

Question 1: Roaming outdoor cats harm wildlife

Question 2: People should keep their cats indoors

Question 3: Pet cats should be spayed or neutered

Question 4: Pet cats should be microchipped

Question 5: Roaming outdoor cats pose a risk to human health

Question 1: Roaming outdoor cats harm wildlife

Question 2: People should keep their cats indoors

Question 3: Pet cats should be spayed or neutered

Question 4: Pet cats should be microchipped

Question 5: Roaming outdoor cats pose a risk to human health

Survey Monkey Data

Code ▼

Question 1: Roaming outdoor cats harm wildlife

A high number strongly agrees whereas a low number disagrees.

Question 1A: Roaming outdoor cats harm wildlife.

Answers: Strongly Agree = 7 Moderately Agree = 6 Slightly Agree = 5 Neither Agree or Disagree = 4 Slightly Disagree = 3 Moderately Disagree = 2 Strongly Disagree = 1

Question 1B: Roaming outdoor cats do not harm wildlife.

Answers: Strongly Agree = 1 Moderately Agree = 2 Slightly Agree = 3 Neither Agree or Disagree = 4 Slightly Disagree = 5 Moderately Disagree = 6 Strongly Disagree = 7

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```
ggplot(data = test, aes(x = "", y = Cnt, fill = Type )) +  
  geom_bar(stat = "identity", position = position_fill()) +  
  geom_text(aes(label = Cnt), position = position_fill(vjust = 0.5)) +  
  coord_polar(theta = "y") +  
  facet_wrap(~ City) +  
  theme(axis.title.x = element_blank(),  
        axis.title.y = element_blank()) +  
  theme(legend.position='bottom') +  
  guides(fill=guide_legend(nrow=2, byrow=TRUE))
```

Error: At least one layer must contain all faceting variables: `City`.

- * Plot is missing `City`
- * Layer 1 is missing `City`
- * Layer 2 is missing `City`

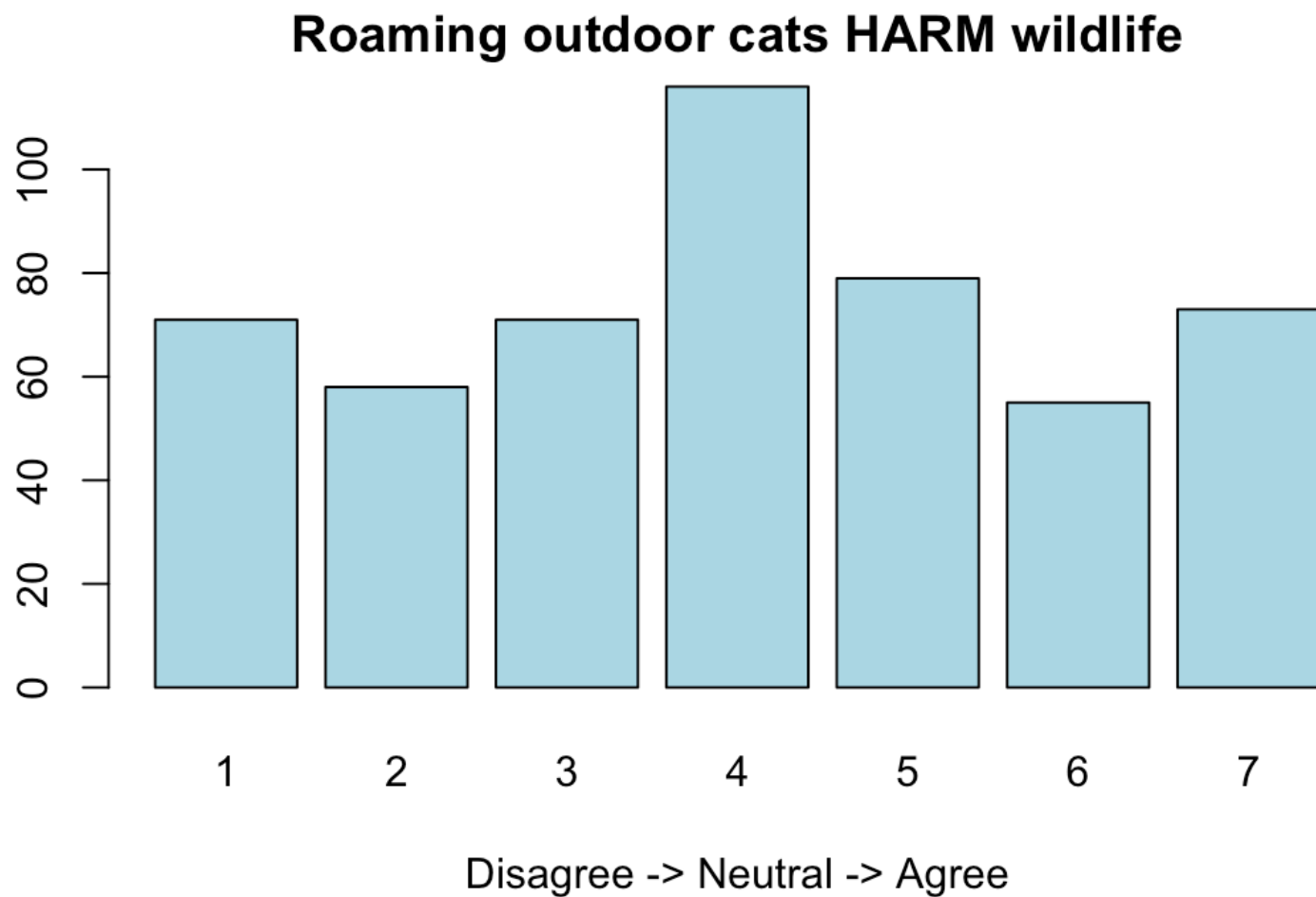
Hide

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```

library(car)
df <- read.csv(file = "Raw_Data.csv")
df$A1Num <- as.numeric(df$A1)
Q1A <- df[df[, "Q1"]=="Roaming outdoor cats harm wildlife",]
Q1A <- Q1A[, c(1,2,3,12:17)]
Q1A$A1Num <- recode(Q1A$A1Num,"1=6;2=2;3=4;4=5;5=3;6=7;7=1")
Q1B <- df[df[, "Q1"]=="Roaming outdoor cats do not harm wildlife",]
Q1B <- Q1B[, c(1,2,3,12:17)]
Q1B$A1Num <- recode(Q1B$A1Num,"1=2;2=6;3=4;4=3;5=5;6=1;7=7")
A <- as.numeric(Q1A$A1Num)
B <- as.numeric(Q1B$A1Num)
barplot(table(A), main = "Roaming outdoor cats HARM wildlife",xlab = "Disagr
ee -> Neutral -> Agree",col = "light blue")

