

Mam, I am taking the msleep data-set for visualization purpose

Description of the data-set

This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage

msleep

Format

A data frame with 83 rows and 11 variables:

name
common name

genus
vore

carnivore, omnivore or herbivore?

order
conservation

the conservation status of the animal

sleep_total

total amount of sleep, in hours

sleep_rem

rem sleep, in hours

sleep_cycle

length of sleep cycle, in hours

awake

amount of time spent awake, in hours

brainwt

brain weight in kilograms

bodywt

body weight in kilograms

Details

Additional variables order, conservation status and vore were added from wikipedia.

Loading the libraries and the data-set

```
```{r}
library(ggplot2) ## msleep is included in ggplot2
library(plotly)
library(data.table)
```

```{r}
print(paste("Attributes of the data-set"))
colnames(df)
```

[1] "Attributes of the data-set"
[1] "name"          "genus"         "vore"          "order"         "conservation" "sleep_total"
[7] "sleep_rem"     "sleep_cycle"   "awake"         "brainwt"       "bodywt"

```{r}
str(df)
```

tibble [83 x 11] (S3:tbl_df/tbl/data.frame)
$ name      : chr [1:83] "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed shrew" ...
$ genus     : chr [1:83] "Acinonyx" "Aotus" "Aplodontia" "Blarina" ...
$ vore      : chr [1:83] "carni" "omni" "herbi" "omni" ...
$ order     : chr [1:83] "Carnivora" "Primates" "Rodentia" "Soricomorpha" ...
$ conservation: chr [1:83] "lc" NA "nt" "lc" ...
$ sleep_total : num [1:83] 12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
$ sleep_rem  : num [1:83] NA 1.8 2.4 2.3 0.7 2.2 1.4 NA 2.9 NA ...
$ sleep_cycle: num [1:83] NA NA NA 0.133 0.667 ...
$ awake     : num [1:83] 11.9 7 9.6 9.1 20 9.6 15.3 17 13.9 21 ...
$ brainwt   : num [1:83] NA 0.0155 NA 0.00029 0.423 NA NA NA 0.07 0.0982 ...
$ bodywt    : num [1:83] 50 0.48 1.35 0.019 600 ...
```

1) Scatter Plot

File list

```
scatterplot.R
boxplot.R
donut.R
barplot.R
piechart.R
histogram.R
```

scatterplot.R

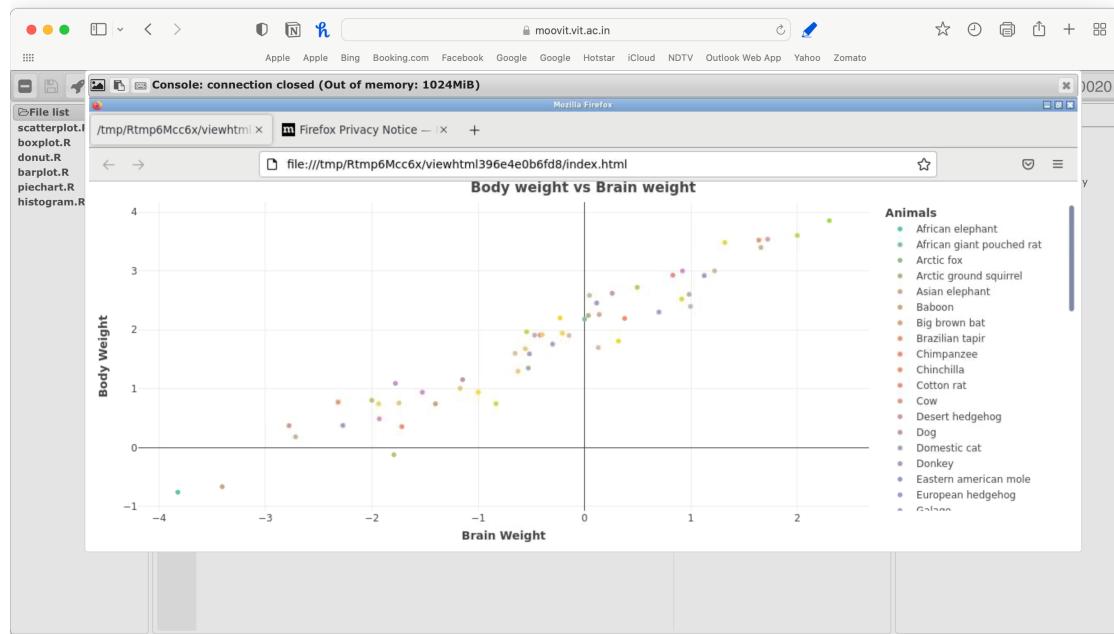
```
1 library(ggplot2) ## msleep is included in ggplot-2
2 library(plotly)
3 library(data.table)
4 library(plotly)
5 library(dplyr)
6
7
8 scatter_plot = plot_ly(data=msleep, x=-(-log10(bodywt)), y=-(-log10(brainwt)), color = ~name,
9   type='scatter', mode='markers') %>%
10   layout(
11     title= list(text = "Body weight vs Brain weight"),
12     legend = list(title = list(text = "Animals")),
13     xaxis = list(title = list(text = "Brain Weight")),
14     yaxis = list(title = list(text = "Body Weight")))
15
16
17 scatter_plot
18
19
```

