

#Question 1

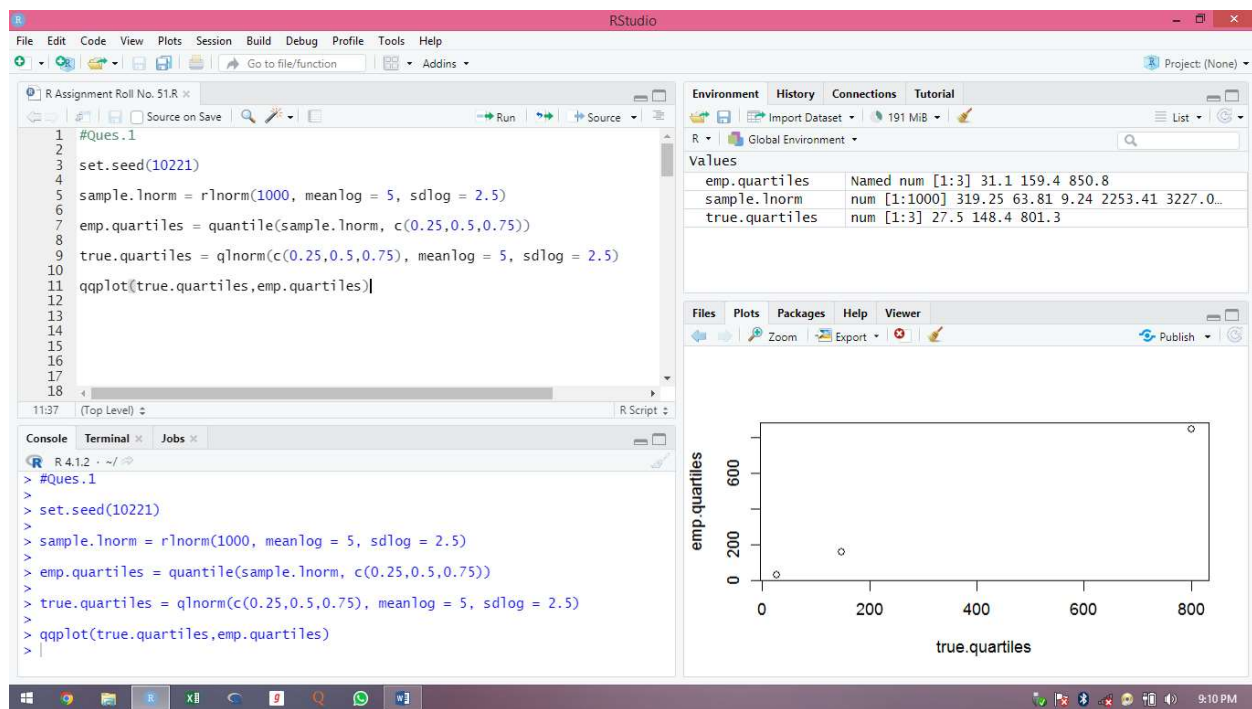
```
set.seed(10221)
```

```
sample.lnorm = rlnorm(1000, meanlog = 5, sdlog = 2.5)
```

```
emp.quantiles = quantile(sample.lnorm, c(0.25,0.5,0.75))
```

```
true.quantiles = qlnorm(c(0.25,0.5,0.75), meanlog = 5, sdlog = 2.5)
```

```
qqplot(true.quantiles,emp.quantiles)
```



#Question 2

```
cars = mtcars
```

```
#a)
```

```
model.a = lm(mpg ~ 1, data = cars)
```

```
#b)
```

```
model.b = lm(mpg ~ wt, data = cars)
```

