

Project

DSK

3/10/2022

Packages

```
library(dplyr)
```

Data

```
library(magrittr)
```

```
## Warning: package 'magrittr' was built under R version 4.1.3
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5      v purrr  0.3.4
## v tibble  3.1.3      v stringr 1.4.0
## v tidyr   1.1.3      v forcats 0.5.1
## v readr   1.4.0
```

```
## Warning: package 'ggplot2' was built under R version 4.1.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x tidyr::extract() masks magrittr::extract()
## x dplyr::filter()  masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## x purrr::set_names() masks magrittr::set_names()
```

```
data <- read.csv("C:/Users/14193/Downloads/Life Expectancy Data.csv") %>%
  filter(Year==2014)
dat=data[,-c(1,2)]
dat$Status=as.factor(dat$Status)
levels(dat$Status)=c("no", "yes")
```

Partitioning The Data

```
RNGkind(sample.kind = "Rounding")
```

```
## Warning in RNGkind(sample.kind = "Rounding"): non-uniform 'Rounding' sampler
## used
```

```
set.seed(0)
```

```
partition.2 <- function(data, prop.train){
  # select a random sample of size = prop.train % of total records
  selected <- sample(1:nrow(data), round(nrow(data)*prop.train), replace = FALSE)
  # create training data which has prop.train % of total records
  data.train <- data[selected,]
  # create validation data
  rest <- setdiff(1:nrow(data), selected)
  data.test <- data[rest,]
  return(list(data.train=data.train, data.test=data.test))
}
```

```
partitioned=partition.2(dat,0.7)
training.data=partitioned$data.train
test.data=partitioned$data.test
```

Imputation on training data and using the attributes of training data on test data

```
sapply(training.data, anyNA)
```

```
##              Status              Life.expectancy
##              FALSE              FALSE
##      Adult.Mortality      infant.deaths
##              FALSE              FALSE
##              Alcohol      percentage.expenditure
##              FALSE              FALSE
##      Hepatitis.B              Measles
##              TRUE              FALSE
##              BMI      under.five.deaths
##              TRUE              FALSE
##              Polio      Total.expenditure
##              FALSE              TRUE
##      Diphtheria      HIV.AIDS
##              FALSE              FALSE
##              GDP      Population
##              TRUE              TRUE
##      thinness..1.19.years      thinness.5.9.years
##              TRUE              TRUE
##      Income.composition.of.resources      Schooling
##              TRUE              TRUE
```

```
# BMI, Total.expenditure, GDP, thinness.5.9, Hepatitis, Population, Income composition, thinnes.1.19, schoolin,
```

```
sapply(test.data, anyNA)
```

```
##              Status              Life.expectancy
##              FALSE              FALSE
##      Adult.Mortality      infant.deaths
##              FALSE              FALSE
##              Alcohol      percentage.expenditure
##              TRUE              FALSE
##      Hepatitis.B              Measles
##              TRUE              FALSE
##              BMI              under.five.deaths
##              TRUE              FALSE
##              Polio      Total.expenditure
##              FALSE              TRUE
##      Diphtheria              HIV.AIDS
##              FALSE              FALSE
##              GDP              Population
##              TRUE              TRUE
##      thinness..1.19.years      thinness.5.9.years
##              TRUE              TRUE
##      Income.composition.of.resources      Schooling
##              TRUE              TRUE
```

```
# HepatitisB,BMI, TOTAL EXPENDITURE,GDP,thinness.5.9,Population,Income composition,Alcohol,thinnes.1.1
```

```
# We will first replace the missing values with the median values of the respective columns.
```

```
med.BMI.train <- median(training.data$BMI, na.rm = TRUE)
training.data$BMI[is.na(training.data$BMI)] <- med.BMI.train
test.data$BMI[is.na(test.data$BMI)] <- med.BMI.train
```

```
med.Hepatitis.train <- median(training.data$Hepatitis.B, na.rm = TRUE)
training.data$Hepatitis.B[is.na(training.data$Hepatitis.B)] <- med.Hepatitis.train
test.data$Hepatitis.B[is.na(test.data$Hepatitis.B)] <- med.Hepatitis.train
```

```
med.total_expenditure.train <- median(training.data$Total.expenditure, na.rm = TRUE)
training.data$Total.expenditure[is.na(training.data$Total.expenditure)] <- med.total_expenditure.train
test.data$Total.expenditure[is.na(test.data$Total.expenditure)] <- med.total_expenditure.train
```

```
med.GDP.train <- median(training.data$GDP, na.rm = TRUE)
training.data$GDP[is.na(training.data$GDP)] <- med.GDP.train
test.data$GDP[is.na(test.data$GDP)] <- med.GDP.train
```

```
med.thinnes1_19.train <- median(training.data$thinness..1.19.years, na.rm = TRUE)
training.data$thinness..1.19.years[is.na(training.data$thinness..1.19.years)] <- med.thinnes1_19.train
test.data$thinness..1.19.years[is.na(test.data$thinness..1.19.years)] <- med.thinnes1_19.train
```

```

med.population.train <- median(training.data$Population, na.rm = TRUE)
training.data$Population[is.na(training.data$Population)] <- med.population.train
test.data$Population[is.na(test.data$Population)] <- med.population.train

med.income.train <- median(training.data$Income.composition.of.resources, na.rm = TRUE)
training.data$Income.composition.of.resources[is.na(training.data$Income.composition.of.resources)] <- med.income.train
test.data$Income.composition.of.resources[is.na(test.data$Income.composition.of.resources)] <- med.income.train

med.under5_deaths.train <- median(training.data$under.five.deaths, na.rm = TRUE)
training.data$under.five.deaths[is.na(training.data$under.five.deaths)] <- med.under5_deaths.train
test.data$under.five.deaths[is.na(test.data$under.five.deaths)] <- med.under5_deaths.train

med.alcohol.train <- median(training.data$Alcohol, na.rm = TRUE)
training.data$Alcohol[is.na(training.data$Alcohol)] <- med.alcohol.train
test.data$Alcohol[is.na(test.data$Alcohol)] <- med.alcohol.train

med.thinness5_9.train <- median(training.data$thinness.5.9.years, na.rm = TRUE)
training.data$thinness.5.9.years[is.na(training.data$thinness.5.9.years)] <- med.thinness5_9.train
test.data$thinness.5.9.years[is.na(test.data$thinness.5.9.years)] <- med.thinness5_9.train

med.schooling.train <- median(training.data$Schooling, na.rm = TRUE)
training.data$Schooling[is.na(training.data$Schooling)] <- med.schooling.train
test.data$Schooling[is.na(test.data$Schooling)] <- med.schooling.train

```

Fitting a model on the training data

```
full_lm <- lm(Life.expectancy~., data=training.data)
```

Residual analysis

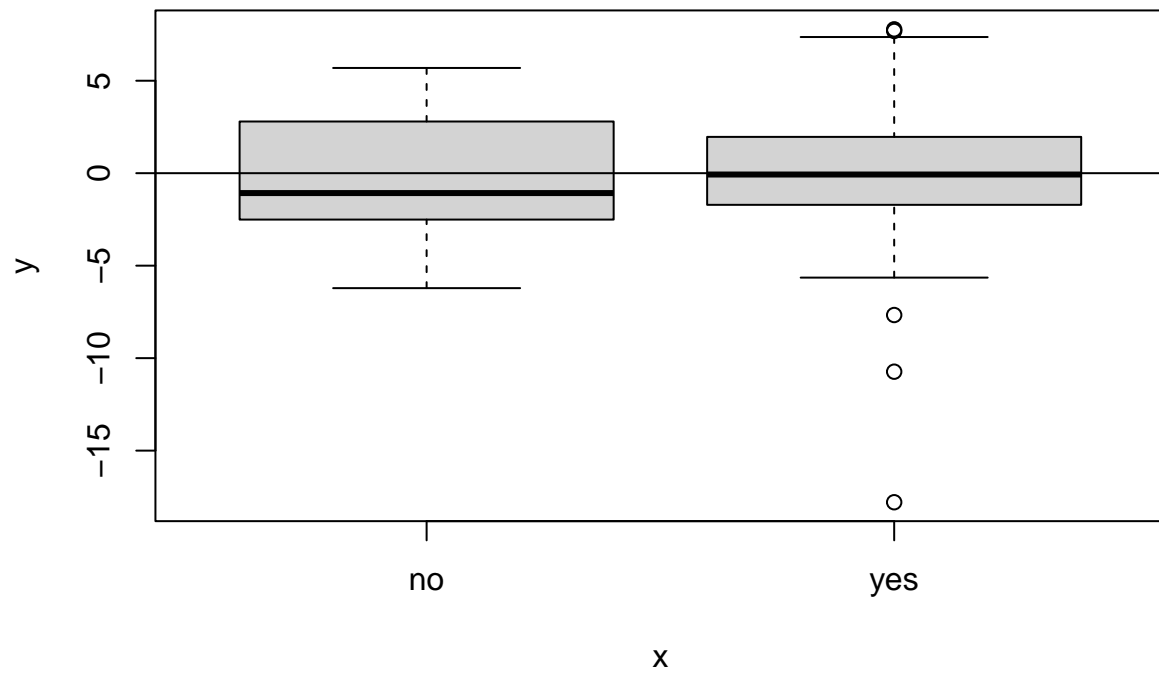
```

## Check for linearity

plot(x=training.data$Status, y=full_lm$residuals,
     main = "Check for linearity \n Residuals vs. Status")
abline(h=0)

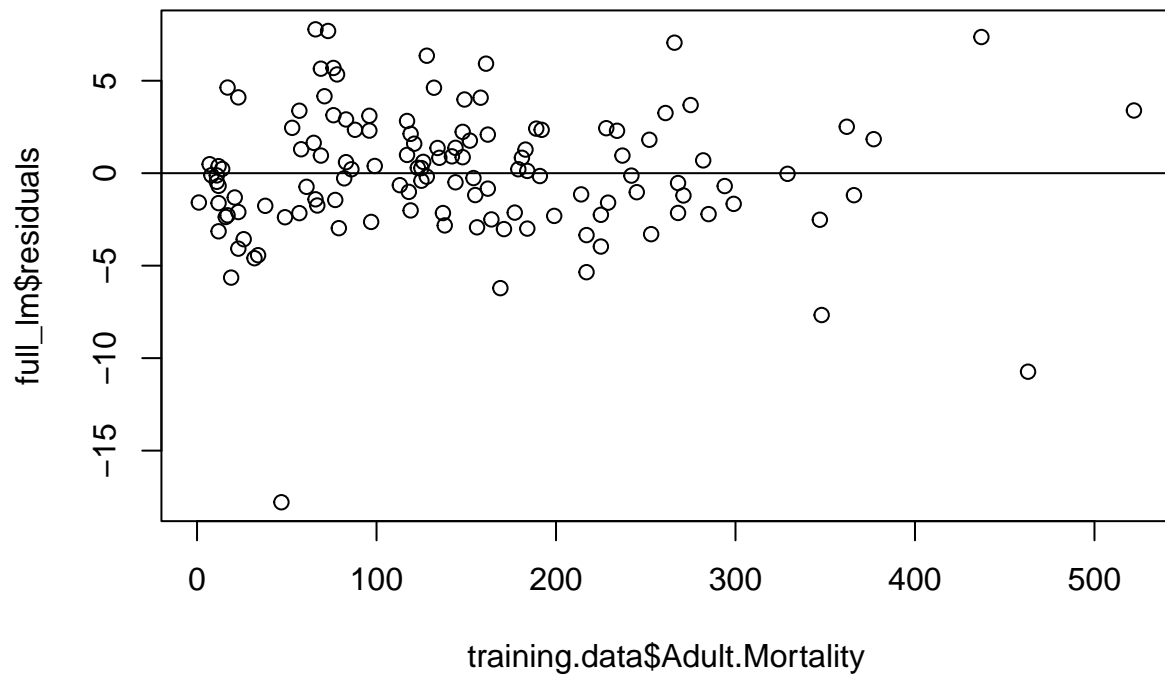
```