Description

Use any of the inbuilt datasets(except Iris) and try the following basic graphs using plotly

1) Scatter plot
2) Bar graph(regular, stacked, group)
3) Histogram
4) Pie chart
5) donut chart
6) Box plot

and any others.
Upload this exercise on VTOP



1) Bar plot

The screenshot shows an RStudio interface. On the left, a file list pane contains files: scatterplot.R, boxplot.R, donut.R, barplot.R, piechart.R, and histogram.R. The main pane displays R code for creating a bar plot:

```
## Bar graph
library(ggplot2)
library(datasets)
library(data.table)
library(plotly)
library(dplyr)

r_barplot = plot_ly(data=df, y=order, type="bar") %>%
  layout(
    title=list(text = "<b>Total sleep time of Animals based on Vore</b>"),
    legend=list(title = list(text="Vore")),
    xaxis = list(title = list(text = "<b>sleep total</b>"), tickformat = "%"),
    yaxis = list(title = list(text = "<b>Count</b>")))
r_barplot
```

Below the code, there is a sidebar with a 'Description' section containing instructions and numbered items 1 through 6, followed by a note about other plots and a link to upload the exercise.

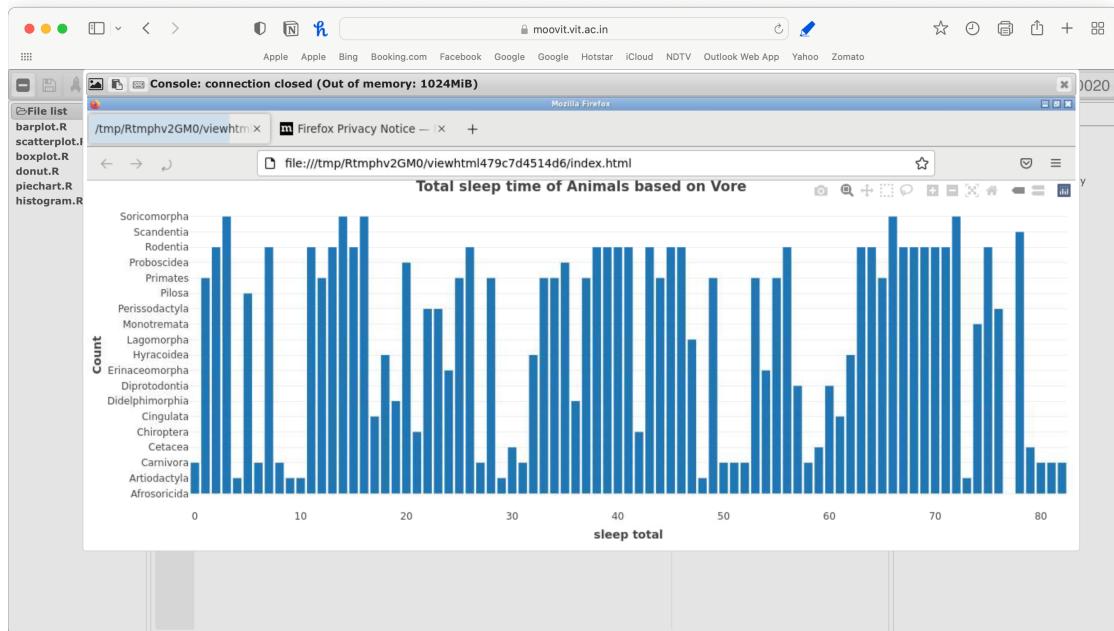
Use any of the inbuilt datasets(except Iris) and try the following basic graphs using plotly