```



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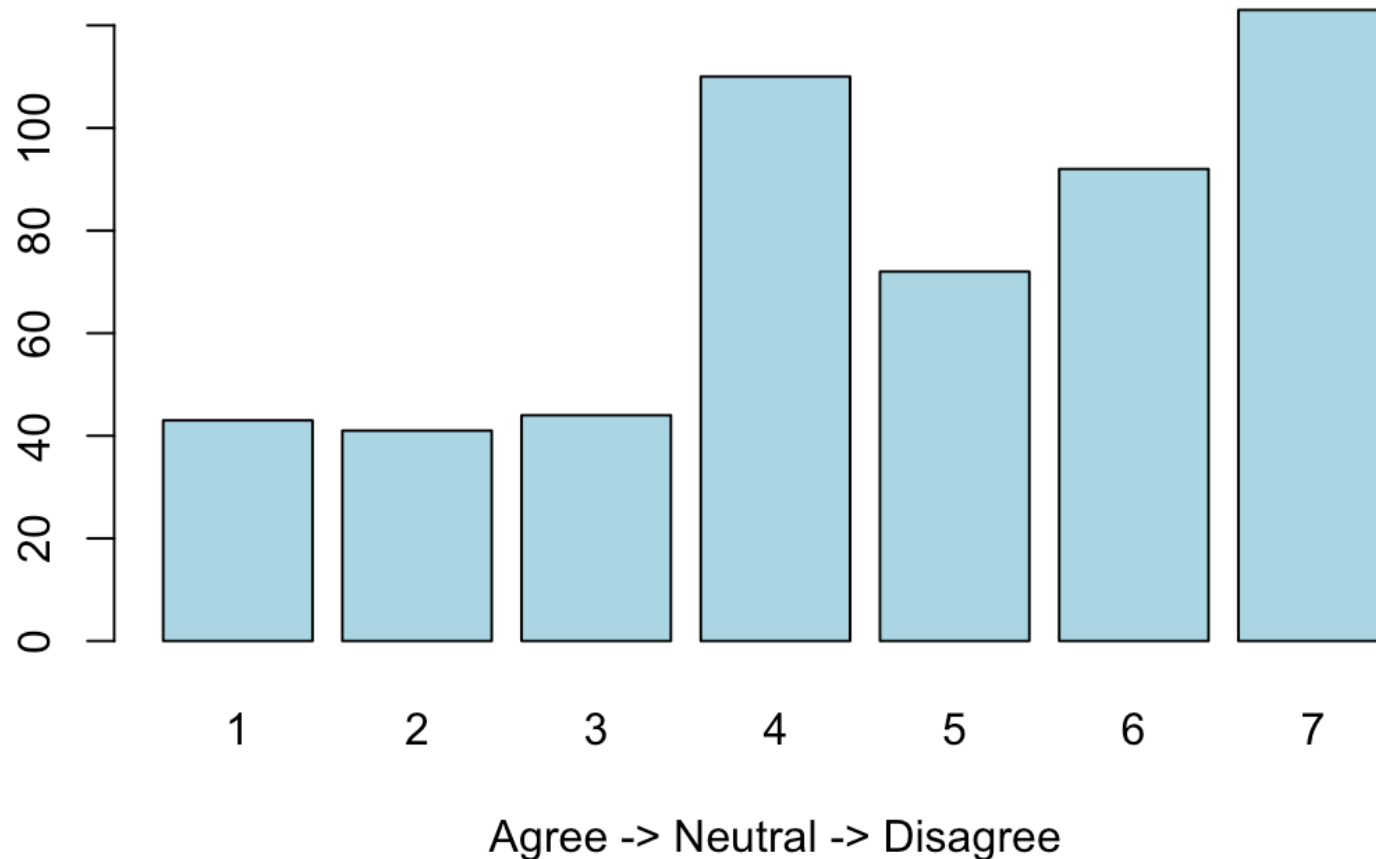
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```

barplot(table(B),main = "Roaming Cats DO NOT harm Wildlife",xlab = "Agree ->
Neutral -> Disagree", col = "light blue")

```

Roaming Cats DO NOT harm Wildlife



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```
Data <- data.frame(
  WtAnswer=c(A, B),
  Question =factor(rep(c("A", "B"), times=c(length(A), length(B))))
)
m <- aov(WtAnswer~Question,data = Data)
summary(m)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Question	1	125	124.54	34.47	5.8e-09 ***
Residuals	1046	3779	3.61		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Hide

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```
shapiro.test(Data$WtAnswer)
```

Shapiro-Wilk normality test

```
data: Data$WtAnswer
W = 0.91976, p-value < 2.2e-16
```

Hide

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```
print("From the output, the p-value < 0.05 implying that the distribution of  
the data are significantly different from normal distribution. In other wor  
ds, we can NOT assume the normality.")
```

```
[1] "From the output, the p-value < 0.05 implying that the distribution of t  
he data are significantly different from normal distribution. In other word  
s, we can NOT assume the normality."
```

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```
kruskal.test(WtAnswer ~ Question, data = Data)
```

Kruskal-Wallis rank sum test

data: WtAnswer by Question

Kruskal-Wallis chi-squared = 34.159, df = 1, p-value = 5.079e-09

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```
print("At .05 significance level, we conclude that the two questions have di  
fferent answers.")
```

```
[1] "At .05 significance level, we conclude that the two questions have diff  
erent answers."
```

Hide

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```
fligner.test(WtAnswer ~ Question, data = Data)
```

Fligner-Killeen test of homogeneity of variances

data: WtAnswer by Question

Fligner-Killeen:med chi-squared = 0.32674, df = 1, p-value = 0.5676

Question 2: People should keep their

cats indoors

A high number strongly agrees whereas a low number disagrees.

Question 2A: People should keep their cats indoors or under a person's control (e.g., leash, catio) while outdoors.

Answers: Strongly Agree = 7 Moderately Agree = 6 Slightly Agree = 5 Neither Agree or Disagree = 4 Slightly Disagree = 3 Moderately Disagree = 2 Strongly Disagree = 1

Question 2B: People need not keep their cats indoors or under a person's control (e.g., leash, catio) while outdoors.