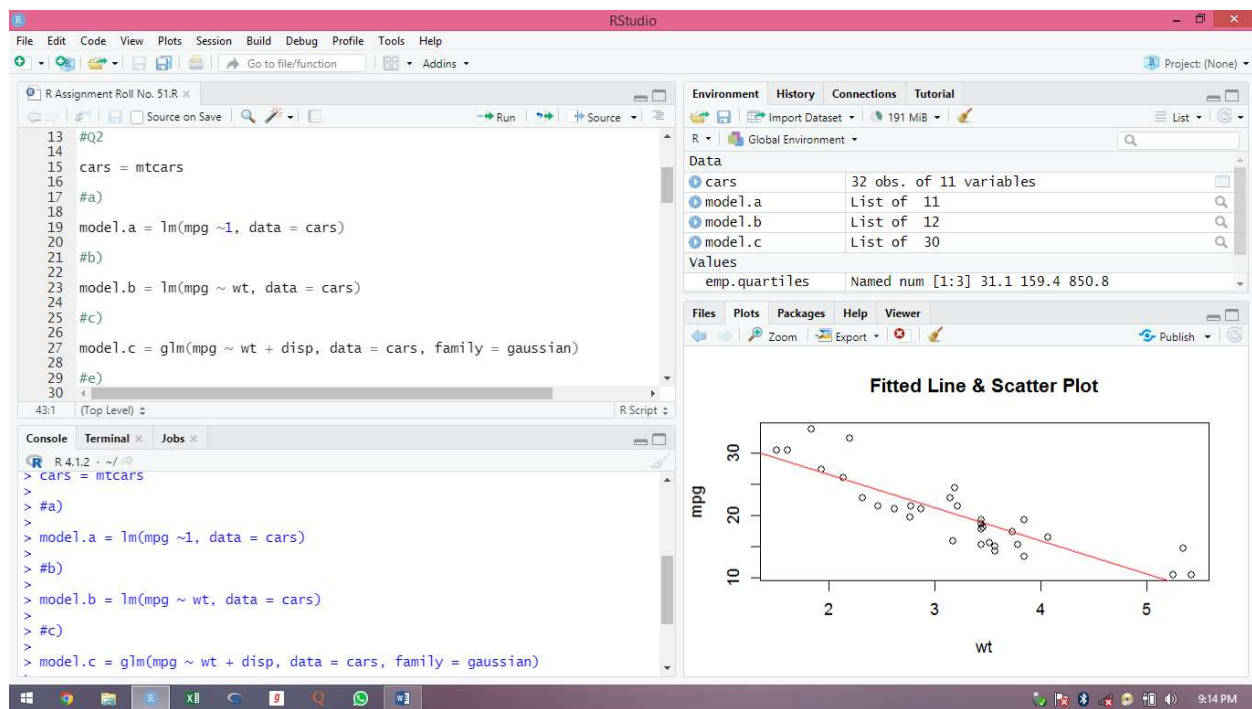
```
#c)
```

```
model.c = glm(mpg ~ wt + disp, data = cars, family = gaussian)
```

```
#e)
```

```
plot(cars$wt, cars$mpg, xlab = "wt", ylab = "mpg", main = "Fitted Line & Scatter Plot")
```

```
abline(model.b, col = "red", pch = 3)
```



