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title: "Practice with Dataframes"
output:
  pdf_document: default
  html_document:
    df_print: paged
editor_options:
  chunk_output_type: inline
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```{r}
#to read data from csv file
bat=read.csv('Data/bats.csv')
str(bat)
```

```{r}
#the chance of a random bat carrying Ebola virus=calculating mean of ebola being true
mean(bat$Ebola=="TRUE")
mean(bat$Ebola=="TRUE")*100
```

```{r}
#for each gene calculating the likelihood that is expressed in a random bat=calculating
mean of gene-1 being true
mean(bat$Gene.1=="TRUE")
mean(bat$Gene.1=="TRUE")*100
```

```{r}
#for each gene calculating the likelihood that is expressed in a random bat=calculating
mean of gene-1 being true
mean(bat$Gene.2=="TRUE")
mean(bat$Gene.2=="TRUE")*100
```

```{r}
#for each gene calculating the likelihood that is expressed in a random bat=calculating
mean of gene-1 being true
mean(bat$Gene.3=="TRUE")
mean(bat$Gene.3=="TRUE")*100
```

```{r}
#for each gene calculating the likelihood that is expressed in a random bat=calculating
mean of gene-1 being true
mean(bat$Gene.4=="TRUE")
mean(bat$Gene.4=="TRUE")*100
```

```{r}
#for each gene calculating the likelihood that is expressed in a random bat=calculating
mean of gene-1 being true
mean(bat$Gene.5=="TRUE")
mean(bat$Gene.5=="TRUE")*100
```

```{r}
#is the presence or absence of any of the genes indicative of a random bat potentially
carrying Ebola virus=conditional probability of bat with gene=true and carrying ebola
virus.i.e ebola=true
mean(bat[bat$Gene.1=="TRUE",]$Ebola=="TRUE")
mean(bat[bat$Gene.1=="TRUE",]$Ebola=="TRUE")*100
```

```{r}

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#is the presence or absence of any of the genes indicative of a random bat potentially
carrying Ebola virus=conditional probability of bat with gene=true and carrying ebola
virus.i.e ebola=true
mean(bat[bat$Gene.2=="TRUE",]$Ebola=="TRUE")
mean(bat[bat$Gene.2=="TRUE",]$Ebola=="TRUE")*100
```


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```{r}
#is the presence or absence of any of the genes indicative of a random bat potentially
carrying Ebola virus=conditional probability of bat with gene=true and carrying ebola
virus.i.e ebola=true
mean(bat[bat$Gene.3=="TRUE",]$Ebola=="TRUE")
mean(bat[bat$Gene.3=="TRUE",]$Ebola=="TRUE")*100
```


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```{r}
#is the presence or absence of any of the genes indicative of a random bat potentially
carrying Ebola virus=conditional probability of bat with gene=true and carrying ebola
virus.i.e ebola=true
mean(bat[bat$Gene.4=="TRUE",]$Ebola=="TRUE")
mean(bat[bat$Gene.4=="TRUE",]$Ebola=="TRUE")*100
```


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```{r}
#is the presence or absence of any of the genes indicative of a random bat potentially
carrying Ebola virus=conditional probability of bat with gene=true and carrying ebola
virus.i.e ebola=true
mean(bat[bat$Gene.5=="TRUE",]$Ebola=="TRUE")
mean(bat[bat$Gene.5=="TRUE",]$Ebola=="TRUE")*100
```


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```{r}
((mean(bat[bat$Gene.1=="TRUE",]$Ebola=="TRUE")-mean(bat$Ebola=="TRUE"))/mean(bat$Ebola))
```



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```{r}
((mean(bat[bat$Gene.2=="TRUE",]$Ebola=="TRUE")-mean(bat$Ebola=="TRUE"))/mean(bat$Ebola))
```


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```{r}
((mean(bat[bat$Gene.3=="TRUE",]$Ebola=="TRUE")-mean(bat$Ebola=="TRUE"))/mean(bat$Ebola))
```


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```{r}
((mean(bat[bat$Gene.4=="TRUE",]$Ebola=="TRUE")-mean(bat$Ebola=="TRUE"))/mean(bat$Ebola))
```


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```{r}
((mean(bat[bat$Gene.5=="TRUE",]$Ebola=="TRUE")-mean(bat$Ebola=="TRUE"))/mean(bat$Ebola))
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