Check for linearity Residuals vs. Status



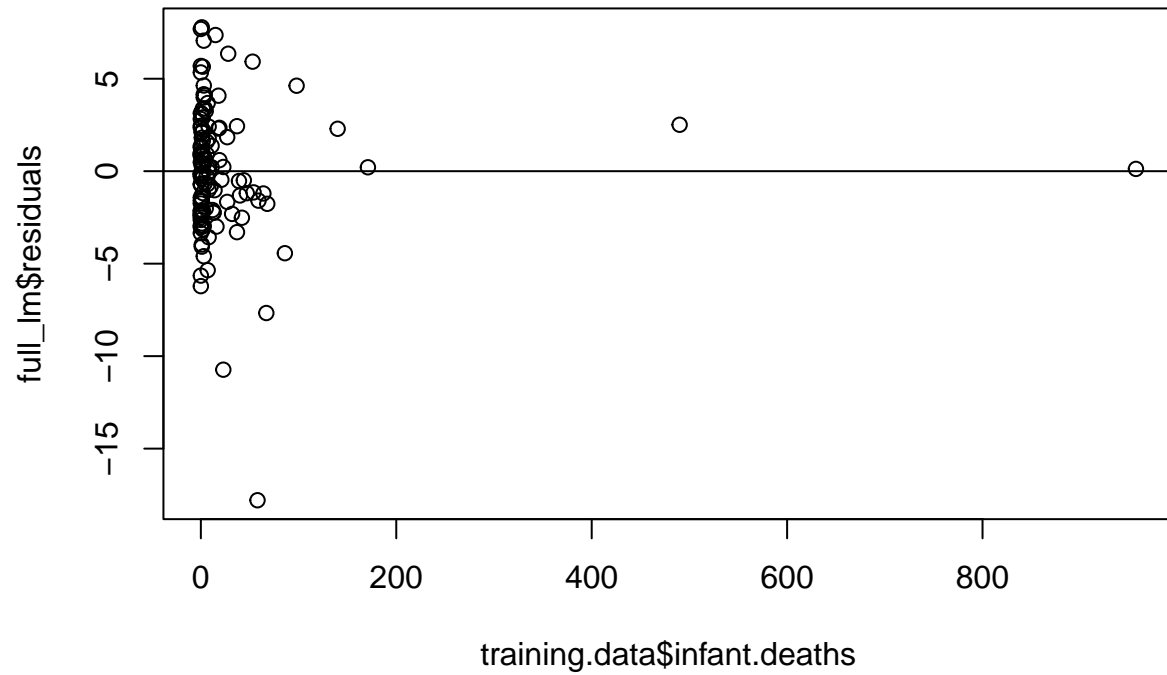
```
plot(training.data$Adult.Mortality, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. adult mortality")  
abline(h=0)
```

Check for linearity Residuals vs. adult mortality



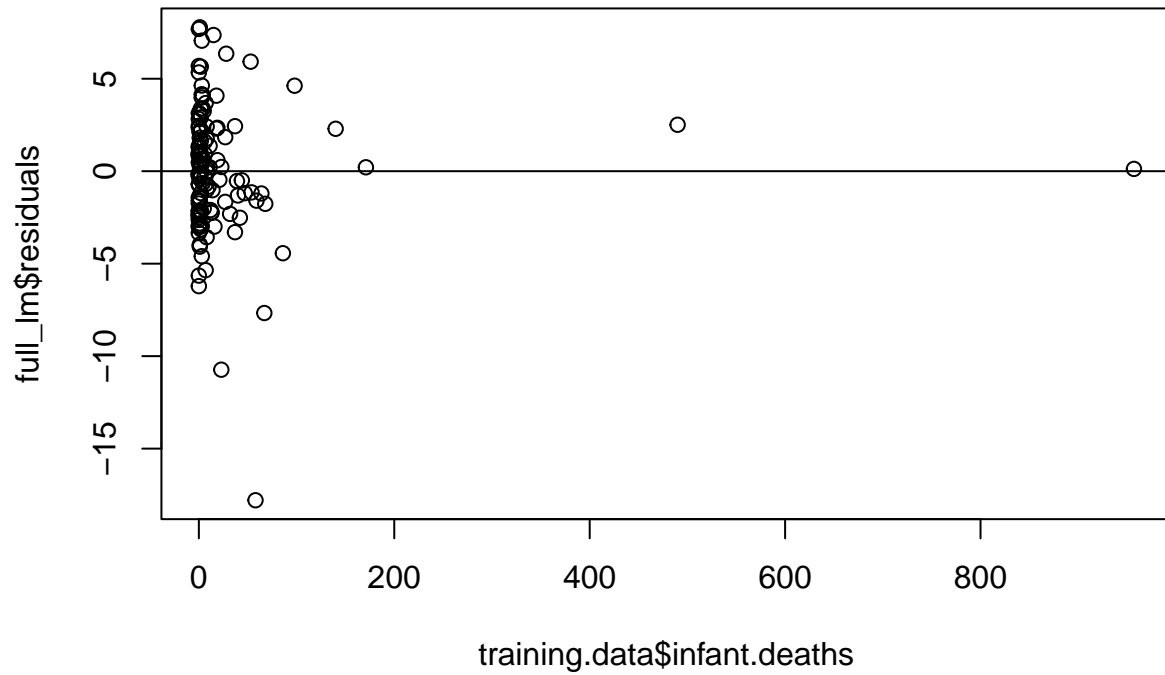
```
plot(training.data$infant.deaths, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. infant deaths")  
abline(h=0)
```

Check for linearity Residuals vs. infant deaths



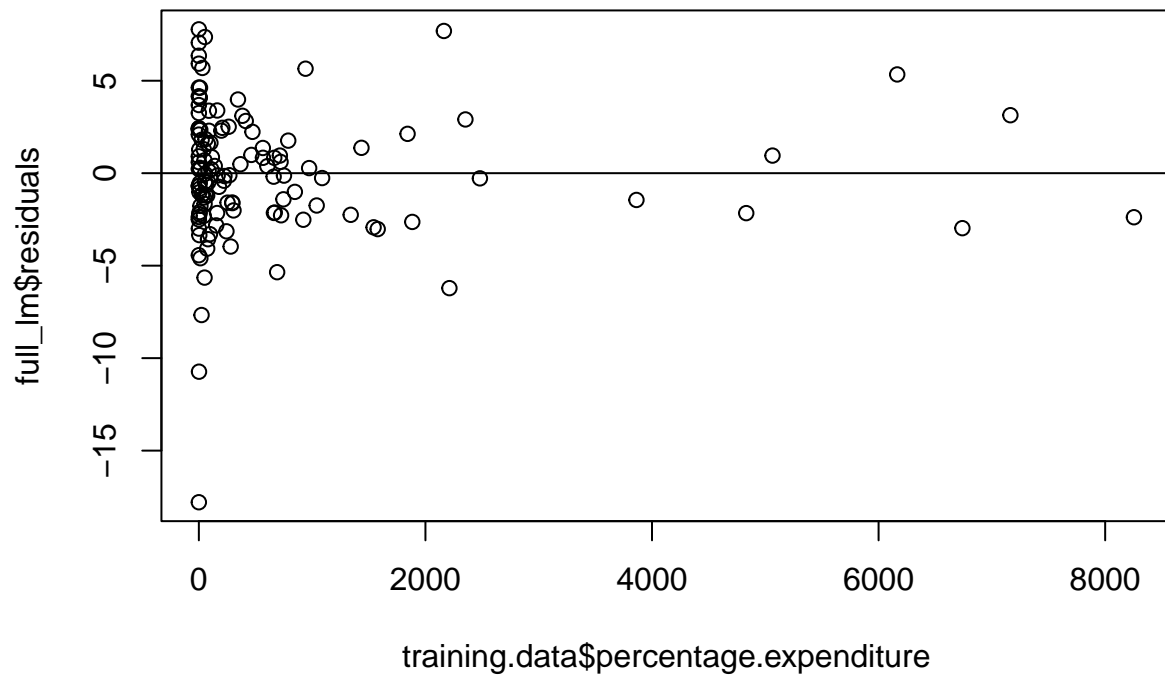
```
plot(training.data$infant.deaths, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. alcohol")  
abline(h=0)
```

