STAT S 670 - Exploratory Data Analysis - Finals

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Solutions

1. Five R's of EDA

   - Resistance : The ability of the statistic/method to have minimum influence from an "Outlier" and remain faithful to the main body of the data points
   - Residuals : Examining Residuals to describe the quality of the fit, if required so using residuals as iterative parameters to update the fit.
   - Reexpression : Using Linear methods of Data Transformation to fit the data to $y = model + Residuals$ so that we might be able to analyse models that deviate from gaussian model
   - Revelation : Using Exploratory tools like Scatter Plots, Histograms, Residual vs Fit plots for data visualization, outlier detection and model conformance cheching.
   - Re-iteration : Iterative data fitting, can be best seen in resistant methods like Resistant Regression and Median polish where Residuals/Row-Column effects are calculated iteratively and consumed in the successive fits.

2. Five Number Summary : Five number summary gives an overall description of the data described by parameters

   - Sample Minimum
   - First Quantile
   - Median
   - Third Quantile
   - Sample Maximum

```
#Generate 10 random numbers with mean 7 and sd 1
set.seed(1)
population <- rnorm(10,7,1)

#display population
print (population)
```

```
##  [1] 6.373546 7.183643 6.164371 8.595281 7.329508 6.179532 7.487429
##  [8] 7.738325 7.575781 6.694612
```

```
#display 5 number summary
fivenum(population)
```

```
## [1] 6.164371 6.373546 7.256576 7.575781 8.595281
```

```
summary(population)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   6.164   6.454   7.257   7.132   7.554   8.595
```

3. Goals for Re-Expressing Data

- Finding a suitable scale for data representation, Eg: Logrithmic, Square root etc for dimplyfying data analyis
- Finding an transformation which promotes symmetry and transforms the data to a known distribution like Gaussian
- Transforms data for straightness, spread etc to emphasis the straightness of an relationship
- Convert complex multiplicative models to simple additive models with reduced complexity, Eg log transform converts a model say $y = ab$ to $\log y = \log a + \log b$
- Changing the scale of measurement to comply with the nature of the data

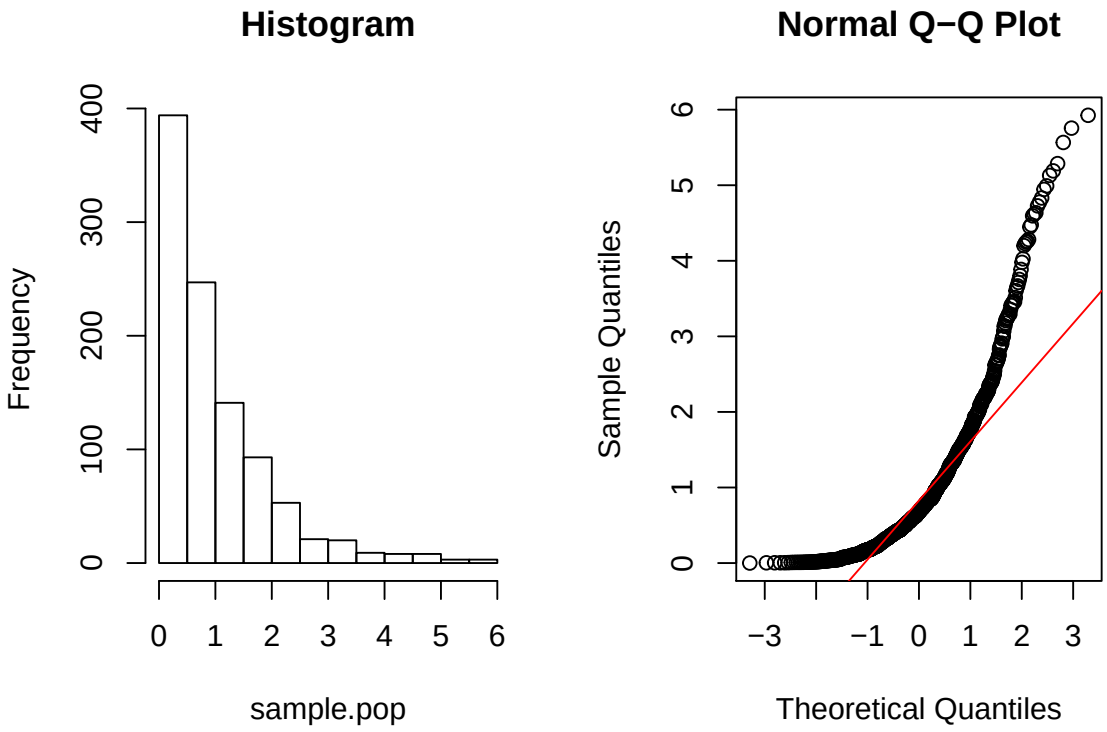
4. Detecting Long-Tailness

   - Long Tailness can be detected using visual methods like Histograms or q-q Plots.

```r
set.seed(123)

#Generate a tailed distribution
sample.pop<-rgamma(1000,shape=1)
par(mfrow=c(1,1),mfcol=c(1,2))

#Plot Histograms and q-q plots
hist(sample.pop,main="Histogram")
qqnorm(sample.pop)
qqline(sample.pop,col="red")
```

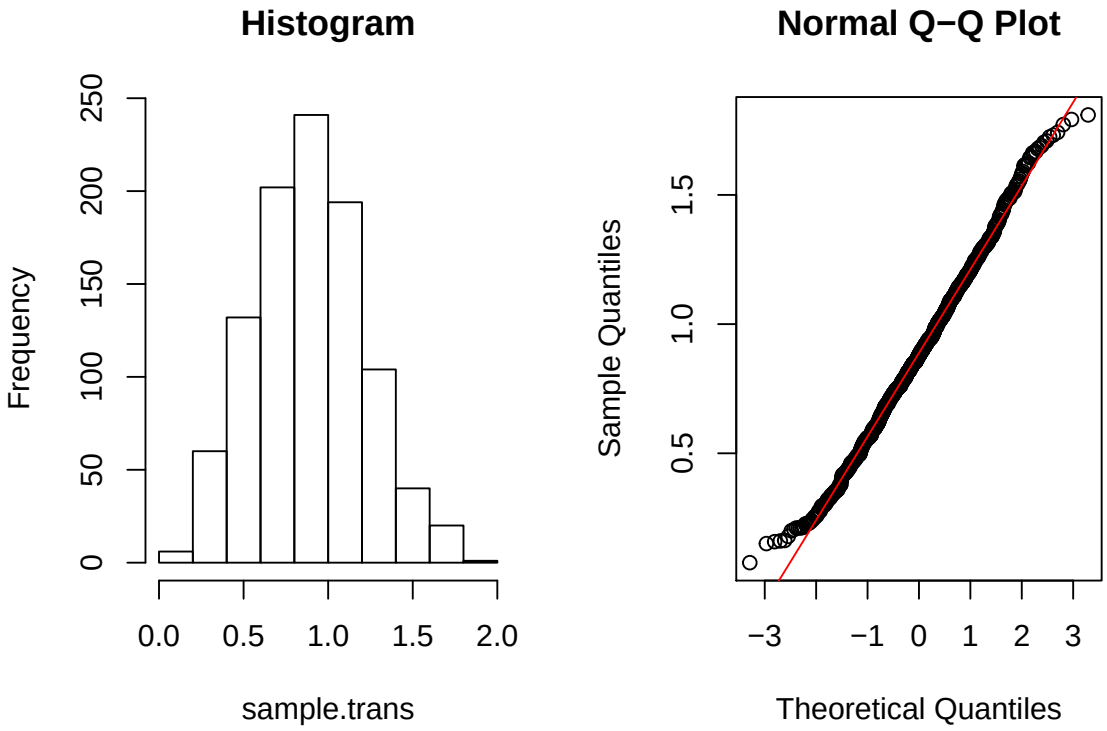


- In the above example it can be seen that the distribution has heavy left tails, and this can be visually seen in both Histogtam and q-q plots.
- Inorder to transform such data, few methods are Tukey's Power Transform, Transform for Symmetry and Transform for Straightness.

- Tukey's power transform involves finding suitable power function to either "Pull In" or "Push out" the data points. example, for the above said distribution, we would need to pull in data, and according to Tukey's Power Transformation a cube root transform would be necessary.

```
# Do a Cube Root Transform
sample.trans<-sample.pop^(1/3)
par(mfrow=c(1,1),mfcol=c(1,2))

#Plot the tail detection visualizations
hist(sample.trans,main="Histogram")
qqnorm(sample.trans)
qqline(sample.trans,col="red")
```



- Other Methods like transforming for straightness and Spread involves plotting an letter value plot and using their fourth spread and midsummaries to calculate required parameters for data transformation.

5. g-h estimates
   From the Theory of G and H estimates,

   - g = 0 indicates no skewness, g $\leq$ 0.25 = Slight Skewness, g ~ 1 implies highly skewed
   - h = 0, No long tails, h $\geq$ 0 then increasingly longer tails

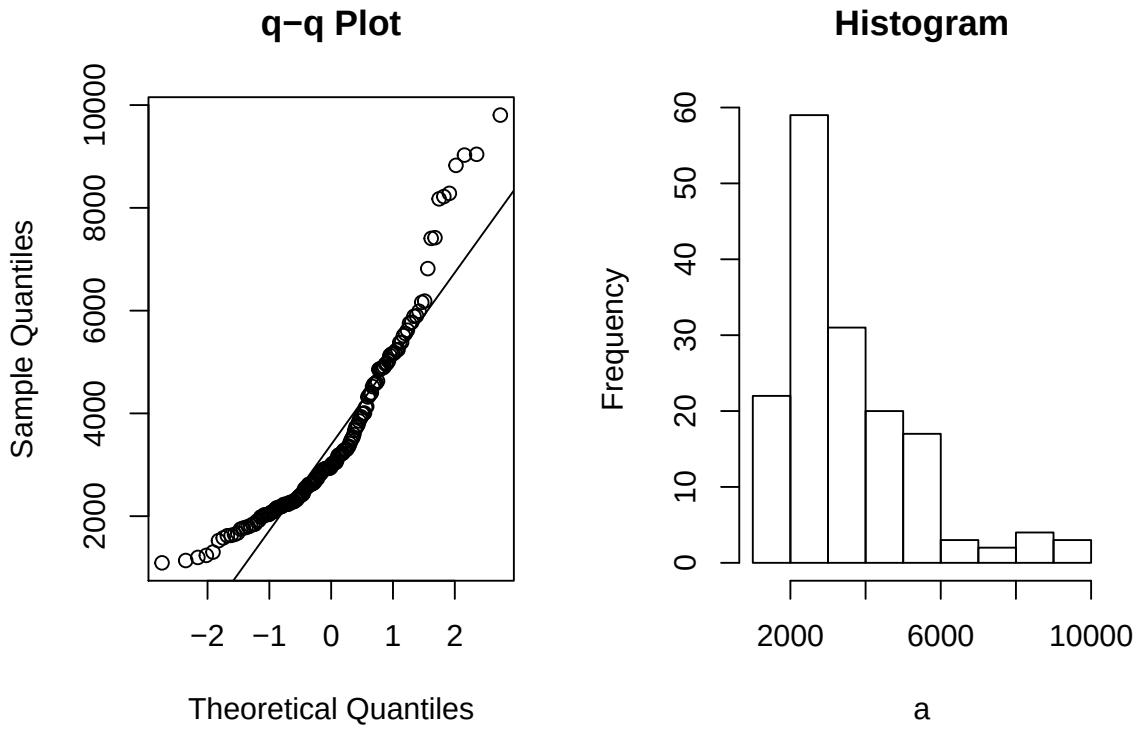
   Given that the given gh estimates,

   - (-0.5,0.3) has negative skewness and has light tails
   - (0.5,0.3) has positive skewness and light tails
   - (1,0.6) has high positive skewness and heavy tails

6.

a) q-q Plot

```
a=c(1092,1137,1197,1237,1301,1523,1577,1619,1626,1644,1672,1748,1768,1780,1796,1816,1843,1844,1902,
# Plot QQ Plot
par(mfrow=c(1,2))
qqnorm(a,main="q-q Plot")
# Plot QQ Line
qqline(a)
#Histogram
hist(a,main="Histogram")
```



By interpeting both Q-Q Plot and the Histogram, it is evident that the distribution of the given populaion has light left tail and an heavy right tail. This is also evident in the histogram.

b)

```
source("lvalprogs.r")
source("rrline.r")
ll<-lval(a)
print(ll)
```

```
##   Depth  Lower  Upper    Mid Spread pseudo-s
## M  81.0 2961.0 2961.0 2961.0      0    0.000
## F  41.0 2265.0 4522.0 3393.5   2257 1673.117
## E  21.0 1983.0 5383.0 3683.0   3400 1477.812
```

