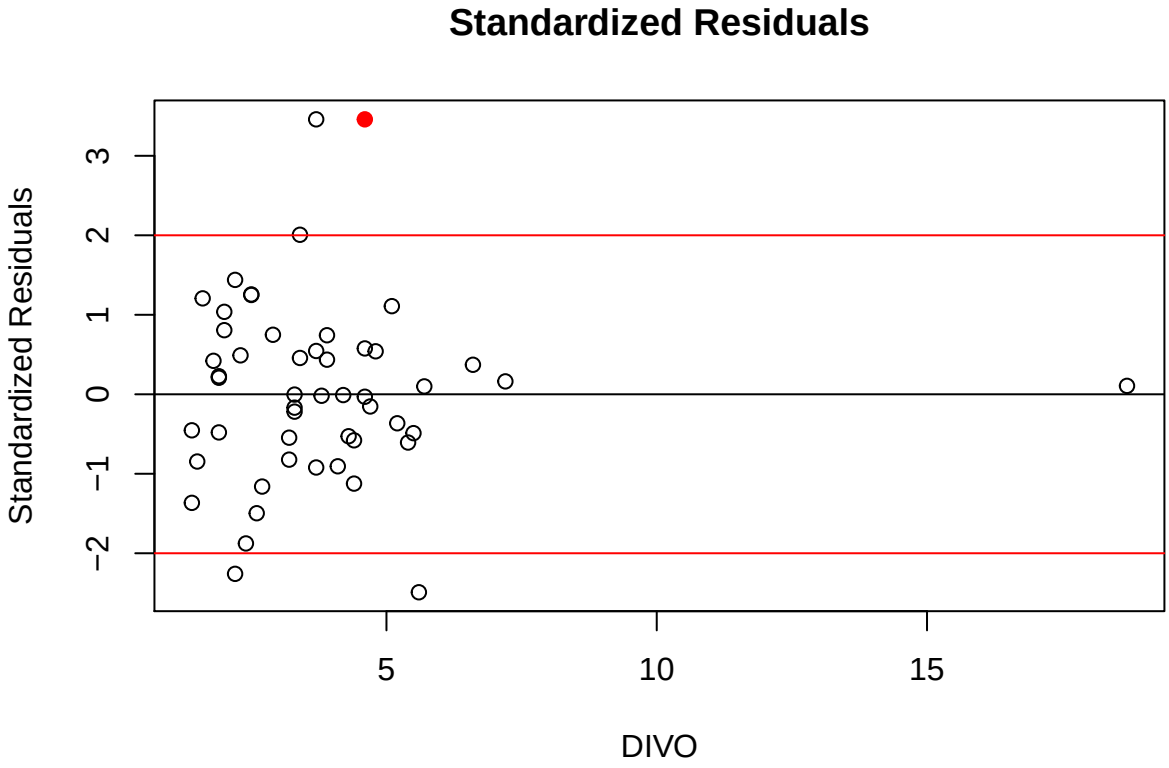
```
#MALE
plot(MALE2, std_res_NoDC, ylab="Standardized Residuals", xlab="MALE", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(MALE[44], std_res_NoDC[44] , col='red', pch = 19)
```



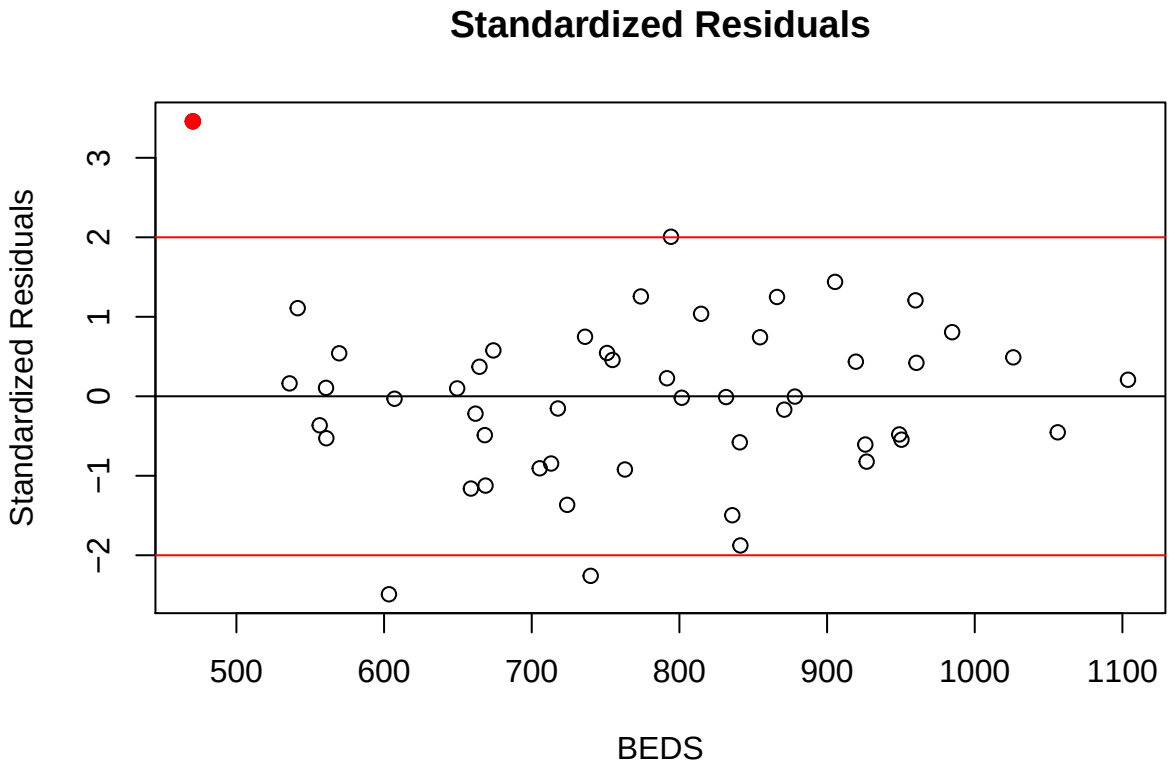

```
#BEDS
plot(BIRTH2, std_res_NoDC, ylab="Standardized Residuals", xlab="BIRTH", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(BIRTH2[44], std_res_NoDC[44] , col='red', pch = 19)
```