Check for linearity Residuals vs. alcohol



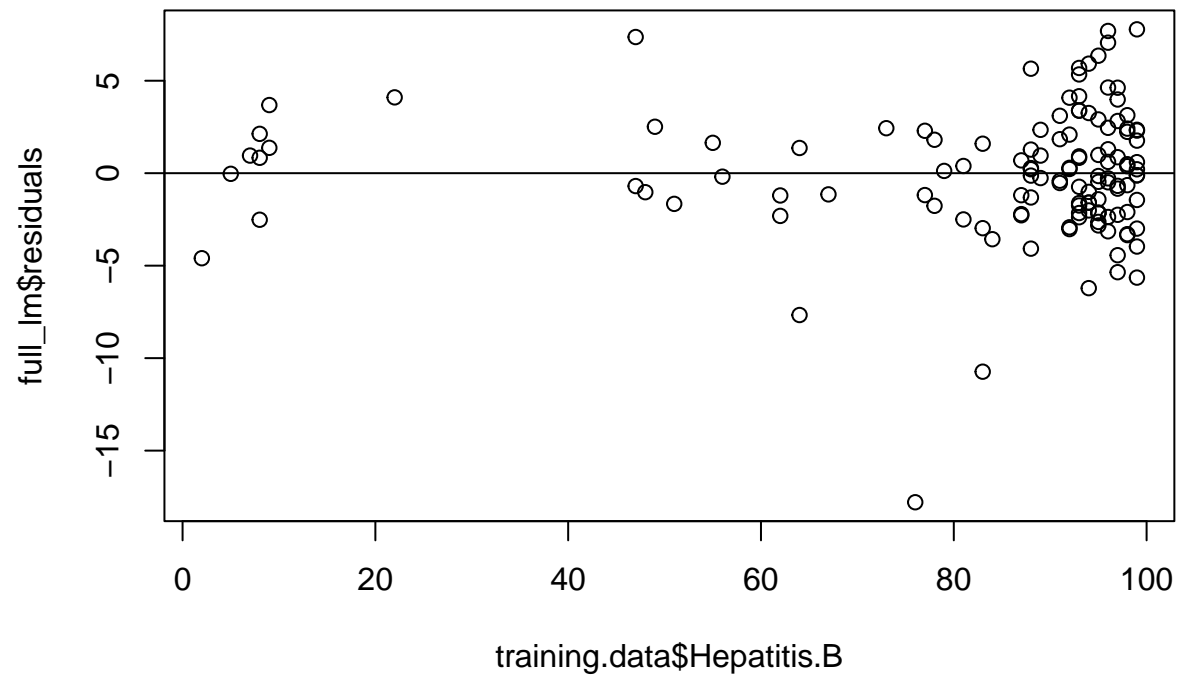
```
plot(training.data$percentage.expenditure, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. percent expenditure")  
abline(h=0)
```


Check for linearity Residuals vs. percent expenditure



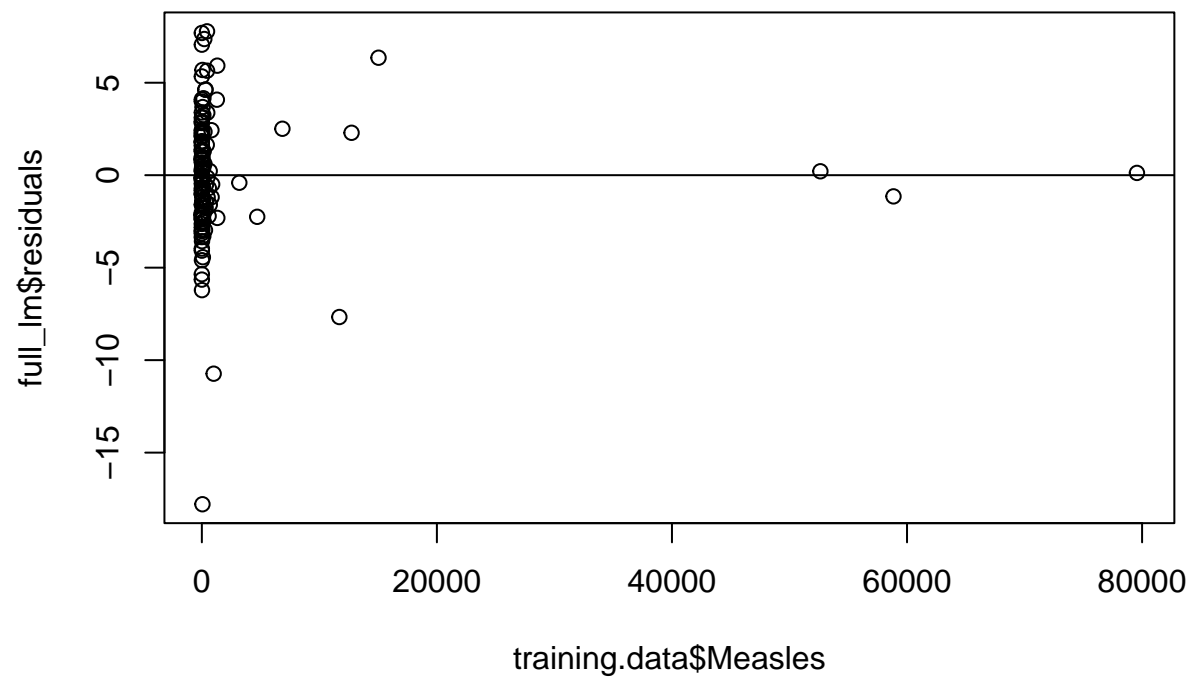
```
plot(training.data$Hepatitis.B, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. hepatitis B")  
abline(h=0)
```

Check for linearity Residuals vs. hepatitis B

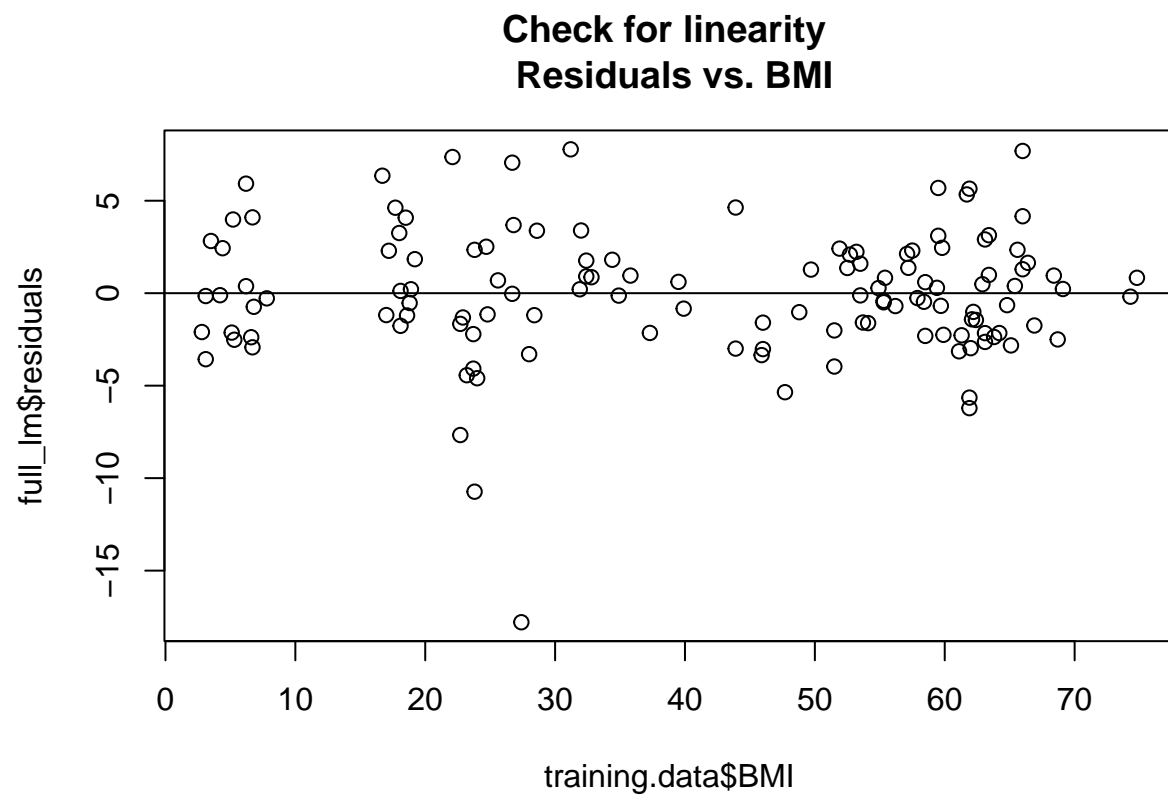


```
plot(training.data$Measles, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. Measles")  
abline(h=0)
```

Check for linearity Residuals vs. Measles

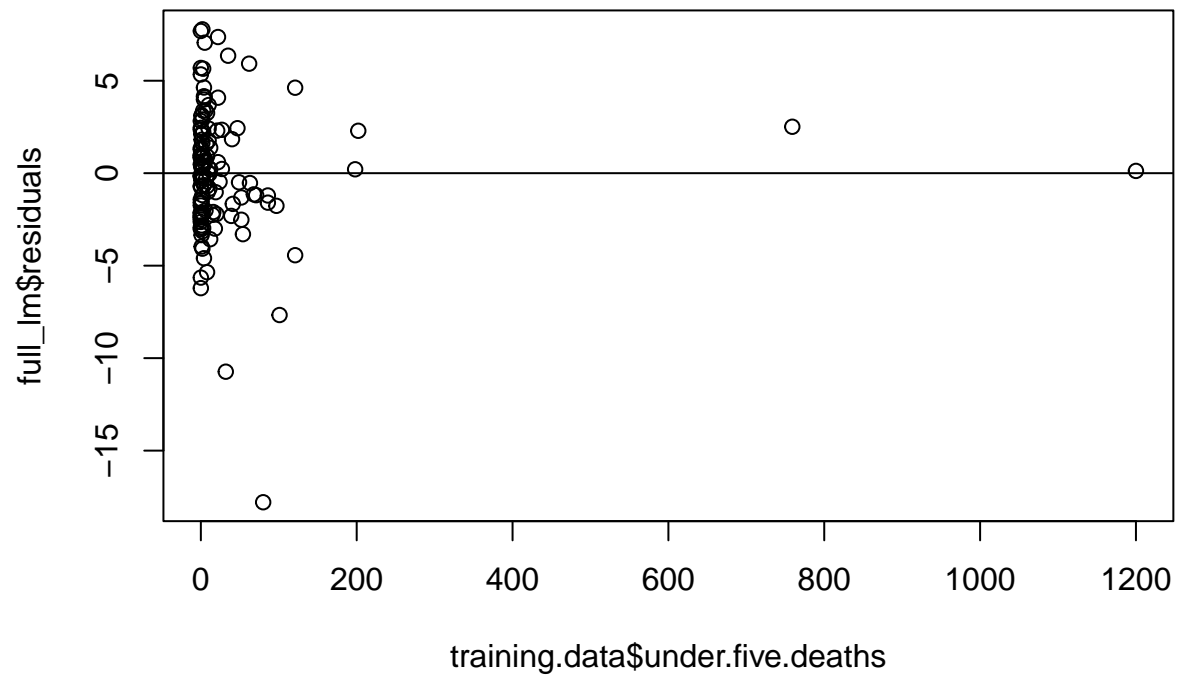


```
plot(training.data$BMI, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. BMI")  
abline(h=0)
```