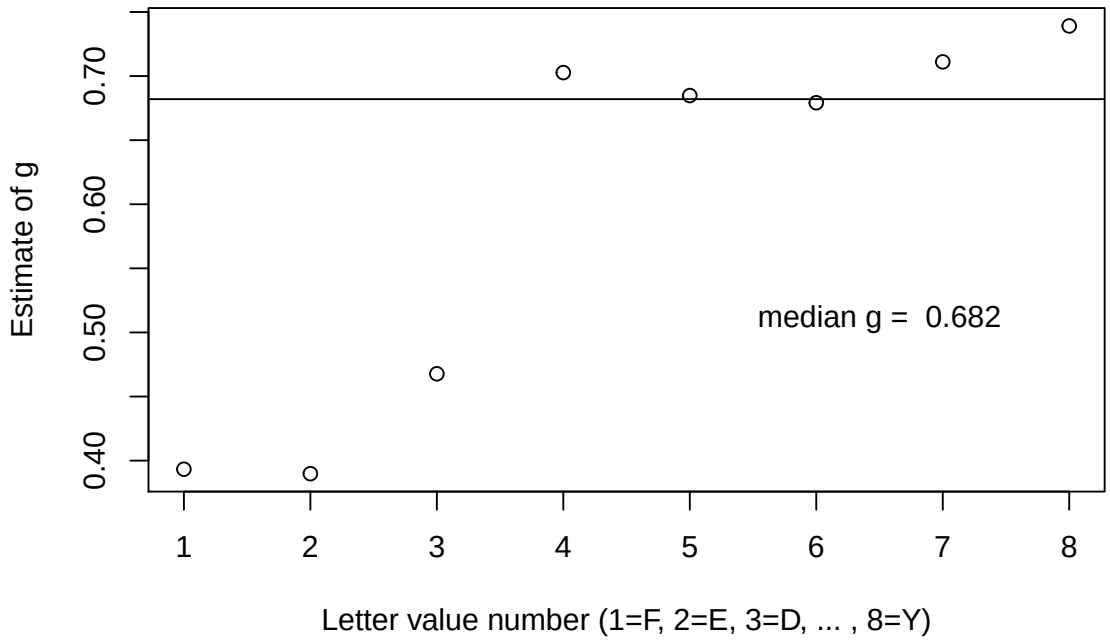
```
## D  11.0 1672.0 6185.0 3928.5   4513 1470.875
## C   6.0 1523.0 8220.0 4871.5   6697 1797.629
## B   3.5 1217.0 8927.0 5072.0   7710 1789.798
## A   2.0 1137.0 9042.0 5089.5   7905 1634.914
## Z   1.5 1114.5 9423.5 5269.0   8309 1561.803
## Y   1.0 1092.0 9805.0 5448.5   8713 1509.720
```

There are 9 Levels, Hence the probability of expected quantile is $\frac{1}{2^9}$

```
pp1 <- 1/2^(1:nrow(ll)-1)
gau1 <- abs(qnorm(pp1))
pp2 <- abs((pp1-1/3)/(nrow(ll)-1 + 1/3))
gau2 <- abs(qnorm(abs(pp2)))
est2.g <- log((ll[,3] - ll[1,2])/(ll[1,2]-ll[,2]))/gau2
print(round(cbind(pp1,pp2,gau1,gau2,est2.g),5))
```

```
##       pp1     pp2    gau1    gau2  est2.g
## M 1.00000 0.08000     Inf 1.40507     NaN
## F 0.50000 0.02000 0.00000 2.05375 0.39330
## E 0.25000 0.01000 0.67449 2.32635 0.38981
## D 0.12500 0.02500 1.15035 1.95996 0.46774
## C 0.06250 0.03250 1.53412 1.84526 0.70271
## B 0.03125 0.03625 1.86273 1.79597 0.68481
## A 0.01562 0.03812 2.15387 1.77287 0.67920
## Z 0.00781 0.03906 2.41756 1.76167 0.71110
## Y 0.00391 0.03953 2.66007 1.75615 0.73910
```

```
#Plot L-Val Values Vs the G estimate
plot(1:8, est2.g[-1],
xlab = "Letter value number (1=F, 2=E, 3=D, ... , 8=Y)",
ylab = "Estimate of g")
abline(h=median(est2.g[-1]))
text(6.5,0.51,paste("median g = ",format(round(median(est2.g[-1]),3))))
```



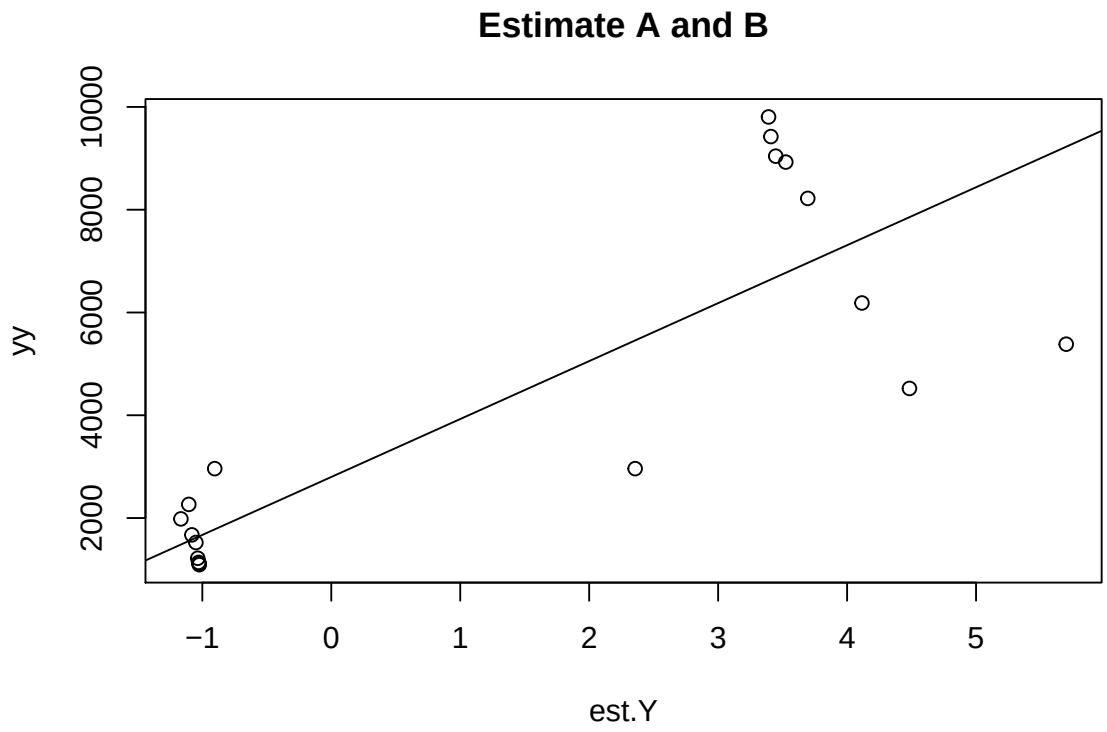

```
# Estimation of g
est.g <- median(est2.g[-1])
print(est.g)
```

```
## [1] 0.6820059
```

```
#Estimation of A and B
zp <- c(rev(qnorm(pp2)),abs(qnorm(pp2)))
yy <- c(rev(ll[,2]),ll[,3])
est.Y <- (exp(est.g*zp)-1)/est.g
#print(cbind(est.Y,yy))
plot(est.Y,yy,main="Estimate A and B")
rr <- run.rrline(est.Y,yy)
```

```
##          a        b |res|
## 1 2798.903 1127.665 27227
## 2    0.000    0.000 27227
## 3    0.000    0.000 27227
## 4    0.000    0.000 27227
## 5    0.000    0.000 27227
##   2798.903 1127.665 27227
```

```
abline(rr$a, rr$b)
```




```
print(paste("A Estimate ",rr$a," B Estimate ",rr$b))
```

```
## [1] "A Estimate  2798.90299991372  B Estimate  1127.6651769943"
```

The G Estimates are as follows, g= 0.68, A= 2796, B=1127.

c) Bootstrap Estimates

```
library(ggplot2)
library(GGally)
g.dist.estimates<-function(sample.pop){
source("lvalprogs.r")
source("rrline.r")
ll<-lval(sample.pop)
pp1 <- 1/2^(1:nrow(ll)-1)
gau1 <- abs(qnorm(pp1))
pp2 <- abs((pp1-1/3)/(nrow(ll)-1 + 1/3))
gau2 <- abs(qnorm(abs(pp2)))
est2.g <- log((ll[,3] - ll[1,2])/(ll[1,2]-ll[,2]))/gau2

# Estimation of g
est.g <- median(est2.g[-1])
p <- c(0.005, 0.01, 0.025, 0.05, 0.1, 0.25, 0.5, 0.75, 0.9, 0.95, 0.975, 0.99, 0.995)
zp <- qnorm(p)
est.Y <- (exp(est.g*zp)-1)/est.g
rr <- run.rrline(est.Y,quantile(sample.pop,p))
#Run Resistant Regression for A and B Estimates
```

```
  return (list(g=est.g,A=rr$a,B=rr$b))
}


bootstrap.g<-function(pops,sims){
  g.est <- c()
  A.est <- c()
  B.est <- c()
  for (i in 1:sims){
boot.sample<-sample(pops,length(pops),replace = TRUE)
r.val <- g.dist.estimates(boot.sample)
g.est[i]<-r.val$g
A.est[i]<-r.val$A
B.est[i]<-r.val$B
  }
  best.g <- mean(g.est)
  g.lower <- best.g - qt(0.95,df=length(g.est)-1)*sd(g.est)
  g.upper <- best.g + qt(0.95,df=length(g.est)-1)*sd(g.est)
  best.A <- mean(A.est)
  A.lower <- best.A - qt(0.95,df=length(A.est)-1)*sd(A.est)
  A.upper <- best.A + qt(0.95,df=length(A.est)-1)*sd(A.est)
  best.B <- mean(B.est)
  B.lower <- best.B - qt(0.95,df=length(B.est)-1)*sd(B.est)
  B.upper <- best.B + qt(0.95,df=length(B.est)-1)*sd(B.est)
  cor.est <- cor (cbind(g.est,A.est,B.est))
  es.plt <- ggpairs(as.data.frame(cbind(g.est,A.est,B.est)))
  return(list(g=best.g,a=best.A,b=best.B,g.lower,g.upper,A.lower,A.upper,B.lower,B.upper,cor.est,es
}



a<-c(1092,1137,1197,1237,1301,1523,1577,1619,1626,1644,1672,1748,1768,1780,1796,1816,1843,1844,1902
bs.val <- bootstrap.g(a,1000)
```

```
print(paste("The g Estimate is ", bs.val[1]))
```

```
## [1] "The g Estimate is  0.641669506755099"
```

```
print(paste(" and Confidence interval is between", bs.val[4],
    " and ", bs.val[5]))
```

```
## [1] " and Confidence interval is between 0.521871831174727  and  0.761467182335472"
```

```
print(paste("The A Estimate is ", bs.val[2]))
```

```
## [1] "The A Estimate is  2913.49184610751"
```

```
print(paste(" and Confidence interval is between", bs.val[6],
    " and ", bs.val[7]))
```

```
## [1] " and Confidence interval is between 2719.53477970354  and  3107.44891251147"
```

```
print(paste("The B Estimate is ", bs.val[3]))
```

```
## [1] "The B Estimate is  1232.00294638049"
```

```
print(paste(" and Confidence interval is between", bs.val[8],
    " and ", bs.val[9]))
```

```
## [1] " and Confidence interval is between 1086.31037266022  and  1377.69552010075"
```

- Correlation Matrix :

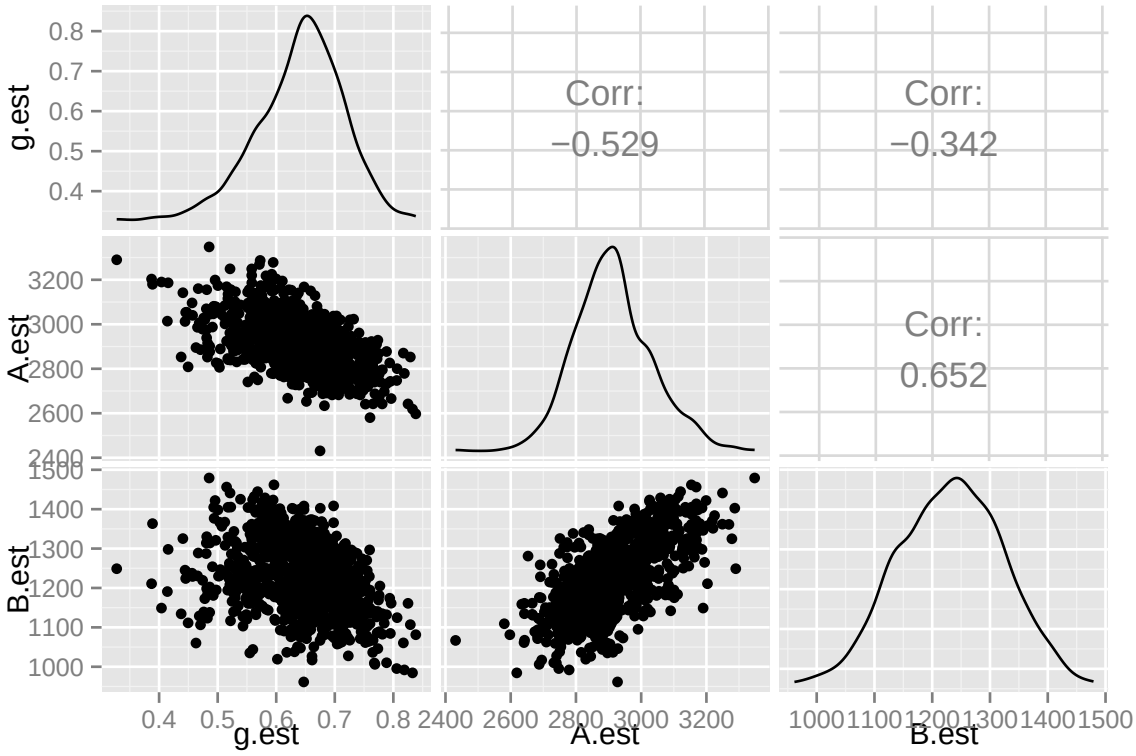
```
print(bs.val[10])
```

```
## [[1]]
##             g.est      A.est      B.est
## g.est  1.0000000 -0.5292720 -0.3418948
## A.est -0.5292720  1.0000000  0.6518705
## B.est -0.3418948  0.6518705  1.0000000
```

