ISyE 6414 Computer Project 2

Kaustubh Mohite (903235166)

1. Motivation Studies

1.1

"Adaptive Estimation of Daily Demands with Complex Calendar Effects for Freight Transportation"

The purpose of the paper is to propose a class of exponential smoothing-based methods (called called damped trend multi-calendar (DTMC) exponential smoothing) for forecasting 'spatial activities' on a daily basis.

These methods can model multiple periodic and non-periodic 'calendar effects', are easier to apply than more sophisticated Auto-regressive Integrated Moving Average (ARIMA) methods, and actually outperform ARIMA methods in terms of forecast accuracy (3 percent lower RMSE than ARIMA; 2 percent lower than single exponential smoothing).

There are three sets of experiments in the study:

- Examining the validity of modelling multiple calendar effects (using only one day-of-the-week effect vs. multiple effects and the corresponding RMSE improvements)
- The relationship between trend-adjusted models and the need for control charts; Conclusion: using dampened trend gives better results than using full trend, and control charts give a slight performance improvement for testing sets
- Testing the effect of each of the control charts under a range of control parameters: EWMA charts give the most consistent and accurate results; Trig charts improve accuracy, but are sensitive to control parameters; Stewart charts provide no improvement

1.2

"Forecasting and Risk Analysis in Supply Chain Management"

The purpose of the paper to explore the application of autoregressive forecasting models to supply chain problems, and, in particular, generalized autoregressive conditional heteroscedasticity (GARCH), of which the writers present a Proof of Concept. The data used is from a supply chain inventory model (spare parts inventory management). The paper uses the '4-stage Beer Distribution Game' simulation model to illustrate Demand Amplification or the Bullwhip effect.

The writers identify four main domains in which GARCH may minimise forecasting errors and fiscal losses:

- Cost of personnel, supply, support
- Planning, programming, budgeting
- Defense program and fiscal guidance development
- Force planning and financial program development

The writers compare the performance of the Classical Linear Regression Model (CLRM) with the Auto-regressive Moving Average (ARMA) model, and GARCH, and find that CLRM is always outperformed by the latter two.

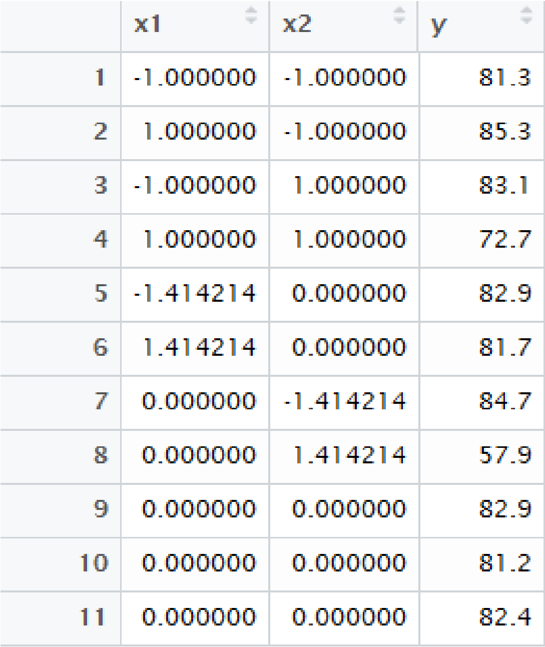
The paper’s temporary conclusion is that GARCH and VAR- MGARCH techniques are promising (and often outperform ARMA), in high-volume and rich data environments that will be made feasible through real time capture (e.g. with RFID tagging and other Automatic Identification Technologies).

2. Model Fitting

MBT Synthesis

Raw Data:

y: dependent variable
x1: [time (in hours) – 12] / 5.6
x2 = [Temperature (in Celsius) – 250] / 20



	x1	x2	y
1	-1.000000	-1.000000	81.3
2	1.000000	-1.000000	85.3
3	-1.000000	1.000000	83.1
4	1.000000	1.000000	72.7
5	-1.414214	0.000000	82.9
6	1.414214	0.000000	81.7
7	0.000000	-1.414214	84.7
8	0.000000	1.414214	57.9
9	0.000000	0.000000	82.9
10	0.000000	0.000000	81.2
11	0.000000	0.000000	82.4

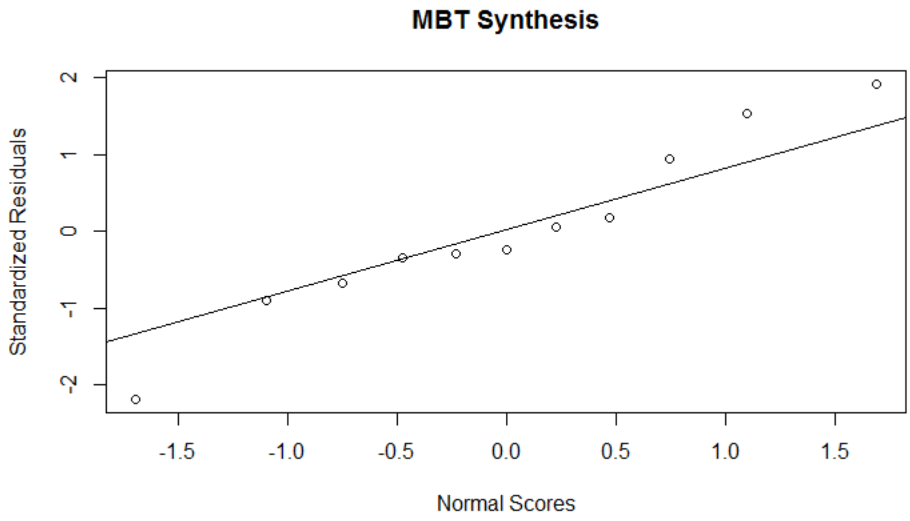
Second order polynomial regression model:

```
Call:
lm(formula = y ~ x1 + x2 + I(x1 * x2) + I(x1 * x1) + I(x2 * x2), data = dfP2)

Residuals:
      1       2       3       4       5       6       7       8       9      10      11 
-0.8997 -2.0755  5.8755  4.6997 -2.7314 -1.0686  2.8908 -6.6908  0.7333 -0.9667  0.2333 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   82.167      2.887  28.466    1e-06 ***
x1            -1.012      1.768  -0.573   0.5917    
x2            -6.088      1.768  -3.444   0.0184 *  
I(x1 * x2)    -3.600      2.500  -1.440   0.2094    
I(x1 * x1)     1.017      2.104   0.483   0.6493    
I(x2 * x2)    -4.483      2.104  -2.131   0.0863 .  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5 on 5 degrees of freedom
Multiple R-squared:  0.8012,	Adjusted R-squared:  0.6024 
F-statistic: 4.031 on 5 and 5 DF,  p-value: 0.07614
```

Y = -1.012(x1) -6.088(x2) - 3.6(x1*x2) +1.017(x1*x1) -4.483(x2*x2)

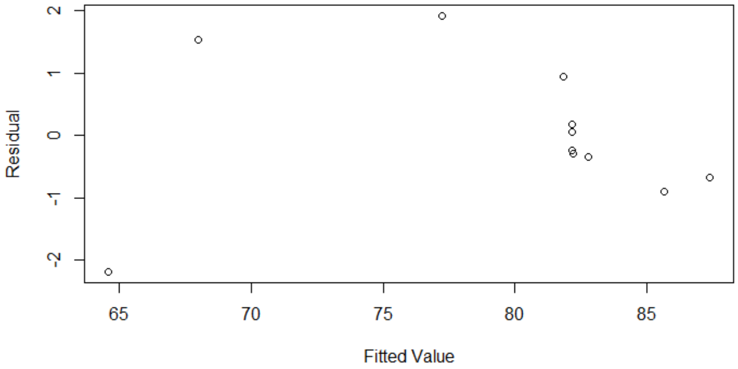
Diagnostics:

a. Normal Probability plot of Standardised Residuals:



