MATH 2780 Chapter 8B Worksheet

Summary

The multiple regression model that is linear in the parameters is $E(y) = \beta_0+\beta_1x_1+\beta_2x_2+\ldots+\beta_kx_k$

Coefficient and Residual Variance Estimation:

$Y = X\beta + E$ $\hat{\beta} = (X'X)^{-1}X'y$ $s^2 = \frac{(y - X\hat{\beta})'(y - X\hat{\beta})}{n-k-1}$ $MSE = s^2,\ s = \sqrt{s^2}$	$Y = \begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_n \end{bmatrix}, X = \begin{bmatrix} 1 & x_{11} & x_{21} & \cdots & x_{kn} \\ 1 & x_{12} & x_{22} & \cdots & x_{k2} \\ 1 & x_{13} & x_{23} & \cdots & x_{k3} \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & x_{1n} & x_{2n} & \cdots & x_{kn} \end{bmatrix}, \beta = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \vdots \\ \beta_k \end{bmatrix}, E = \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \\ \vdots \\ \varepsilon_n \end{bmatrix}$

Regression Residuals: Residuals are $\hat{\varepsilon}_i = y_i - \hat{\beta}_0 - \hat{\beta}_1x_1 - \ldots - \hat{\beta}_kx_k$, $s^2 = \sum(y_i - \hat{y}_i)^2 / (n-k-1)$.

Detecting Lack of Fit: 1) Plot $\hat{\varepsilon}_i$'s (y-axis) against x_{ji}'s (x-axis). 2) Plot $\hat{\varepsilon}_i$'s (y-axis) against $\hat{y}_i$'s (x-axis).
3) In each plot, look for trends, dramatic changes, and/or >5% of residuals outside $\pm 1.96s$ of 0.

Partial Residuals: For the jth independent variable, x_j, is $\hat{\varepsilon}_i^* = \hat{\varepsilon}_i + \hat{\beta}_j x_{ji}$. Plot $\hat{\varepsilon}_i^*$'s vs. x_j for pattern.

Detecting Unequal Variances: Assumption is that $var(\varepsilon_i)=\sigma^2$, $i=1,\ldots,n$.
Transformation of y: 1) Poisson $Var(y) \propto E(y)$, $\sqrt{y}$. 2) Binomial $Var(y_i)=E(y_i)[1-E(y_i)]/n_i$, $\sin^{-1}(y)$.
3) Multiplicative $Var(y)=[E(y)]^2\sigma^2$, $\ln(y)$.
Hypothesis test: H_0: $\sigma_1^2 / \sigma_2^2 = 1$ vs. H_1: $\sigma_1^2 / \sigma_2^2 \neq 1$,
σ_1^2=variance of 1st half, σ_1^2=variance of 2nd half. $F = (Larger\ s^2) / (Smaller\ s^2)$.
Reject H_0 if $F > F_{\alpha,n/2-k-1,n/2-k-1}$.

Checking the Normality Assumption:
1. Histogram for the residuals. Inspect for looking like normal curve.
2. Stem-and- leave plot of the residuals. Inspect for looking like normal curve.
3. Normal probability plot (QQ plot). Plot ε_i vs. $E(\varepsilon_i)$ assuming normality.
$z_i = \Phi^{-1}\left((i-3/8)/(n+1/4)\right)$
Inspect for points looking like fit a line indicating normality satisfied.
Some possible transformations: $\sqrt{y}$, $log(y)$, $1/y$, and $1/\sqrt{y}$.

Detecting Outliers and Identifying Influential Observations:
The standardized residual $z_i = \hat{\varepsilon}_i / s = (y_i - \hat{y}_i) / s$
An observation with a standardized residual that is larger than 3s (in absolute value).
The studentized residual
$z_i^* = \hat{\varepsilon}_i / (s\sqrt{1-h_i}) = (y_i - \hat{y}_i) / (s\sqrt{1-h_i})$
where h_i (called leverage) is h_i=ith diagonal element of $X(X'X)X'$.
The **leverage** of the ith observation is h_i, associated with y_i in the equation
$\hat{y}_i = h_1y_1 + h_2y_2 + \cdots + h_iy_i + \cdots + h_ny_n$. **The Rule of Thumb:** $h_i > 2(k+1)/n$ is outlier

Cook's Distance D_i. A large D_i value of indicates that the observed y_i value has strong influence on the estimated β coefficients. Compare D_i to the F distribution with $v_1=k+1$ and $v_2=n-k-1$.
$D_i = [(y_i - \hat{y}_i)^2 / [(k+1)MSE]][h_i / (1-h_i)^2]$

Detecting Residual Correlation:
We can test for temporal autocorrelation with the **Durbin-Watson Test**.