- 1) Scatter plot
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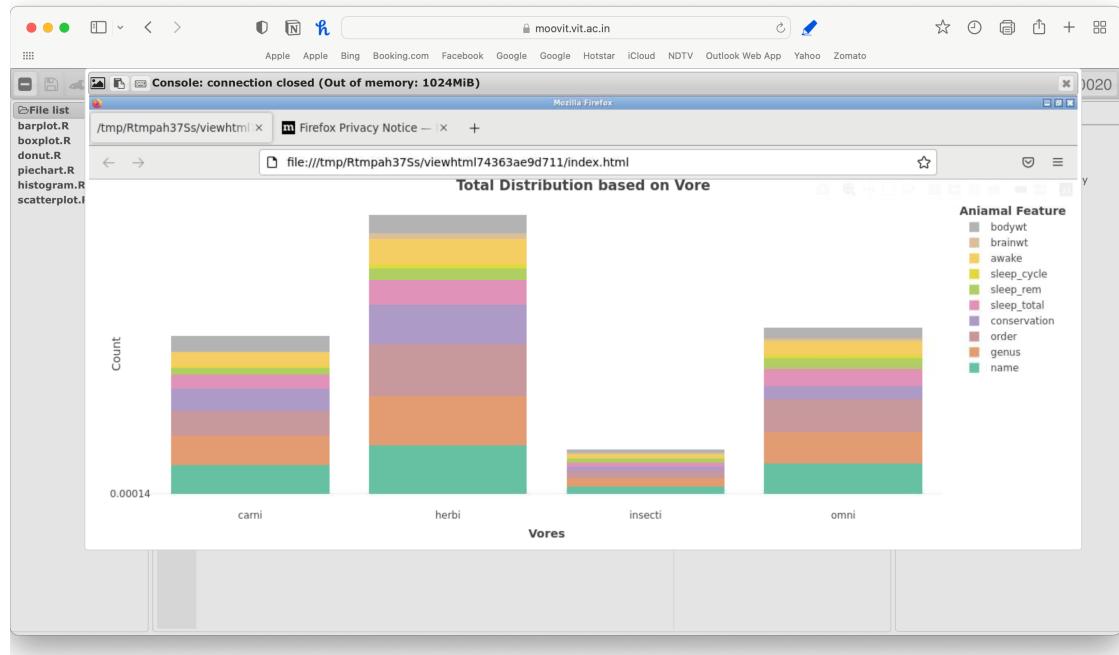
and any others.
Upload this exercise on VTOP

