MATH 588

HW5

Md Ismail Hossain

3/06/2022

Question 1

a

```
library(Sleuth3)
pyg = case1302
# Number of rows and columns
dim(pyg)
```

```
## [1] 29  3
```

```
# Head of the data
head(pyg)
```

```
##   Company     Treat Score
## 1      C1 Pygmalion  80.0
## 2      C1   Control  63.2
## 3      C1   Control  69.2
## 4      C2 Pygmalion  83.9
## 5      C2   Control  63.1
## 6      C2   Control  81.5
```

```
names(pyg) <- tolower(names(pyg))
summary(aov(score~company*treat,pyg))
```

```
##               Df Sum Sq Mean Sq F value Pr(>F)
## company        9  671.0    74.6   1.437 0.2990
## treat          1  338.9   338.9   6.530 0.0309 *
## company:treat  9  311.5    34.6   0.667 0.7221
## Residuals      9  467.0    51.9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

b

$H_0 : \mu_{B1} = ... = \mu_{B10}$

The p-value is greater than 0.05. So, null hypothesis cannot be rejected.

```
summary(aov(score~company,pyg))
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## company      9    671   74.55   1.268  0.315
## Residuals   19   1117   58.81
```

c

```
summary(aov(score~company+treat,pyg))
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## company      9  671.0    74.6   1.724 0.1556
## treat        1  338.9   338.9   7.835 0.0119 *
## Residuals   18  778.5    43.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

H_0 : There is no treatment effect.
H_1 : Treatment effect is significant.

At 5% level of significance we can reject the null hypothesis because the calculated p-value is 0.0119. So, treatment effect is statistically significant.

d

$MS_R = 43.3$ is the best estimate of the residual.

e

```
summary(aov(score~treat+company,pyg))
```

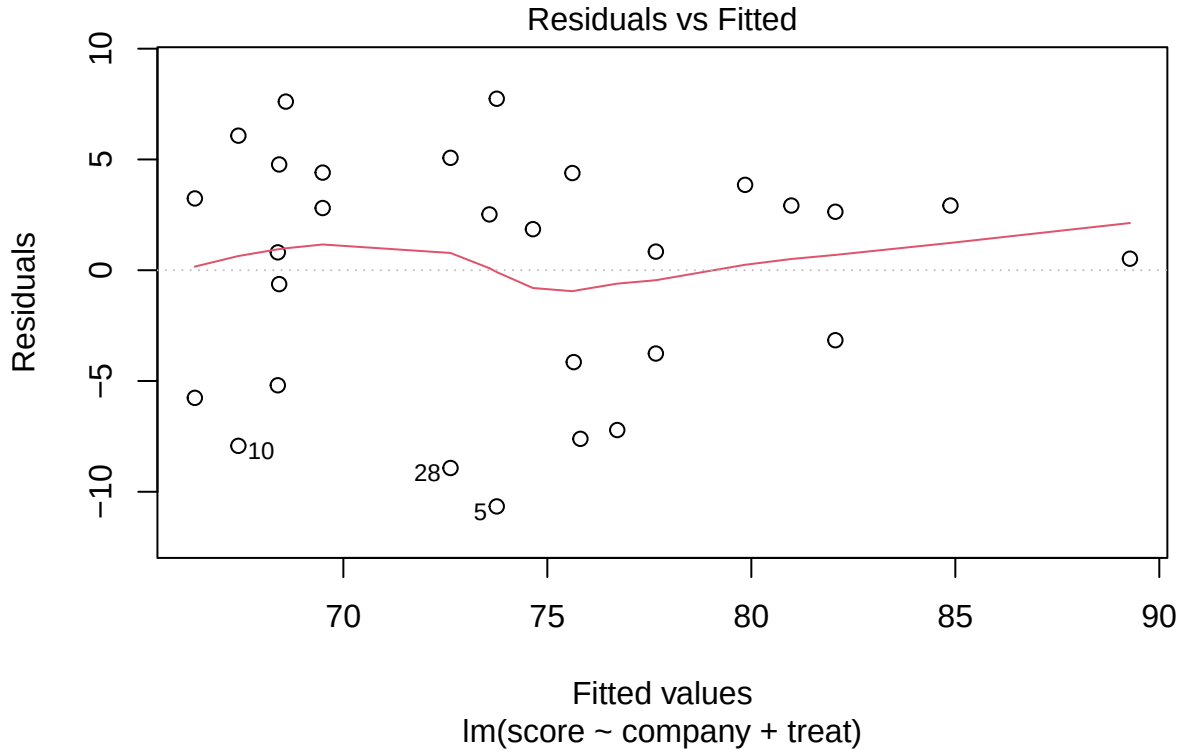
```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treat        1  327.3   327.3   7.569 0.0131 *
## company      9  682.5    75.8   1.753 0.1484
## Residuals   18  778.5    43.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, the p-value for treatment is 0.0131 if we put treatment before company.

f