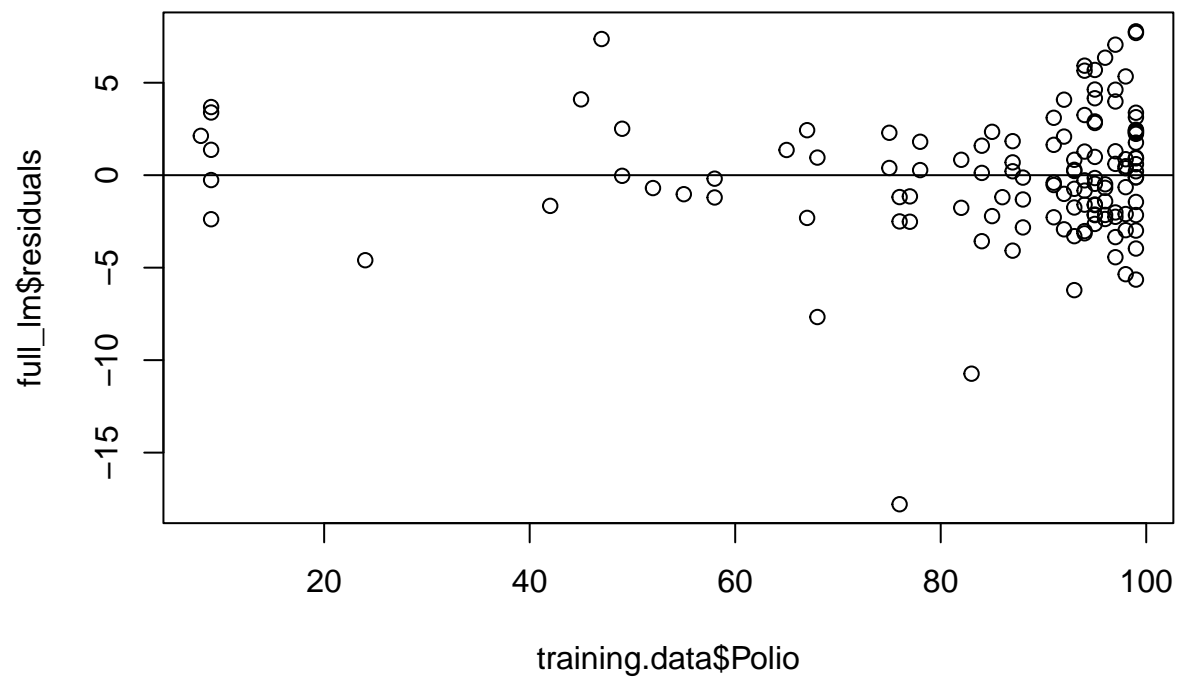
```
plot(training.data$under.five.deaths, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. under five deaths")  
abline(h=0)
```

Check for linearity Residuals vs. under five deaths



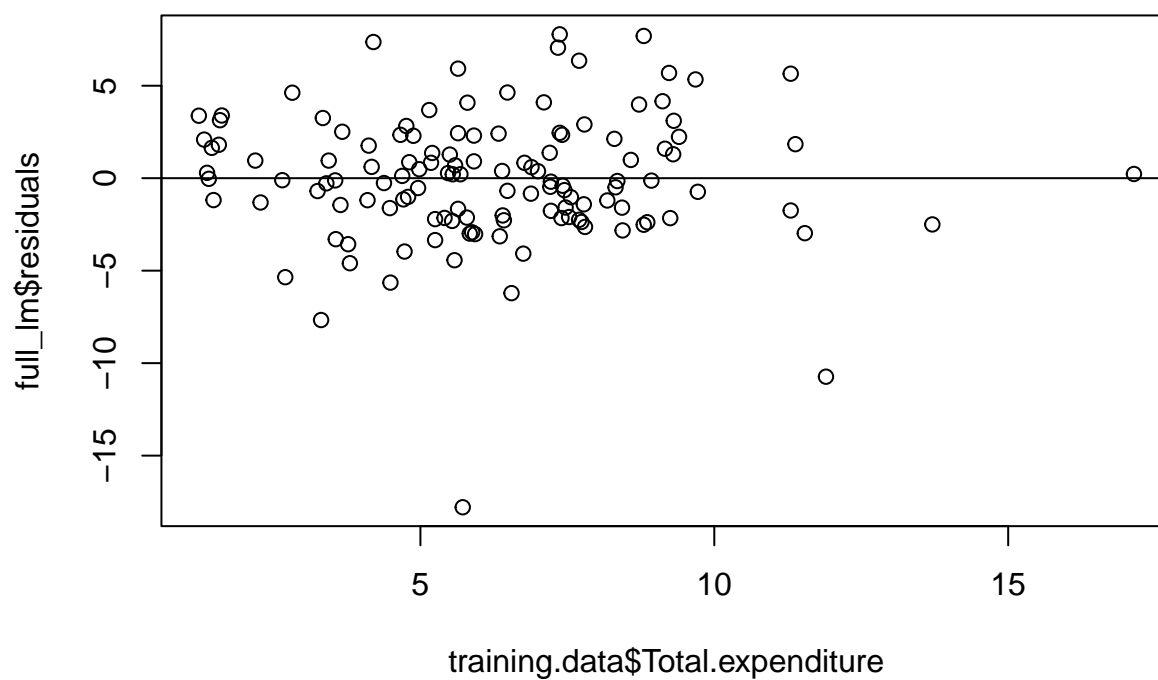
```
plot(training.data$Polio, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. Polio")  
abline(h=0)
```

Check for linearity Residuals vs. Polio



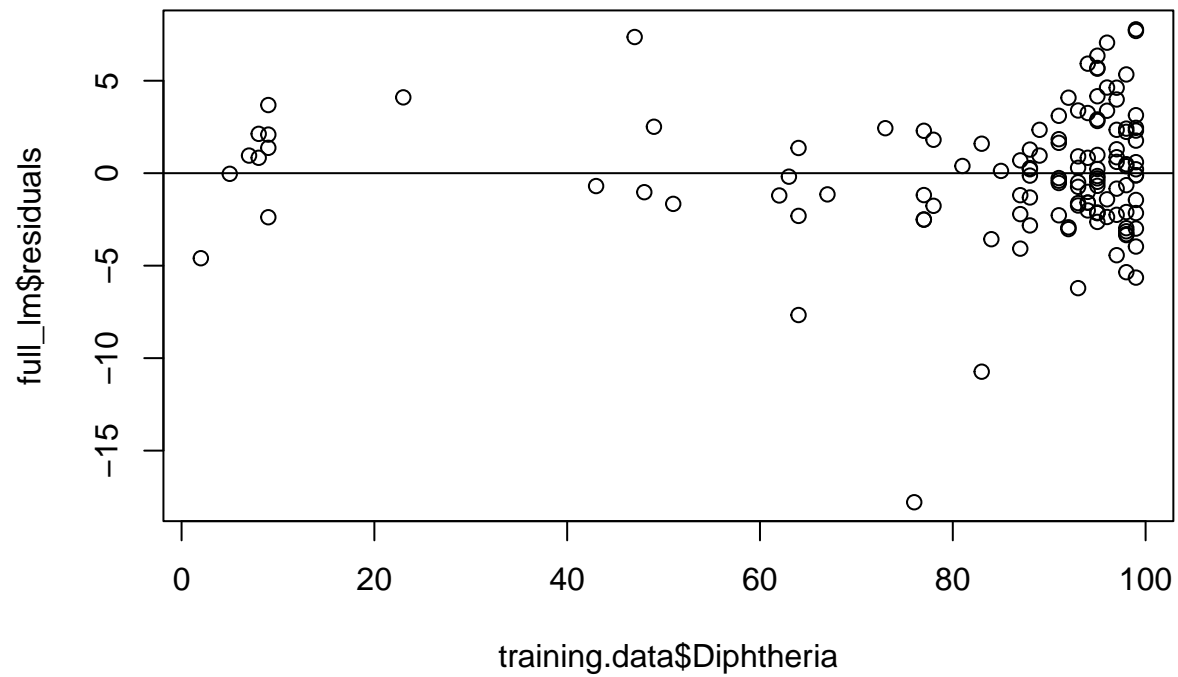
```
plot(training.data$Total.expenditure, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. total expenditure")  
abline(h=0)
```

Check for linearity Residuals vs. total expenditure



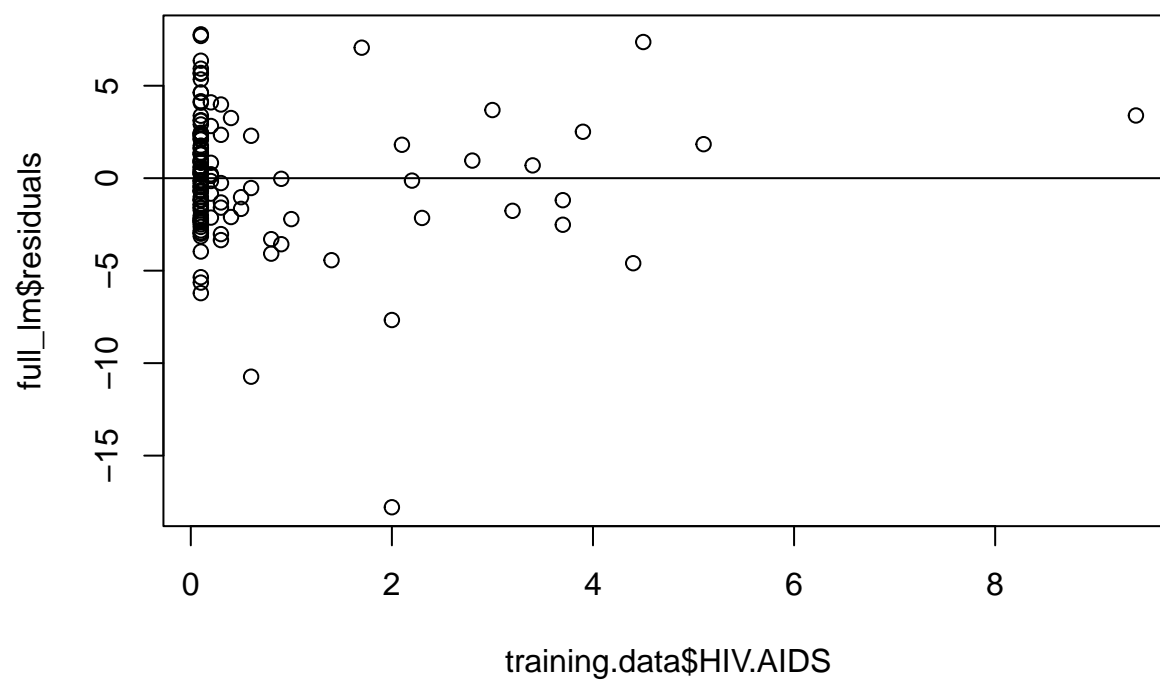
```
plot(training.data$Diphtheria, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. Diphtheria")  
abline(h=0)
```

