Advanced Data Analysis
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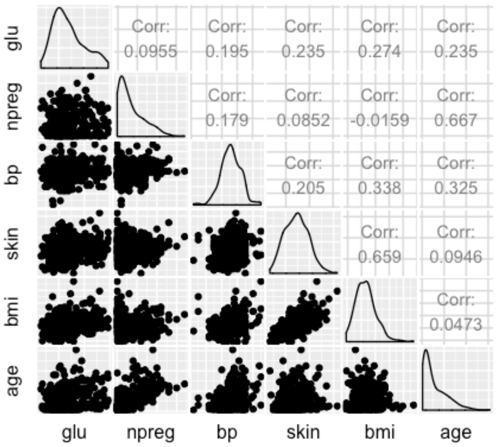
1. Consider the Pima.te dataset

   a). Fit a multiple linear regression model:
   The model: glu = 56.9314 – 0.8753npreg + 0.1039bp + 0.2626skin + 0.7958bmi + 0.7638age

```
> summary(LinearModel)

Call:
lm(formula = glu ~ npreg + bp + skin + bmi + age, data =
Pima.te)

Residuals:
    Min      1Q  Median      3Q     Max
-61.285 -20.556  -4.356  17.370  76.509

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  56.8314    10.3090   5.513 7.19e-08 ***
npreg        -0.8753     0.6475  -1.352  0.17735
bp            0.1039     0.1385   0.750  0.45353
skin          0.2626     0.2164   1.214  0.22575
bmi           0.7958     0.3020   2.636  0.00880 **
age           0.7638     0.2068   3.693  0.00026 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 28.6 on 326 degrees of freedom
Multiple R-squared:  0.1338,  Adjusted R-squared:  0.1205
F-statistic: 10.07 on 5 and 326 DF,  p-value: 5.575e-09
```

b). State and assess the validity of the underlying assumptions:

➢ Linearity/functional form, including the need for any interaction terms:



From the scatter plot, we find that bp, skin, bmi, and age have linear relationship with glu, while npreg do not have linear relationship with glu. Thus the linearity form is not appropriate. R-square is 0.1338, not very good.

For the interaction terms:

First, add all interactions into model:

```
> summary(LinearModelwithAllInteractions)

Call:
lm(formula = glu ~ npreg + bp + skin + bmi + age + npreg * bp + 
    npreg * skin + npreg * bmi + npreg * age + bp * skin + bp * 
    bmi + bp * age + skin * bmi + skin * age + bmi * age, data = Pima.te)

Residuals:
    Min      1Q  Median      3Q     Max 
-63.424 -19.930  -4.356  19.575  75.418 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)  
(Intercept) -1.679e+01  4.855e+01  -0.346   0.7298  
npreg        2.116e+00  5.318e+00   0.398   0.6909  
bp           7.623e-01  6.614e-01   1.153   0.2500  
skin         1.504e+00  1.384e+00   1.087   0.2780  
bmi          5.571e-01  1.702e+00   0.327   0.7437  
age          2.924e+00  1.631e+00   1.793   0.0740 .
npreg:bp    -2.026e-02  5.869e-02  -0.345   0.7302  
npreg:skin  -1.323e-02  9.023e-02  -0.147   0.8835  
npreg:bmi   -2.978e-02  1.130e-01  -0.263   0.7924  
npreg:age    7.744e-04  5.998e-02   0.013   0.9897  
bp:skin      8.502e-03  1.829e-02   0.465   0.6424  
bp:bmi      -3.677e-03  1.813e-02  -0.203   0.8394  
bp:age      -2.441e-02  1.714e-02  -1.424   0.1555  
skin:bmi    -1.341e-02  2.034e-02  -0.659   0.5102  
skin:age    -4.546e-02  2.583e-02  -1.760   0.0793 .
bmi:age      3.097e-02  3.639e-02   0.851   0.3954  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 28.58 on 316 degrees of freedom
Multiple R-squared:  0.1615,	Adjusted R-squared:  0.1217 
F-statistic: 4.058 on 15 and 316 DF,  p-value: 8.889e-07
```