$d = \sum_{t=2}^{n}(\hat{\varepsilon}_t - \hat{\varepsilon}_{t-1})^2 / \sum_{t=1}^{n}\hat{\varepsilon}_t^2 \approx \underbrace{2(1-\hat{\rho})}_{\text{Large } n}$	H_0: $\rho \leq 0$ vs. H_a: $\rho > 0$, Reject $d < d_{L,\alpha}$ H_0: $\rho \geq 0$ vs. H_a: $\rho < 0$, Reject $(4-d) < d_{L,\alpha}$ H_0: $\rho = 0$ vs. H_a: $\rho \neq 0$, Reject $d < d_{L,\alpha/2}$ or $(4-d) < d_{L,\alpha/2}$

1. Range of d: $0 \leq d \leq 4$.
2. If residuals are uncorrelated, $d \approx 2$.
3. If residuals are positively correlated, $d < 2$, and if the correlation is very strong, $d \approx 0$.
4. If residuals are negatively correlated, $d > 2$, and if the correlation is very strong, $d \approx 4$.

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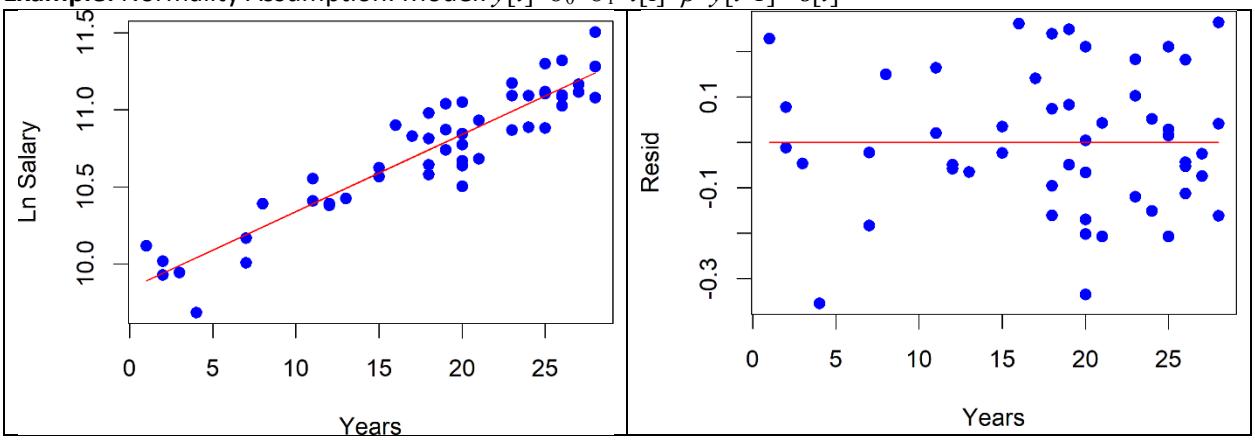
Example: Normality Assumption. Model: $y[i]=b_0+b_1*t[\mathrm{i}]+\rho*y[i\text{-}1]+\varepsilon[i]$



Run R code and examine results.

read data
parse out variables
Fit logarithmic model
get residuals
#scatter plot with line
histogram of residuals
stem and leaf of residuals
QQ plot
manual QQ plot
R function QQ plot
Shapiro-Wilks Test
Kolmogorov-Smirnov test
Lilliefors test
Anderson-Darling test
D'Agostino-Pearson test
Jarque-Bera test

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```
# read data
mydata <- read.delim("SOCWORK.txt",header=TRUE)

# parse out variables
n <- nrow(mydata)
k <- 1
x1<- c(mydata[,1])#Experience
y2<- c(mydata[,3])#Ln Salary

#scatter plot with line
plot(x1,y2,xlab='Years',ylab='Ln
Salary',pch=19,col="blue")
points(x1,mymodel$fitted.values,col='red',type="l")

# Fit logarithmic model
Mymodel<-lm(y2~x1)
summary(mymodel)$coefficients[,]

# get residuals
res<-summary(mymodel)$residuals
sortres<-sort(res)
write.csv(sortres,file="socresidln.csv")
c(mean(res),sd(res))

#scatter plot with line
plot(x1,res,xlab='Years',ylab=Residals',pch=19,
col="blue")
points(x1,rep(0,length(x1)),col='red',type="l")

# histogram of residuals
hist(res,breaks=seq(from=-
0.376,to=0.274,by=0.05),col="blue")

# stem and leaf of residuals
stem(res,scale=1.5)

# QQ plot
a   <-3/8 #a<-3/8 if n<=10, a<-1/2 if n>10
A   <-(seq(from=1,to=n)-a)/(n+1-2*a)
MSE <-anova(mymodel)['Residuals','Mean Sq']
Eres<-qnorm(A) #*sqrt(MSE)
```