```
part_c_model = lm(score~company+treat,pyg)

plot(part_c_model, which=c(1,1))
```

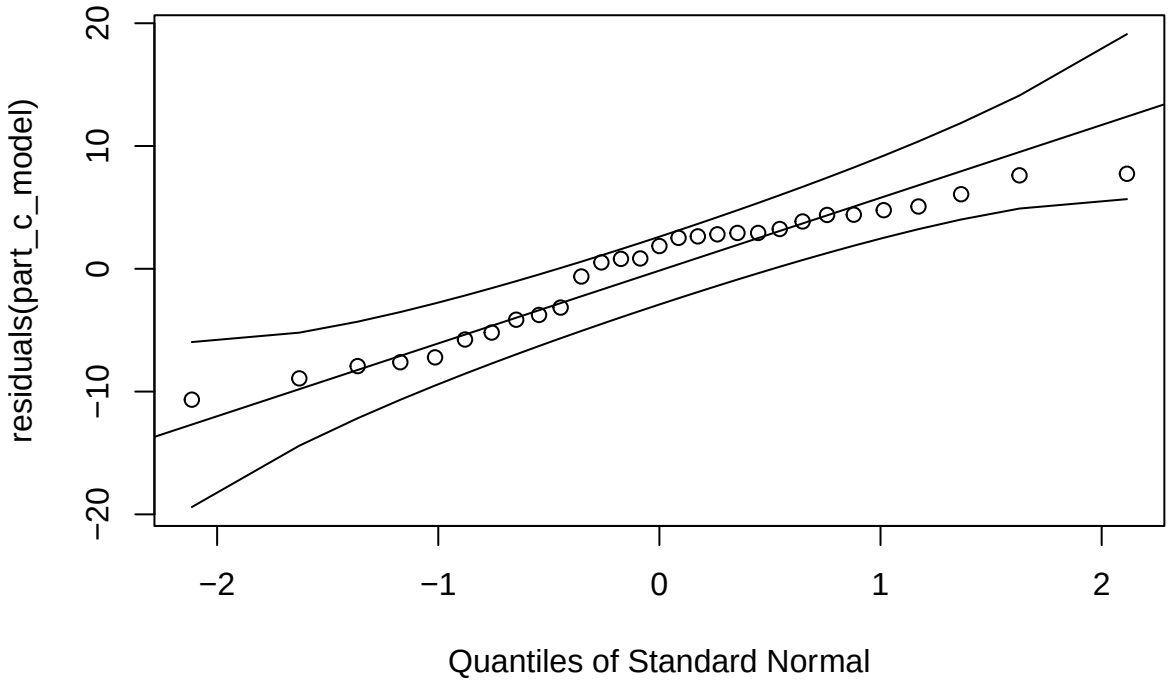


The residual Vs fitted plot seems good because we are not observing any unusual pattern in the upper part

and lower part of the zero line.

g

```
source("http://www.stat.cmu.edu/~hseltman/files/qqn.R")
qqn(residuals(part_c_model))
```



Other than very few observation in lower and upper tail the plot looks fine.

h

```
summary(aov(score~company+treat,pyg))
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## company      9  671.0    74.6   1.724 0.1556
## treat        1  338.9   338.9   7.835 0.0119 *
## Residuals   18  778.5    43.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(aov(score~treat,pyg))
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## treat        1  327.3   327.3   6.049 0.0206 *
## Residuals   27 1461.0    54.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

When we are using the company+treatment model then the degree of freedom for residual become lesser than the model where we are only use treatment. As a result when we are dividing the residual sum of square value using it's degree of freedom then the calculated sum of square become lower for company+treatment model. Finally when we try to find the F-statistic, by dividing all the mean square using residual sum of square it finding a higher F-statistics value for treatment in treatment+company model. So we are getting a smaller p-value for the treatment+company model. This smaller p-value increasing the power because residual mean square is nothing but the σ^2 which we want as smaller as possible. So, smaller p-value indicating a more power of the analysis.