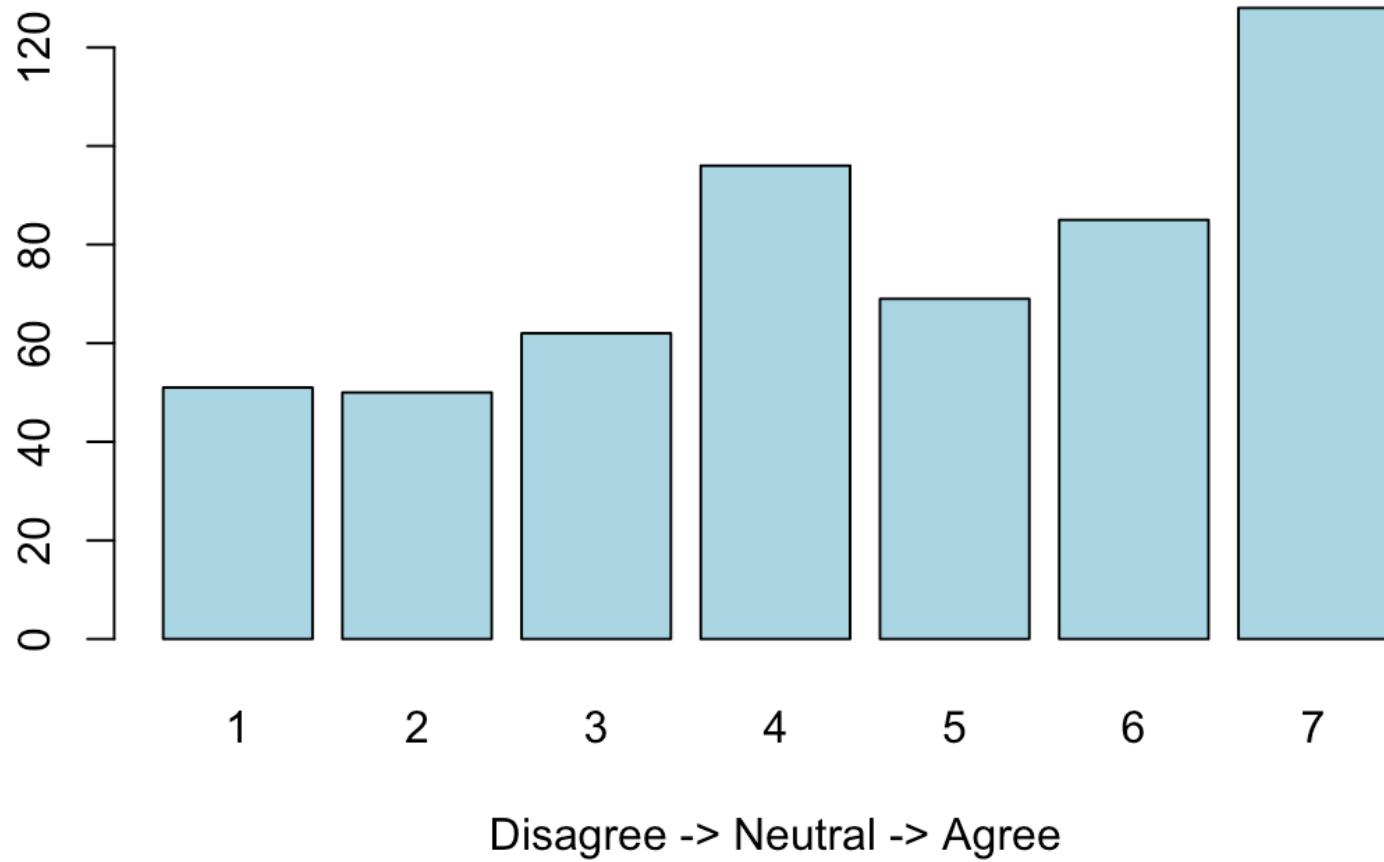
Answers: Strongly Agree = 1 Moderately Agree = 2 Slightly Agree = 3 Neither Agree or Disagree = 4 Slightly Disagree = 5 Moderately Disagree = 6 Strongly Disagree = 7

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```
df <- read.csv(file = "Raw_Data.csv")
df$A2Num <- as.numeric(df$A2)
Q2A <- df[df[, "Q2"]=="People should keep their cats indoors or under a person's control (e.g., leash, catio) while outdoors",]
Q2A <- Q2A[, c(1,4,5,12:17)]
Q2A$A2Num <- recode(Q2A$A2Num, "1=6;2=2;3=4;4=5;5=3;6=7;7=1")
Q2B <- df[df[, "Q2"]=="People need not keep their cats indoors or under a person's control (e.g., leash, catio) while outdoors",]
Q2B <- Q2B[, c(1,4,5,12:17)]
Q2B$A2Num <- recode(Q2B$A2Num, "1=2;2=6;3=4;4=3;5=5;6=1;7=7")
A <- as.numeric(Q2A$A2Num)
B <- as.numeric(Q2B$A2Num)
barplot(table(A), main = "People SHOULD keep their cats indoors", xlab = "Disagree -> Neutral -> Agree", col = "light blue")
```

People SHOULD keep their cats indoors

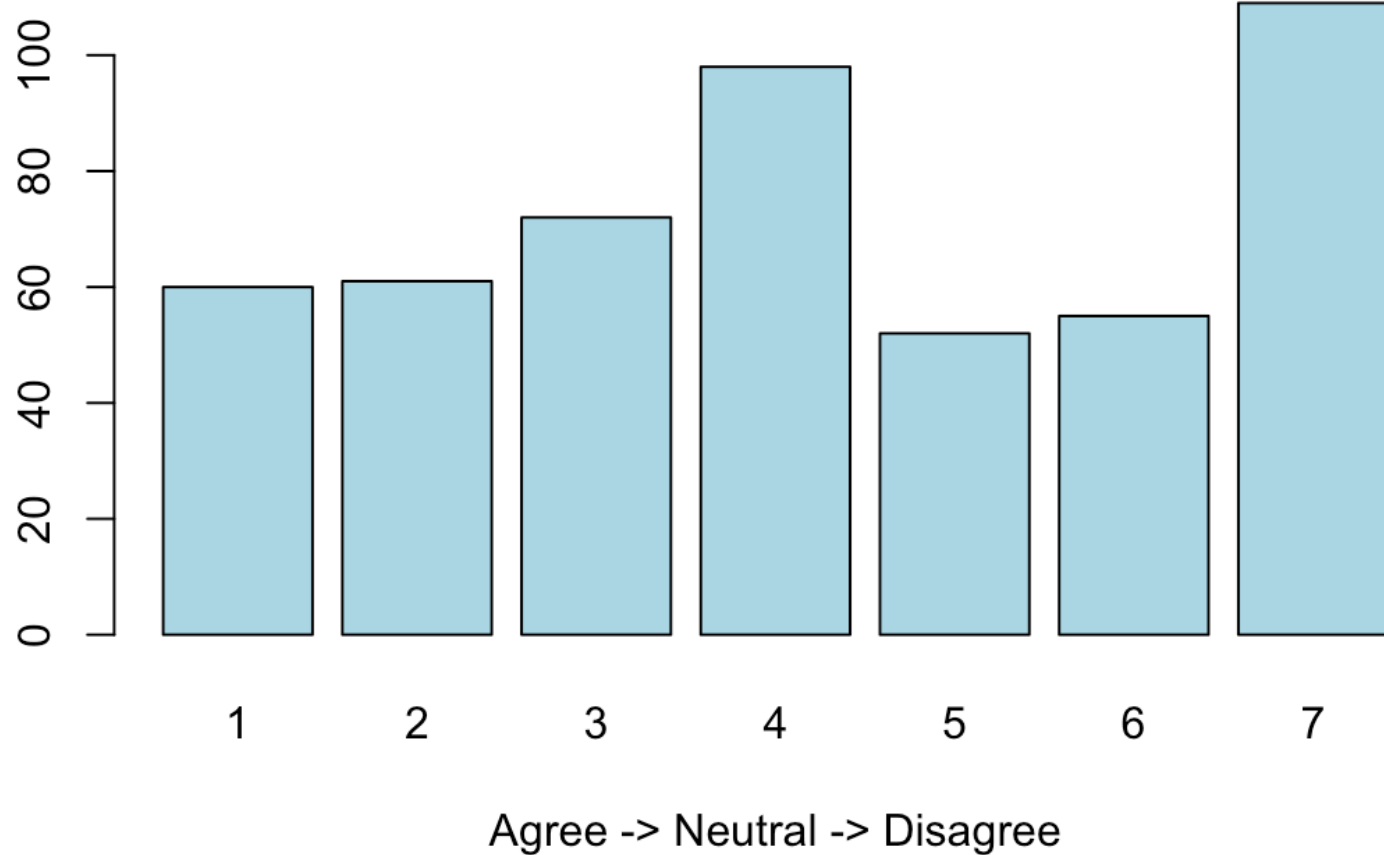


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```
barplot(table(B),main = "People need NOT keep their cats indoors",xlab = "Agree -> Neutral -> Disagree", col = "light blue")
```