```
# manual QQ plot
qqline<-lm(Eres~sortres)
plot(sortres,Eres,xlab='RESIDUAL',ylab='Normal Score',
    pch=19,col="blue",xlim=c(-0.40,0.40),ylim=c(-2.5,2.5))
abline(qqline,col='red')

# R function QQ plot
qqnorm(res,pch=19,col="blue",ylim=c(-0.40,0.40),xlim=c(-
2.5,2.5))
qqline(res,col="red")

# Shapiro-Wilks Test
shapiro.test(res)

# Kolmogorov-Smirnov test
ks.test(res,"pnorm")

# Lilliefors test
library(nortest)
lillie.test(res)

# Anderson-Darling test
ad.test(res)

# D'Agostino-Pearson test
meanres<-mean(res)
sdres  <-sd(res)
skewres<-sum(((res-meanres)/sdres)^3)/n    # 0 for normal
kurtres<-sum(((res-meanres)/sdres)^4)/(n-1)# 3 for nor-
mal
pearson.test(res)

# Jarque-Bera test
install.packages('tseries')
library('tseries')
jarque.bera.test(res)
```

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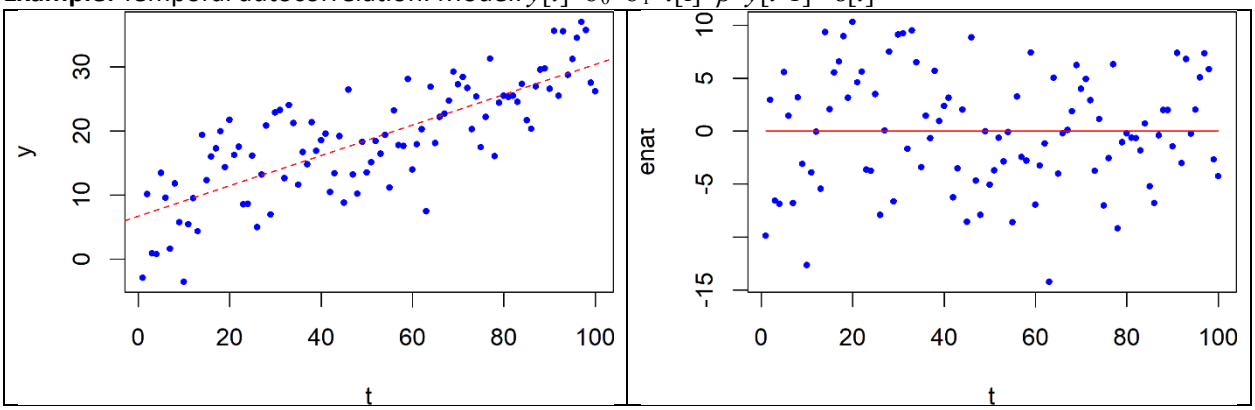
Example: Temporal autocorrelation. Model: $y[i]=b_0+b_1*t[i]+\rho*y[i-1]+\varepsilon[i]$



Run R code and examine results.

Simulate autoregressive(p) residual correlation

Set seed to same default value

Generate data

y[i]=b0+b1*t[i]+rho*y[i-p]+ e[i]

Regression Model

Examine residuals

Estimated AR(1) correlation

Durbin-Watson Test AR(1)

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```r
# Simulate autoregressive(p) residual correlation
install.packages('lmtest') # for DW test

# Set seed to same default value
set.seed(NULL)
alph <- 0.05

# Generate data
n    <-100# sample length
b0   <-5 # y-intercept
b1   <-0.1 # slope coefficient
sigma<-5 # error std
p    <-3 # AR order
rho  <-0.5 # AR correlation

# y[i]=b0+b1*t[i]+rho*y[i-p]+ e[i]
t <- (0-p+1):n
y <- rep(0,n+p)
e <- sigma*rnorm(n+p)
for (i in (1+p):length(t)){
  y[i]<-b0+b1*t[i]+rho*y[i-p]+e[i]
}
y <- tail(y,-p) # Remove first p
t <- tail(t,-p) # Remove first p
df<-cbind(t,y)

# Regression Model
model1 <- lm(y ~ t)
plot(t,y,pch=19,cex =.5,col="blue",xlab='t',ylab='y')
abline(lm(y~t),col='red',lty=2)

# Examine residuals
ehat    <- model1$residuals
cbind(mean(ehat),sd(ehat))
plot(t,ehat,pch=19,cex
=.5,col="blue",xlab='t',ylab='ehat')
points(t,rep(0,length(y)),col='red',type="l")

# Estimated AR(1) correlation
lmacf<-acf(ehat,lag.max=5)
lmacf$acf
cor(ehat[1:(n-p)],ehat[(1+p):n])
```

```r
# Durbin-Watson Test AR(1)
library(lmtest)
dwlm<-dwtest(y~t,exact=TRUE,alternative='greater')
dwlm
d<-dwlm$statistic
1-d/2
```