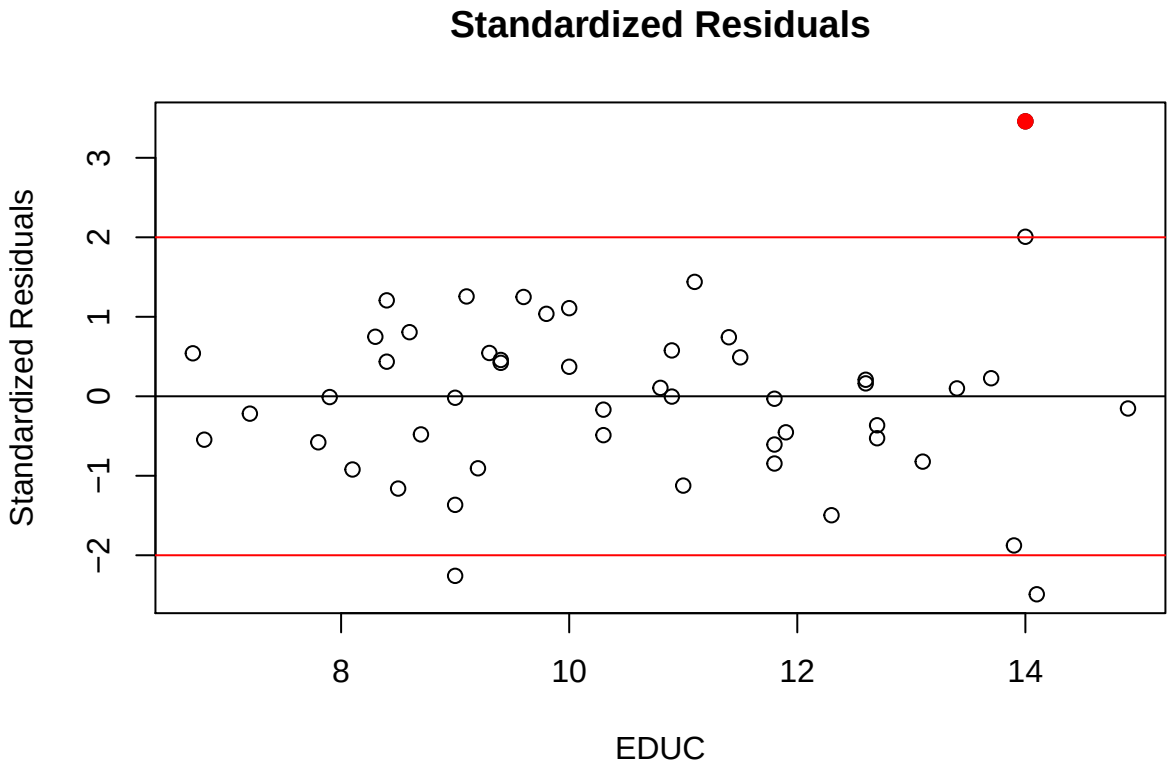

```
#DIVO
plot(DIVO2, std_res_NoDC, ylab="Standardized Residuals", xlab="DIVO", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(DIVO[44], std_res_NoDC[44] , col='red', pch = 19)
```