- Pairs Plot:

```
print(bs.val[11])
```

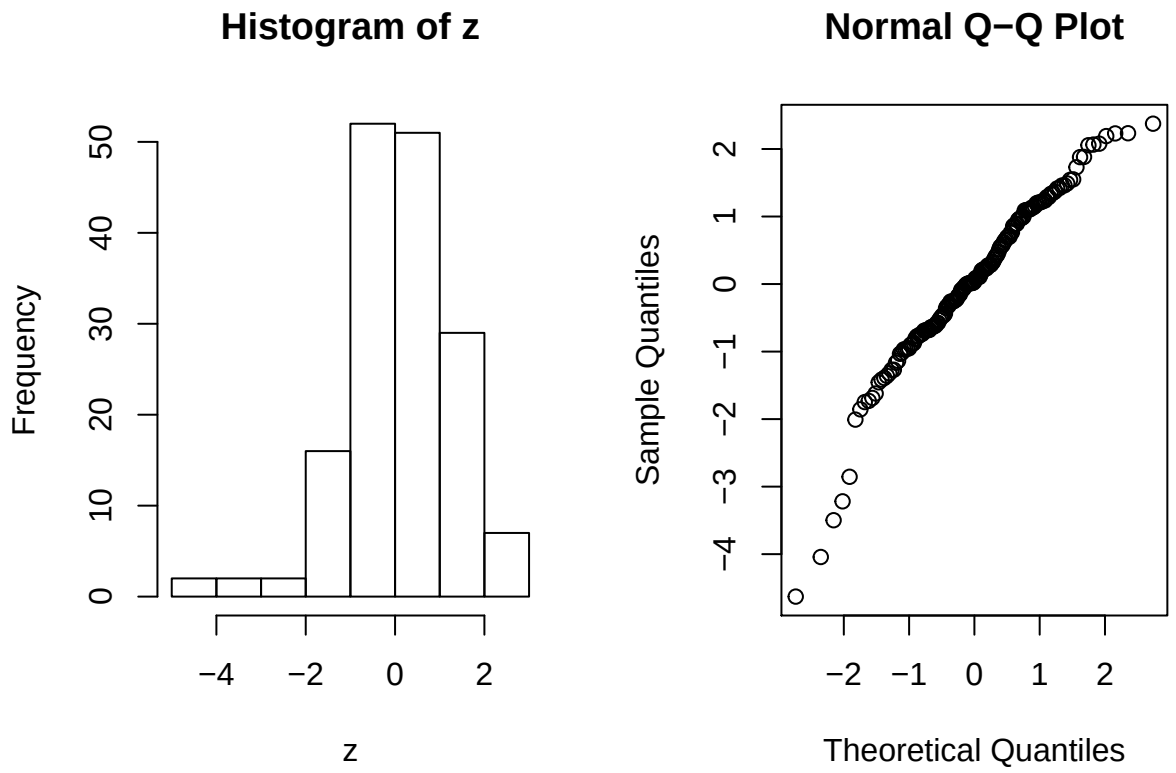
```
## [[1]]
```



D) Transforming back to Normalcy :

Given the values, transforming this to normalcy.

```
g<-bs.val$g
A<-bs.val$a
B<-bs.val$b
z<- 1/g*log(((a-A)*g)/B +1)
par(mfrow=c(1,2))
hist(z)
qqnorm(z)
```



Once transformed, both the tails are now less affected and is near to the normal distribution. However, there is still skewness in the left tail.

E) GoF Tests + Pearson's Test

```
  gof.pearson=function (x,nbins) {
n = length(x)
m = floor(n/nbins)
k = n - m*nbins # This is the remainder
xx=sort(x)
index = rep(1:nbins,m)
if(k >0){ d=sample(1:nbins,k,replace=FALSE);
index=c(index,d) }
bincount=as.numeric(table(index))
binindicies = cumsum(bincount)
```

```
    binbreaks = rev(rev(xx[binindicies])[-1])
    binbreaks = c(-Inf,binbreaks,Inf)
    bins=cut(x,breaks=binbreaks)
    internalbreaks = rev(rev(xx[binindicies])[-1])
    p = pnorm(internalbreaks,mean(x),sd(x))
    p = c(p[1],diff(p),1-pnorm(max(internalbreaks),mean(x),sd(x)))
    exp = n*p
    df = data.frame(bin=levels(bins),bincount=bincount,prob=p,expectedcount=exp)
    chisqstat = sum((bincount - exp)^2/exp)
    pval = 1- pchisq(chisqstat,nbins-1)
    output = list(df=df,chisq=chisqstat,pval=pval)
    output = list(df=df,chisq=chisqstat,pval=pval)
    }
    out.p<-gof.pearson(z,2*sqrt(length(z))) #usinf Velleman rule
    out.p
```

```
## $df
##                bin bincount       prob expectedcount
## 1     (-Inf,-2.01]        6 0.04068310      6.549979
## 2    (-2.01,-1.41]        7 0.06676198     10.748678
## 3    (-1.41,-1.14]        7 0.05004384      8.057058
## 4   (-1.14,-0.899]        7 0.05360335      8.630139
## 5   (-0.899,-0.75]        6 0.03826684      6.160961
## 6   (-0.75,-0.681]        6 0.01903148      3.064068
## 7  (-0.681,-0.613]        6 0.01922849      3.095786
## 8  (-0.613,-0.462]        6 0.04520750      7.278407
## 9   (-0.462,-0.26]        7 0.06411529     10.322562
## 10  (-0.26,-0.179]        7 0.02680290      4.315267
## 11 (-0.179,-0.044]        6 0.04527012      7.288489
## 12 (-0.044,0.0141]        7 0.01965413      3.164315
## 13  (0.0141,0.102]        6 0.02987868      4.810468
## 14   (0.102,0.216]        6 0.03823414      6.155697
## 15    (0.216,0.28]        6 0.02146109      3.455235
## 16    (0.28,0.417]        6 0.04479630      7.212205
## 17   (0.417,0.621]        7 0.06365008     10.247663
## 18   (0.621,0.759]        6 0.04010828      6.457433
## 19   (0.759,0.948]        6 0.05072748      8.167125
## 20    (0.948,1.09]        6 0.03506716      5.645812
## 21     (1.09,1.15]        6 0.01345869      2.166850
## 22     (1.15,1.24]        6 0.01752753      2.821932
## 23     (1.24,1.42]        7 0.03445175      5.546732
## 24     (1.42,1.73]        6 0.04507174      7.256550
## 25     (1.73, Inf]        6 0.07689808     12.380590
##
## $chisq
## [1] 33.46522
##
## $pval
## [1] 0.1036767
```

- ECDF Based

```r
library("goftest")
#Kolmogorov Test
ks.test(z,"pnorm")
```

```
## Warning in ks.test(z, "pnorm"): ties should not be present for the
## Kolmogorov-Smirnov test
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  z
## D = 0.08551, p-value = 0.1897
## alternative hypothesis: two-sided
```

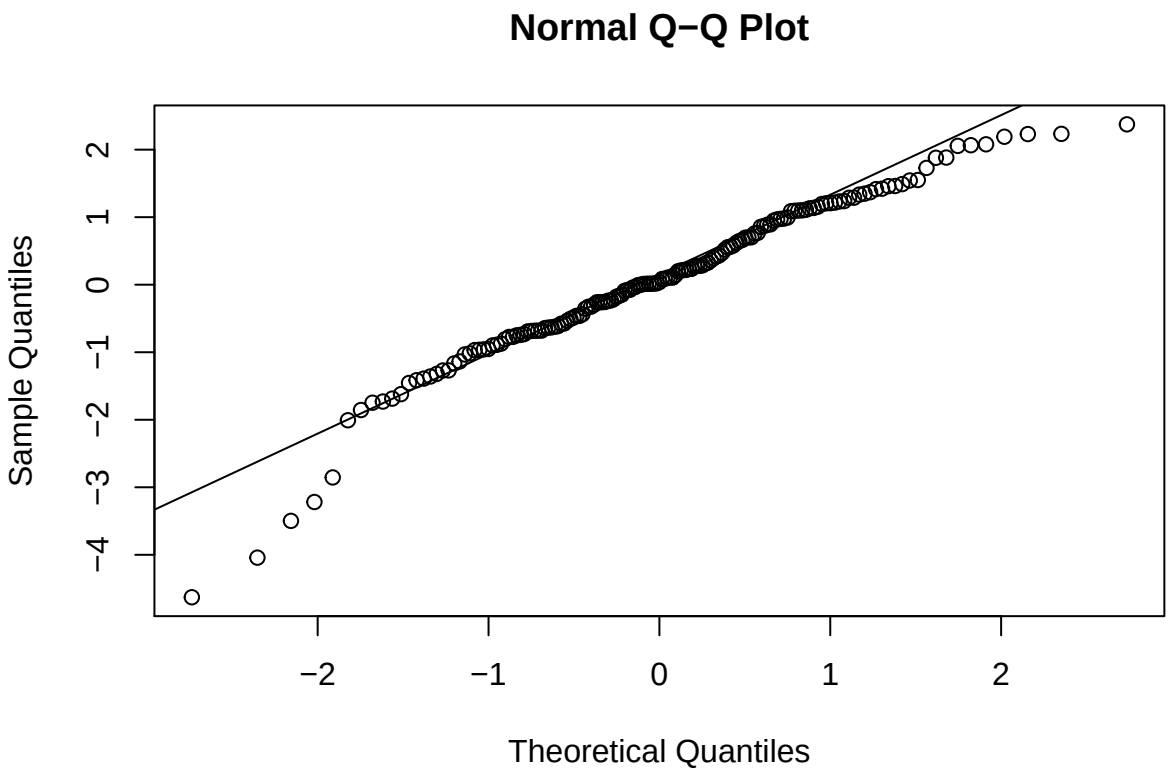
```r
#Anderson-Darling Test
ad.test(z,"pnorm")
```

```
##
##  Anderson-Darling test of goodness-of-fit
##  Null hypothesis: Normal distribution
##
## data:  z
## An = 1.7337, p-value = 0.1294
```

```r
#Cramer-von-Mises Test
cvm.test(z,"pnorm")
```

```
##
##  Cramer-von Mises test of goodness-of-fit
##  Null hypothesis: Normal distribution
##
## data:  z
## omega2 = 0.20164, p-value = 0.2645
```

```r
#Correlation of the QQ Data test
qqnorm(z)
qqline(z)
```



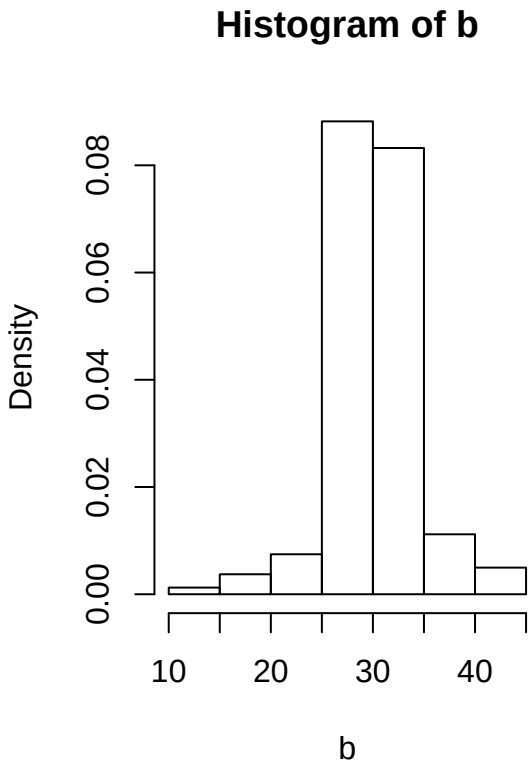

```
#Shapiro Wilk's Test
shapiro.test(z)
```

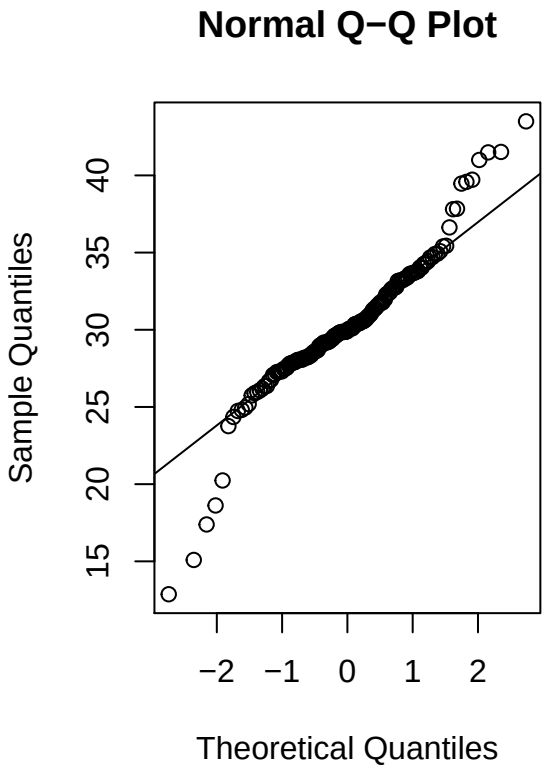
```
##
##  Shapiro-Wilk normality test
##
## data:  z
## W = 0.95878, p-value = 0.0001055
```

- Inferences : Wilks Test : p-values suggest that the distribution is normal.
- P values from ECDF Tests doesn't suggest that much normality as the shapiro-wilks Test.
- Pearson Gof: On a smaller sample size, Pearson GoF Tests doesn't perform quite well. This can be identified from the test results and the p-value.
- q-q Plot: Easiest of the above GoFs, visual way of interpreting normality. Can be seen that the has slight lower tails, however the data seems more normal than it was without transformation.