People need NOT keep their cats indoors



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```
Data <- data.frame(
  WtAnswer=c(A, B),
  Question =factor(rep(c("A", "B"), times=c(length(A), length(B))))
)
m <- aov(WtAnswer~Question,data = Data)
summary(m)
```

```
              Df Sum Sq Mean Sq F value    Pr(>F)
Question         1      31   30.700     7.665 0.00573 **
Residuals    1046     4190    4.005
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
shapiro.test(Data$WtAnswer)
```

Shapiro-Wilk normality test

```
data:  Data$WtAnswer
W = 0.90762, p-value < 2.2e-16
```

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```
print("From the output, the p-value < 0.05 implying that the distribution of
the data are significantly different from normal distribution. In other wor
ds, we can NOT assume the normality.")
```

```
[1] "From the output, the p-value < 0.05 implying that the distribution of t
he data are significantly different from normal distribution. In other word
s, we can NOT assume the normality."
```

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```
kruskal.test(WtAnswer ~ Question, data = Data)
```



```
Kruskal-Wallis rank sum test
```

```
data: WtAnswer by Question
```

```
Kruskal-Wallis chi-squared = 7.4214, df = 1, p-value = 0.006445
```

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```
print("At .05 significance level, we conclude that the two questions have different answers.")
```

```
[1] "At .05 significance level, we conclude that the two questions have different answers."
```

Question 3: Pet cats should be spayed or neutered

A high number strongly agrees whereas a low number disagrees.

Question 3A: Pet cats should be spayed or neutered unless intended for breeding.

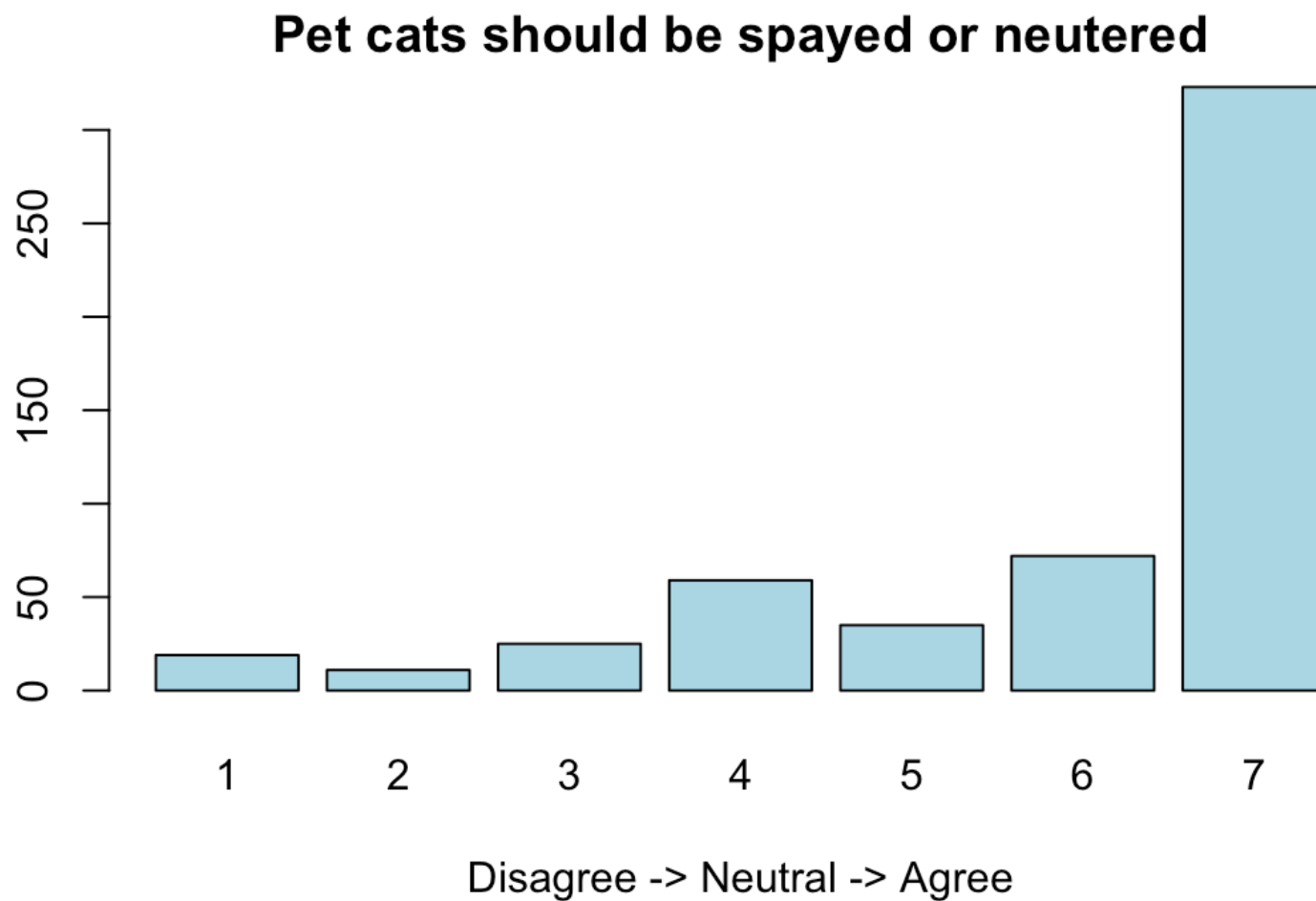
Answers: Strongly Agree = 7 Moderately Agree = 6 Slightly Agree = 5 Neither Agree or Disagree = 4 Slightly Disagree = 3 Moderately Disagree = 2 Strongly Disagree = 1

Question 3B: Pet cats not intended for breeding need not be spayed or neutered.