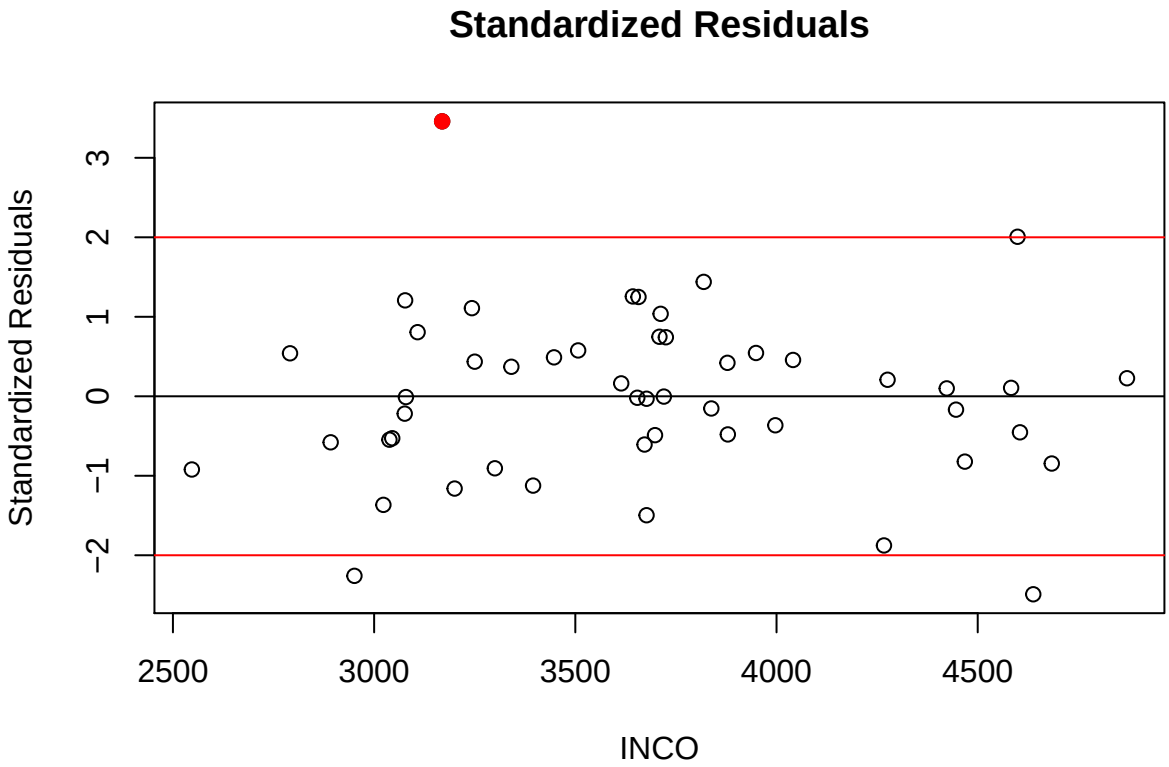

```
#BEDS
plot(BEDS2, std_res_NoDC, ylab="Standardized Residuals", xlab="BEDS", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(BEDS2[44], std_res_NoDC[44] , col='red', pch = 19)
```




```
#EDUC
plot(EDUC2, std_res_NoDC, ylab="Standardized Residuals", xlab="EDUC", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(EDUC2[44], std_res_NoDC[44] , col='red', pch = 19)
```




```
#INCO
plot(INCO2, std_res_NoDC, ylab="Standardized Residuals", xlab="INCO", main="Standardized Residuals")
abline(0, 0)
abline(2, 0, col=c("red"))
abline(-2, 0, col=c("red"))
points(INCO2[44], std_res_NoDC[44] , col='red', pch = 19)
```




ALL

Data corresponding to this STATE has very standardized residual values. Difference between observations and expected values is large.

3g)

```
dat3 <- subset(dat2, STATE != 'UT')
LIFE3 <- dat3$LIFE
MALE3 <- dat3$MALE
BIRTH3 <- dat3$BIRTH
DIVO3 <- dat3$DIVO
BEDS3 <- dat3$BEDS
EDUC3 <- dat3$EDUC
INCO3 <- dat3$INCO
MLR_NoDC_NoUT <- lm(formula = LIFE3 ~ MALE3+ BIRTH3 + DIVO3 + BEDS3 + EDUC3 + INCO3, data=dat3)
```

$R^2$ is higher without UT data. Therefore this model explains the proportion of variability explained by the regression, better. Predictor have coefficients chnaged:

```
MLR_NoDC_NoUT$coefficients
```

```
##   (Intercept)         MALE3        BIRTH3         DIVO3         BEDS3
## 68.2344178920  0.1494306784 -0.6334939159 -0.1116666651 -0.0007407427
##         EDUC3         INCO3
##  0.2163469795 -0.0003390279
```

Vs

```
MLR$coefficients
```

```
##   (Intercept)          MALE         BIRTH          DIVO          BEDS
## 70.5577812704  0.1261018758 -0.5160557876 -0.1965375074 -0.0033392036
##          EDUC          INCO
##  0.2368222541 -0.0003612011
```