Check for linearity Residuals vs. Diphtheria



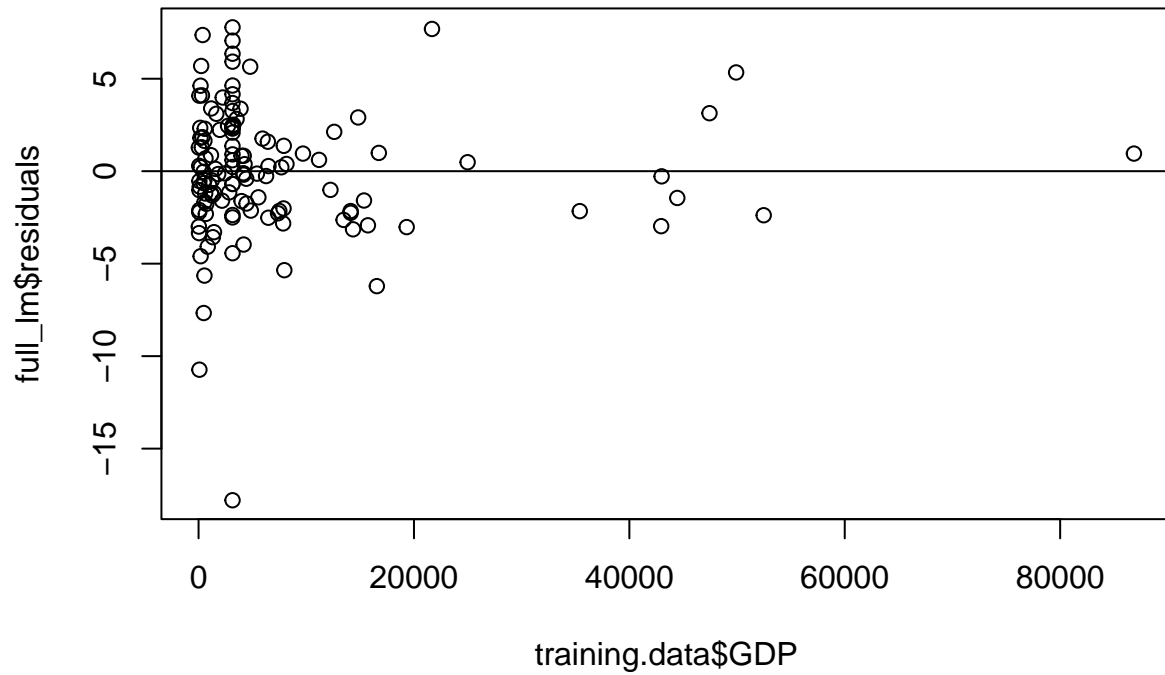
```
plot(training.data$HIV.AIDS, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. HIV/AIDS")  
abline(h=0)
```


Check for linearity Residuals vs. HIV/AIDS



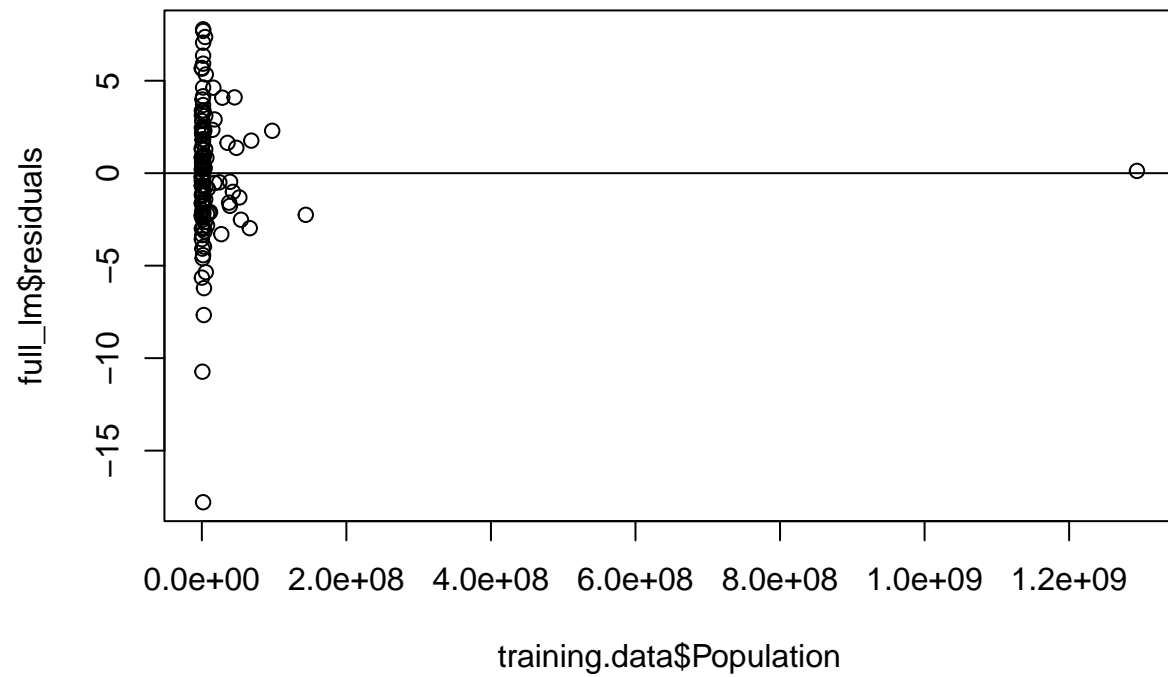
```
plot(training.data$GDP, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. GDP")  
abline(h=0)
```

Check for linearity Residuals vs. GDP



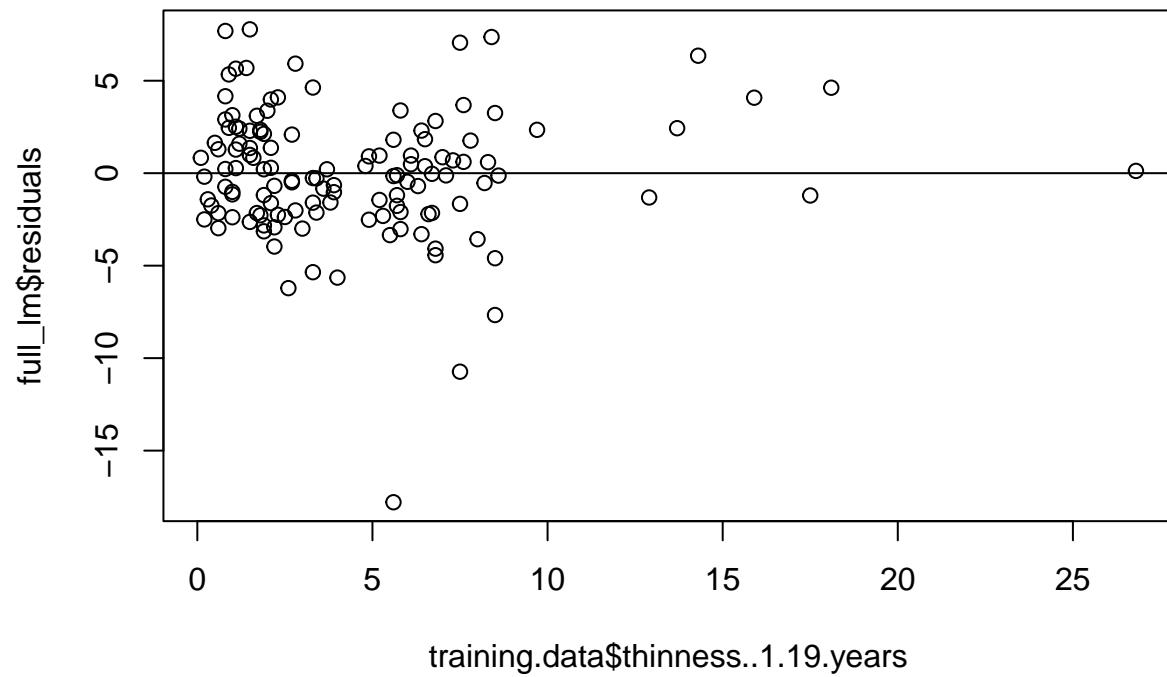
```
plot(training.data$Population, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. population")  
abline(h=0)
```

Check for linearity Residuals vs. population



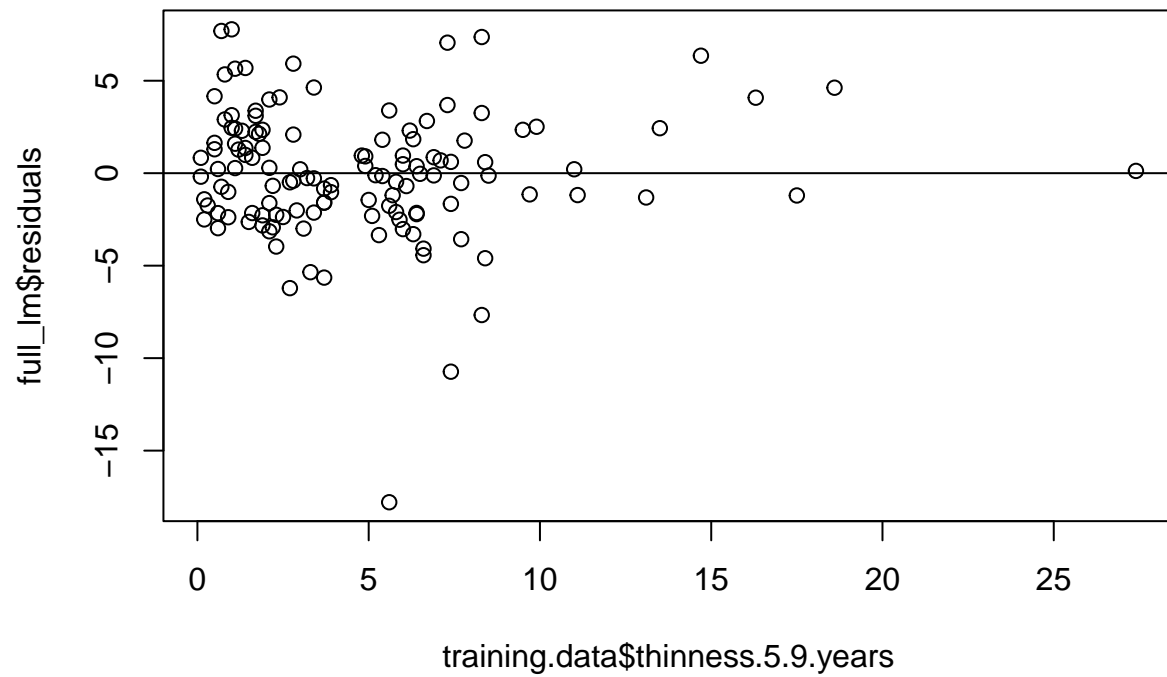
```
plot(training.data$thinness..1.19.years, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. thinness.1.19 years")  
abline(h=0)
```