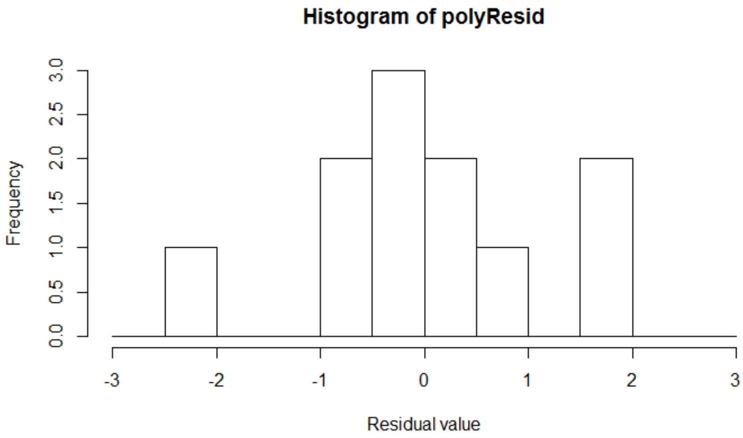
Inference: Standardised residuals approximate the normal distribution.

b. Standardised fitted values vs. residuals:



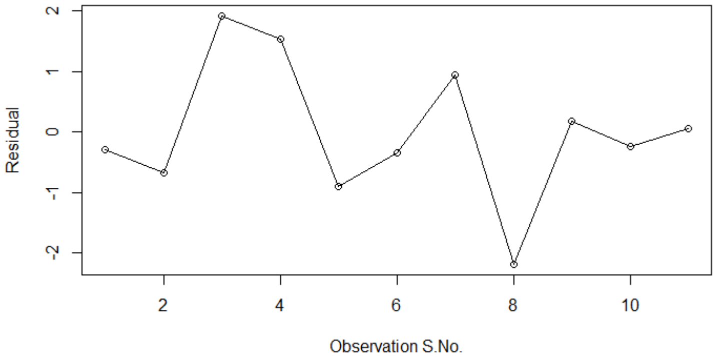
Inference: Residuals seem to be random w.r.t. Fitted Values

c. Histogram of residual values:



Inference: Residuals are approximately normally distributed, with mean = 0

d. Observation sequence vs. residuals:



Inference: no trend seen

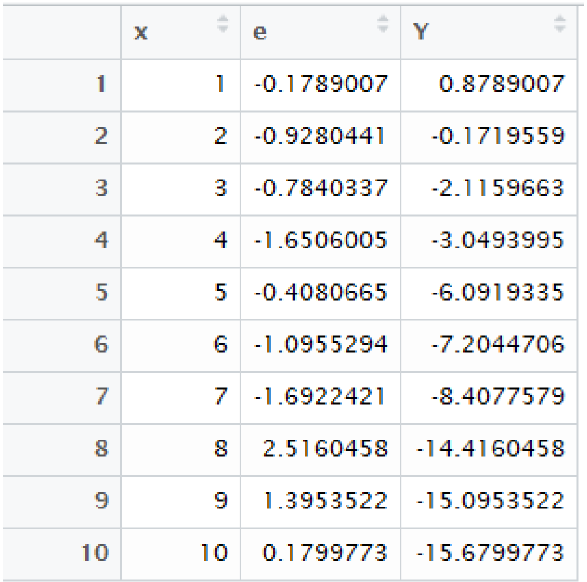
3. **Simulation Studies**

A]

Raw Data:

e: simulated normal distribution with mean = 0, s.d. = 1

Y = 2.5 – 1.8 x + *e*



	x	e	Y
1	1	-0.1789007	0.8789007
2	2	-0.9280441	-0.1719559
3	3	-0.7840337	-2.1159663
4	4	-1.6506005	-3.0493995
5	5	-0.4080665	-6.0919335
6	6	-1.0955294	-7.2044706
7	7	-1.6922421	-8.4077579
8	8	2.5160458	-14.4160458
9	9	1.3953522	-15.0953522
10	10	0.1799773	-15.6799773

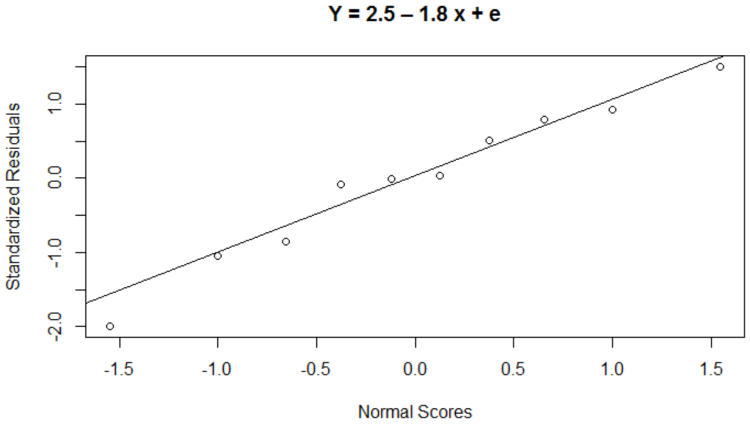
Simple Linear Regression Model:

Y ~ x

```
Call:
lm(formula = Y ~ x)

Residuals:
     Min       1Q   Median       3Q      Max 
-2.24759 -0.70597  0.01161  0.83188  1.74747 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)   3.9373     0.8478   4.644  0.00166 ** 
x            -2.0132     0.1366 -14.734 4.43e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.241 on 8 degrees of freedom
Multiple R-squared:  0.9645,	Adjusted R-squared:   0.96 
F-statistic: 217.1 on 1 and 8 DF,  p-value: 4.426e-07
```

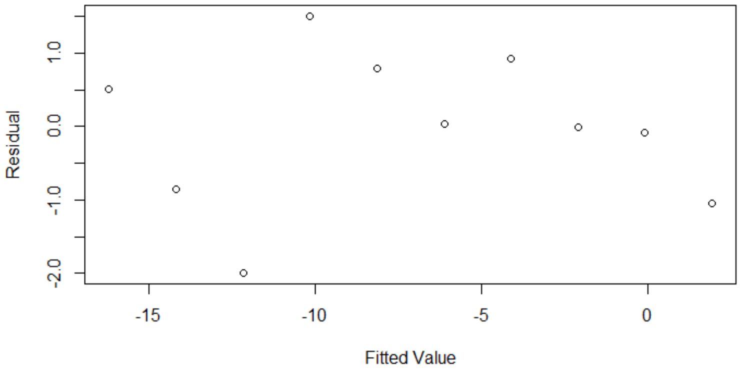
Diagnostics:

a. Normal Probability plot of Standardised Residuals:



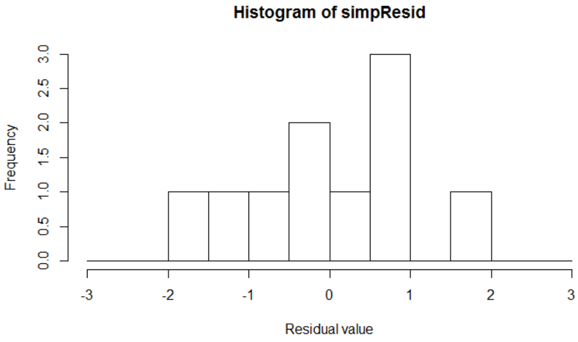
Inference: Standardised residuals approximate the normal distribution.

b. Standardised fitted values vs. residuals:



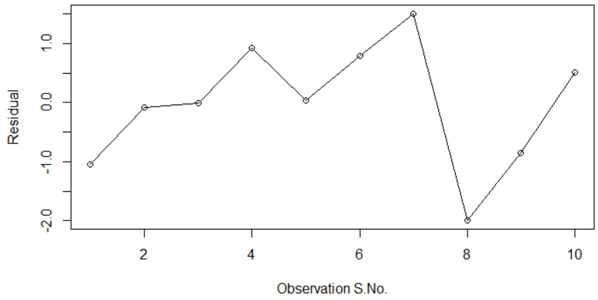
Inference: Residuals seem to be random w.r.t. Fitted Values

c. Histogram of residual values:



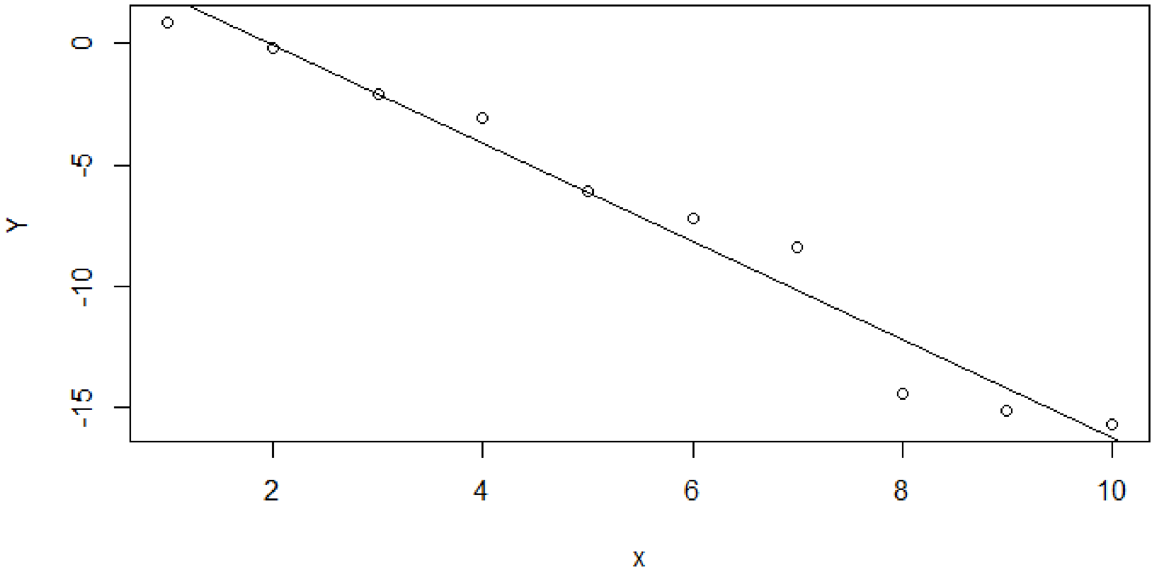
Inference: Residuals are approximately normally distributed, with mean = 0

d. Observation sequence vs. residuals:



Inference: no trend seen

Plotting the regression line over the data



Comment: The regression line seems to be well-balanced, with positive as well as negative residual values (points above as well as below)

B] Finding alternative sigma

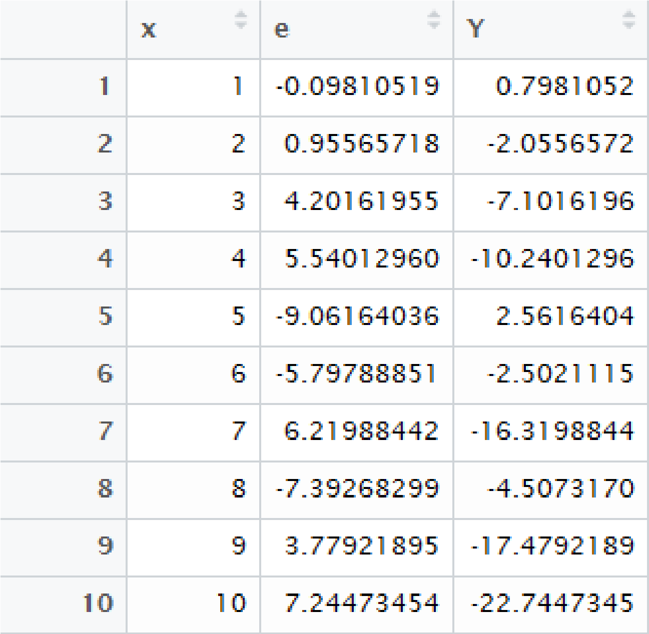
By simulating multiple data sets with different values of *sigma*, and examining the respective regression models (value of p statistic for the coefficient estimate of x) we arrive at:

sigma = 8

Updated raw data

e: simulated normal distribution with mean = 0, s.d. = 1

Y = 2.5 – 1.8 x + *e*



	x	e	Y
1	1	-0.09810519	0.7981052
2	2	0.95565718	-2.0556572
3	3	4.20161955	-7.1016196
4	4	5.54012960	-10.2401296
5	5	-9.06164036	2.5616404
6	6	-5.79788851	-2.5021115
7	7	6.21988442	-16.3198844
8	8	-7.39268299	-4.5073170
9	9	3.77921895	-17.4792189
10	10	7.24473454	-22.7447345

Regression Model:

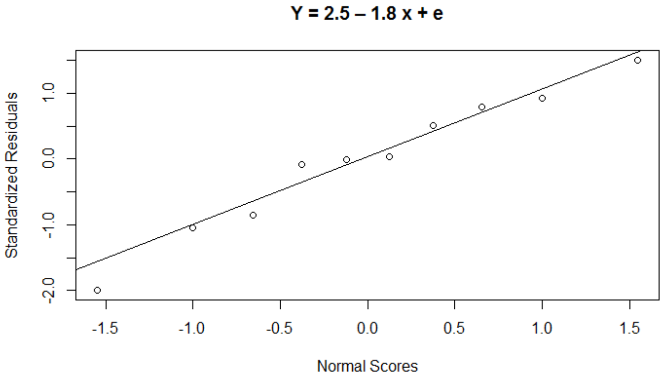
```
Call:
lm(formula = Y ~ x)

Residuals:
     Min       1Q   Median       3Q      Max 
-17.9808  -5.6477   0.0929   6.6551  13.9798 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)  
(Intercept)   13.999      6.782   2.064   0.0729 .
x             -3.506      1.093  -3.207   0.0125 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 9.928 on 8 degrees of freedom
Multiple R-squared:  0.5625,	Adjusted R-squared:  0.5078 
F-statistic: 10.29 on 1 and 8 DF,  p-value: 0.01248
```

Inference: p statistic of the estimate of the coefficient x is 0.0125

Hence, the estimate is statistically significant for alpha=0.1 (10%), but insignificant for alpha = 0.01 (1%)

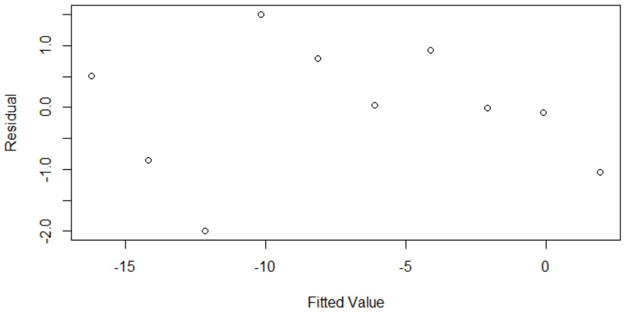
Diagnostics:

a. Normal Probability plot of Standardised Residuals:



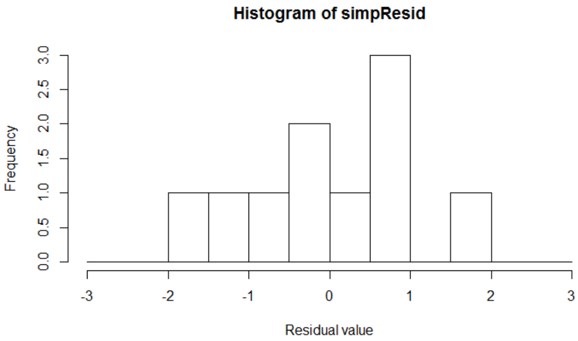
Inference: Standardised residuals approximate the normal distribution.

b. Standardised fitted values vs. residuals:



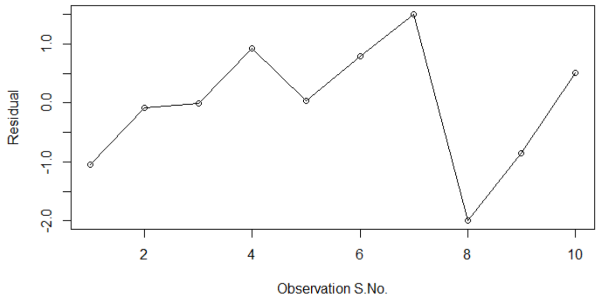
Inference: Residuals seem to be random w.r.t. Fitted Values

c. Histogram of residual values:



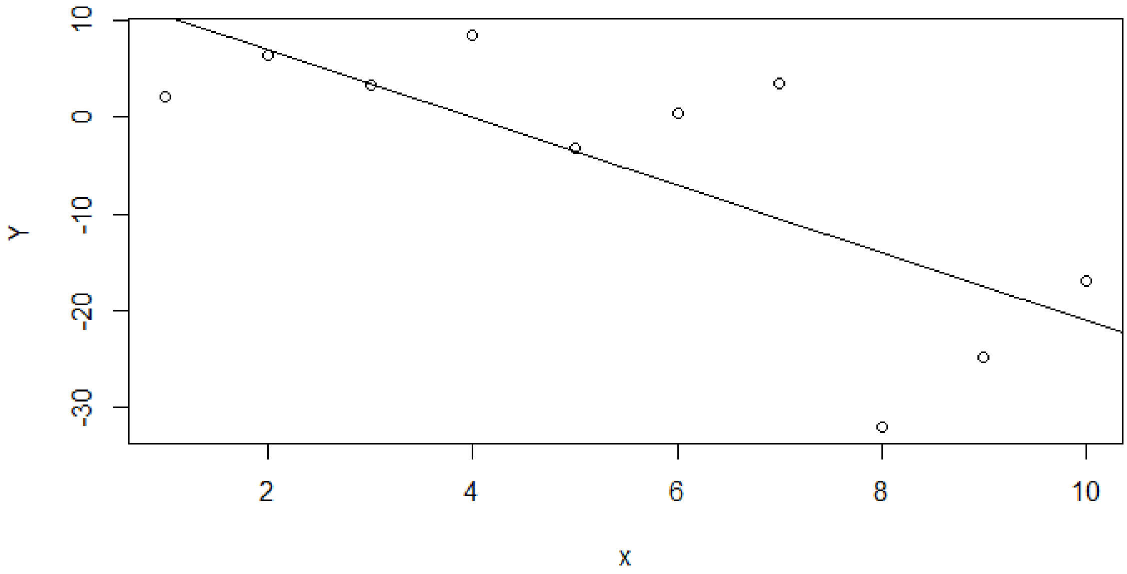
Inference: Residuals are approximately normally distributed, with mean = 0

d. Observation sequence vs. residuals:



Inference: no trend seen

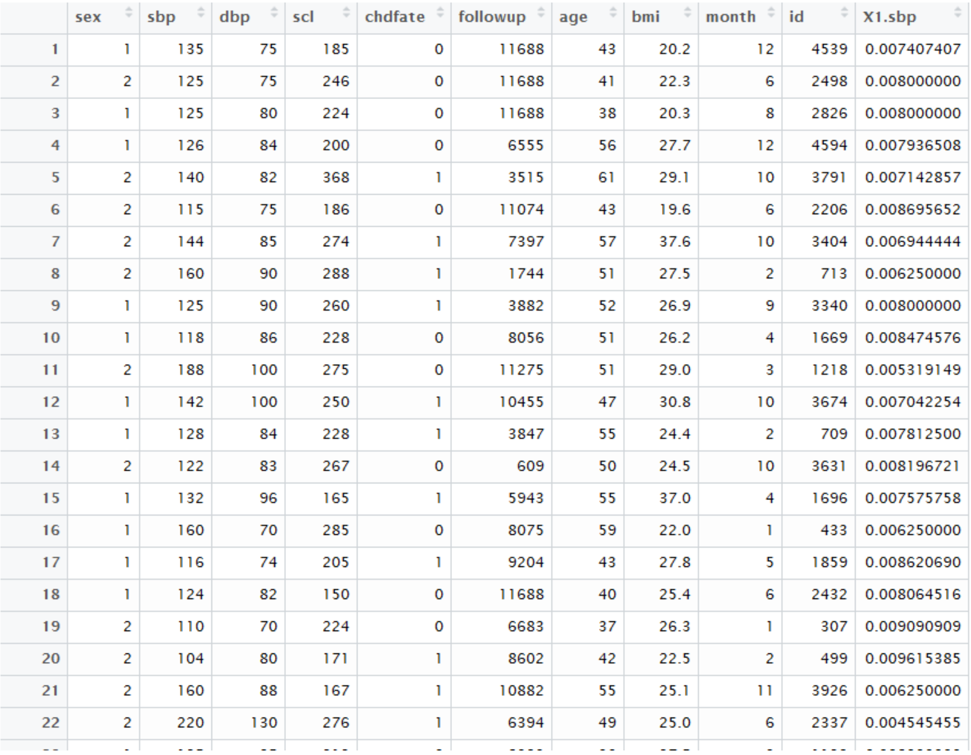
Plotting the regression line over the data



Comment: The regression line seems to be fairly balanced, with positive as well as negative residual values (points above as well as below). The residual values are larger than the earlier case (when e: sd = 1)

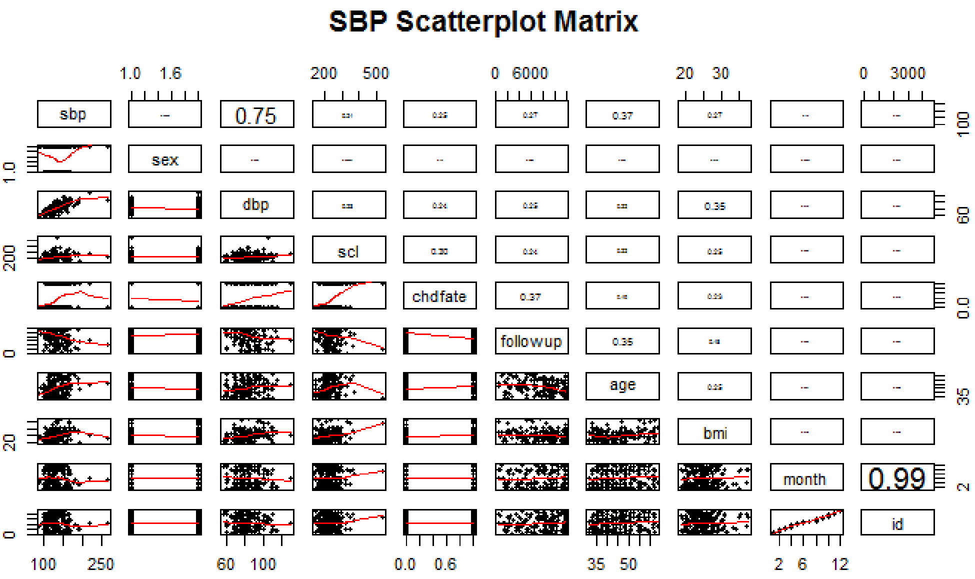
4. Real-life Data Analysis for Variable Selections