7) H- Distribution

```
b =c(12.87,15.09,17.39,18.62,20.24,23.76,24.35, 24.74,24.81,24.96,25.19,25.75,25.89,25.97, 26.07,26.19,
par(mfrow=c(1,2))
hist(b,prob=TRUE)
qqnorm(b)
qqline(b)
```

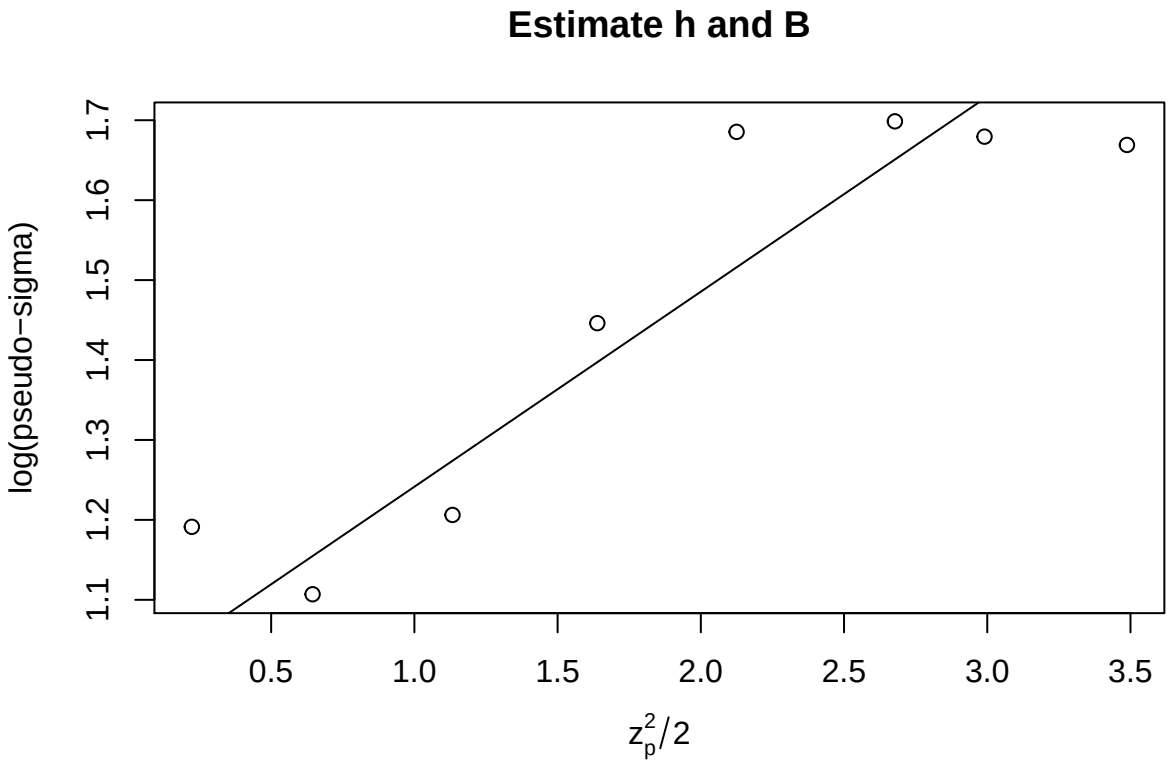




From the interpretation of the q-q plot, it is clear that the distribution has tails.

- Normal Estimates for A, B and h

```
est.h<-function(b){
  source("lvalprogs.r")
  source("rrline.r")
  ll <- lval(b)
  n<-length(b)
  gh2.data <- b
  ll.gh2 <- lval(gh2.data)
  yy.gh2 <- log(ll.gh2[-1,6])
  xx.gh2 <- (qnorm((ll.gh2[-1,1] - 1/3)/(161 + 1/3)))^2/2
  plot(xx.gh2,yy.gh2,main="Estimate h and B",
    ylab="log(pseudo-sigma)", xlab=expression(z[p]^2/2))
  rr <- run.rrline(xx.gh2,yy.gh2)
   abline(rr$a, rr$b)
  return(list(h=rr$b,A=median(b),B=exp(rr$a)))
}
normal.h<-est.h(b)
```




```
##          a       b   |res|
## 1  1.08115 0.20809 0.69095
## 2 -0.08373 0.03595 0.74816
## 3  0.00000 0.00000 0.74816
## 4  0.00000 0.00000 0.74816
## 5  0.00000 0.00000 0.74816
##    0.99741 0.24404 0.74816
```

```
print (paste("H estimate is",normal.h$h))
```

```
## [1] "H estimate is 0.24404266941269"
```

```
print (paste("A estimate is",normal.h$A))
```

```
## [1] "A estimate is 29.92"
```

```
print (paste("B estimate is",normal.h$B))
```

```
## [1] "B estimate is 2.71126231385263"
```

```
est.h<-function(b){
  source("lvalprogs.r")
  source("rrline.r")
```

```
  ll <- lval(b)
  n<-length(b)
  gh2.data <- b
  ll.gh2 <- lval(gh2.data)
  yy.gh2 <- log(ll.gh2[-1,6])
  xx.gh2 <- (qnorm((ll.gh2[-1,1] - 1/3)/(161 + 1/3)))^2/2
  #plot(xx.gh2,yy.gh2,main="Estimate h and B",
   #  ylab="log(pseudo-sigma)", xlab=expression(z[p]^2/2))
  rr <- run.rrline(xx.gh2,yy.gh2)

  return(list(h=rr$b,A=median(b),B=exp(rr$a)))
}

bootstrap.h<-function(pop,sims){
  library(GGally)
  est.h <-c()
  est.A <-c()
  est.B <-c()
  for (i in 1:sims){
    b<-sample(pop,length(pop),replace = TRUE)
    b.sample <- est.h(b)
    est.h[i]<- b.sample$h
    est.A[i]<- b.sample$A
    est.B[i]<- b.sample$B
  }
  best.h <- mean(est.h)
  g.lower <- best.h - qt(0.95,df=length(est.h)-1)*sd(est.h)
  g.upper <- best.h + qt(0.95,df=length(est.h)-1)*sd(est.h)
  best.A <- mean(est.A)
  A.lower <- best.A - qt(0.95,df=length(est.A)-1)*sd(est.A)
  A.upper <- best.A + qt(0.95,df=length(est.A)-1)*sd(est.A)
  best.B <- mean(est.B)
  B.lower <- best.B - qt(0.95,df=length(est.B)-1)*sd(est.B)
  B.upper <- best.B + qt(0.95,df=length(est.B)-1)*sd(est.B)
  cor.est <- cor (cbind(est.h,est.A,est.B))
  es.plt <- ggpairs(as.data.frame(cbind(est.h,est.A,est.B)))
  return(list(h=best.h,A=best.A,B=best.B,gcil=g.lower,gciu=g.upper,Acil=A.lower,Aciu=A.upper,bcil=B.lowe
}
s <- bootstrap.h(b,1000)
```

- Estimates for A, B and H and Their 90 % Confidence Intervals

```
print(paste("The H estimate is ",s$h))
```

```
## [1] "The H estimate is  0.192731211674053"
```

```
print(paste("C.I is between",s$gcil," and ",s$gciu))
```

```
## [1] "C.I is between 0.106892537807329  and  0.278569885540777"
```

```r
print(paste("The A estimate is ",s$A))
```

```
## [1] "The A estimate is  29.99515"
```

```r
print(paste("C.I is between",s$Acil," and ",s$Aciu))
```

```
## [1] "C.I is between 29.6154082490898  and  30.3748917509102"
```

```r
print(paste("The B estimate is ",s$B))
```

```
## [1] "The B estimate is  2.94842740518267"
```

```r
print(paste("C.I is between",s$bcil," and ",s$bciu))
```

```
## [1] "C.I is between 2.32254814641151  and  3.57430666395383"
```

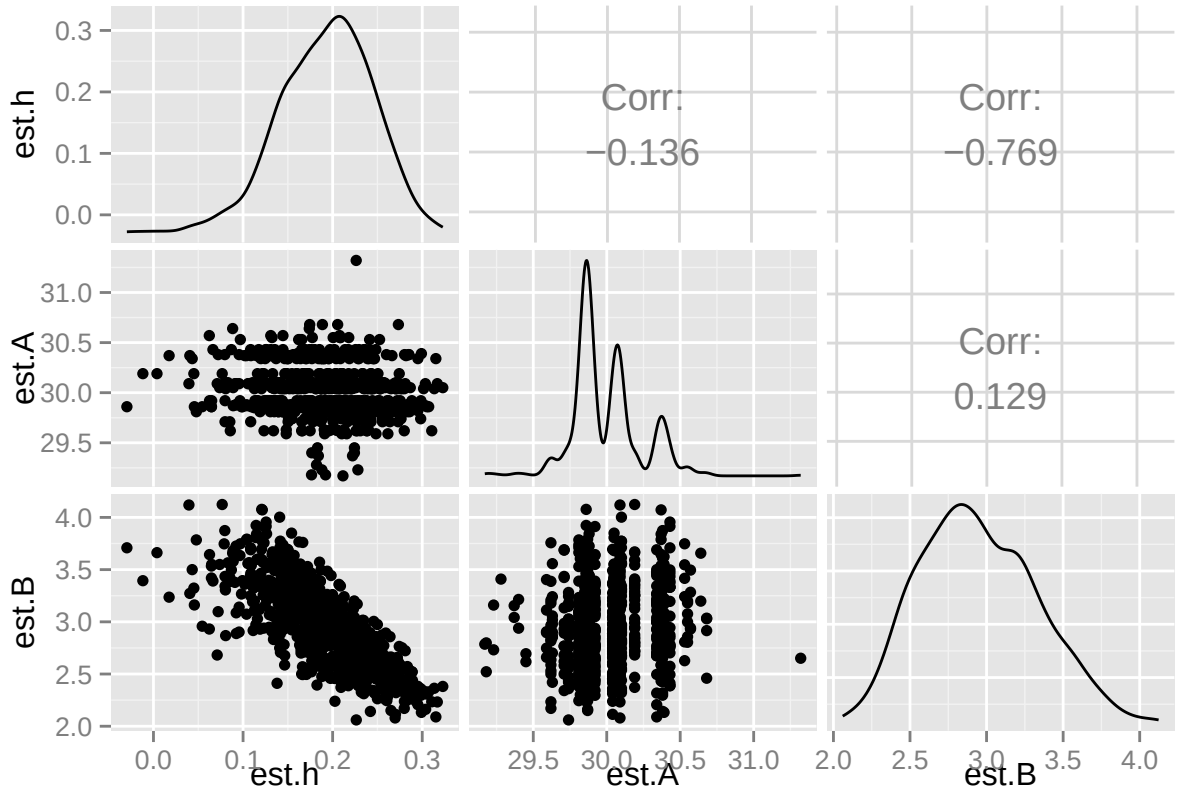
- Co-Relation Pairs

```r
#Co-Relation Plot
s$cor.est
```

```
##            est.h      est.A      est.B
## est.h  1.0000000 -0.1359497 -0.7693468
## est.A -0.1359497  1.0000000  0.1285403
## est.B -0.7693468  0.1285403  1.0000000
```