Check for linearity Residuals vs. thinness.1.19 years



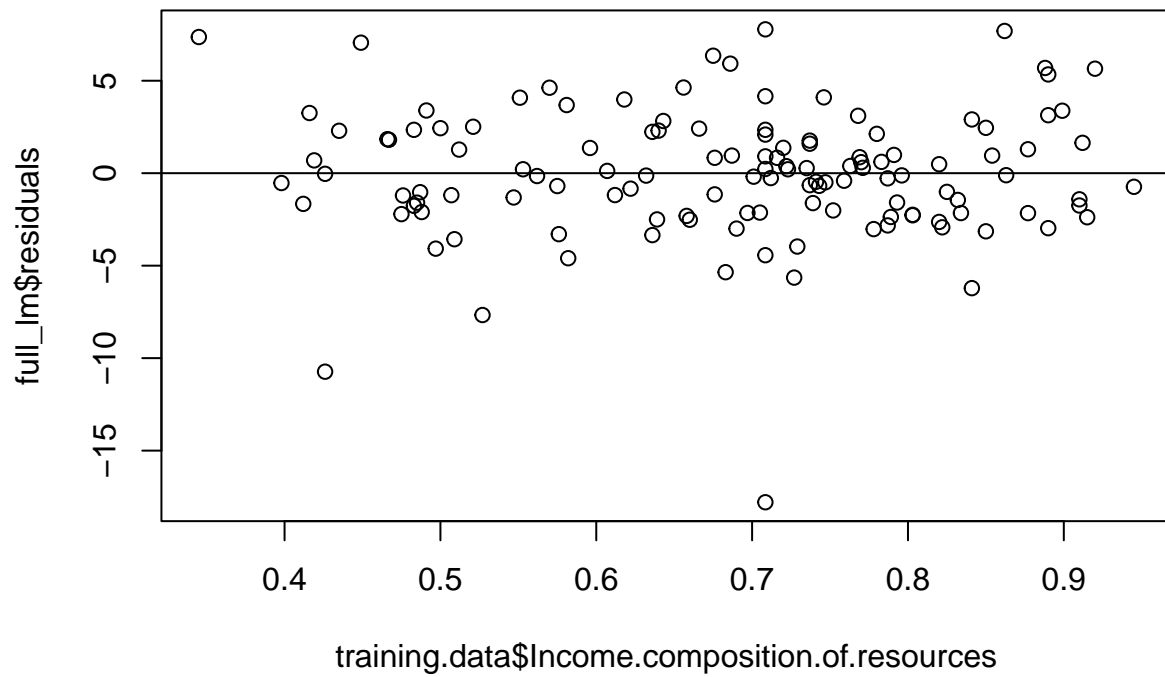
```
plot(training.data$thinness.5.9.years, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. thinness.5.19 years")  
abline(h=0)
```

Check for linearity Residuals vs. thiness.5.19 years



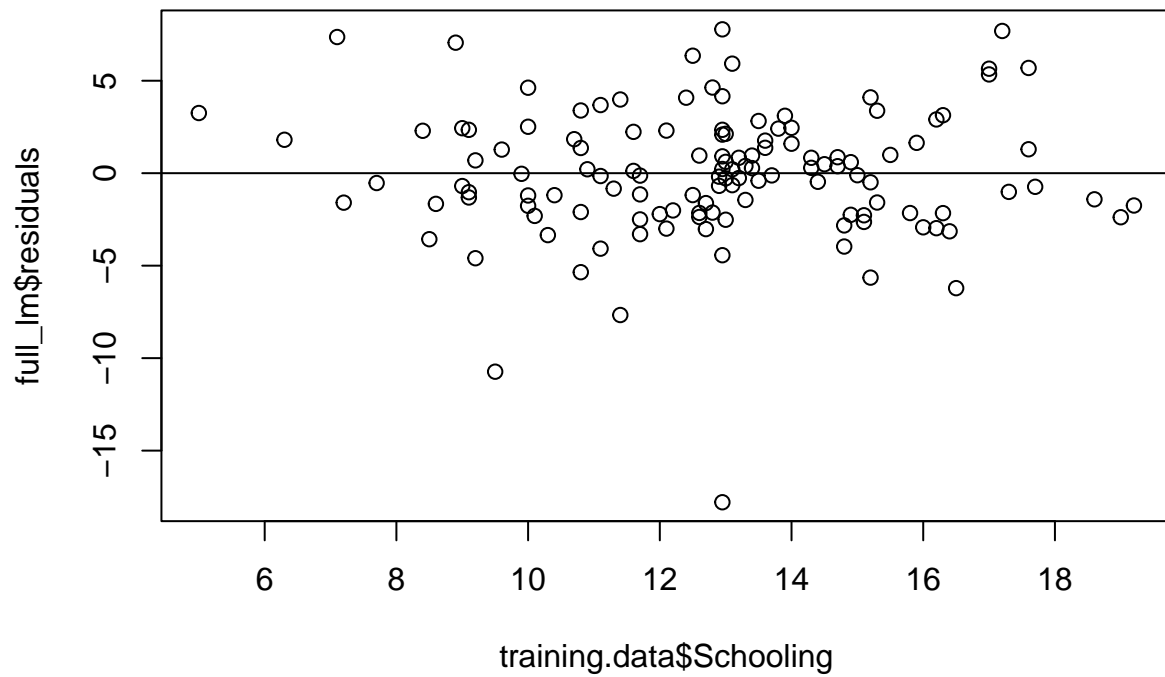
```
plot(training.data$Income.composition.of.resources, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. Income composition of resources")  
abline(h=0)
```

Check for linearity Residuals vs. Income composition of resources



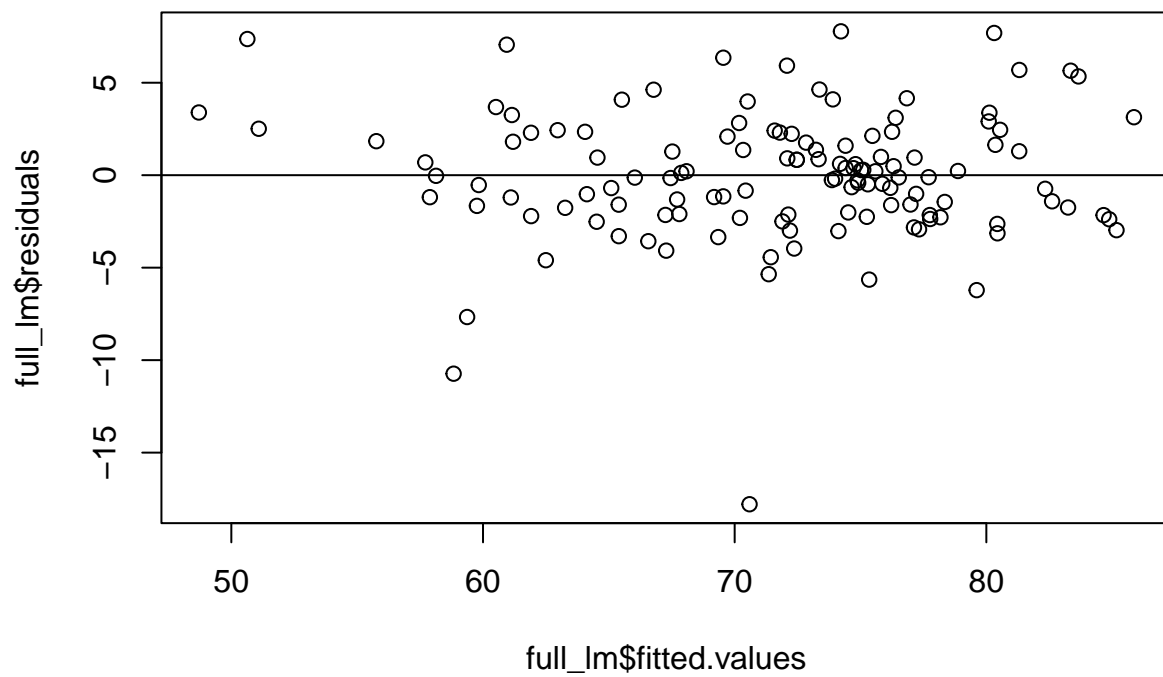
```
plot(training.data$Schooling, full_lm$residuals,  
      main = "Check for linearity \n Residuals vs. Schooling")  
abline(h=0)
```