Executing the code one-by-one plots

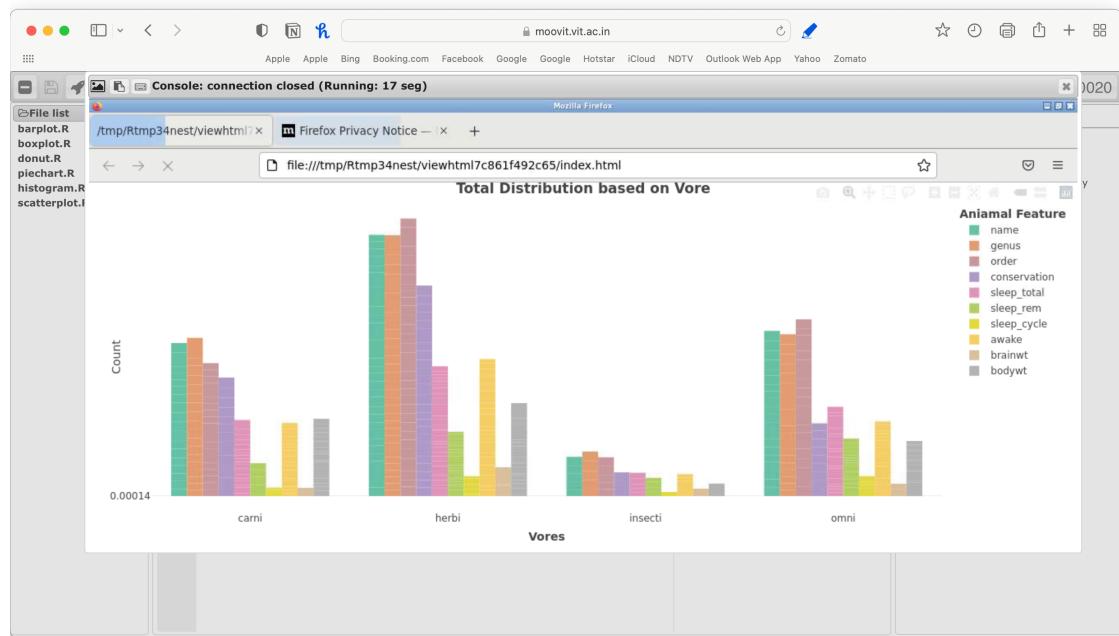
Bar-Chart



Stacked Bar-Chart



Grouped Bar-Chart



2) Histogram Plot

The screenshot shows a web-based R environment. On the left, a file list contains files like histogram.R, barplot.R, scatterplot.R, boxplot.R, donut.R, and piechart.R. The main area displays the following R code:

```
1 library(ggplot2)
2 library(datasets)
3 library(data.table)
4 library(plotly)
5 library(dplyr)
6
7 histogram_plot = plot_ly(data = msleep, x = ~sleep_total, name=vore, type="histogram") %>%
8   layout(
9     title= list(text = "<b>Total sleep time of Animals based on Vore"),
10    legend = list(title = list(text= '<b>Vore')),
11    xaxis = list(title = list(text = '<b>sleep total')), 
12    yaxis = list(title = list(text = '<b>Count')))
```

