1.(a)

> Data=read.table("F:/1.txt",header=T)

> plot(Data$Week,Data$Hits,xlab="Week",ylab="Hits")



> x=Data$Week

> y=Data$Hits

(b)

> cor(x,y,method=”s”)

[1] 0.3217489

(c)

> cor.test(x,y,method='s')

Spearman's rank correlation rho

data: x and y

S = 4842.713, p-value = 0.05945

alternative hypothesis: true rho is not equal to 0

sample estimates:

rho

0.3217489

Warning message:

In cor.test.default(x, y, method = "s") :

Cannot compute exact p-value with ties

Fail to reject the Null assumption.

2.(a)

> library(base)

> data(cars)

> plot(cars$speed,cars$dist,xlab="speed",ylab="dist",main="cars")



(b)

> x=cars$speed

> y=cars$dist

> model=lm(y~x)

> model

Call:

lm(formula = y ~ x)

Coefficients:

(Intercept) x

-17.579 3.932

(c)

>abline(model)



(d)

> residuals<-residuals(model)

> fit=fitted(model)

> data=data.frame(residuals,fit)

> head(data,n=5)

residuals fit

1 3.849460 -1.849460

2 11.849460 -1.849460

3 -5.947766 9.947766

4 12.052234 9.947766

5 2.119825 13.880175

(e)

> plot(data$fit,data$resduals,main="Fitted VS Residual plot",xlab="fit",ylab="residual")



(f)

>  model2<-lm(y~-1+x) # No intercept model

> model2

Call:

lm(formula = y ~ -1 + x)

Coefficients:

x

2.909

(g)

> coef(model)

(Intercept) x

-17.579095 3.932409

> coef(model2)

x

2.909132

(h)

> xnew=21

> xnew=as.data.frame(xnew)

> colnames(xnew)<-"x"

> predict(model, xnew, interval="pred")

fit lwr upr

1 65.00149 33.42257 96.5804

3.

**(a)**

> library(MASS)

> data(mammals)

> x=mammals$body

> y=mammals$brain

> model=lm(y~x)

> model

Call:

lm(formula = y ~ x)

Coefficients:

(Intercept) x

91.0044 0.9665

(b)

> confint(model,level=0.95)

2.5 % 97.5 %

(Intercept) 3.8862623 178.122530

x 0.8711564 1.061836

(c)

>confint(model,level=0.9)

5 % 95 %

(Intercept) 18.2433254 163.765467

x 0.8868684 1.046124

(d)

> residuals<-residuals(model)

> plot(residuals)



(e)

> which( residuals==max(residuals))

19

19

> subset(mammals, mammals$brain==mammals$brain[19])

body brain

Asian elephant 2547 4603

4.(a)

>plot(log(mammals$brain),log(mammals$body),main="logBrain VS logBody plot",xlab="logbrain",ylab="logbody")



(b)

> x=log(mammals$brain)

> y=log(mammals$body)

> model=lm(y~x)

> model

Call:

lm(formula = y ~ x)

Coefficients:

(Intercept) x

-2.509 1.225

The equation is y=-2.509+1.225x

5.

> x=0:9

> y=c(98,135,162,178,221,232,283,300,374,395)

> plot(x,y)



Therefore, the linear relationship appears adequate.

> model=lm(y~x)

> model

Call:

lm(formula = y ~ x)

Coefficients:

(Intercept) x

91.56 32.50

> abline(model)



(b)

> library(MASS)

> b=boxcox(model)



> model2=lm(y^0.5~x)

> boxcox(model2)



(c)

> plot(x,y^0.5)

> abline(model2)



(d)

> residuals<-residuals(model)

> fit=fitted(model)

> data=data.frame(residuals,fit)

> plot(data$fit,data$resduals,main="Fitted VS Residual plot",xlab="fit",ylab="residual")



(e)

> model2=lm(y~-1+x)

> model2

Call:

lm(formula = y ~ -1 + x)

Coefficients:

x

46.95