Check for linearity Residuals vs. Schooling



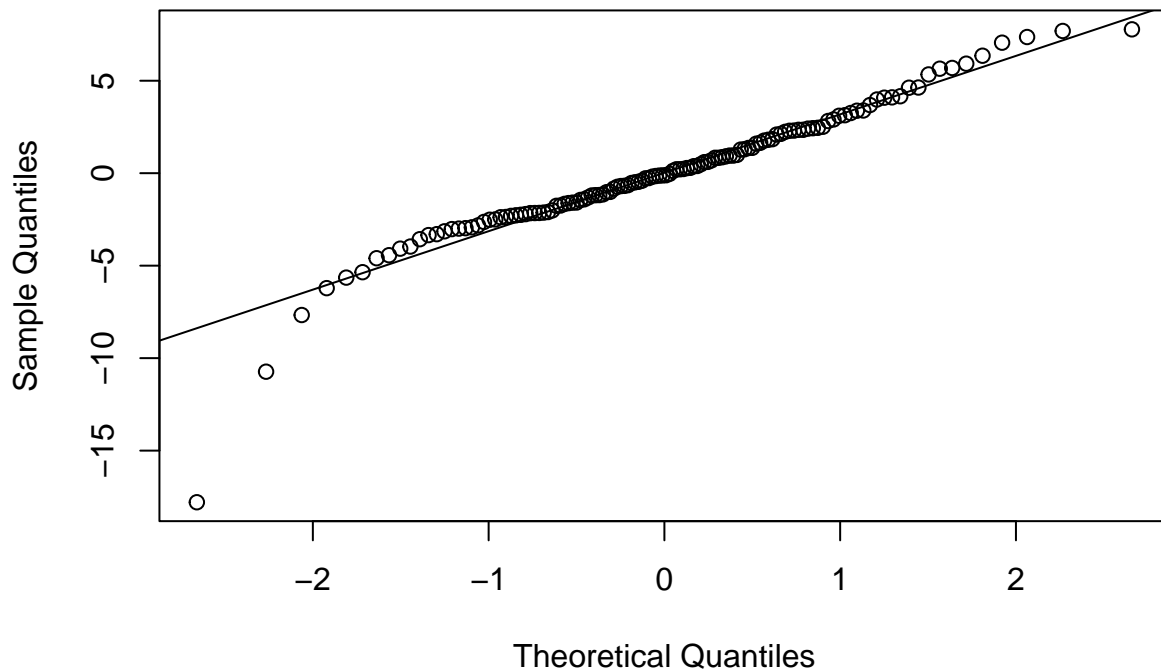
```
## Check for zero mean and constant variance of random error
plot(full_lm$fitted.values, full_lm$residuals,
     main = "Check for 0 mean and constant var \n Residual vs. fitted value")
abline(h=0)
```

Check for 0 mean and constant var Residual vs. fitted value



```
## Check for normality of random error  
qqnorm(full_lm$residuals)  
qqline(full_lm$residuals)
```


Normal Q-Q Plot



Definitely needs a transformation as only some of the linearity plots are satisfactory. We are okay with constant variance.

Applying the transformations

```
##### lets log transformation on response variable #####

new.training.data <- training.data
new.training.data$infant.deaths <- new.training.data$infant.deaths^(0.5)

new.training.data$Alcohol <- new.training.data$Alcohol^(0.5)
new.training.data$percentage.expenditure <- new.training.data$percentage.expenditure^(0.5)
new.training.data$Hepatitis.B <- new.training.data$Hepatitis.B^(0.5)

new.training.data$Measles <- new.training.data$Measles^(0.5)

new.training.data$under.five.deaths <- new.training.data$under.five.deaths^(0.5)

new.training.data$Polio <- new.training.data$Polio^(0.5)

new.training.data$Diphtheria <- new.training.data$Diphtheria^(0.5)

new.training.data$HIV.AIDS <- new.training.data$HIV.AIDS^(0.5)
```

```

new.training.data$GDP <- new.training.data$GDP^(0.5)

new.training.data$Population <- new.training.data$Population^(0.5)

new.training.data$Measles <- new.training.data$Measles^(0.5)

new.training.data$thinness..1.19.years <- new.training.data$thinness..1.19.years^(0.5)

new.training.data$thinness.5.9.years <- new.training.data$thinness.5.9.years^(0.5)

new_full_lm <- lm(Life.expectancy ~ . , data = new.training.data)
summary(new_full_lm )

```

```

##
## Call:
## lm(formula = Life.expectancy ~ . , data = new.training.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.7063  -1.8244  -0.0269   1.9422   8.2850
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    64.3986943   4.9449310   13.023  < 2e-16 ***
## Statusyes      -1.6957714   1.1237354   -1.509  0.134206
## Adult.Mortality -0.0173878   0.0046392   -3.748  0.000288 ***
## infant.deaths   1.4079174   1.3622143    1.034  0.303655
## Alcohol         0.2239293   0.3393691    0.660  0.510761
## percentage.expenditure 0.0449840   0.0372694    1.207  0.230071
## Hepatitis.B     -0.0484411   0.3703135   -0.131  0.896168
## Measles         0.1774388   0.1521522    1.166  0.246105
## BMI             -0.0068524   0.0205970   -0.333  0.740012
## under.five.deaths -1.4182176   1.1554574   -1.227  0.222338
## Polio           -0.1175258   0.3068245   -0.383  0.702444
## Total.expenditure 0.0591599   0.1448075    0.409  0.683685
## Diphtheria      0.3366212   0.3806582    0.884  0.378491
## HIV.AIDS        -3.7587663   0.8945574   -4.202  5.47e-05 ***
## GDP             -0.0028250   0.0136520   -0.207  0.836455
## Population      0.0001081   0.0001338    0.808  0.420705
## thinness..1.19.years -0.1676508   1.0140479   -0.165  0.868995
## thinness.5.9.years -1.1891533   1.0657718   -1.116  0.266998
## Income.composition.of.resources 20.4447935   7.7396298    2.642  0.009477 **
## Schooling       -0.0380177   0.3247116   -0.117  0.907013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.608 on 108 degrees of freedom
## Multiple R-squared:  0.8423, Adjusted R-squared:  0.8146
## F-statistic: 30.37 on 19 and 108 DF,  p-value: < 2.2e-16

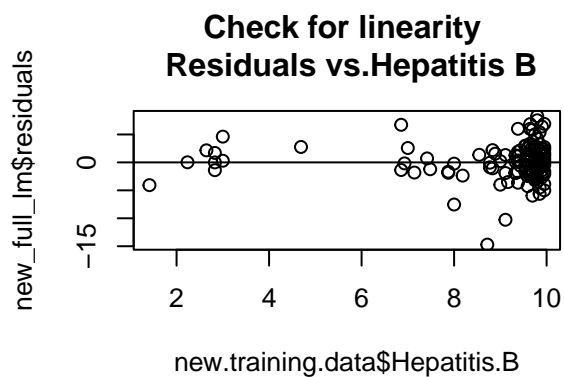
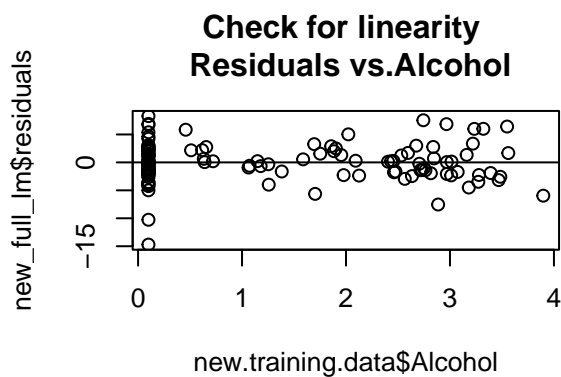
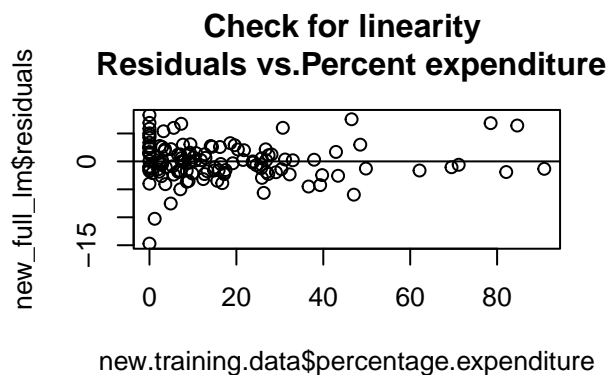
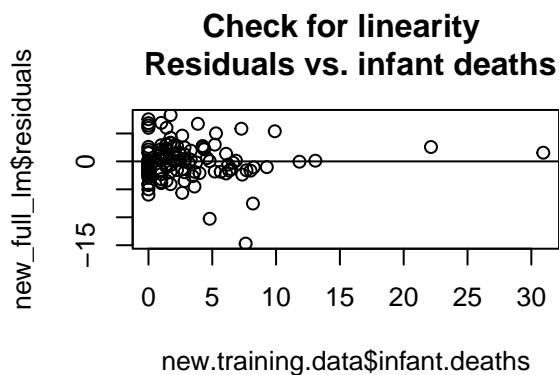
```

```
## Check for linearity
par(mfcol = c(2, 2))
plot(new.training.data$infant.deaths, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. infant deaths")
abline(h=0)

plot(new.training.data$Alcohol, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs.Alcohol")
abline(h=0)

plot(new.training.data$percentage.expenditure, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs.Percent expenditure")
abline(h=0)

plot(new.training.data$Hepatitis.B, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs.Hepatitis B")
abline(h=0)
```



```
plot(new.training.data$Measles, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs.measles")
abline(h=0)
```