- Pairs Plot

```r
#Pairs Plot
print(s$es.plt)
```



8) Transform For Normality and GoF Tests

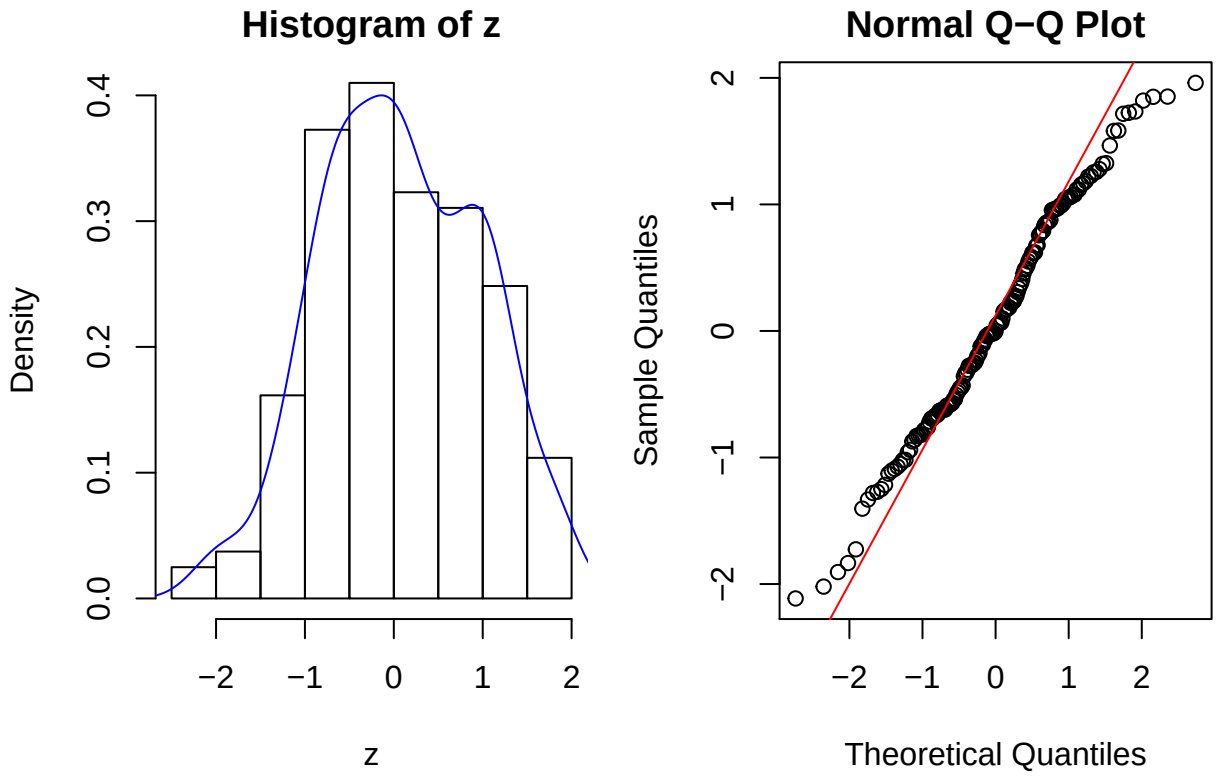
```
HDistBackXform=function(h,A,B,data){
####################################
#  This function will allow you to back solve for Z
#  under any H-distribution transform
#  the Values h, A, and B are the estimated values of
#  the H-distribution parameters.  In this program
#  data is a vector of data.
####################################

n=length(data)
 #using Veleman's rule
output=numeric(n)
g=function(z){z*exp(h*z^2)-((x-A)/B)}
# Begin loop on i where data[i] is the ith data value
for(i in 1:n){
x=data[i]
obj=uniroot(g,interval=c(-6,6))
output[i]=obj$root
}
return(output)
}

h<-normal.h$h
```

```
A<-normal.h$A
B<-normal.h$B

z<-HDistBackXform(h,A,B,b)
par(mfrow=c(1,2),mar = c(4, 4, 2, 1), oma = c(0, 0, 2, 0))
hist(z,prob=TRUE)
lines(density(z),col="blue")
qqnorm(z)
qqline(z,col="red")
```



- Veleman's Rule for Pearson's GoF

```
noofbins=2*sqrt(length(z))
out<-gof.pearson(z,noofbins)
out
```

```
## $df
##                 bin bincount       prob expectedcount
## 1      (-Inf,-1.4]         6 0.04775222      7.688107
## 2     (-1.4,-1.13]         6 0.03979728      6.407362
## 3    (-1.13,-1.02]         6 0.02108262      3.394302
## 4    (-1.02,-0.82]         7 0.04762529      7.667671
## 5   (-0.82,-0.692]         6 0.03691758      5.943731
## 6  (-0.692,-0.624]         7 0.02180950      3.511329
```

```
## 7  (-0.624,-0.569]        7 0.01842103      2.965786
## 8  (-0.569,-0.449]        6 0.04318942      6.953497
## 9  (-0.449,-0.306]        6 0.05622901      9.052870
## 10 (-0.306,-0.251]        6 0.02309947      3.719014
## 11  (-0.251,-0.11]        6 0.06031892      9.711347
## 12 (-0.11,-0.0258]        6 0.03739291      6.020259
## 13     (-0.0258,0]        6 0.01152358      1.855296
## 14       (0,0.154]        7 0.06903701     11.114959
## 15   (0.154,0.222]        6 0.03039341      4.893339
## 16   (0.222,0.337]        7 0.05022699      8.086545
## 17   (0.337,0.515]        7 0.07382803     11.886314
## 18   (0.515,0.621]        6 0.04081552      6.571299
## 19   (0.621,0.791]        6 0.05949567      9.578803
## 20   (0.791,0.954]        6 0.04892302      7.876607
## 21   (0.954,0.994]        6 0.01079519      1.738025
## 22    (0.994,1.07]        6 0.01975675      3.180837
## 23     (1.07,1.18]        6 0.02491813      4.011818
## 24     (1.18,1.33]        7 0.02649182      4.265183
## 25     (1.33, Inf]        7 0.08015963     12.905700
##
## $chisq
## [1] 48.79955
##
## $pval
## [1] 0.002337613
```

9) Estimation of Mode:

```
data = rnorm(100, 3, 2)

getGaussianMax = function(data){
  d = density(data, kernel="gaussian")
  index = which(d$y == max(d$y), arr.ind =TRUE)
  ans = d$x[index]
  return(ans)
}

calculatePseudoValues = function(data) {
  n = length(data)
  y.all = getGaussianMax(data)
  PV = numeric(n)
  for( i in 1:n) {
    yminusi = getGaussianMax(data[-i])
    PV[i] = n*y.all - (n-1)*yminusi
  }
  return(PV)
}

PVAll = calculatePseudoValues(data)
n = length(PVAll)
print(paste("The Mode is ",mean(PVAll) ))
```

```
## [1] "The Mode is  2.23153558113482"
```

```r
#Jack Knife Estimates

jackKnifeEstimate = mean(PVAll)
varJK = sum((PVAll - jackKnifeEstimate)^2)/(n*(n-1))
seJK = sqrt(varJK)
print(paste("The Standard Error of Jackknife Estimator",seJK))
```

```
## [1] "The Standard Error of Jackknife Estimator 0.4260511378212"
```

```r
#Bootstrap Estimates'
getbootstrapestimate = function(data, sims) {
  theta = numeric(sims)
  varTheta = numeric(sims)

  n = length(data)
  index = 1:n
  for (i in 1:sims){
    sampleindex= sample(index,n,replace=TRUE)
    theta[i] = mean(getGaussianMax(data[sampleindex]))
  }

 return(list(thetaBS = mean(theta), varBS = var(theta), seBS = sqrt(var(theta))))
}

BS = getbootstrapestimate(data, 100)$seBS
print(paste("The Standard Error of Bootstrap Estimates",BS))
```

```
## [1] "The Standard Error of Bootstrap Estimates 0.541847270210404"
```

- It can be seen from the abive numbers that, here Jackknifing performed better than bootstrapping for the given dataset

10) Fitting an Resistant Regression Line

- Raison d'etre of Resistant Regression is to be not to be influenced by the outliers or aberrant values.
- Following are the steps to perform an resistant regression
  - sort the values of x and divide these into three groups ie $(x_L, yL), (x_M, y_M), (x_R, y_R)$
  - Find the resistant summary statistic ie median (median x,median y) in the extremes , ie R and L extremes
  - The Slope is given by the following expression. All statistics are median here. $b = \frac{y_R - yL}{x_R - xL}$
  - The Intercept is given as follows, $a_0 = \frac{1}{3}[(y_L - b_0 x_L) + (y_M - b_0 x_M) + (y_R - b_0 x_R)]$
  - The residuals are then ireratively used to adjust the regression parameteres till an threshold is reached.
- Advantages of Resistant Regression:
  - Less susceptible to the effect of outliers as median is more robust than mean
  - Asymptotically efficient than OLS per step
- Disadvantages of Resistant Regression:
  - Its an iterative process, hence requires iterations

- Computations directly corresponds to resistance required. Eg, More groups can be used for RR. This requires more computational power
- No formulic solution. Hence RR methods iterates before converging.

11) Jackknifing and Bootstrapping:

- Both Jackknifing and Bootstrapping are re-sampling methods used to find variance, bias and standard estimate of almost all types of statistic/estimators. Historically Jackknife was the predecessor of bootstrapping. Following are the ways in which they are similar,
- **Sampling**
  - Jackknifing: The sample for jackknifing is calculated with leave one out and calculate the estimate with rest of the values.
  - Bootstrapping: Bootstrapping instead follows an broader approach of re-sampling the distribution. The sampling is done with replacement from the sample poplulation. The key idea is that multiple sampling of the sample poplulation directly represents the true distribution of the sample. Thus generally bootstrapping gives an better estimate of the two
  - *Consequece* : Bootstrapping gives an better estimate and better model for understanding variability and bias. However since due to the nature of sampling, the estimates differ every time the method was repeated. However Jackknifing always produces an exact result.
- *Obtaining Estimates and Standard Errors* : Due to the nature of sampling, bootstrapping requires more space and computational complexity. However Jackkife produces easier asymptotic complexity and reproduceable results.
- Jackkinfing is mainly used to understand the bias of an point estimator. However bootstrapping helps simulating the true distribution, hence can be applied for nearly all estimation methods.

12) Inventions Dataset

a) Tablate the dataset

```
library(e1071)
library(vcd)
```

```
## Loading required package: grid
```

```
library(kequate)
```

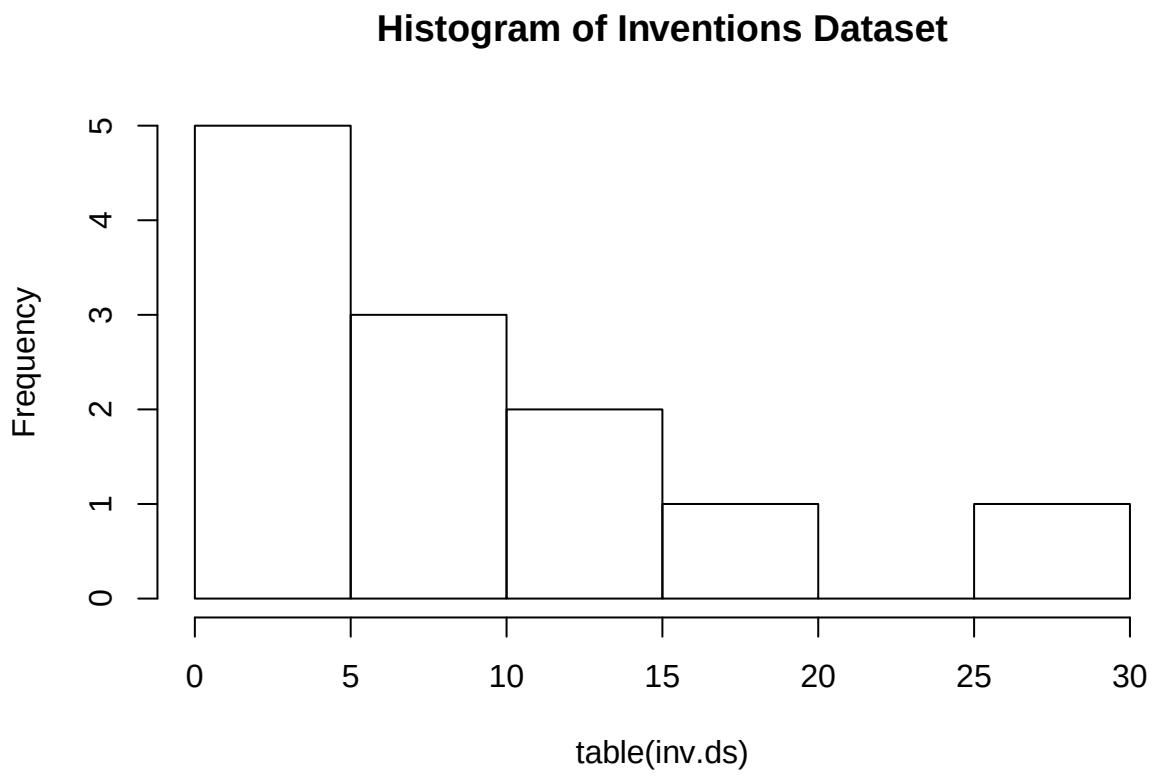
```
## Loading required package: ltm
## Loading required package: MASS
## Loading required package: msm
## Loading required package: polycor
## Loading required package: mvtnorm
## Loading required package: sfsmisc
```

```
inv.ds <- c(5,3,0,2,0,3,2,3,6,1,2,1,2,1,3,3,3,5,2,4,
                    4,0,2,3,7,12,3,10,9,2,3,7,7,2,3,3,6,2,4,3,
                    5,2,2,4,0,4,2,5,2,3,3,6,5,8,3,6,6,0,5,2,
                    2,2,6,3,4,4,2,2,4,7,5,3,3,0,2,2,2,1,3,4,
                    2,2,1,1,1,2,1,4,4,3,2,1,4,1,1,1,0,0,2,0)

# Tabulation of inventions
table(inv.ds)
```