Sample of Raw Data:



	sex	sbp	dbp	scl	chdfate	followup	age	bmi	month	id	X1.sbp
1	1	135	75	185	0	11688	43	20.2	12	4539	0.007407407
2	2	125	75	246	0	11688	41	22.3	6	2498	0.008000000
3	1	125	80	224	0	11688	38	20.3	8	2826	0.008000000
4	1	126	84	200	0	6555	56	27.7	12	4594	0.007936508
5	2	140	82	368	1	3515	61	29.1	10	3791	0.007142857
6	2	115	75	186	0	11074	43	19.6	6	2206	0.008695652
7	2	144	85	274	1	7397	57	37.6	10	3404	0.006944444
8	2	160	90	288	1	1744	51	27.5	2	713	0.006250000
9	1	125	90	260	1	3882	52	26.9	9	3340	0.008000000
10	1	118	86	228	0	8056	51	26.2	4	1669	0.008474576
11	2	188	100	275	0	11275	51	29.0	3	1218	0.005319149
12	1	142	100	250	1	10455	47	30.8	10	3674	0.007042254
13	1	128	84	228	1	3847	55	24.4	2	709	0.007812500
14	2	122	83	267	0	609	50	24.5	10	3631	0.008196721
15	1	132	96	165	1	5943	55	37.0	4	1696	0.007575758
16	1	160	70	285	0	8075	59	22.0	1	433	0.006250000
17	1	116	74	205	1	9204	43	27.8	5	1859	0.008620690
18	1	124	82	150	0	11688	40	25.4	6	2432	0.008064516
19	2	110	70	224	0	6683	37	26.3	1	307	0.009090909
20	2	104	80	171	1	8602	42	22.5	2	499	0.009615385
21	2	160	88	167	1	10882	55	25.1	11	3926	0.006250000
22	2	220	130	276	1	6394	49	25.0	6	2337	0.004545455

Matrix scatter plot – variable correlation:

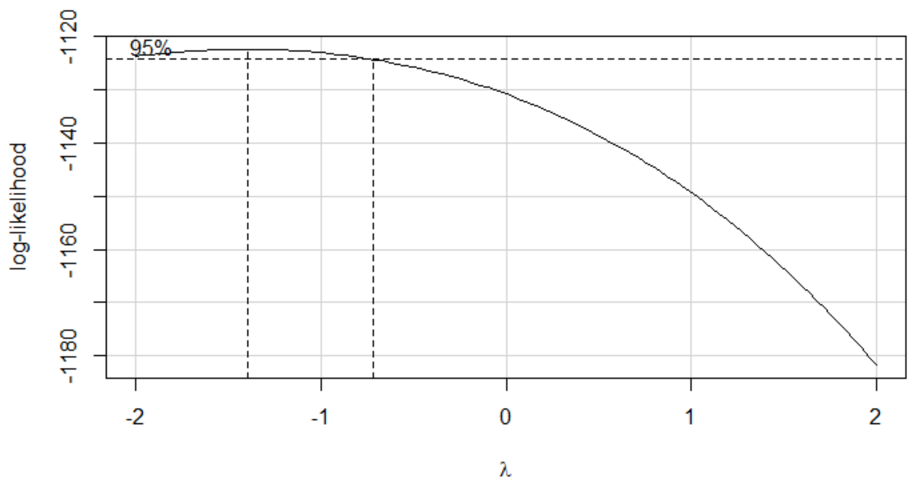


Inference: Variables *month* and *id* are almost identical: correlation coefficient = 0.99

Variables *sbp* and *dbp* are highly correlated: correlation coefficient = 0.75

Variables bmi and scl are not evenly distributed – crowded towards the left. Hence using inverse transformation.

Box Cox Transform of dependent variable *sbp*



Inference: Based on the plot, we select lambda = -1, and take inverse of variable *sbp*

Eliminating multicollinearity using VIF:

We calculate VIF value for each independent variable, based on a full regression model (i.e. model involving all available independent variables)

```
vif(linRegFullSBP)
      sex       dbp   scl_inv   chdfate  followup       age   bmi_inv     month        id 
 1.042867  1.258584  1.193355  1.295479  1.334374  1.251730  1.222040 61.268017 60.971757 
```

We find that variables month and id have very high VIF, hence we eliminate one of them – id

```
vif(linRegFullSBP)
     sex      dbp  scl_inv  chdfate followup      age  bmi_inv    month 
1.028791 1.249625 1.192292 1.265258 1.328000 1.251716 1.215426 1.041857 
```

Forward Stepwise Variable Selection:

We start with a ‘null’ regression model (output ~ 1), and use forward stepwise selection (based on AIC value).

```
Start:  AIC=-2672.4
X1.sbp ~ 1

           Df  Sum of Sq        RSS     AIC
+ dbp       1 1.6918e-04 0.00012075 -2844.7
+ age       1 4.4971e-05 0.00024496 -2703.9
+ bmi_inv   1 2.9537e-05 0.00026039 -2691.8
+ chdfate   1 2.3017e-05 0.00026691 -2686.9
+ scl_inv   1 2.1798e-05 0.00026813 -2685.9
+ followup  1 2.1006e-05 0.00026892 -2685.4
<none>                   0.00028993 -2672.4
+ month     1 2.4620e-06 0.00028747 -2672.1
+ id        1 1.6520e-06 0.00028828 -2671.5
+ sex       1 5.5900e-07 0.00028937 -2670.8

Step:  AIC=-2844.7
X1.sbp ~ dbp

           Df  Sum of Sq        RSS     AIC
+ age       1 1.5807e-05 0.00010495 -2870.6
+ chdfate   1 3.0492e-06 0.00011770 -2847.8
+ scl_inv   1 2.7441e-06 0.00011801 -2847.3
+ followup  1 2.0307e-06 0.00011872 -2846.1
<none>                   0.00012075 -2844.7
+ bmi_inv   1 6.7770e-07 0.00012008 -2843.8
+ month     1 3.6070e-07 0.00012039 -2843.3
+ sex       1 2.5460e-07 0.00012050 -2843.1
+ id        1 2.4670e-07 0.00012051 -2843.1

Step:  AIC=-2870.62
X1.sbp ~ dbp + age

           Df  Sum of Sq        RSS     AIC
+ chdfate   1 1.3767e-06 0.00010357 -2871.2
+ month     1 1.0958e-06 0.00010385 -2870.7
<none>                   0.00010495 -2870.6
+ id        1 8.8473e-07 0.00010406 -2870.3
+ scl_inv   1 5.1993e-07 0.00010443 -2869.6
+ sex       1 3.0894e-07 0.00010464 -2869.2
+ followup  1 4.1900e-08 0.00010490 -2868.7
+ bmi_inv   1 1.2640e-08 0.00010493 -2868.6

Step:  AIC=-2871.25
X1.sbp ~ dbp + age + chdfate

           Df  Sum of Sq        RSS     AIC
+ month     1 1.1788e-06 0.00010239 -2871.5
<none>                   0.00010357 -2871.2
+ id        1 9.1965e-07 0.00010265 -2871.0
+ sex       1 4.5820e-07 0.00010311 -2870.1
+ scl_inv   1 2.3211e-07 0.00010334 -2869.7
+ followup  1 2.4570e-08 0.00010354 -2869.3
+ bmi_inv   1 7.6000e-10 0.00010357 -2869.2

Step:  AIC=-2871.52
X1.sbp ~ dbp + age + chdfate + month

           Df  Sum of Sq        RSS     AIC
<none>                   0.00010239 -2871.5
+ id        1 8.0610e-07 0.00010158 -2871.1
+ sex       1 4.4451e-07 0.00010195 -2870.4
+ scl_inv   1 2.6444e-07 0.00010213 -2870.0
+ followup  1 9.8070e-08 0.00010229 -2869.7
+ bmi_inv   1 3.0000e-11 0.00010239 -2869.5

Call:
lm(formula = X1.sbp ~ dbp + age + chdfate + month, data = dfSBPData)

Coefficients:
(Intercept)          dbp          age      chdfate        month  
  1.473e-02   -6.572e-05   -3.429e-05   -1.902e-04    2.126e-05  
```

Final model:

sbp_inv ~ dbp + age + chdfate + month

All subsets variable selection:

We start with the ‘full’ regression model, and use all subsets variable selection.