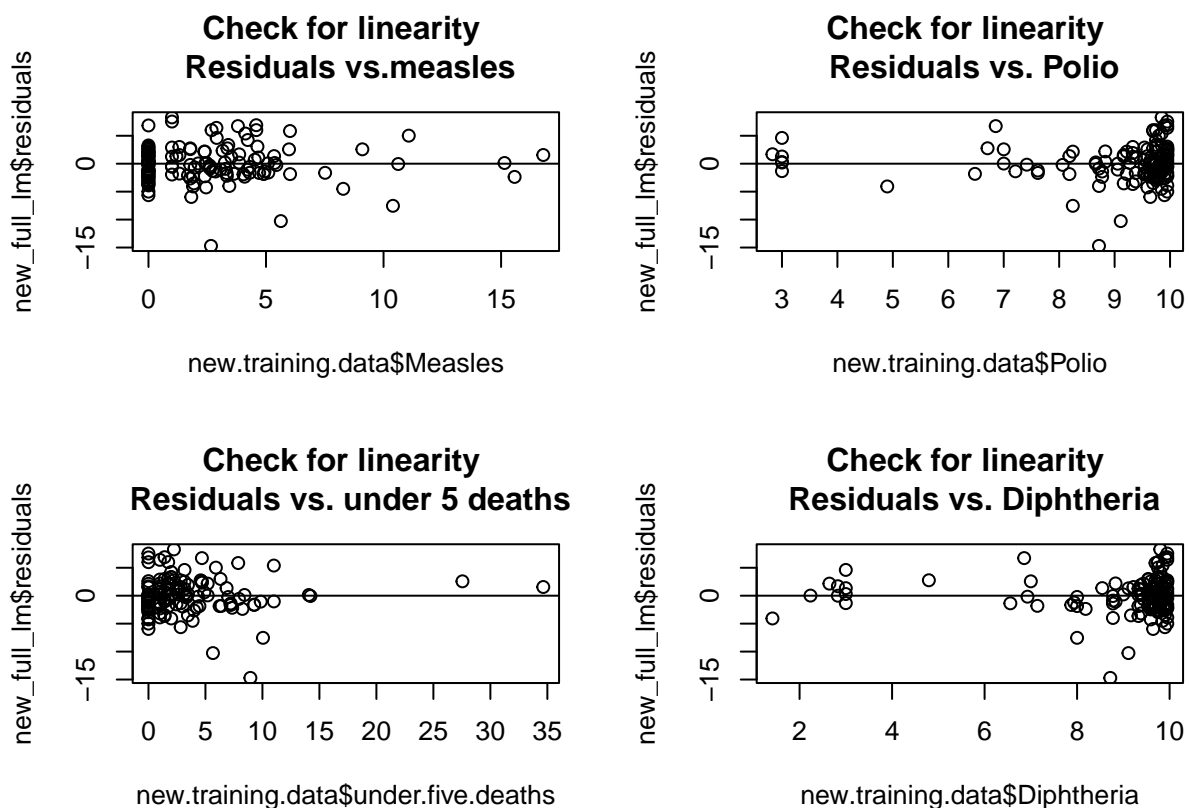
```

plot(new.training.data$under.five.deaths, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. under 5 deaths")
abline(h=0)

plot(new.training.data$Polio, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. Polio")
abline(h=0)

plot(new.training.data$Diphtheria, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. Diphtheria")
abline(h=0)

```



```

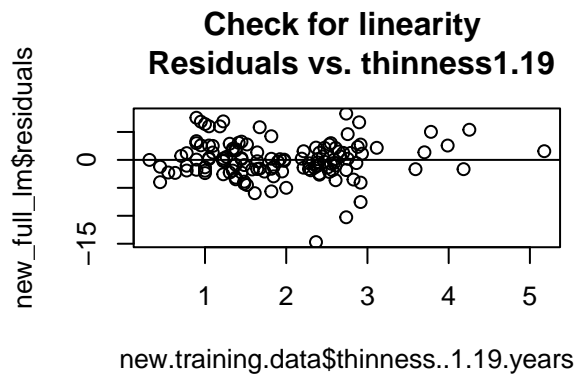
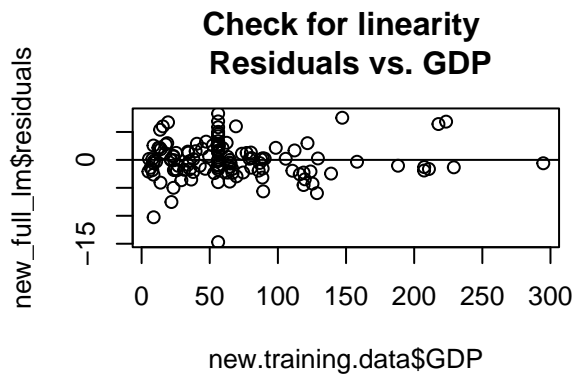
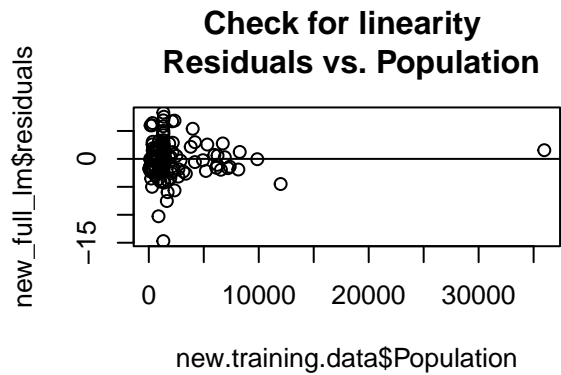
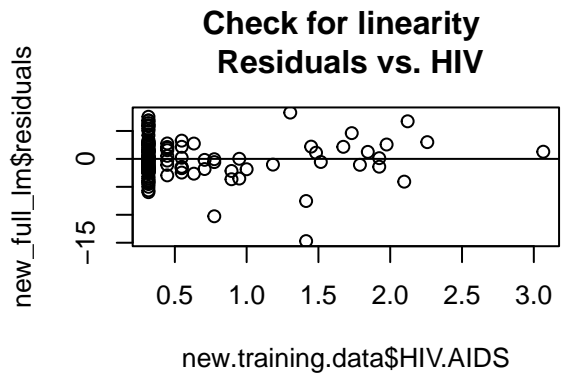
plot(new.training.data$HIV.AIDS, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. HIV")
abline(h=0)

plot(new.training.data$GDP, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. GDP")
abline(h=0)

plot(new.training.data$Population, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. Population")
abline(h=0)

```

```
plot(new.training.data$thinness..1.19.years, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. thinness1.19")
abline(h=0)
```



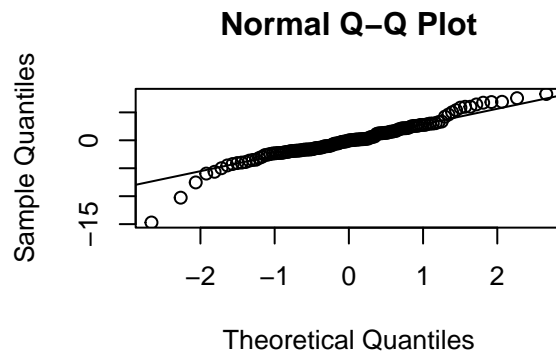
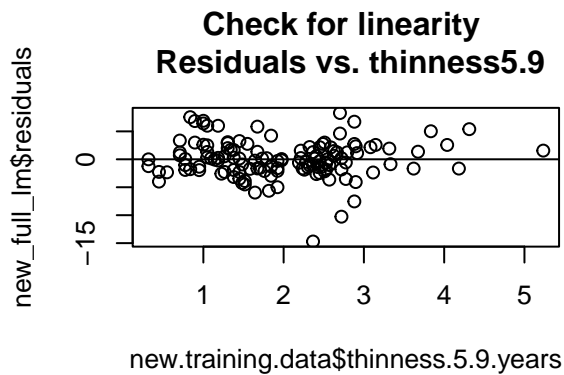
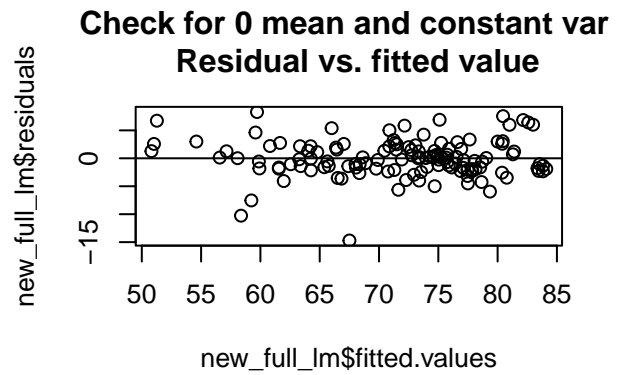
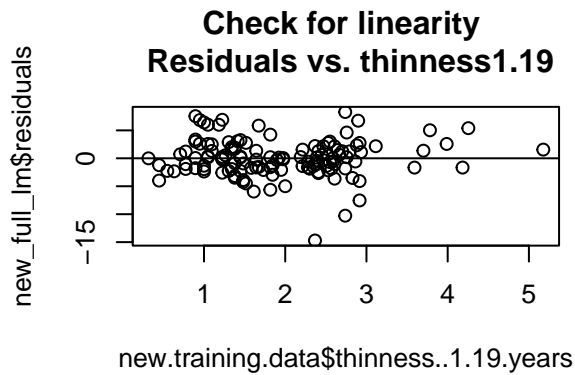
```
plot(new.training.data$thinness..1.19.years, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. thinness1.19")
abline(h=0)
```

```
plot(new.training.data$thinness.5.9.years, new_full_lm$residuals,
     main = "Check for linearity \n Residuals vs. thinness5.9")
abline(h=0)
```

```
# Check for zero mean and constant variance of random error
plot(new_full_lm$fitted.values, new_full_lm$residuals,
     main = "Check for 0 mean and constant var \n Residual vs. fitted value")
```

```
abline(h=0)
```

```
## Check for normality of random error
qqnorm(new_full_lm$residuals)
qqline(new_full_lm$residuals)
```



So, the new training model is

```
summary(new_full_lm)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ ., data = new.training.data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.7063  -1.8244  -0.0269   1.9422   8.2850
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    64.3986943   4.9449310   13.023 < 2e-16 ***
## Statusyes     -1.6957714   1.1237354   -1.509  0.134206
## Adult.Mortality -0.0173878   0.0046392   -3.748  0.000288 ***
## infant.deaths   1.4079174   1.3622143    1.034  0.303655
## Alcohol         0.2239293   0.3393691    0.660  0.510761
```

```

## percentage.expenditure      0.0449840  0.0372694   1.207  0.230071
## Hepatitis.B                 -0.0484411  0.3703135  -0.131  0.896168
## Measles                     0.1774388  0.1521522   1.166  0.246105
## BMI                        -0.0068524  0.0205970  -0.333  0.740012
## under.five.deaths          -1.4182176  1.1554574  -1.227  0.222338
## Polio                      -0.1175258  0.3068245  -0.383  0.702444
## Total.expenditure           0.0591599  0.1448075   0.409  0.683685
## Diphtheria                  0.3366212  0.3806582   0.884  0.378491
## HIV.AIDS                   -3.7587663  0.8945574  -4.202  5.47e-05 ***
## GDP                        -0.0028250  0.0136520  -0.207  0.836455
## Population                  0.0001081  0.0001338   0.808  0.420705
## thinness..1.19.years       -0.1676508  1.0140479  -0.165  0.868995
## thinness.5.9.years         -1.1891533  1.0657718  -1.116  0.266998
## Income.composition.of.resources 20.4447935  7.7396298   2.642  0.009477 **
## Schooling                   -0.0380177  0.3247116  -0.117  0.907013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.608 on 108 degrees of freedom
## Multiple R-squared:  0.8423, Adjusted R-squared:  0.8146
## F-statistic: 30.37 on 19 and 108 DF,  p-value: < 2.2e-16

```

Adjusted R _squared is pretty high.Residual standard error is also low.

We will work on this model.