Answers: Strongly Agree = 1 Moderately Agree = 2 Slightly Agree = 3 Neither Agree or Disagree = 4 Slightly Disagree = 5 Moderately Disagree = 6 Strongly Disagree = 7

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```
df <- read.csv(file = "Raw_Data.csv")
df$A3Num <- as.numeric(df$A3)
Q3A <- df[df[, "Q3"]=="Pet cats should be spayed or neutered unless intended
for breeding",]
Q3A <- Q3A[, c(1,6,7,12:17)]
Q3A$A3Num <- recode(Q3A$A3Num,"1=6;2=2;3=4;4=5;5=3;6=7;7=1")
Q3B <- df[df[, "Q3"]=="Pet cats not intended for breeding need not be spayed
or neutered",]
Q3B <- Q3B[, c(1,6,7,12:17)]
Q3B$A3Num <- recode(Q3B$A3Num,"1=2;2=6;3=4;4=3;5=5;6=1;7=7")
A <- as.numeric(Q3A$A3Num)
B <- as.numeric(Q3B$A3Num)
barplot(table(A), main = "Pet cats should be spayed or neutered", xlab = "Di
sagree -> Neutral -> Agree",col = "light blue")
```

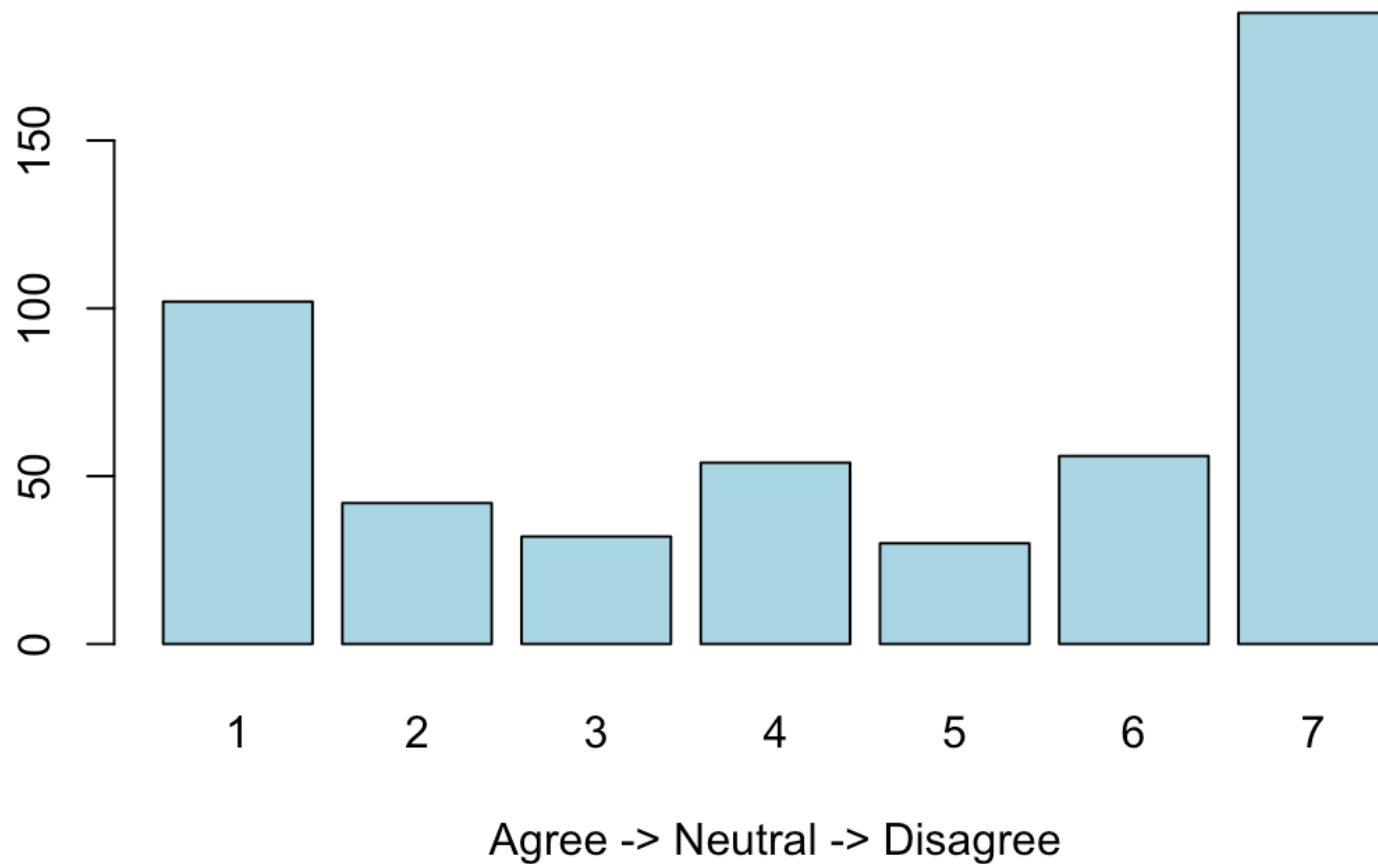


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```
barplot(table(B),main = "Pet cats need not be spayed or neutered",xlab = "Ag
ree -> Neutral -> Disagree", col = "light blue")
```

Pet cats need not be spayed or neutered



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```
Data <- data.frame(
  WtAnswer=c(A, B),
  Question =factor(rep(c("A", "B"), times=c(length(A), length(B))))
)
m <- aov(WtAnswer~Question,data = Data)
summary(m)
```

```
          Df Sum Sq Mean Sq F value Pr(>F)
Question    1    481   480.8   115.1 <2e-16 ***
Residuals 1046   4370     4.2
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
shapiro.test(Data$WtAnswer)
```

Shapiro-Wilk normality test

```
data:  Data$WtAnswer
W = 0.76684, p-value < 2.2e-16
```

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```
print("From the output, the p-value < 0.05 implying that the distribution of  
the data are significantly different from normal distribution. In other wor  
ds, we can NOT assume the normality.")
```

```
[1] "From the output, the p-value < 0.05 implying that the distribution of t  
he data are significantly different from normal distribution. In other word  
s, we can NOT assume the normality."
```

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```
kruskal.test(WtAnswer ~ Question, data = Data)
```

Kruskal-Wallis rank sum test

```
data: WtAnswer by Question  
Kruskal-Wallis chi-squared = 87.577, df = 1, p-value < 2.2e-16
```

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```
print("At .05 significance level, we conclude that the two questions have di  
fferent answers.")
```

```
[1] "At .05 significance level, we conclude that the two questions have diff  
erent answers."
```

Question 4: Pet cats should be microchipped

A high number strongly agrees whereas a low number disagrees.

Question 4A: Pet cats should be microchipped (a microchip is a small identification device inserted under the animal's skin).