Question 2

```
stp <- read.delim("E:/NMT MS/Spring 22/MATH 588/Home_Work/Spring-2022---MATH-588-01-Advanced-Data-Analys


dim(stp) # 30 6
```

```
## [1] 30  6
```

```
sapply(stp, class)
```

```
##     Order     Block    Height Frequency    RestHR        HR
## "numeric" "numeric" "numeric" "numeric" "numeric" "integer"
```

```
# Order Block Height Frequency RestHR HR
# "integer" "integer" "integer" "integer" "integer" "integer"
stp$Block = factor(stp$Block)
stp$Height = factor(stp$Height, labels=c("Low","High"))
stp$Frequency = factor(stp$Frequency, labels=c("Low","Med","High"))
summary(stp)
```

```
##      Order       Block  Height   Frequency     RestHR           HR
##  Min.   : 1.00   1:5   Low :15   Low :10   Min.   :60.00   Min.   : 75.0
##  1st Qu.: 8.25   2:5   High:15   Med :10   1st Qu.:72.75   1st Qu.: 93.0
##  Median :15.50   3:5             High:10   Median :81.00   Median : 99.0
##  Mean   :15.50   4:5                       Mean   :80.00   Mean   :107.4
##  3rd Qu.:22.75   5:5                       3rd Qu.:87.00   3rd Qu.:122.2
##  Max.   :30.00   6:5                       Max.   :96.00   Max.   :153.0
```

a

```
with(stp, table(Height, Frequency, Block))
```

```
## , , Block = 1
##
##       Frequency
## Height Low Med High
##   Low    1   1    1
##   High   1   1    0
##
## , , Block = 2
##
##       Frequency
## Height Low Med High
##   Low    1   1    1
##   High   1   0    1
```

```
##
## , , Block = 3
##
##       Frequency
## Height Low Med High
##   Low    0   1    1
##   High   1   1    1
##
## , , Block = 4
##
##       Frequency
## Height Low Med High
##   Low    1   0    1
##   High   1   1    1
##
## , , Block = 5
##
##       Frequency
## Height Low Med High
##   Low    1   1    1
##   High   0   1    1
##
## , , Block = 6
##
##       Frequency
## Height Low Med High
##   Low    1   1    0
##   High   1   1    1
```

In each block we observed 1 observation per cell and the missing observation is located in different position.

b

```
with(stp, table(Height, Frequency))
```

```
##       Frequency
## Height Low Med High
##   Low    5   5    5
##   High   5   5    5
```

Looks like it's a "Balanced" design.

c

```
summary(aov(HR~Block+Frequency+Height,stp))
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Block        5   4511     902   16.20 1.37e-06 ***
## Frequency    2   3035    1518   27.26 1.46e-06 ***
## Height       1   3406    3406   61.17 1.18e-07 ***
## Residuals   21   1169      56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(aov(HR~Frequency+Block+Height,stp))
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Frequency    2   3728    1864   33.48 2.94e-07 ***
## Block        5   3818     764   13.71 5.13e-06 ***
## Height       1   3406    3406   61.17 1.18e-07 ***
## Residuals   21   1169      56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(aov(HR~Block+Height+Frequency,stp))
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Block        5   4511     902   16.20 1.37e-06 ***
## Height       1   3406    3406   61.17 1.18e-07 ***
## Frequency    2   3035    1518   27.26 1.46e-06 ***
## Residuals   21   1169      56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Among these 3 combination we observed that the Height and Residuals are unchanged. The Block and Frequency sum of square changed when we are changing the position.

d

$df_B = df_{Block} + df_H + df_F = 5 + 1 + 2 = 8$
$SS_B = SS_{Block} + SS_H + SS_F = 4511 + 3406 + 3035 = 10952$
$MS_B = SS_B/df_B = 10952/8 = 1369$
$df_T = df_B + df_W = 8 + 21 = 29$
$SS_T = SS_B + SS_W = 10952 + 1169.2 = 12121.2$

e