#Question 3

```
set.seed(2919)
```

```
s = rnorm(100,5,2.5)
```

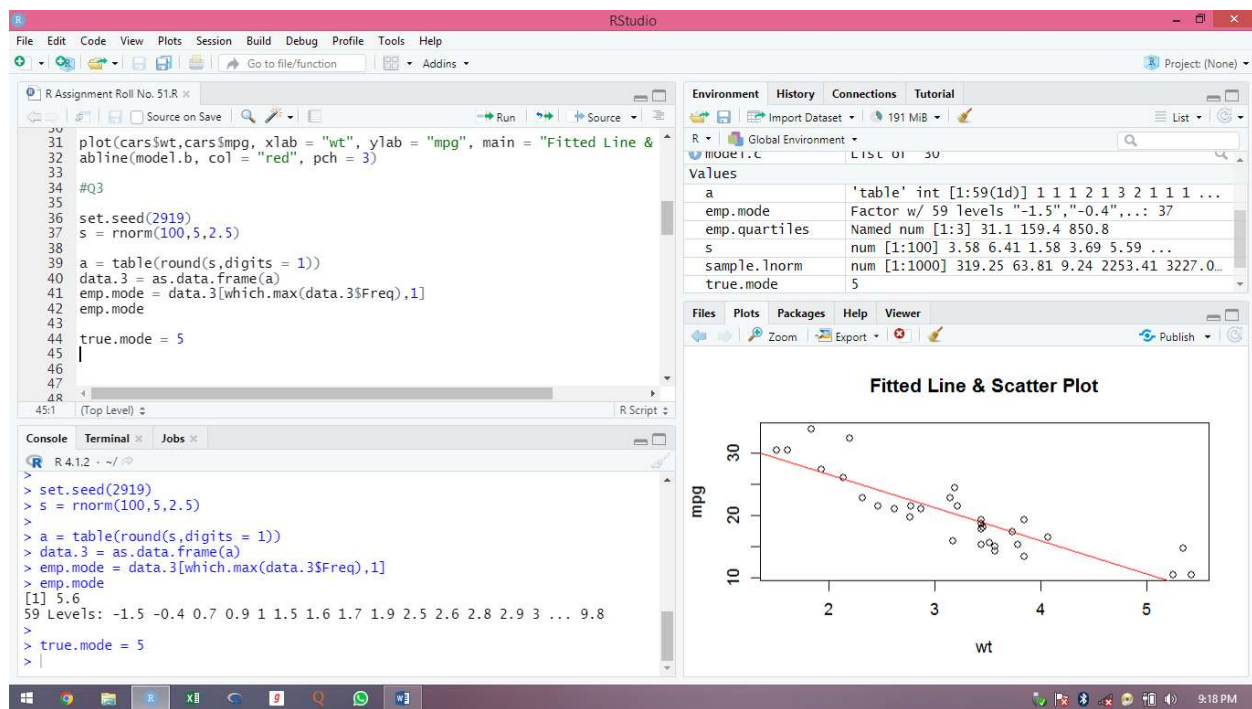
```
a = table(round(s,digits = 1))
```

```
data.3 = as.data.frame(a)
```

```
emp.mode = data.3[which.max(data.3$Freq),1]
```

```
emp.mode
```

```
true.mode = 5
```



#Question 4

```
X = c(0:6)
```

```
Obs.Frequency = c(739280,185309,23349,1937,114,1,3)
```

```
lambda.hat = sum(X*Obs.Frequency)/sum(Obs.Frequency)
```

```
chisq.test(Obs.Frequency,p = dpois(0:6,lambda.hat))
```

"Since p value is even less than 1%, we have sufficient evidence to reject

H0 i.e the sample is not from Poisson Distribution"

The screenshot displays the RStudio interface with the following components:

- Source Editor:** Contains R code for Question 4, including variable assignment and a chi-squared test. Line 54 is highlighted.
- Environment:** Lists objects in the Global Environment, including 'cars', 'data.3', 'model.a', 'model.b', 'model.c', and 'Values'.
- Console:** Shows the output of the chi-squared test, including the p-value (4.88e-06) and a warning message about the chi-squared approximation.
- Terminal:** Displays the command prompt and the execution of the R script.

```
#Q4
46
47
48
49 X = c(0:6)
50 Obs.Frequency = c(739280,185309,23349,1937,114,1,3)
51 lambda.hat = sum(X*Obs.Frequency)/sum(Obs.Frequency)
52 chisq.test(Obs.Frequency,p = dpois(0:6,lambda.hat))
53 "Since p value is even less than 1%, we have sufficient evidence to reject
54 H0 i.e the sample is not from Poisson Distribution"
55
56
57
58
59
60
61
62
63
```

Environment:

Object	Class	Size
cars	data.frame	32 obs. of 11 variables
data.3	data.frame	59 obs. of 2 variables
model.a	lm	List of 11
model.b	lm	List of 12
model.c	lm	List of 30
Values	table	int [1:59(1d)] 1 1 1 2 1 3 2 1 1 1 ...
emp.mode	Factor	w/ 59 levels "-1.5", "-0.4", ...: 37
emp.quantiles	Named num	[1:3] 31.1 159.4 850.8
lambda.hat	num	0.250840795669021
Obs.Frequency	num	[1:7] 739280 185309 23349 1937 114 ...
s	num	[1:100] 3.58 6.41 1.58 3.69 5.59 ...
sample.lnorm	num	[1:1000] 319.25 63.81 9.24 2253.41 3227.0...
true.mode	int	5
true.quantiles	num	[1:3] 27.5 148.4 801.3
X	int	[1:7] 0 1 2 3 4 5 6

Console:

```
R 4.1.2 ~ /
Chi-squared test for given probabilities

data: Obs.Frequency
X-squared = 34.721, df = 6, p-value = 4.88e-06

Warning message:
In chisq.test(Obs.Frequency, p = dpois(0:6, lambda.hat)) :
  chi-squared approximation may be incorrect
> "Since p value is even less than 1%, we have sufficient evidence to reject
+ H0 i.e the sample is not from Poisson Distribution"
[1] "Since p value is even less than 1%, we have sufficient evidence to reject
\nH0 i.e the sample is not from Poisson Distribution"
>
```

#Question 5

```
library(MASS)
```

```
Animals = Animals
```

```
View(Animals)
```

```
?MASS::Animals
```

#a)

"Body Weight and Brain Weight are positively correlated"

#c)

```
model.5 = lm(body ~ brain, data = Animals)
```

```
summary(model.5)
```

```
confint(model.5, level = 0.90)
```

"Since $0.6 <$ upper limit of 5% one-tailed test, we do not reject the hypothesis.

"

#d)

```
Animals$brain = Animals$brain/1000
```

```
t.test(Animals$body,Animals$brain, alternative = "greater",var.equal = T,  
      conf.level = 0.99)
```

"Since 0 is included in C.I, mean body weight is not always greater than mean
brain weight

"

#e)

```
qqnorm(Animals$body)
```

```
qqline(Animals$body)
```

```
qqnorm(Animals$brain)
```

```
qqline(Animals$brain)
```

"From the QQPlots it is indeed true that Brain weights are more likely to
follow normal distribution"

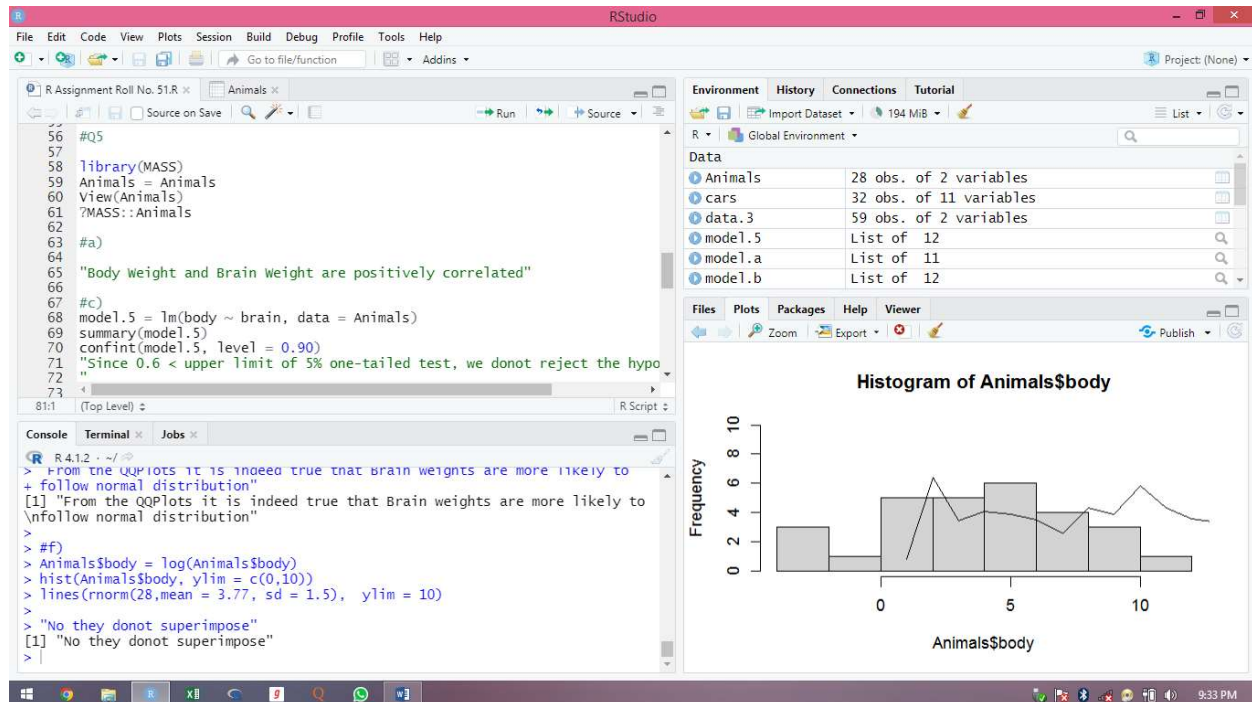
#f)

```
Animals$body = log(Animals$body)
```

```
hist(Animals$body, ylim = c(0,10))
```

```
lines(rnorm(28,mean = 3.77, sd = 1.5), ylim = 10)
```