Answers: Strongly Agree = 7 Moderately Agree = 6 Slightly Agree = 5 Neither Agree or Disagree = 4
Slightly Disagree = 3 Moderately Disagree = 2 Strongly Disagree = 1

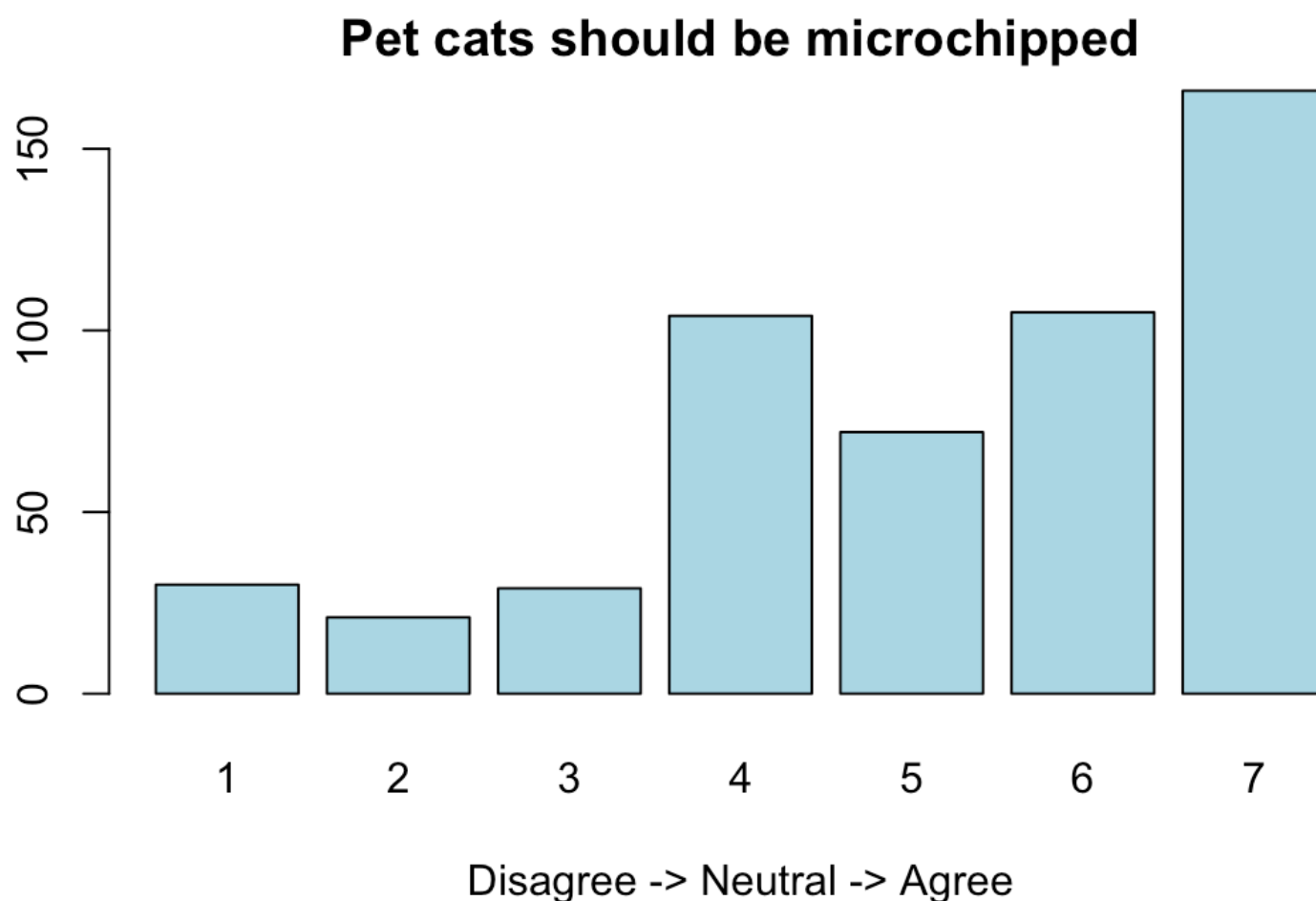
Question 4B: Pet cats need not be microchipped (a microchip is a small identification device inserted under the animal's skin).

Answers: Strongly Agree = 1 Moderately Agree = 2 Slightly Agree = 3 Neither Agree or Disagree = 4 Slightly Disagree = 5 Moderately Disagree = 6 Strongly Disagree = 7

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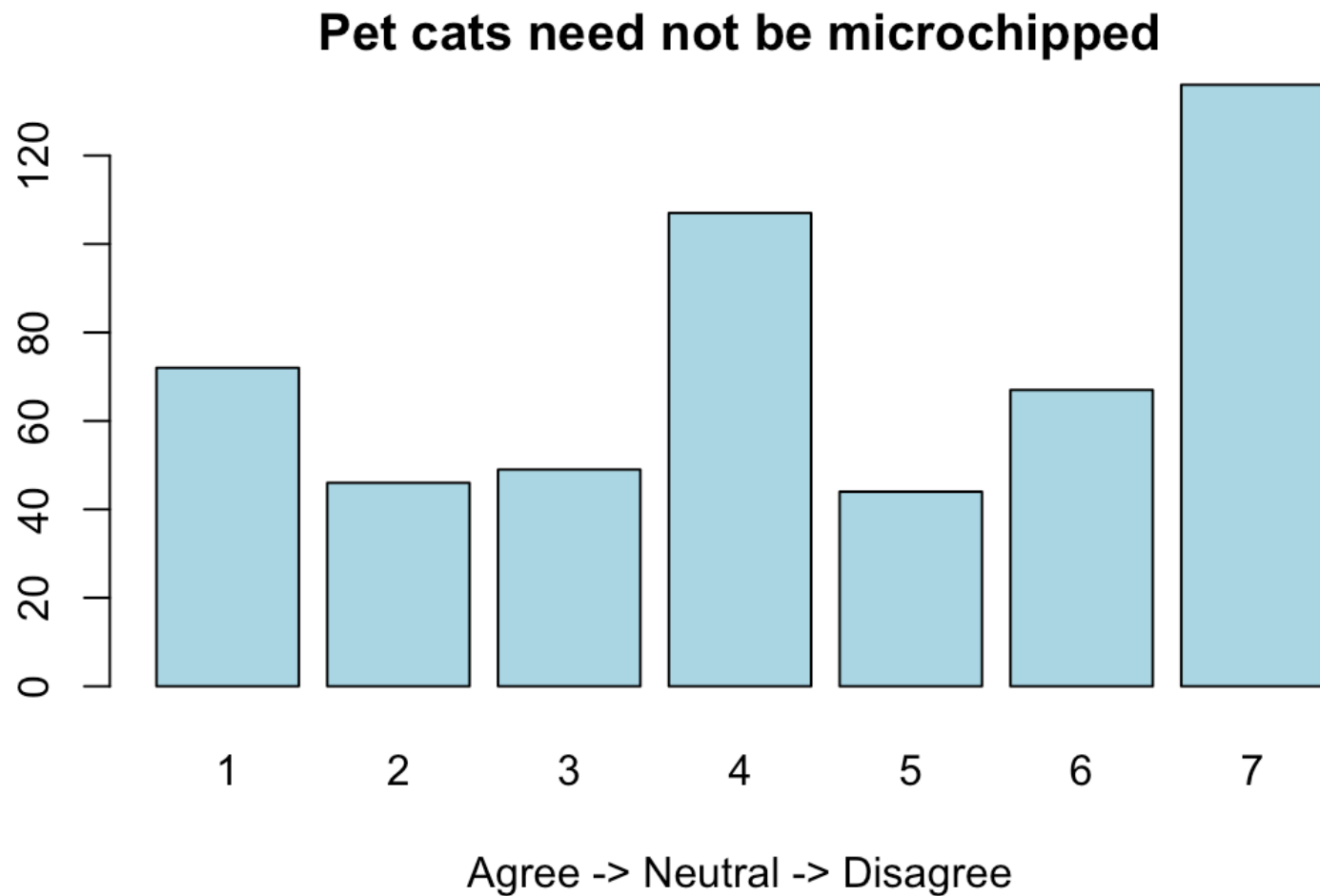
```
df <- read.csv(file = "Raw_Data.csv")
df$A4Num <- as.numeric(df$A4)
Q4A <- df[df[, "Q4"]=="Pet cats should be microchipped (a microchip is a small identification device inserted under the animal's skin)<br>",]
Q4A <- Q4A[, c(1,8,9,12:17)]
Q4A$A4Num <- recode(Q4A$A4Num, "1=6;2=2;3=4;4=5;5=3;6=7;7=1")
Q4B <- df[df[, "Q4"]=="Pet cats need not be microchipped (a microchip is a small identification device inserted under the animal's skin)",]
Q4B <- Q4B[, c(1,8,9,12:17)]
Q4B$A4Num <- recode(Q4B$A4Num, "1=2;2=6;3=4;4=3;5=5;6=1;7=7")
A <- as.numeric(Q4A$A4Num)
B <- as.numeric(Q4B$A4Num)
barplot(table(A), main = "Pet cats should be microchipped", xlab = "Disagree -> Neutral -> Agree", col = "light blue")
```