```
summary(aov(HR~Block+Frequency*Height,stp))
```

```
##                  Df Sum Sq Mean Sq F value   Pr(>F)
## Block             5   4511     902  19.794 6.12e-07 ***
## Frequency         2   3035    1518  33.297 6.17e-07 ***
## Height            1   3406    3406  74.733 5.20e-08 ***
## Frequency:Height  2    303     152   3.327   0.0577 .
## Residuals        19    866      46
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

H_0 : There is no interaction effect.
H_1 : Interaction effect is statistically significant.

At 5% level of significance we cannot reject the null hypothesis and conclude that there is no interaction effect.

f

```
mi=aov(HR~Block+Frequency+Height+Frequency:Height, stp)
coefficients(mi)
```

```
##              (Intercept)                   Block2                   Block3
##                    81.90                    -3.50                    -5.25
##                   Block4                   Block5                   Block6
##                    23.00                    16.25                    -7.25
##             FrequencyMed            FrequencyHigh               HeightHigh
##                    12.25                    20.00                    20.50
##  FrequencyMed:HeightHigh FrequencyHigh:HeightHigh
##                    -6.00                     9.75
```

```
sqrt(vcov(mi)["FrequencyHigh:HeightHigh", "FrequencyHigh:HeightHigh"])
```

```
## [1] 6.162813
```

```
summary.lm(mi)
```

```
##
## Call:
## aov(formula = HR ~ Block + Frequency + Height + Frequency:Height,
##     data = stp)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -11.400  -4.775   0.225   4.100   9.350
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 81.900      4.088  20.035 3.09e-14 ***
## Block2                      -3.500      4.358  -0.803 0.431813
## Block3                      -5.250      4.358  -1.205 0.243094
## Block4                      23.000      4.358   5.278 4.29e-05 ***
## Block5                      16.250      4.358   3.729 0.001423 **
## Block6                      -7.250      4.358  -1.664 0.112580
## FrequencyMed                12.250      4.358   2.811 0.011151 *
## FrequencyHigh               20.000      4.358   4.590 0.000200 ***
## HeightHigh                  20.500      4.358   4.704 0.000154 ***
## FrequencyMed:HeightHigh     -6.000      6.163  -0.974 0.342497
## FrequencyHigh:HeightHigh     9.750      6.163   1.582 0.130137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.751 on 19 degrees of freedom
## Multiple R-squared:  0.9286, Adjusted R-squared:  0.891
## F-statistic:  24.7 on 10 and 19 DF,  p-value: 8.423e-09
```

```
qt(0.975, 19)
```

```
## [1] 2.093024
```

```
high = 9.75 + 2.09*(6.163)
low = 9.75 - 2.09*(6.163)
paste("95% CI is:", low, "to",high)
```

```
## [1] "95% CI is: -3.13067 to 22.63067"
```

We are 95% confident that the difference in the rise of heart rate from low to high steps is between 3 beats per minute smaller and 23 bpm larger when comparing high frequency to low frequency.

If the subject matter expert conclude that 23 is not that high then we would go with the model without

intercation and if they suggest otherwise then we should consider more sample.

g

```
summary(aov(HR~Block+Frequency+Height,stp))
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## Block        5   4511     902   16.20 1.37e-06 ***
## Frequency    2   3035    1518   27.26 1.46e-06 ***
## Height       1   3406    3406   61.17 1.18e-07 ***
## Residuals   21   1169      56
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The frequency and Heights seems statistically significant at 5 level of significance because p-value lower than 0.05.

h

```
#install.packages("gmodels")
library(gmodels)
levels(stp$Frequency)
```

```
## [1] "Low"  "Med"  "High"
```

```
s0 = aov(HR~Block+Frequency+Height,stp)
contr = rbind(HvsML = c(-1/2, -1/2, 1), MvsL = c(-1, 1, 0))
round( fit.contrast(s0, "Frequency", contr, conf.int=0.95), 3)
```