We find that bp*age and skin*age may have interactions, thus we construct a model with these two interactions.

```
> summary(LinearModelwithTwoInteractions)

Call:
lm(formula = glu ~ npreg + bp + skin + bmi + age + bp * age + 
    skin * age, data = Pima.te)

Residuals:
   Min     1Q Median     3Q    Max 
-61.52 -20.00  -4.30  18.24  75.77 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -24.73944   32.36098  -0.764 0.445136    
npreg        -0.79329    0.64643  -1.227 0.220643    
bp            0.80056    0.40276   1.988 0.047690 *  
skin          1.33841    0.53688   2.493 0.013169 *  
bmi           0.74008    0.30027   2.465 0.014231 *  
age           3.61883    1.08370   3.339 0.000938 ***
bp:age       -0.02360    0.01243  -1.899 0.058449 .  
skin:age     -0.03636    0.01583  -2.296 0.022293 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 28.31 on 324 degrees of freedom
Multiple R-squared:  0.1567,	Adjusted R-squared:  0.1385 
F-statistic: 8.604 on 7 and 324 DF,  p-value: 1.104e-09
```

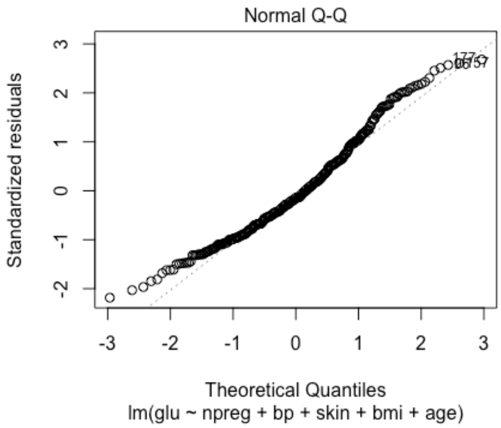
We find that only skin*age have significantly difference. Thus we construct a model only contain one interaction.

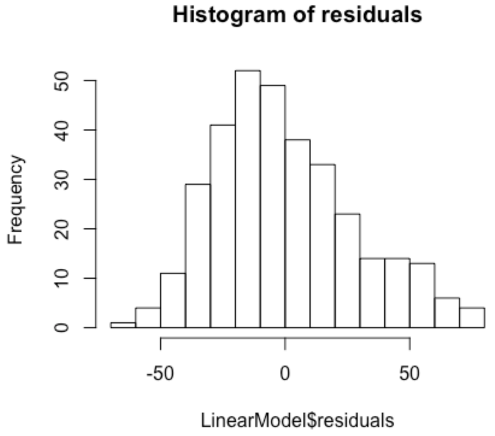
```
> summary(LinearModelwithOneInteractions)

Call:
lm(formula = glu ~ npreg + bp + skin + bmi + age + skin * age, 
    data = Pima.te)

Residuals:
    Min      1Q  Median      3Q     Max 
-64.849 -20.820  -4.357  17.453  75.701 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 28.66509   16.07608   1.783  0.07550 .  
npreg       -0.70926    0.64750  -1.095  0.27416    
bp           0.08158    0.13795   0.591  0.55466    
skin         1.38493    0.53847   2.572  0.01056 *  
bmi          0.73039    0.30143   2.423  0.01593 *  
age          1.78530    0.49410   3.613  0.00035 ***
skin:age    -0.03614    0.01590  -2.273  0.02366 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 28.42 on 325 degrees of freedom
Multiple R-squared:  0.1474,	Adjusted R-squared:  0.1316 
F-statistic: 9.362 on 6 and 325 DF,  p-value: 1.76e-09
```

Thus skin*age is an important interaction to the glu.