Criteria: Mallow’s C_p

```
Subset selection object
Call: regsubsets.formula(X1.sbp ~ sex + dbp + scl + chdfate + followup + 
    age + bmi + month, data = dfSBPData, nbest = 10)
8 Variables  (and intercept)
         Forced in Forced out
sex          FALSE      FALSE
dbp          FALSE      FALSE
scl          FALSE      FALSE
chdfate      FALSE      FALSE
followup     FALSE      FALSE
age          FALSE      FALSE
bmi          FALSE      FALSE
month        FALSE      FALSE
10 subsets of each size up to 8
Selection Algorithm: exhaustive
          sex dbp scl chdfate followup age bmi month
1  ( 1 )  " " "*" " " " "     " "      " " " " " " "
1  ( 2 )  " " " " " " " "     " "      "*" " " " "
1  ( 3 )  " " " " " " " "     " "      " " "*" " "
1  ( 4 )  " " " " " " "*"     " "      " " " " " "
1  ( 5 )  " " " " " " " "     "*"      " " " " " "
1  ( 6 )  " " " " "*" " "     " "      " " " " " "
1  ( 7 )  " " " " " " " "     " "      " " " " "*"
1  ( 8 )  "*" " " " " " "     " "      " " " " " "
2  ( 1 )  " " "*" " " " "     " "      "*" " " " "
2  ( 2 )  " " "*" " " "*"     " "      " " " " " "
2  ( 3 )  " " "*" " " " "     "*"      " " " " " "
2  ( 4 )  " " "*" "*" " "     " "      " " " " " "
2  ( 5 )  " " "*" " " " "     " "      " " "*" " "
2  ( 6 )  " " "*" " " " "     " "      " " " " "*"
2  ( 7 )  "*" "*" " " " "     " "      " " " " " "
2  ( 8 )  " " " " " " " "     " "      "*" "*" " "
2  ( 9 )  " " " " " " "*"     " "      "*" " " " "
2  ( 10 ) " " " " "*" " "     " "      "*" " " " "
3  ( 1 )  " " "*" " " "*"     " "      "*" " " " "
3  ( 2 )  " " "*" " " " "     " "      "*" " " "*"
3  ( 3 )  "*" "*" " " " "     " "      "*" " " " "
3  ( 4 )  " " "*" "*" " "     " "      "*" " " " "
3  ( 5 )  " " "*" " " " "     "*"      "*" " " " "
3  ( 6 )  " " "*" " " " "     " "      "*" "*" " "
3  ( 7 )  " " "*" " " "*"     "*"      " " " " " "
3  ( 8 )  " " "*" "*" "*"     " "      " " " " " "
3  ( 9 )  " " "*" " " "*"     " "      " " " " "*"
3  ( 10 ) "*" "*" " " "*"     " "      " " " " " "
4  ( 1 )  " " "*" " " "*"     " "      "*" " " "*"
4  ( 2 )  "*" "*" " " "*"     " "      "*" " " " "
4  ( 3 )  " " "*" "*" "*"     " "      "*" " " " "
4  ( 4 )  " " "*" "*" " "     " "      "*" " " "*"
4  ( 5 )  " " "*" " " "*"     "*"      "*" " " " "
4  ( 6 )  "*" "*" " " " "     " "      "*" " " "*"
4  ( 7 )  " " "*" " " "*"     " "      "*" "*" " "
4  ( 8 )  " " "*" " " " "     " "      "*" "*" "*"
4  ( 9 )  " " "*" " " " "     "*"      "*" " " "*"
4  ( 10 ) "*" "*" "*" " "     " "      "*" " " " "
5  ( 1 )  "*" "*" " " "*"     " "      "*" " " "*"
5  ( 2 )  " " "*" " " "*"     "*"      "*" " " "*"
5  ( 3 )  " " "*" "*" "*"     " "      "*" " " "*"
5  ( 4 )  " " "*" " " "*"     " "      "*" "*" "*"
5  ( 5 )  "*" "*" "*" "*"     " "      "*" " " " "
5  ( 6 )  "*" "*" " " "*"     "*"      "*" " " " "
5  ( 7 )  "*" "*" " " "*"     " "      "*" "*" " "
5  ( 8 )  "*" "*" "*" " "     " "      "*" " " "*"
5  ( 9 )  " " "*" "*" "*"     "*"      "*" " " " "
5  ( 10 ) " " "*" "*" "*"     " "      "*" "*" " "
6  ( 1 )  "*" "*" " " "*"     "*"      "*" " " "*"
6  ( 2 )  "*" "*" "*" "*"     " "      "*" " " "*"
6  ( 3 )  "*" "*" " " "*"     " "      "*" "*" "*"
```

```
6  ( 4 )  " " "*" "*" "*"    "*"      "*" " " "*"
6  ( 5 )  " " "*" " " "*"    "*"      "*" "*" "*"
6  ( 6 )  " " "*" "*" "*"    " "      "*" "*" "*"
6  ( 7 )  "*" "*" "*" "*"    "*"      "*" " " " "
6  ( 8 )  "*" "*" "*" "*"    " "      "*" "*" " "
6  ( 9 )  "*" "*" " " "*"    "*"      "*" "*" " "
6  ( 10 ) "*" "*" "*" " "    " "      "*" "*" "*"
7  ( 1 )  "*" "*" "*" "*"    "*"      "*" " " "*"
7  ( 2 )  "*" "*" " " "*"    "*"      "*" "*" "*"
7  ( 3 )  "*" "*" "*" "*"    " "      "*" "*" "*"
7  ( 4 )  " " "*" "*" "*"    "*"      "*" "*" "*"
7  ( 5 )  "*" "*" "*" "*"    "*"      "*" "*" " "
7  ( 6 )  "*" "*" "*" " "    "*"      "*" "*" "*"
7  ( 7 )  "*" "*" "*" "*"    "*"      " " "*" "*"
7  ( 8 )  "*" " " "*" "*"    "*"      "*" "*" "*"
8  ( 1 )  "*" "*" "*" "*"    "*"      "*" "*" "*"
```

```
[1]  30.443125 262.335719 291.784542 303.322984 307.077927 314.409607 341.698211 345.251380
 [9]   2.932627  26.750270  28.651770  29.709875  31.105644  31.769773  31.967827 236.744818
[17] 240.407999 250.704721   2.362348   2.886762   4.355835   4.484827   4.854393   4.917190
[25]  27.238162  27.626258  27.871986  27.875341   2.161601   3.506902   4.280291   4.315312
[33]   4.316468   4.336998   4.351641   4.862286   4.876316   5.932746   3.331706   3.978503
[41]   4.027517   4.155719   5.449584   5.455222   5.501482   5.793662   6.223080   6.260792
[49]   5.138314   5.229669   5.329457   5.812300   5.973397   6.012582   7.387964   7.438721
[57]   7.450132   7.787414   7.007572   7.136563   7.221993   7.797472   9.377081   9.787386
[65]  32.445018 217.700972   9.000000
```

We find that the value of C_p is lowest for the model:

sbp_inv ~ dbp + age + chdfate

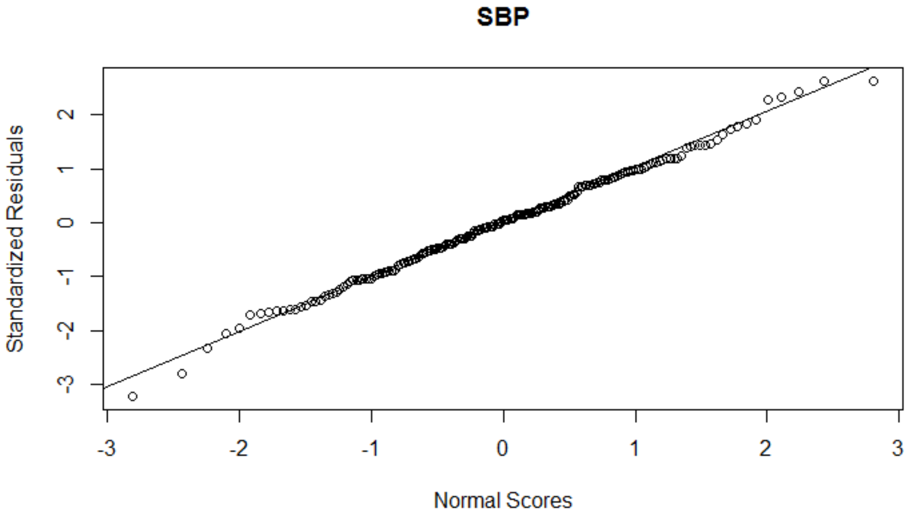
Final Regression Model:

sbp _inv ~ dbp + chdfate + age

```
Call:
lm(formula = X1.sbp ~ dbp + chdfate + age, data = dfSBPData)

Residuals:
       Min         1Q     Median         3Q        Max 
-2.307e-03 -4.794e-04  3.369e-05  5.120e-04  1.897e-03 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  1.486e-02  4.070e-04  36.512  < 2e-16 ***
dbp         -6.637e-05  4.266e-06 -15.559  < 2e-16 ***
chdfate     -1.846e-04  1.147e-04  -1.610    0.109    
age         -3.328e-05  6.451e-06  -5.159 6.09e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.0007288 on 195 degrees of freedom
Multiple R-squared:  0.6428, Adjusted R-squared:  0.6373 
F-statistic:   117 on 3 and 195 DF,  p-value: < 2.2e-16
```