"No they don't superimpose"



#Question 6

```
data = matrix(c(40, 20, 10,
```

```
30, 35, 15,
```

```
30, 45, 25), 3,3,byrow = T)
```

```
row.names(data) = c("SSC","Graduate","PG")
```

```
colnames(data) = c("A","B","C")
```

```
chisq.test(data)
```

"Here p value is even less than 1%. Therefore, party affiliation is not independent of education level."

RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins

Project (None)

R Assignment Roll No. 51.R Animals

```
94 hist(Animals$body, ylim = c(0,10))
95 lines(rnorm(28,mean = 3.77, sd = 1.5), ylim = 10)
96
97 "No they donot superimpose"
98
99 #Q6
100
101 data = matrix(c(40, 20, 10,
102                30, 35, 15,
103                30, 45, 25), 3,3,byrow = T)
104 row.names(data) = c("SSC", "Graduate", "PG")
105 colnames(data) = c("A", "B", "C")
106
107 chisq.test(data)
108 "Here p value is even less than 1%. Therefore, party affiliation is not
109 independent of education level."
110
```

110:1 (Top Level) R Script

Console Terminal Jobs

```
> chisq.test(data)
Pearson's Chi-squared test

data: data
X-squared = 13.415, df = 4, p-value = 0.009416

> "Here p value is even less than 1%. Therefore, party affiliation is not
+ independent of education level."
[1] "Here p value is even less than 1%. Therefore, party affiliation is not\ni
ndependent of education level."
>
```

Environment History Connections Tutorial

R Global Environment

Data

Animals	28 obs. of 2 variables
cars	32 obs. of 11 variables
data	num [1:3, 1:3] 40 30 30 20 35 45 10 15 25
data.3	59 obs. of 2 variables
model.5	List of 12
model.a	List of 11
model.b	List of 12
model.c	List of 30

Values

a	'table' int [1:59(1d)] 1 1 1 2 1 3 2 1 1 1 ...
emp.mode	Factor w/ 59 levels "-1.5","-0.4",...: 37
emp.quantiles	Named num [1:3] 31.1 159.4 850.8
lambda.hat	0.250840795669021
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s	num [1:100] 3.58 6.41 1.58 3.69 5.59 ...
sample.lnorm	num [1:1000] 319.25 63.81 9.24 2253.41 3227.0...
true.mode	5
true.quantiles	num [1:3] 27.5 148.4 801.3
X	int [1:7] 0 1 2 3 4 5 6

Files Plots Packages Help Viewer

9:35 PM