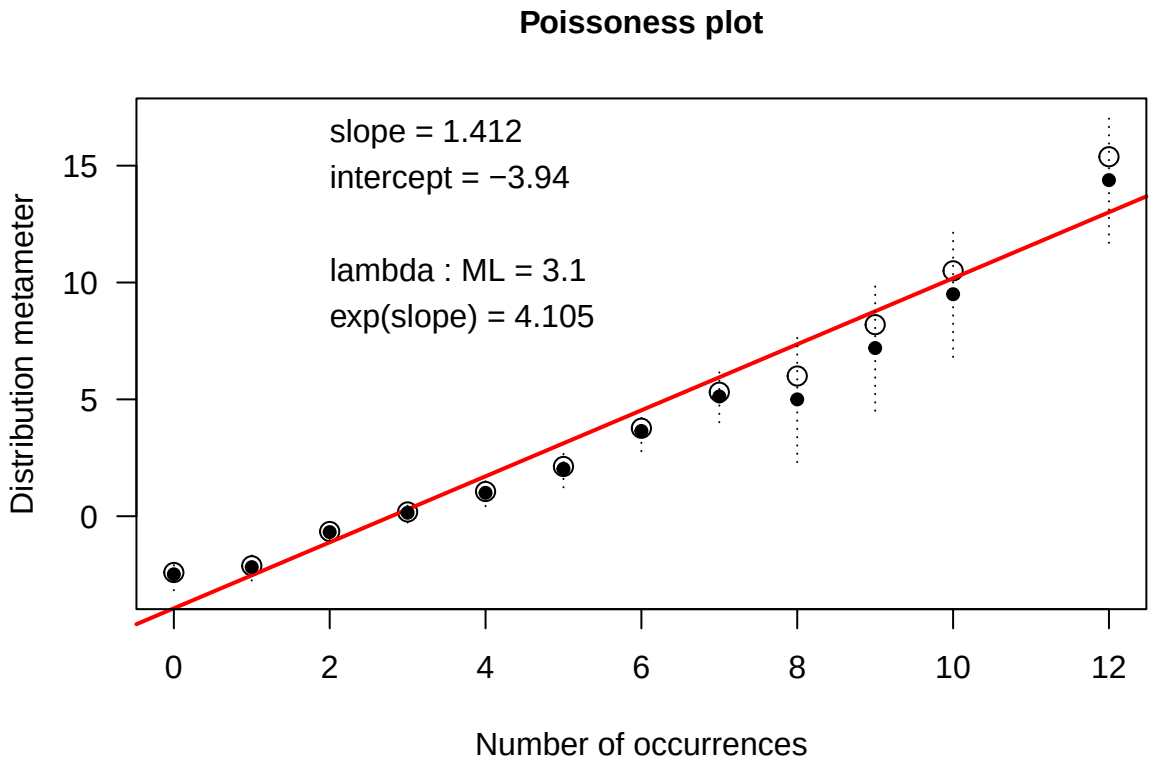
```
## inv.ds
##  0  1  2  3  4  5  6  7  8  9 10 12
##  9 12 26 20 12  7  6  4  1  1  1  1
```

```
#Histogram of the distibution:
hist(table(inv.ds),main="Histogram of Inventions Dataset")
```



b) Poissonness Plot

```
# Draw Poisson Plot
distplot(table(inv.ds), type = "poisson")
```




```
skewness(table(inv.ds))
```

```
## [1] 0.8758157
```

```
kurtosis(table(inv.ds))
```

```
## [1] -0.4820701
```

```
# Freeman Tukey Residuals
ft.res<-FTres(table(inv.ds), sapply(as.array(table(inv.ds)),function(x){1.142*x-3.94}))
```

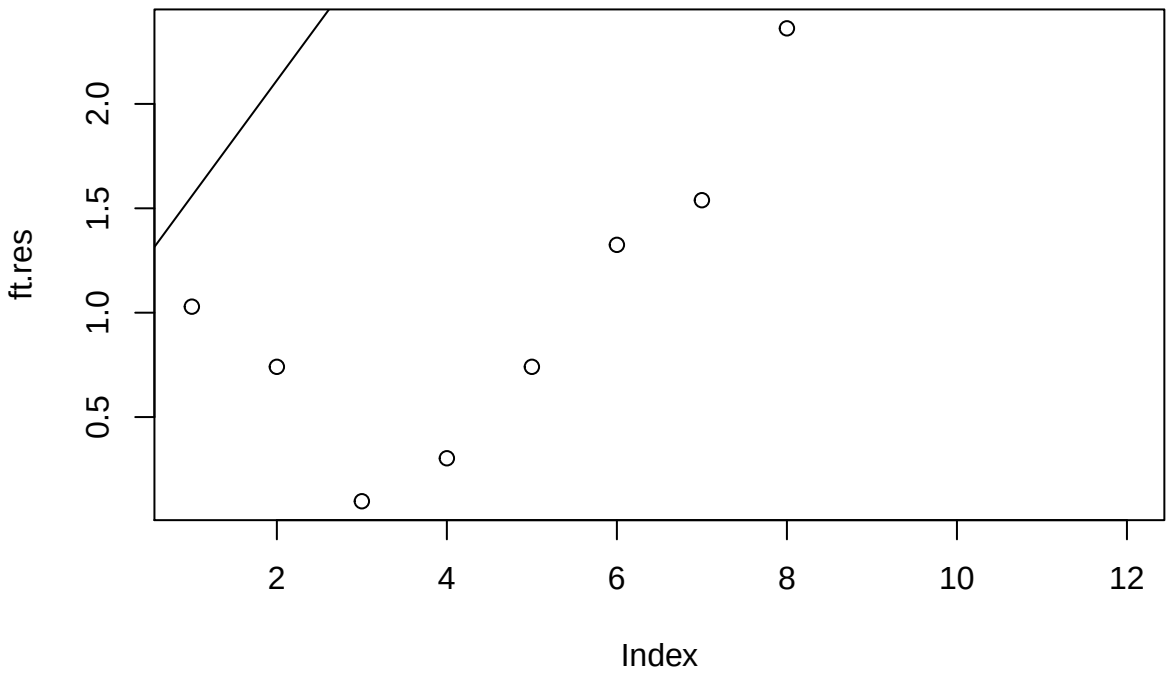
```
## Warning in sqrt(4 * fit[i] + 1): NaNs produced

## Warning in sqrt(4 * fit[i] + 1): NaNs produced

## Warning in sqrt(4 * fit[i] + 1): NaNs produced

## Warning in sqrt(4 * fit[i] + 1): NaNs produced
```

```
plot(ft.res)
qqline(ft.res)
```



13) Median Polish for Co2 Data

```
r1<-c(16,13.6,16.2,14.2,9.3,15.1,10.6,12,11.3,10.5,7.7,10.6)
r2<-c(30.4,27.3,32.4,24.1,27.3,21,19.2,22,19.4,14.9,11.4,18)
r3<-c(34.8,37.1,40.3,30.3,35,38.1,26.2,30.6,25.8,18.1,12.3,17.9)
r4<-c(37.2,41.8,42.1,34.6,38.8,34,30,31.8,27.9,18.9,13,17.9)
r5<-c(35.3,40.6,42.9,32.5,38.6,38.9,30.9,32.4,28.5,19.5,12.5,17.9)
r6<-c(39.2,41.4,43.9,35.4,37.5,39.6,32.4,31.1,28.1,22.2,13.7,18.9)
r7<-c(39.7,44.3,45.5,38.7,42.4,41.4,35.5,31.5,27.8,21.9,14.4,19.9)

df<-rbind(r1,r2,r3,r4,r5,r6,r7)
colnames(df)<-c(111,211,311,412,512,612,721,821,921,1022,1122,1222)
rownames(df)<-c(95,175,250,350,500,675,1000)
results<-medpolish(df)
```

```
## 1: 174.4
## 2: 162.35
## Final: 161.5375
```

```
results
```

```
##
## Median Polish Results (Dataset: "df")
##
```

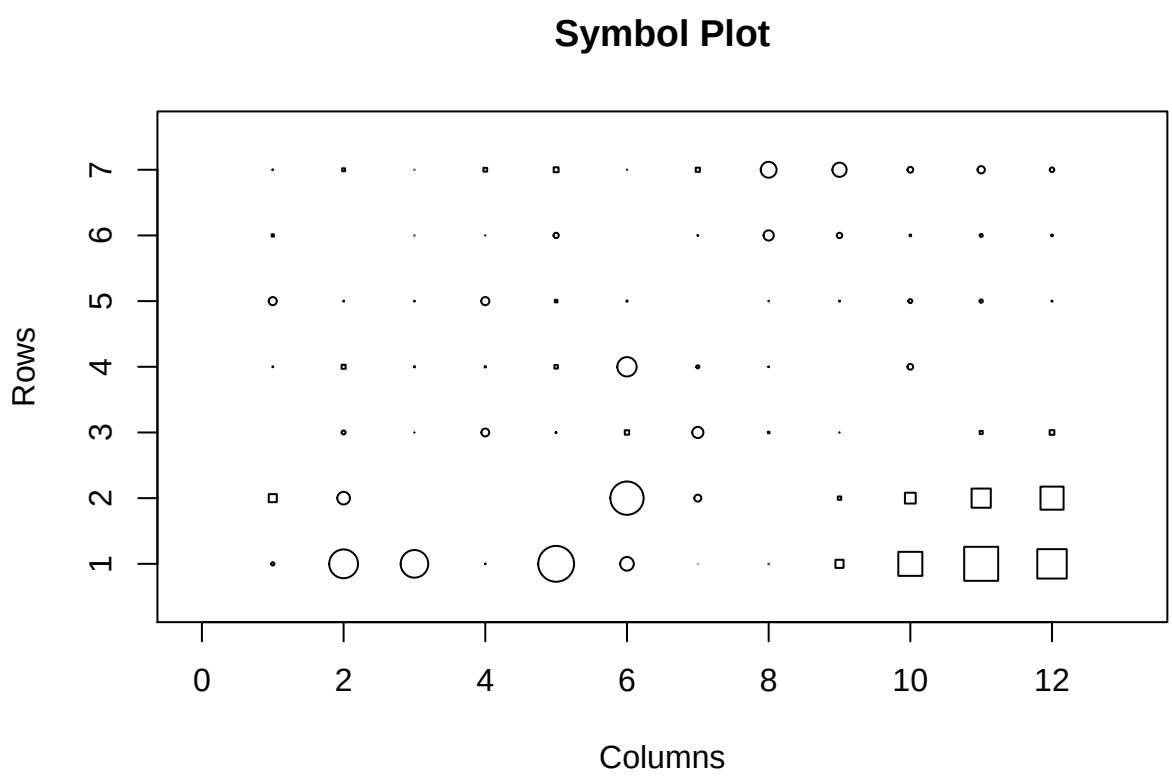
```
## Overall: 33.0125
##
## Row Effects:
##       95      175      250      350      500      675     1000
## -20.1375  -9.9625  -2.0500   0.0000   0.2125   1.3750   3.0000
##
## Column Effects:
##      111      211      311      412      512      612      721      821
##   3.8375   7.0125   9.3500   1.0500   4.2500   5.2125  -2.3250  -1.0500
##      921     1022     1122     1222
##  -5.1125 -12.8625 -20.0125 -15.1125
##
## Residuals:
##          111     211     311     412     512     612     721     821
## 95   -0.7125 -6.2875 -6.0250  0.2750 -7.8250 -2.9875  0.0500  0.1750
## 175   3.5125 -2.7625  0.0000  0.0000  0.0000 -7.2625 -1.5250  0.0000
## 250   0.0000 -0.8750 -0.0125 -1.7125 -0.2125  1.9250 -2.4375  0.6875
## 350   0.3500  1.7750 -0.2625  0.5375  1.5375 -4.2250 -0.6875 -0.1625
## 500  -1.7625  0.3625  0.3250 -1.7750  1.1250  0.4625  0.0000  0.2250
## 675   0.9750  0.0000  0.1625 -0.0375 -1.1375  0.0000  0.3375 -2.2375
## 1000 -0.1500  1.2750  0.1375  1.6375  2.1375  0.1750  1.8125 -3.4625
##          921    1022    1122    1222
## 95    3.5375 10.4875 14.8375 12.8375
## 175   1.4625  4.7125  8.3625 10.0625
## 250  -0.0500  0.0000  1.3500  2.0500
## 350   0.0000 -1.2500  0.0000  0.0000
## 500   0.3875 -0.8625 -0.7125 -0.2125
## 675  -1.1750  0.6750 -0.6750 -0.3750
## 1000 -3.1000 -1.2500 -1.6000 -1.0000
```