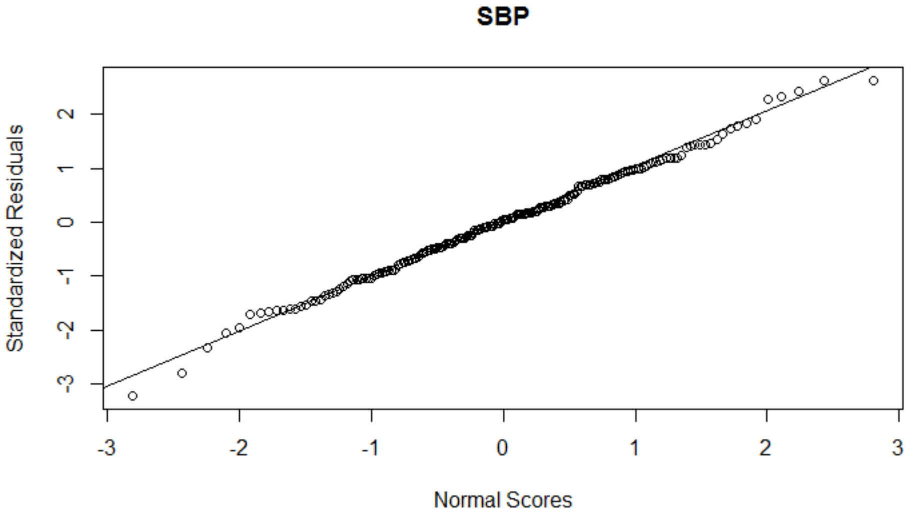
Diagnostics:

a. Normal Probability plot of Standardised Residuals:



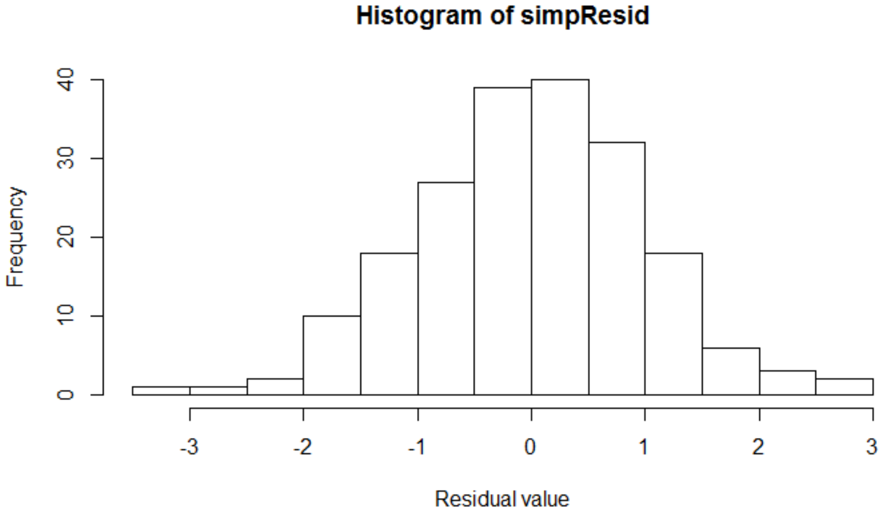
Inference: Standardised residuals approximate the normal distribution.

b. Standardised fitted values vs. residuals:



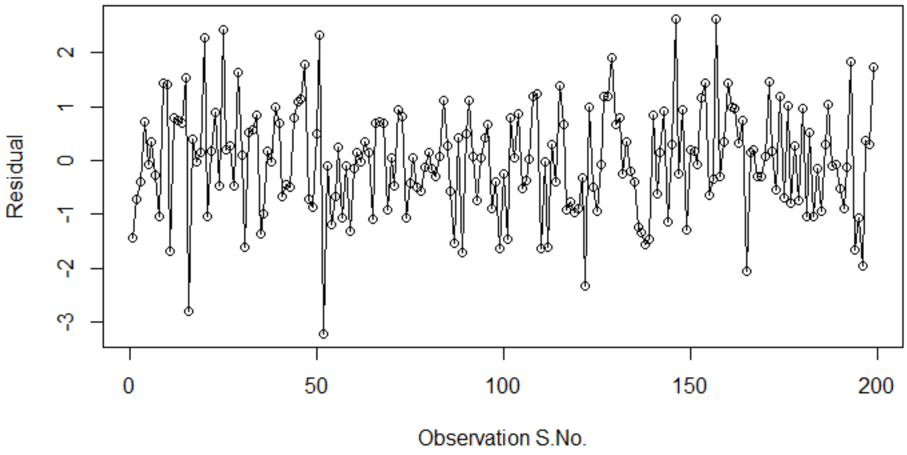
Inference: Residuals seem to be random w.r.t. Fitted Values

c. Histogram of residual values:



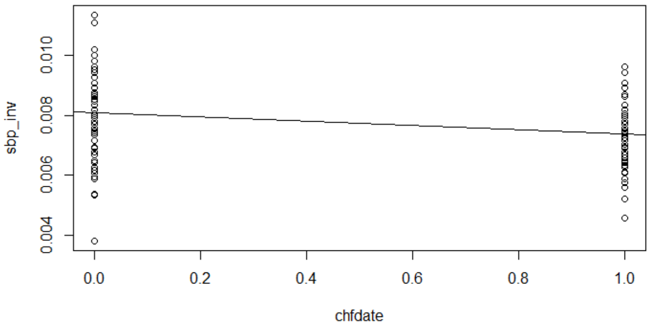
Inference: Residuals are approximately normally distributed, with mean = 0

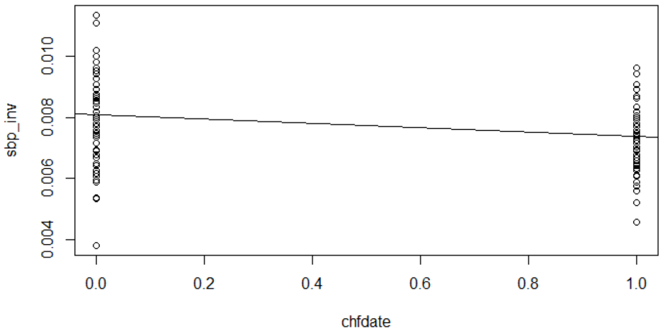
d. Observation sequence vs. residuals:

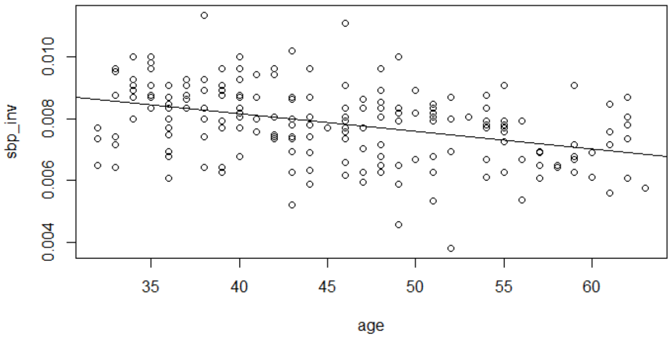


Inference: no trend seen

Plotting the regression line over the data – one independent variable at a time:







Comment: The regression lines seem to be well-balanced, with positive as well as negative residual values (points above as well as below)

Appendix

1. R code for Q2

CP2Q2.R

```
setwd("C:/Users/Kaustubh/Documents/Regression Models/CP2")
x1 <- c(-1, 1, -1, 1, -1.4142136, 1.4142136, 0, 0, 0, 0, 0)
x2 <- c(-1, -1, 1, 1, 0, 0, -1.4142136, 1.4142136, 0, 0, 0)
y <- c(81.3, 85.3, 83.1, 72.7, 82.9, 81.7, 84.7, 57.9, 82.9, 81.2, 82.4)
dfP2 <- data.frame(x1, x2, y)
polyRegModel <- lm(y ~ x1 + x2 + I(x1*x2) + I(x1*x1) + I(x2*x2), data = dfP2)
summary(polyRegModel)
#Calculate standardised residuals, and use in normal probability plot
polyResid <- rstandard(polyRegModel)
qqnorm(polyResid, ylab="Standardized Residuals", xlab="Normal Scores", main="MBT Synthesis")
qqline(polyResid)

# Standardised fitted values vs. residuals
plot(fitted.values(polyRegModel), polyResid, xlab = "Fitted Value", ylab = "Residual")

#histogram of residual values
hist(polyResid, breaks = seq(-3,3,0.5), xlab = "Residual value")

#Observation order vs. standardised residuals
plot(seq(1,11,1), polyResid, xlab = "Observation S.No.", ylab = "Residual", type = "o")
```

2. R code for Q3

CP2Q3.R

```
set.seed(54321)
#Generating random errors - normal with mean 0 and sd = 1
e <- rnorm(10, 0, 1)

#Generating vector of input values
x <- seq(1,10,1)

#Calculating Y by formula: Y = 2.5 – 1.8 x + e
Y <- vector(mode = "numeric", length = 10)
Y <- 2.5 - (1.8*x) - e

dfProb3 <- data.frame(x,e,Y)

#Fitting a simple regression model
simpRegModel <- lm(Y~x)
```

```
# examining the regression model

summary(simpRegModel)


#Calculate standardised residuals, and use in normal probability plot

simpResid <- rstandard(simpRegModel)


qqnorm(simpResid, ylab="Standardized Residuals", xlab="Normal Scores", main="Y = 2.5 – 1.8 x + e")

qqline(simpResid)


# Standardised fitted values vs. residuals


plot(fitted.values(simpRegModel), simpResid, xlab = "Fitted Value", ylab = "Residual")


#histogram of residual values

hist(simpResid, breaks = seq(-3,3,0.5), xlab = "Residual value")


#Observation order vs. standardised residuals

plot(seq(1,10,1), simpResid, xlab = "Observation S.No.", ylab = "Residual", type = "o")


#Plotting the regression line over the data

plot(x,Y)

abline(lm(Y ~ x))





##############################################

#Finding alternative sigma

##############################################


set.seed(54321)


#Generating random errors - normal with mean 0 and sd = 1

e <- rnorm(10, 0, 8)


#Generating vector of input values

x <- seq(1,10,1)


#Calculating Y by formula: Y = 2.5 – 1.8 x + e

Y <- vector(mode = "numeric", length = 10)

Y <- 2.5 - (1.8*x) - e


dfProb3b <- data.frame(x,e,Y)


#Fitting a simple regression model

simpRegModel <- lm(Y~x)


# examining the regression model
```

```
summary(simpRegModel)


#Calculate standardised residuals, and use in normal probability plot

simpResid <- rstandard(simpRegModel)


qqnorm(simpResid, ylab="Standardized Residuals", xlab="Normal Scores", main="Y = 2.5 – 1.8 x + e")

qqline(simpResid)


# Standardised fitted values vs. residuals


plot(fitted.values(simpRegModel), simpResid, xlab = "Fitted Value", ylab = "Residual")


#histogram of residual values

hist(simpResid, breaks = seq(-3,3,0.5), xlab = "Residual value")


#Observation order vs. standardised residuals

plot(seq(1,10,1), simpResid, xlab = "Observation S.No.", ylab = "Residual", type = "o")


#Plotting the regression line over the data

plot(x,Y)

abline(lm(Y ~ x))
```

3. R code for Q4

CP2Q4.R

```
#Reading the data set
dfSBPData <- read.csv("CP_Data_P4_052114.csv", header = TRUE)

head(dfSBPData)


# matrix scatter plot of all possible input variables
# source: https://www.r-bloggers.com/scatterplot-matrices-in-r/
# panel.smooth function is built in.
# panel.cor puts correlation in upper panels, size proportional to correlation
panel.cor <- function(x, y, digits=2, prefix="", cex.cor, ...)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- abs(cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  txt <- paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
  text(0.5, 0.5, txt, cex = cex.cor * r)
}

# Plot #2: same as above, but add loess smoother in lower and correlation in upper
pairs(~sbp+sex+dbp+scl+chdfate+followup+age+bmi+month+id, data=dfSBPData,
      lower.panel=panel.smooth, upper.panel=panel.cor,
      pch=20, main="SBP Scatterplot Matrix")

#Based on the scatter plot, scl and bmi data points are crowded together respectively, hence we transform scl (inverse)
dfSBPData$scl_inv <- (1/dfSBPData$scl)
dfSBPData$bmi_inv <- (1/dfSBPData$bmi)


#Box Cox transformation of the dependent variable sbp
install.packages("car")
library(car)
boxCox(dfSBPData$sbp~1)

#From the graph, we get lambda = -1
#therefore, transformed sbp = 1/sbp

# fit first model - all input variables included

linRegFullSBP <- lm(X1.sbp ~ sex + dbp + scl_inv + chdfate + followup + age + bmi_inv + month + id, data = dfSBPData)
vif(linRegFullSBP)
```

```
# Eliminate input variable id, since VIF for month and id are high (very high correlation)
linRegFullSBP <- lm(X1.sbp ~ sex + dbp + scl_inv + chdfate + followup + age + bmi_inv + month, data = dfSBPData)
vif(linRegFullSBP)

# Forward Stepwise variable selection:
linRegNullSBP <- lm(X1.sbp ~ 1, data = dfSBPData)
step(linRegNullSBP, scope=list(lower=linRegNullSBP, upper = linRegFullSBP), direction="forward", trace = 10)

#All subsets variable selection:
install.packages("leaps")
library(leaps)
leaps<-regsubsets(X1.sbp ~ sex + dbp + scl + chdfate + followup + age + bmi + month, data=dfSBPData, nbest=10)

summary(leaps)
summary(leaps)$cp

#Final model
linRegFinSBP <- lm(X1.sbp ~ dbp + chdfate + age , data = dfSBPData)

summary(linRegFinSBP)


#Diagnostics

#Calculate standardised residuals, and use in normal probability plot
simpResid <- rstandard(linRegFinSBP)

qqnorm(simpResid, ylab="Standardized Residuals", xlab="Normal Scores", main="SBP")
qqline(simpResid)

# Standardised fitted values vs. residuals

plot(fitted.values(linRegFinSBP), simpResid, xlab = "Fitted Value", ylab = "Residual")

#histogram of residual values
hist(simpResid, xlab = "Residual value")

#Observation order vs. standardised residuals
plot(seq(1,199,1), simpResid, xlab = "Observation S.No.", ylab = "Residual", type = "o")

#Plotting the regression line over the data
plot(dfSBPData$chdfate,dfSBPData$X1.sbp, xlab = "chfdate", ylab = "sbp_inv")
abline(lm(dfSBPData$X1.sbp ~ dfSBPData$chdfate))

plot(dfSBPData$dbp,dfSBPData$X1.sbp, xlab = "dbp", ylab = "sbp_inv")
abline(lm(dfSBPData$X1.sbp ~ dfSBPData$dbp))


plot(dfSBPData$age,dfSBPData$X1.sbp, xlab = "age", ylab = "sbp_inv")
abline(lm(dfSBPData$X1.sbp ~ dfSBPData$age))
```