- Normality:

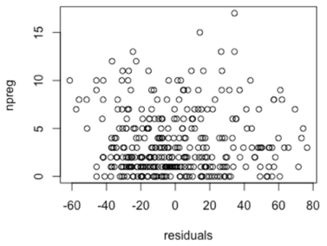
From the Q-Q plot is nearly a line, and the histogram is almost a normal distribution, thus the normality assumption is validated.

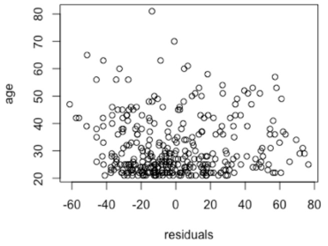


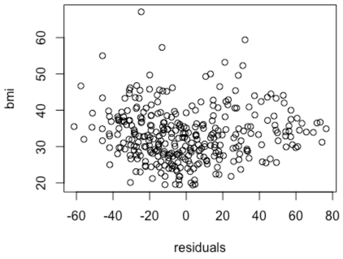


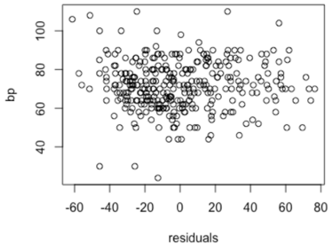
- Homoscedasticity:

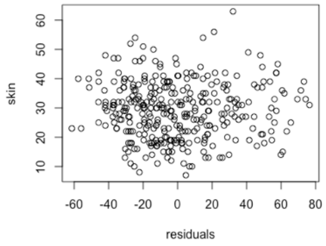
The residuals vs predictors plots indicate that the variance is constant.











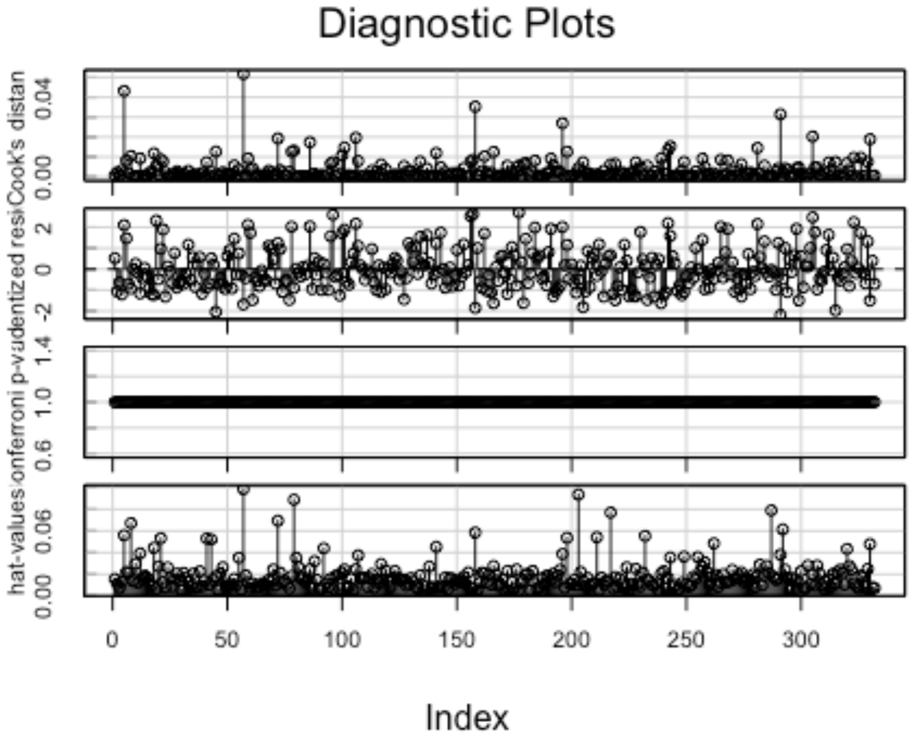
- Uncorrelated error:

The Durbin-Watson Test have a p-value = 0.558, which indicates that it rejects the null hypothesis and the observations are uncorrelated.

```
> durbinWatsonTest(LinearModel)
 lag Autocorrelation D-W Statistic p-value
   1        0.029888      1.937881   0.558
 Alternative hypothesis: rho != 0
```

- Check for outliers and influential points:

Influential points can be detected by Cook's distance. According to the plot below, there are 2 influential points: the first one is an outlier and a high leverage point, and the second one is a high leverage point.



c). Propose remedial measures in case of violations of any of the underlying assumptions

- Linearity:
  - Transformations, basis functions: such as log, smoothing splines
  - Non-linear models
  - Other predictors
- Normality:

    - Transformations, basis functions: such as log, smoothing splines
    - Robust regression methods
- Homoscedasticity:
    - Transformations, basis functions: such as log, smoothing splines
    - Build variance structure into model: weighted least squares
- Uncorrelated error:
    - Transformation: Cochrane-Orcutt Procedure
    - Use models that incorporate the correlation structure: Generalized Estimating Equations
- Outliers and Influential Points:
    - Delete the outliers
    - Use robust regression methods: lease median of squares regression

d). Compare the Lease Median of Squares Regression and Linear Regression models:
The coefficients between linear regression and lease median of squares regression are quite different. This method is more robust for outliers and influential points. Compare to the result in a, the model has a higher breakdown point.

```
> coef(LeastMedianModel)
(Intercept)       npreg          bp        skin         bmi 
 47.7888316   1.9123228   0.3207494   1.2400925  -0.3783237 
        age 
  0.2133375 
> coef(LinearModel)
(Intercept)       npreg          bp        skin         bmi 
 56.8313661  -0.8753016   0.1039174   0.2626200   0.7958464 
        age 
  0.7638058 
```

Code:

```
library('MASS')
data("Pima.te")
Pima.te <- Pima.te[c('glu', 'npreg', 'bp', 'skin', 'bmi', 'age')]
# a) Fit a multiple linear regression model
LinearModel <- lm(glu ~ npreg + bp + skin + bmi + age, data = Pima.te)
summary(LinearModel)

# b) State and assess the validity of the underlying assumptions
# Linearity
library(GGally)
ggpairs(Pima.te)

# interaction
LinearModelwithAllInteractions = lm(glu ~ npreg + bp + skin + bmi + age +
npreg*bp + npreg*skin + npreg*bmi +
                                        npreg*age + bp*skin + bp*bmi+ bp*age
+ skin*bmi + skin*age + bmi*age, data = Pima.te)
summary(LinearModelwithAllInteractions)
LinearModelwithTwoInteractions = lm(glu ~ npreg + bp + skin + bmi + age +
bp*age + skin*age, data = Pima.te)
summary(LinearModelwithTwoInteractions)
LinearModelwithOneInteractions = lm(glu ~ npreg + bp + skin + bmi + age +
skin*age, data = Pima.te)
summary(LinearModelwithOneInteractions)




# Non-normality
hist(LinearModel$residuals, main = 'Histogram of residuals')
qqnorm(LinearModel$residuals)

# Homoscedasticity
plot(LinearModel$residuals, Pima.te$npreg, xlab = 'residuals', ylab =
'npreg')
plot(LinearModel$residuals, Pima.te$bp, xlab = 'residuals', ylab = 'bp')
plot(LinearModel$residuals, Pima.te$skin, xlab = 'residuals', ylab = 'skin')
plot(LinearModel$residuals, Pima.te$bmi, xlab = 'residuals', ylab = 'bmi')
plot(LinearModel$residuals, Pima.te$age, xlab = 'residuals', ylab = 'age')

# Uncorrelated error
library(car)
durbinWatsonTest(LinearModel)


# Check for outliers and influential points
infIndexPlot(LinearModel)



# c Least Median of Squares Regression
LeastMedianModel <- lmsreg(glu ~ npreg + bp + skin + bmi + age, data =
Pima.te)
summary(LeastMedianModel)
coef(LeastMedianModel)
coef(LinearModel)
```