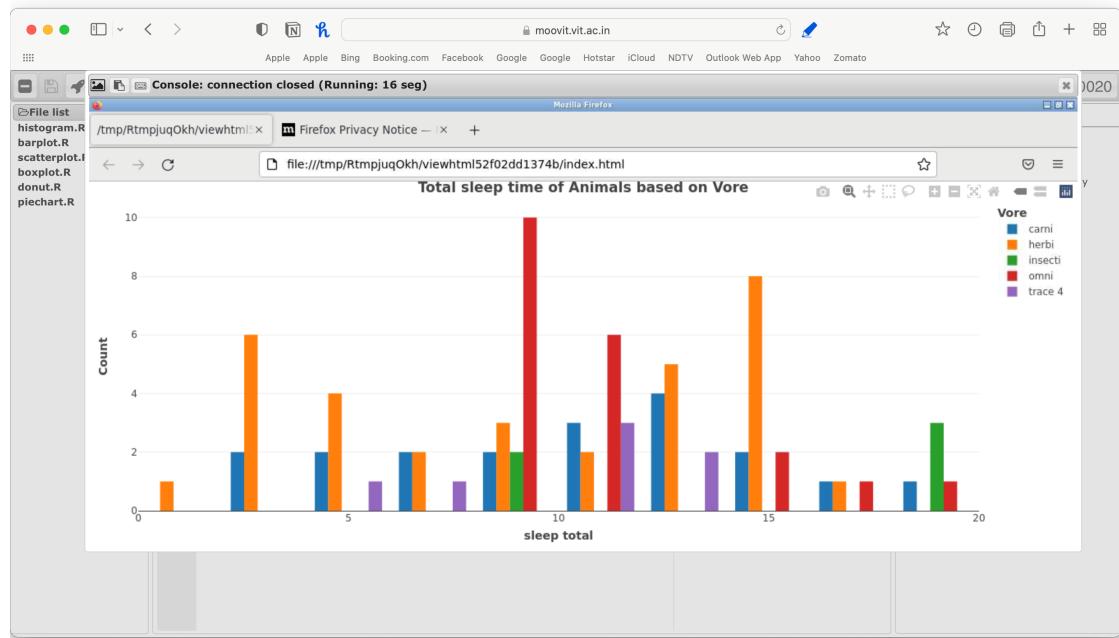
To the right, a 'Description' panel provides instructions:

Use any of the inbuilt datasets(except Iris) and try the following basic graphs using plotly

- 1) Scatter plot
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- 3) Histogram
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and any others.

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3) Pie-Chart

Screenshot of RStudio showing the code for generating a pie chart and its execution results.

The code in the script pane:

```
library(ggplot2)
library(datasets)
library(data.table)
library(plotly)
library(dplyr)

## pie-chart
df_order<-data.frame(table(msleep$order))
pie_chart = plot_ly(type='pie', labels=df_order$Var1, values=df_order$Freq,
textinfo="label+percent", insidetextorientation='radial') %>%
layout(
    title= list(text = "<b>Order Distributions</b>"),
    legend = list(title = list(text= '<b>Order</b>')))

pie_chart
```

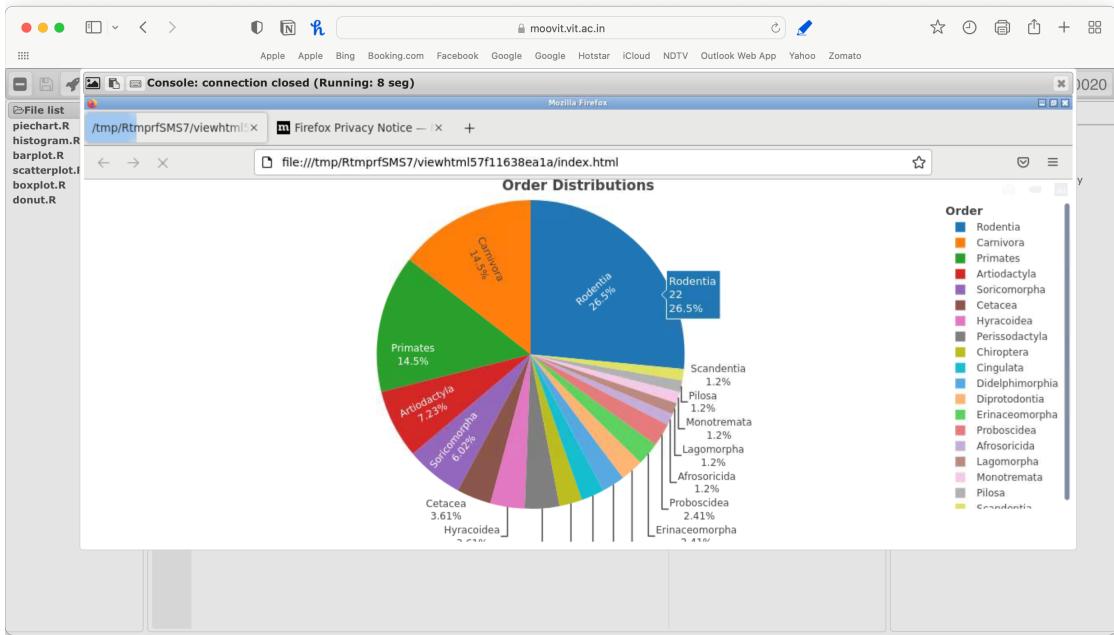
The results pane shows the generated pie chart titled "Order Distributions".