The Row and Column effects of the Dataset are as above. Regarding the patterns in residuals,

```
  symbolPlot<-function(mat){
  result<-medpolish(mat)
  res<-c(result$residuals)
  genNos<-expand.grid(1:7,1:12)
  plotvar<-cbind(genNos$Var2,genNos$Var1,res)
  pos<-plotvar[plotvar[,3]>=0,]
  max<-sum(abs(pos[,3]))
  symbols(pos[,1],pos[,2],squares = 3*(abs(pos[,3]/(max))),inches = FALSE,xlab="Columns",ylab="Rows",ma
  pos<-plotvar[plotvar[,3]<0,]
  symbols(pos[,1],pos[,2],circles = 3*(abs(pos[,3]/(max))),inches = FALSE,add = TRUE)
}

symbolPlot(df)
```

```
## 1: 174.4
## 2: 162.35
## Final: 161.5375
```



- It can be seen that there are no visible patterns in the residuals, which is good. ie the model explains the variability and the data well.

b) Measure to calculate variability:

```
Analog_R_Square<- 1-((sum(abs(results$residuals))) /(sum(abs(df-results$overall))))
print(paste("Variability Measure, Analog R Square :",Analog_R_Square))
```

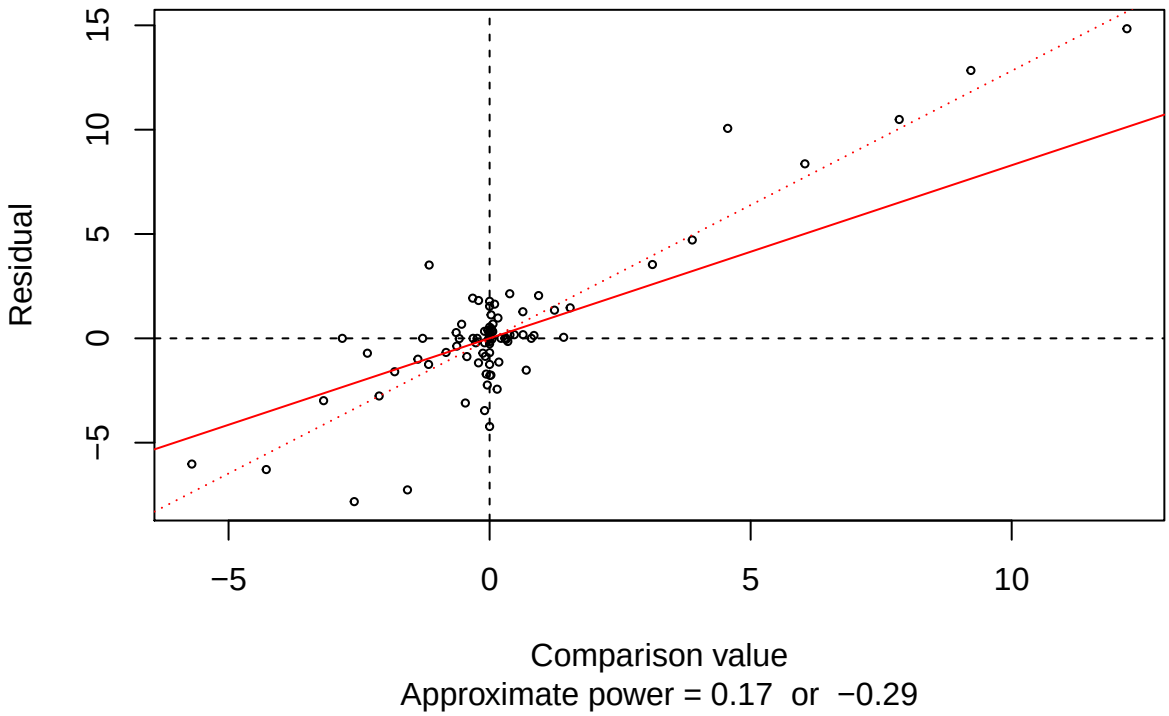
```
## [1] "Variability Measure, Analog R Square : 0.808064755680974"
```

c) Diagnostic Plot:

```
diag.MP <- function(fit){
  source("rrline.r")
  fit.comp <- matrix(fit$row,ncol=1) %*% matrix(fit$col,nrow=1)/fit$overall
  plot(fit.comp, fit$res,xlab="Comparison value",ylab="Residual",cex=0.5)
  abline(v=0,h=0,lty=2)
  ls <- lm(c(fit$res)~c(fit.comp))
  abline(ls,col="red",lty=3)
  rr <- run.rrline(fit.comp,fit$res,iter=10)
  abline(rr$a, rr$b, col="red")
  pwr1 <- 1 - rr$b
  pwr2 <- 1 - ls$coef[2]
  title("",paste("Approximate power =",format(round(pwr1,2))," or ", format(round(pwr2,2))))
```

```
}

diag.MP(results)
```




```
##           a        b    |res|
##  1  0.01939  0.90105 104.3848
##  2 -0.01756 -0.08196 108.8667
##  3  0.00145  0.01096 108.2604
##  4 -0.00011 -0.00083 108.3064
##  5  0.00001  0.00006 108.3029
##  6  0.00000  0.00000 108.3032
##  7  0.00000  0.00000 108.3032
##  8  0.00000  0.00000 108.3032
##  9  0.00000  0.00000 108.3032
## 10  0.00000  0.00000 108.3032
##     0.00318  0.82928 108.3032
```

- Diagnostic plots help to indicate a power transform for "Transform for additivity".
- With median polish as conext, diagnostic plot have comparision values $\frac{a_i b_i}{m}$ vs the residual when the model for additivity is $y_{ij} = m + a_i + b_j + r_{ij}$, where m,$a_i, b_j$ are resistantly determined estimates for the common value
- And $r_{ij} = y_{ij} - (m + a_i + b_j)$ the residuals from additive fit.

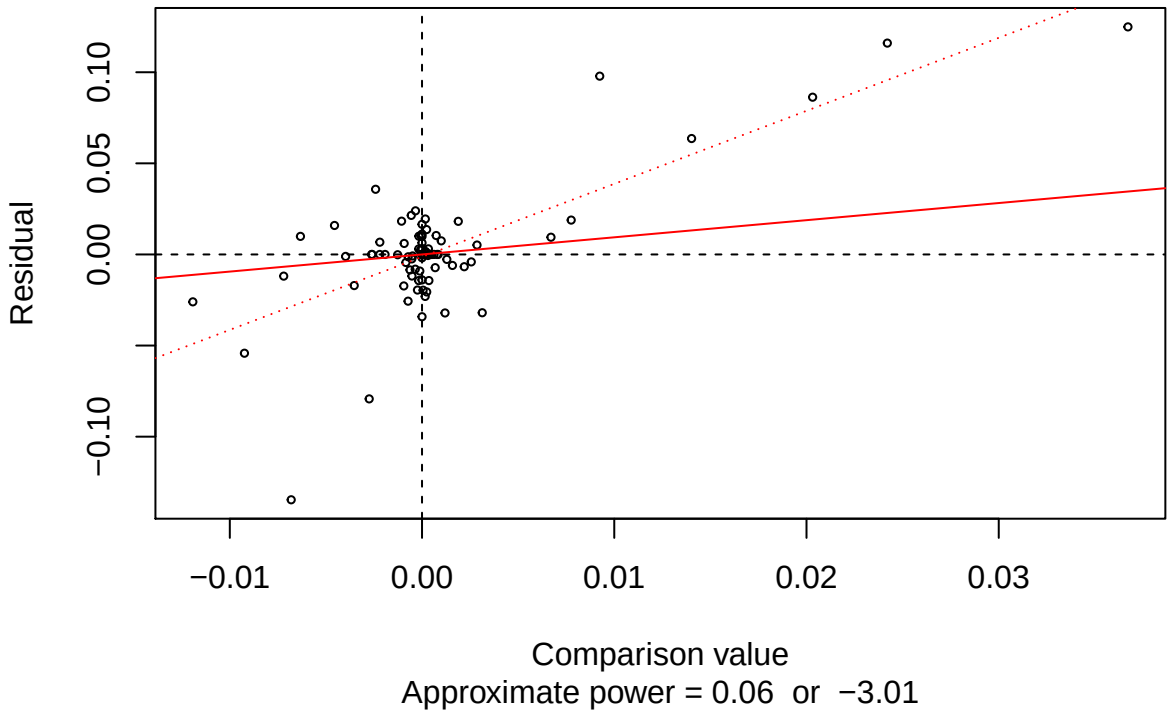
d) Re-Expression as suggested by Diagnostic Plot.

- As suggested by the diagnostic plot, an re-expression is done as follows,

```
#Power Transform
df.t<-(df)^(0.17)
results.t<-medpolish(df.t)
```

```
## 1: 1.76713
## 2: 1.487822
## Final: 1.47599
```

```
#Diagnostic Plot of Transformed Data
diag.MP(results.t)
```




```
##    a       b   |res|
##  1 0 0.35964 1.42878
##  2 0 0.20010 1.40399
##  3 0 0.13288 1.38757
##  4 0 0.08825 1.37667
##  5 0 0.05861 1.36943
##  6 0 0.03892 1.36462
##  7 0 0.02585 1.36143
##  8 0 0.01717 1.35930
##  9 0 0.01140 1.35790
## 10 0 0.00757 1.35696
##    0 0.94037 1.35696
```

```
Analog_R_Square<- 1-((sum(abs(results.t$residuals))) /(sum(abs(df.t-results.t$overall))))
print(paste("Variability Explained after Re-Expression : ",Analog_R_Square))
```

```
## [1] "Variability Explained after Re-Expression :  0.847646504570185"
```

- Also the the residuals are near zero, which is expected.

e) Stem-Leaf Plots

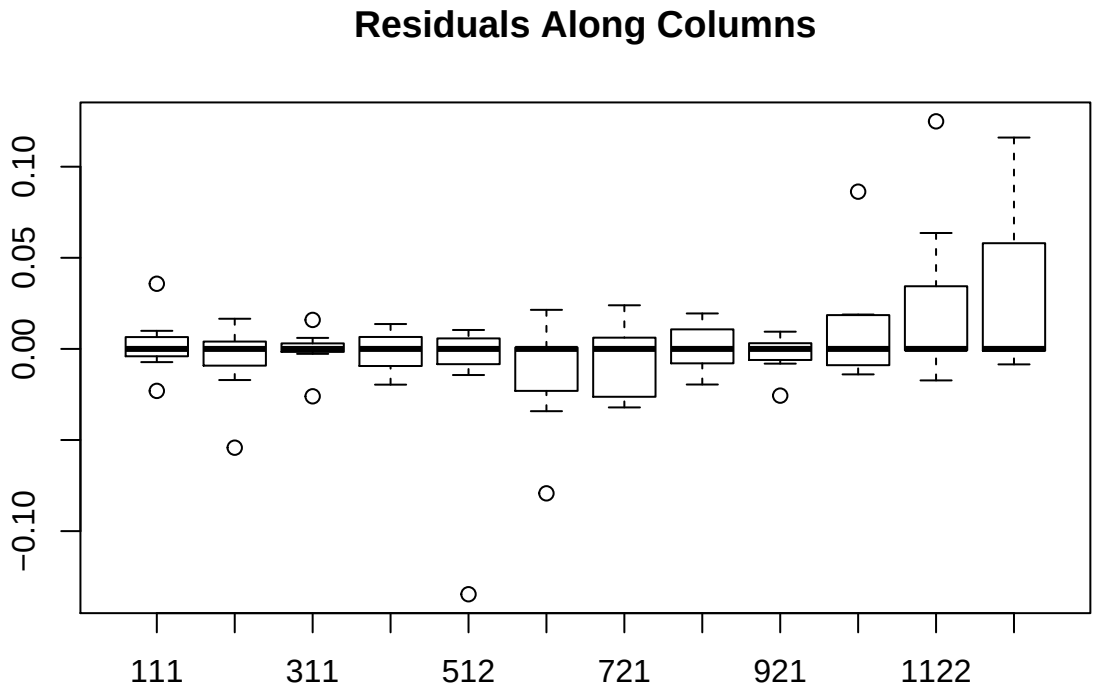
```
stem(results.t$residuals,2)
```

```
##
##   The decimal point is 2 digit(s) to the left of the |
##
##   -12 | 5
##   -10 |
##    -8 |
##    -6 | 9
##    -4 | 4
##    -2 | 422663100
##    -0 | 774442298877644322111100
##     0 | 000000000000001122333566779000001467899
##     2 | 146
##     4 |
##     6 | 4
##     8 | 68
##    10 | 6
##    12 | 5
```