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```
barplot(table(B),main = "Pet cats need not be microchipped",xlab = "Agree -> Neutral -> Disagree", col = "light blue")
```

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```
Data <- data.frame(
  WtAnswer=c(A, B),
  Question =factor(rep(c("A", "B"), times=c(length(A), length(B))))
)
m <- aov(WtAnswer~Question,data = Data)
summary(m)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Question	1	142	141.55	37.41	1.35e-09 ***
Residuals	1046	3958	3.78		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

[Hide](#)[Hide](#)

```
shapiro.test(Data$WtAnswer)
```

Shapiro-Wilk normality test

```
data: Data$WtAnswer  
W = 0.88019, p-value < 2.2e-16
```

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```
print("From the output, the p-value < 0.05 implying that the distribution of  
the data are significantly different from normal distribution. In other wor  
ds, we can NOT assume the normality.")
```

```
[1] "From the output, the p-value < 0.05 implying that the distribution of t  
he data are significantly different from normal distribution. In other word  
s, we can NOT assume the normality."
```

Hide

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```
kruskal.test(WtAnswer ~ Question, data = Data)
```

Kruskal-Wallis rank sum test

```
data: WtAnswer by Question  
Kruskal-Wallis chi-squared = 29.942, df = 1, p-value = 4.452e-08
```

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```
print("At .05 significance level, we conclude that the two questions have di  
fferent answers.")
```

```
[1] "At .05 significance level, we conclude that the two questions have diff  
erent answers."
```

Question 5: Roaming outdoor cats pose a risk to human health

A high number strongly agrees whereas a low number disagrees.

Question 5A: Roaming outdoor cats pose a risk to human health.

Answers: Strongly Agree = 7 Moderately Agree = 6 Slightly Agree = 5 Neither Agree or Disagree = 4 Slightly Disagree = 3 Moderately Disagree = 2 Strongly Disagree = 1

Question 5B: Roaming outdoor cats do not pose a risk to human health.

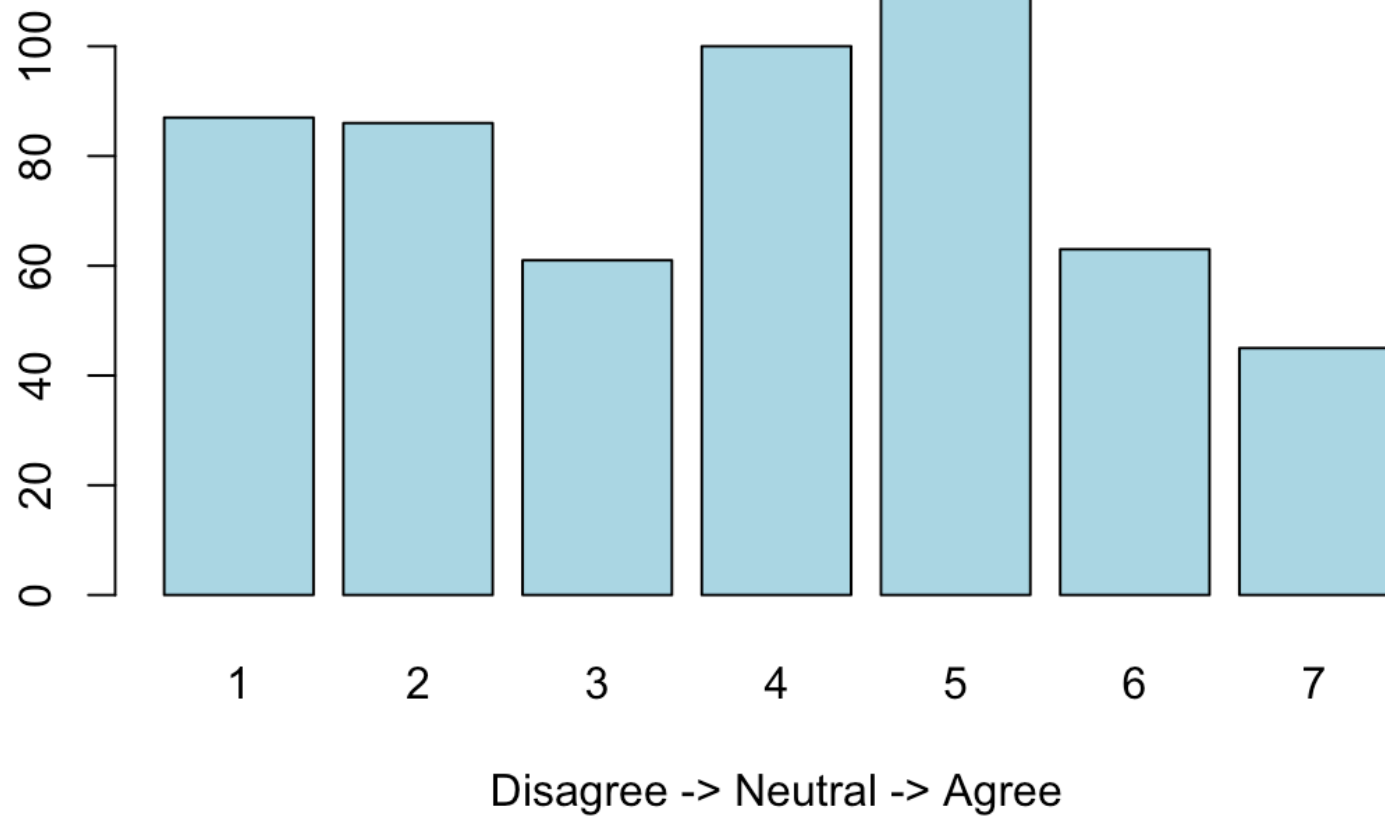
Answers: Strongly Agree = 1 Moderately Agree = 2 Slightly Agree = 3 Neither Agree or Disagree = 4 Slightly Disagree = 5 Moderately Disagree = 6 Strongly Disagree = 7