Description pane (right):

Use any of the inbuilt datasets(except iris) and try the following basic graphs using plotly

- 1) Scatter plot
- 2) Bar graph(regular, stacked, group)
- 3) Histogram
- 4) Pie chart
- 5) donut chart
- 6) Box plot

and any others.
Upload this exercise on VTOP



4) Donut chart

Screenshot of a web-based R environment showing the code for creating a donut chart and its resulting visualization.

The code in the editor:

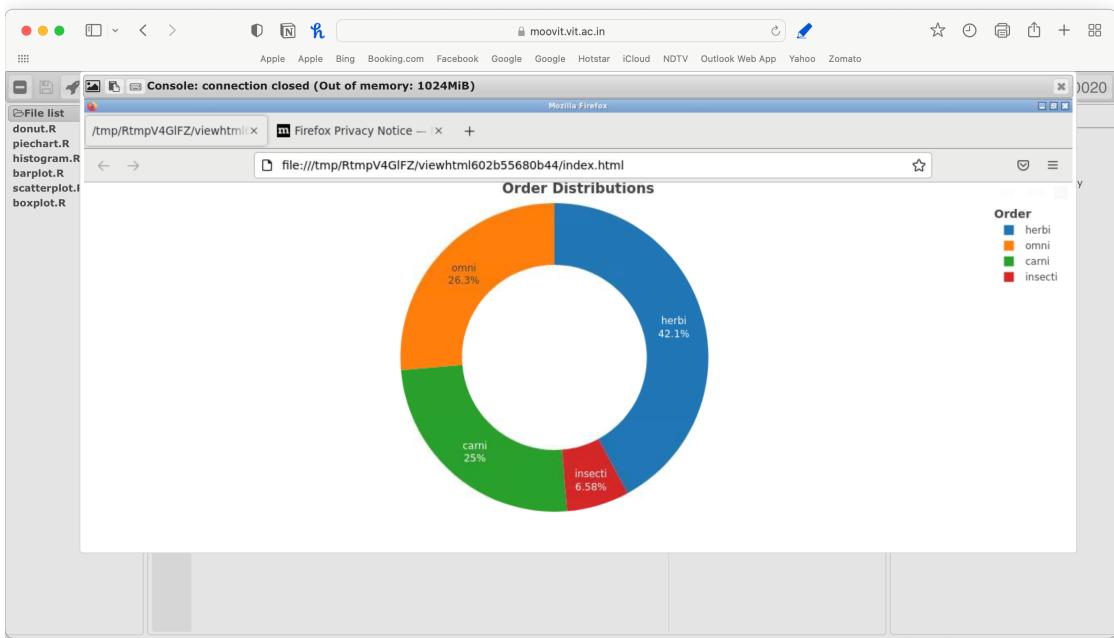
```
library(ggplot2)
library(datasets)
library(data.table)
library(plotly)
library(dplyr)

df_vore = data.frame(table(msleep$vore))
donut_chart = plot_ly(df=df_vore[, values=df_vore$Freq,
                                cex.info=~label+percent()]) %>%
  add_pie(hole = 0.6) %>%
  layout(
    title= list(text = "<b>Order Distributions</b>"),
    legend = list(title = list(text= '<b>Order</b>')))
```