```
##                Estimate Std. Error t value Pr(>|t|) lower CI upper CI
## FrequencyHvsML    20.25      2.950   6.865    0.000   14.116   26.384
## FrequencyMvsL      9.25      3.406   2.716    0.013    2.167   16.333
## attr(,"class")
## [1] "fit_contrast"
```

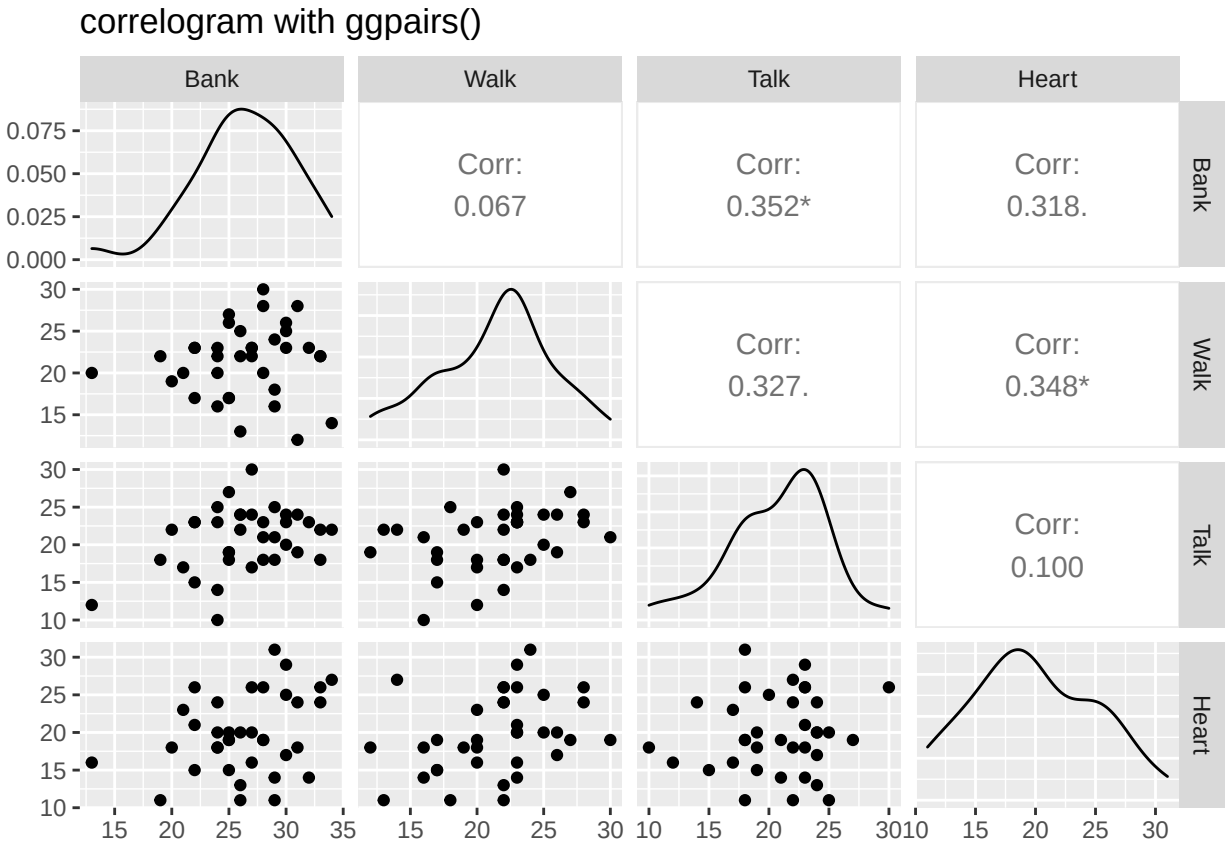
i

c(1, -1) is the only possible contrast with 1 df which test $\mu_{H1} = \mu_{H2}$, and that is the same null hypothesis as the 1 df F test shown in the Height line of the ANOVA table.

Question 3

a