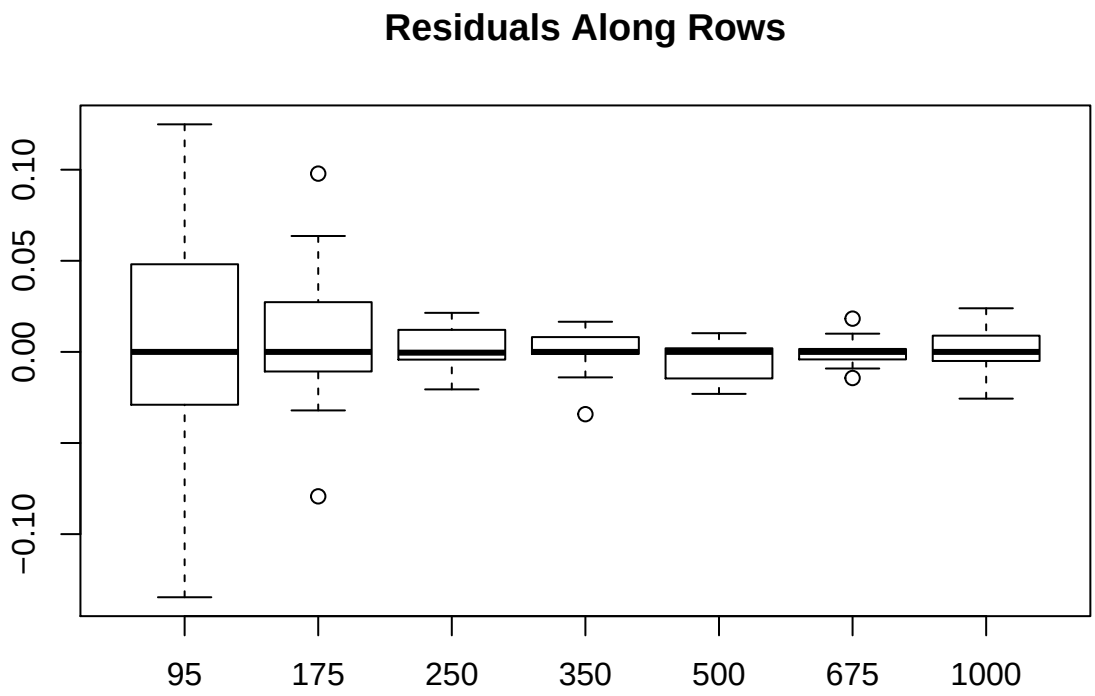
- There are not many outliers, however the first entry 5 seems to be an outlier.

f) Box Plots for Residual Analysis

```
boxplot(results.t$residuals,main = "Residuals Along Columns")
```




```
boxplot(t(results.t$residuals),main = "Residuals Along Rows")
```

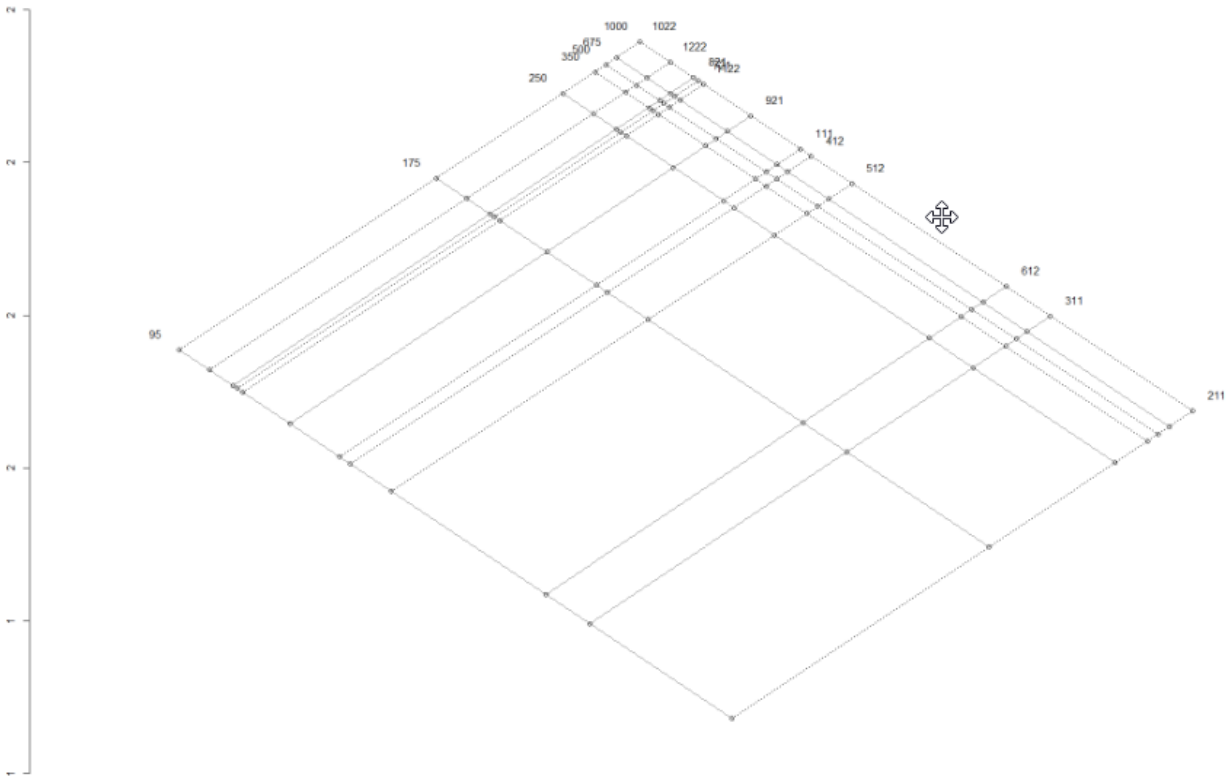


g) Forget-it Plot

```
forgetitplot <- function(outmpol,outlim=0,...) {
  # outmpol is output of medpolish in library(eda) or library(stats)
  # be sure to assign dimnames to matrix being polished
  oldpar <- par()
  par(fig=c(0,.7,0,1))
  nc <- length(outmpol$col)
  nr <- length(outmpol$row)
  a <- rep(outmpol$row,nc)
  b <- rep(outmpol$col,rep(nr,nc))
  sqrt2 <- sqrt(2)
  ab <- cbind((a-b)/sqrt2,(a+b)/sqrt2)
  xrange <- range(ab[,1]) + c(-.1,.1)*(max(ab[,1])-min(ab[,1]))
  yrange <- range(ab[,2]) + c(-.1,.1)*(max(ab[,2])-min(ab[,2]))
  dx <- (xrange[2]-xrange[1])/50
  dy <- (yrange[2]-yrange[1])/50
  plot(ab[,1],ab[,2],axes=F,xlim=xrange,ylim=yrange,xlab="",ylab="",...)
  segments((min(a)-outmpol$col)/sqrt2, (min(a)+outmpol$col)/sqrt2,
           (max(a)-outmpol$col)/sqrt2, (max(a)+outmpol$col)/sqrt2,lty=3)
  segments((outmpol$row-min(b))/sqrt2, (outmpol$row+min(b))/sqrt2,
           (outmpol$row-max(b))/sqrt2, (outmpol$row+max(b))/sqrt2,lty=3)
  # segments((outmpol$row)/sqrt2-min(b), (outmpol$row)/sqrt2+min(b),
  #          (outmpol$row)/sqrt2-max(b), (outmpol$row)/sqrt2+max(b),lty=3)
  yrowloc <-  rep(max(b),nr)
```

```
  xrowloc <-  outmpol$row
  # text((xrowloc-yrowloc)/sqrt2-dx,dy+(xrowloc+yrowloc)/sqrt2,format(1:nr))
  text((xrowloc-yrowloc)/sqrt2-dx,dy+(xrowloc+yrowloc)/sqrt2,
       names(sort(outmpol$row)))
  xcolloc <- rep(max(a),nc)
  ycolloc <- outmpol$col
  # text(dx+(xcolloc-ycolloc)/sqrt2,dy+(xcolloc+ycolloc)/sqrt2,format(1:nc))
  text(dx+(xcolloc-ycolloc)/sqrt2,dy+(xcolloc+ycolloc)/sqrt2,
       names(sort(outmpol$col)))
  ynames <- format(round(outmpol$overall + sqrt2*pretty(ab[,2])))
  axis(2,at=pretty(ab[,2]),labels=ynames)
  # add vertical lines when there is an outlier
  if(abs(outlim) > 1e-4) {
    out.index <- which(abs(outmpol$res) > outlim, arr.ind=T)
    # find (r,c) for outlier indices
    zz.x <- outmpol$row[out.index[,1]]
    zz.y <- outmpol$col[out.index[,2]]
    # outlier points at (zz.x-zz.y)/sqrt2, (zz.x+zz.y)/sqrt2
    # draw segment from here to end of residual
    segments((zz.x-zz.y)/sqrt2, (zz.x+zz.y)/sqrt2,
             (zz.x-zz.y)/sqrt2, (zz.x+zz.y)/sqrt2 + outmpol$res[out.index])
  }
  par <- oldpar
  invisible()
}

#forgetitplot(results.t)
```



- Co2 of type 1000 had the maximum effect at plant 0311
- C02 of type 95 is more infulential than the others.

h) Boost Strap Estimates for Median Polish Overall:

```
vectorize.medpolish<-function(residuals.mp){
  residualslist <- c(residuals.mp)
  residuals.ret <- c()
  for (i in 1:nrow(residuals.mp)){
    residuals.ret <- rbind(residuals.ret,c(sample(residualslist,ncol(residuals.mp),replace = TRUE)))
  }
  return (residuals.ret)
}


bootstrap.medpolish<-function(mat,sims){
  nrows <- nrow(mat)
  ncols <- ncol (mat)
  row.est <- matrix(0,nrow=sims,ncol=nrows)
  col.est <- matrix(0,nrow=sims,ncol=ncols)
  overall.est <- c()
  org.result<-medpolish(mat)
  sample.mat <- org.result$residuals
  sample.result <- org.result
  for (j in 1:sims){
    new.residuals <- vectorize.medpolish(sample.mat)
    bs.mat <- new.residuals+t(rbind(sample.result$row,sample.result$row,sample.result$row,sample.result$
    sample.result <- medpolish(bs.mat,maxiter = 1000)
    sample.mat<-sample.result$residuals
    #print(row.est[j,])
    #print(bs.mat)
    #print(c(sample.result$row))
    row.est[j,]<-c(sample.result$row)
    col.est[j,]<-c(sample.result$col)
    overall.est[j]<-sample.result$overall
  }
  return(list(row.est=row.est,col.est=col.est,overall.est=overall.est))
}

b<-bootstrap.medpolish(df,50)

overall.serror<-sd(b$overall.est)/sqrt(length(df))
b.rowest<-rbind(c(mean(b$row.est[,1]),mean(b$row.est[,2]),mean(b$row.est[,3]),mean(b$row.est[,4]),mean(
colnames(b.rowest)<-rownames(df)
b.colest<-rbind(c(mean(b$col.est[,1]),mean(b$col.est[,2]),mean(b$col.est[,3]),mean(b$col.est[,4]),mean(
colnames(b.colest)<-colnames(df)
b.serowest<-rbind(c(mean(b$row.est[,1])/sqrt(length(b$row.est[,1])),mean(b$row.est[,2])/sqrt(length(b$r
colnames(b.serowest)<-rownames(df)
b.secolest<-rbind(c(mean(b$col.est[,1])/sqrt(length(b$col.est[,1])),mean(b$col.est[,2])/sqrt(length(b$c
colnames(b.secolest)<-colnames(df)
```

```
## [1] "Bootstrap Estimates for overall :  33.5475810618335"
```

```
## [1] "The standard error of Bootstrap Estimates 0.0486387314618759"
```

```
## [1] "-------------------------------------------------"

## [1] "Boot strapped Row Estimates:"

##             95       175       250        350       500     675     1000
## [1,] -18.65091 -9.580678 -1.802223 0.01963037 0.8639511 1.93773 2.771877

## [1] "Bootstrapped Column Estimates:"

##            111      211      311       412     512      612       721
## [1,] 0.1553666 15.19159 7.047301 0.9811789 3.30727 4.162722 -3.944642
##             821       921      1022      1122      1222
## [1,] 0.06968543 -6.244833 -13.33086 -18.37562 -17.03355

## [1] "-------------------------------------------------"

## [1] "Standard Errors for Row estimates"

##             95       175        250         350       500       675
## [1,] -2.637636 -1.354912 -0.2548729 0.002776154 0.1221811 0.2740364
##           1000
## [1,] 0.3920026

## [1] "Standard Errors for Column estimates"

##             111      211       311       412       512       612
## [1,] 0.02197216 2.148415 0.9966388 0.1387597 0.4677186 0.5886977
##             721         821        921      1022      1122      1222
## [1,] -0.5578566 0.009855008 -0.8831527 -1.885269 -2.598706 -2.408907
```