The right panel contains a list of exercises:

- 1) Scatter plot
- 2) Bar graph(regular, stacked, group)
- 3) Histogram
- 4) Pie chart
- 5) donut chart
- 6) Box plot

and any others.
Upload this exercise on VTOP



5) Box Plot

The screenshot shows an RStudio interface. On the left, a file list pane contains files: scatterplot.R, barplot.R, histogram.R, piechart.R, donut.R, boxplot.R, and scatterplot.R. The main code editor pane displays the following R code:

```
1 library(ggplot2)
2 library(datasets)
3 library(data.table)
4 library(plotly)
5 library(dplyr)
6
7 box_plot<-plot_ly(data=msleep, y=sleep_total, color=vore, type='box') %>%
8   layout(
9     title = list(text = "Total sleep time Distribution in Vore Basis"),
10    legend = list(title = list(text = 'Vore')),
11    xaxis = list(title = list(text = 'Vore')),
12    yaxis = list(title = list(text = 'Sleep Total Distribution')))
13
14 box_plot|
```

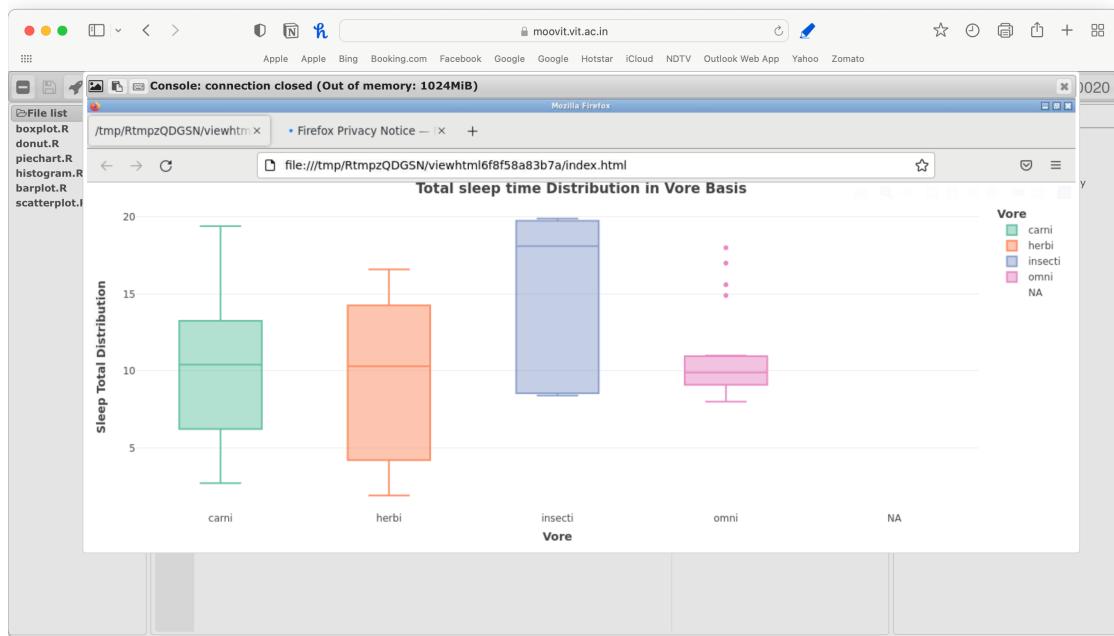
To the right of the code editor is a 'Description' panel with the following content:

Use any of the inbuilt datasets(except iris) and try the following basic graphs using plotly

- 1) Scatter plot
- 2) Bar graph(regular, stacked, group)
- 3) Histogram
- 4) Pie chart
- 5) donut chart
- 6) Box plot

and any others.

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Mam, I am also including the work done on <https://moovit.vit.ac.in/>