```
#install.packages("GGally")
library(GGally)
# Check correlations (as scatterplots), distribution and print corrleation coefficient
ggpairs(ex0914, title="correlogram with ggpairs()")
```



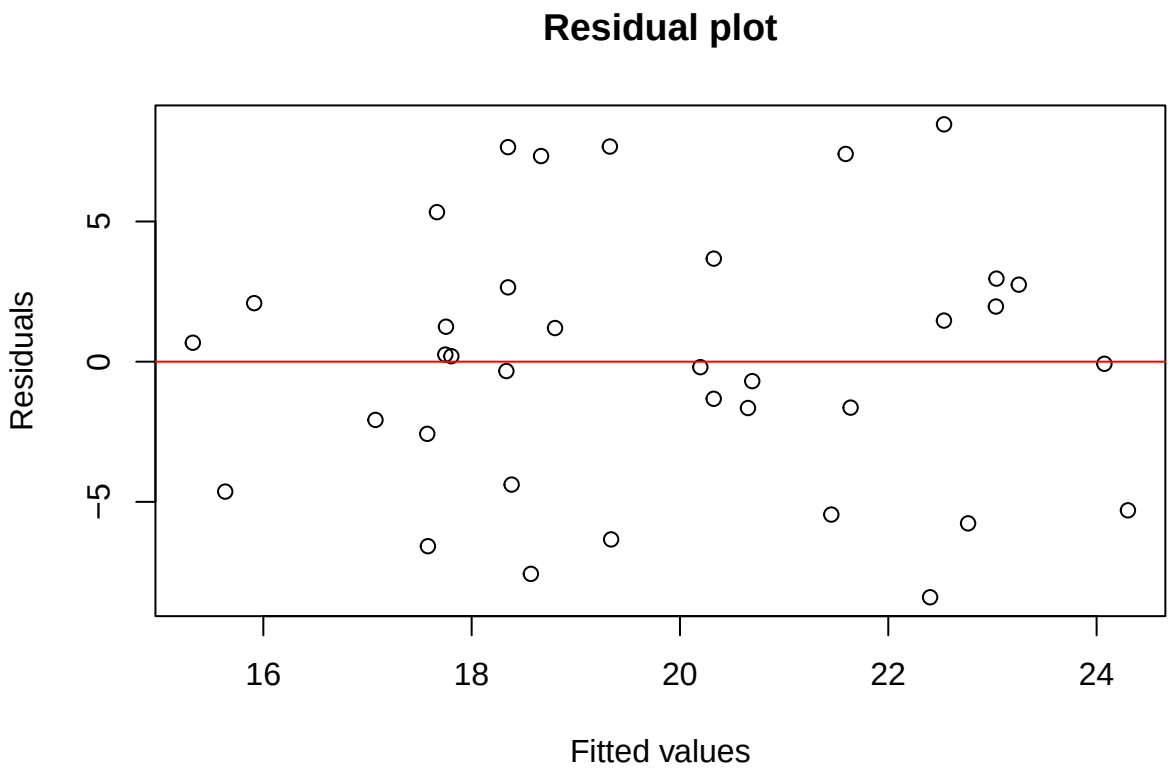
b

```
fit <- lm(Heart~Bank+Walk+Talk,data=ex0914)
```

The fitted model is: $Heart = 3.1787 + 0.4052 * Bank + 0.4516 * Walk - 0.1796 * Talk$

c

```
{plot(resid(fit)~predict(fit),xlab="Fitted values",ylab="Residuals",main="Residual plot")
abline(0,0, col = "red")}
```



The residual seems randomly allocated. We can not see any unusual pattern or outlier observation.

d

The summary of the regression model presented below:

```
summary(fit)
```

```
##
## Call:
## lm(formula = Heart ~ Bank + Walk + Talk, data = ex0914)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.4014 -3.0263  0.0602  2.6748  8.4646
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.1787     6.3369   0.502   0.6194
## Bank          0.4052     0.1971   2.056   0.0480 *
## Walk          0.4516     0.2009   2.248   0.0316 *
## Talk         -0.1796     0.2222  -0.808   0.4249
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.805 on 32 degrees of freedom
## Multiple R-squared:  0.2236, Adjusted R-squared:  0.1509
```

```
## F-statistic: 3.073 on 3 and 32 DF,  p-value: 0.04162
```

From this summary table we observed that the calculated R squared value is 0.2236 which doesn't seems very high. Talk is not statistically significant at 5% level of significance in predicting the Heart disease. So, more independent variable needed to be introduced to increase the model predictability.