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```
df <- read.csv(file = "Raw_Data.csv")
df$A5Num <- as.numeric(df$A5)
Q5A <- df[df[, "Q5"] == "Roaming outdoor cats pose a risk to human health<br>",
]
Q5A <- Q5A[, c(1, 10, 11, 12:17)]
Q5A$A5Num <- recode(Q5A$A5Num, "1=6;2=2;3=4;4=5;5=3;6=7;7=1")
Q5B <- df[df[, "Q5"] == "Roaming outdoor cats do not pose a risk to human health",
]
Q5B <- Q5B[, c(1, 10, 11, 12:17)]
Q5B$A5Num <- recode(Q5B$A5Num, "1=2;2=6;3=4;4=3;5=5;6=1;7=7")
A <- as.numeric(Q5A$A5Num)
B <- as.numeric(Q5B$A5Num)
barplot(table(A), main = "Roaming outdoor cats pose a risk to human health",
xlab = "Disagree -> Neutral -> Agree", col = "light blue")
```


Roaming outdoor cats pose a risk to human health

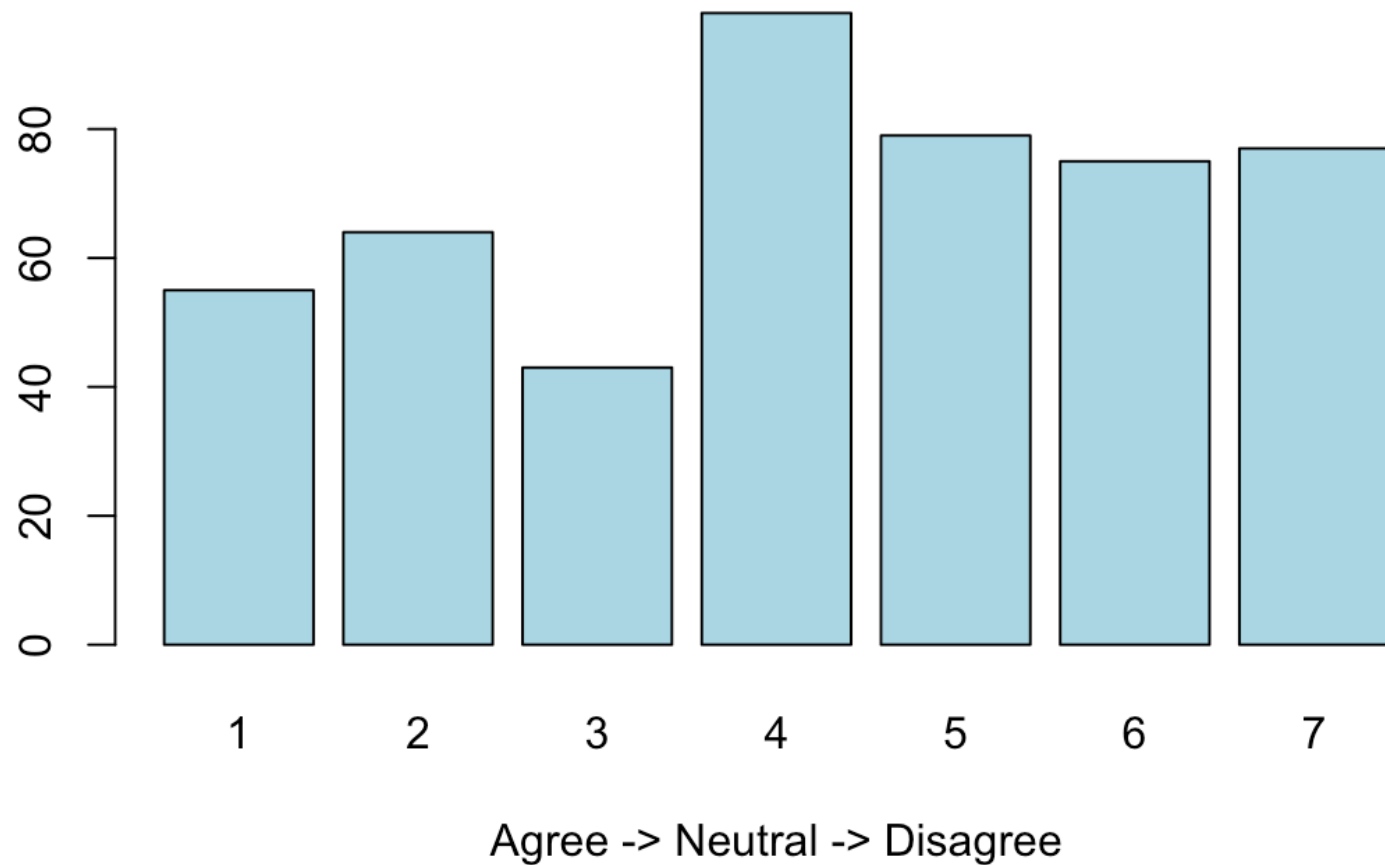


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```
barplot(table(B),main = "Roaming outdoor cats do not pose a risk to human health",xlab = "Agree -> Neutral -> Disagree", col = "light blue")
```

Roaming outdoor cats do not pose a risk to human health



Hide

Hide

```
Data <- data.frame(
  WtAnswer=c(A, B),
  Question =factor(rep(c("A", "B"), times=c(length(A), length(B))))
)
m <- aov(WtAnswer~Question,data = Data)
summary(m)
```

```
              Df Sum Sq Mean Sq F value    Pr(>F)
Question         1      56    56.28   15.62 8.28e-05 ***
Residuals    1046     3770     3.60
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hide

Hide

```
shapiro.test(Data$WtAnswer)
```

Shapiro-Wilk normality test

```
data:  Data$WtAnswer
W = 0.92644, p-value < 2.2e-16
```

Hide

Hide

```
print("From the output, the p-value < 0.05 implying that the distribution of
the data are significantly different from normal distribution. In other wor
ds, we can NOT assume the normality.")
```

```
[1] "From the output, the p-value < 0.05 implying that the distribution of t
he data are significantly different from normal distribution. In other word
s, we can NOT assume the normality."
```

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```
kruskal.test(WtAnswer ~ Question, data = Data)
```

Kruskal-Wallis rank sum test

data: WtAnswer by Question

Kruskal-Wallis chi-squared = 14.935, df = 1, p-value = 0.0001113

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```
print("At .05 significance level, we conclude that the two questions have different answers.")
```

```
[1] "At .05 significance level, we conclude that the two questions have different answers."
```