

# 19MID0020 Plots

Code

```
library(ggplot2) ## msleep is included in ggplot-2
library(plotly)
```

Hide

Attaching package: 'plotly'

The following object is masked from 'package:ggplot2':

last\_plot

The following object is masked from 'package:stats':

filter

The following object is masked from 'package:graphics':

layout

Hide

library(data.table)

data.table 1.14.2 using 1 threads (see ?getDTthreads). Latest news: r-datatable.com  
\*\*\*\*\*  
This installation of data.table has not detected OpenMP support. It should still work but in single-threaded mode.  
This is a Mac. Please read https://mac.r-project.org/openmp/. Please engage with Apple and ask them for support.  
Check r-datatable.com for updates, and our Mac instructions here: https://github.com/Rdatatable/data.table/wiki/Installation. After several years of many reports of installation problems on Mac, it's time to gingerly point out that there have been no similar problems on Windows or Linux.  
\*\*\*\*\*

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df = msleep

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print(paste("Attributes of the data-set"))

[1] "Attributes of the data-set"

Hide

colnames(df)

[1] "name" "genus" "vore" "order" "conservation" "sleep\_total"  
[7] "sleep\_cycle" "sleep\_rem" "awake" "brainwt" "bodywt"

Hide

str(df)

tibble [83 × 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 "lc" NA "lc" NA "lc" NA ...  
\$ 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 NA NA 0.133 0.667 ...  
\$ sleep\_cycle : num [1:83] 11.9 7 9 9.1 28 9 8 18.2 17 13.9 21 ...  
\$ awake : num [1:83] NA 0.0155 NA 0.0802 0.425 NA NA 0.07 0.0982 ...  
\$ brainwt : num [1:83] 50 0.48 1.35 0.019 600 ...  
\$ bodywt : num [1:83] 50 0.48 1.35 0.019 600 ...

## 1) Scatter Plot

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scatter\_plot = plot\_ly(data=msleep, x=~(-log10(bodywt)), y=~(-log10(brainwt)), color = ~name, type='scatter',mode='markers') %>%  
 layout(  
 title= list(text = "<b>Body weight vs Brain weight"),  
 legend = list(title = list(text = "<b>Animals"),  
 xaxis = list(title = list(text = "<b>Brain Weight"),  
 yaxis = list(title = list(text = "<b>Body Weight")))  
 )  
 scatter\_plot

Warning: Ignoring 27 observations  
Warning in RColorBrewer::brewer.pal(N, "Set2") :  
n too large, allowed maximum for palette Set2 is 8  
Returning the palette you asked for with that many colors  
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## 2) Barchart

Hide

head(df)

name	genus	vore	order	conservation	sleep_total	sleep_rem
<chr>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>
Cheetah	Acinonyx	carni	Carnivora	lc	12.1	NA
Owl monkey	Aotus	omni	Primates	NA	17.0	1.8
Mountain beaver	Aplodontia	herbi	Rodentia	nt	14.4	2.4
Greater short-tailed shrew	Blarina	omni	Soricomorpha	lc	14.9	2.3
Cow	Bos	herbi	Artiodactyla	domesticated	4.0	0.7
Three-toed sloth	Bradypus	herbi	Pilosa	NA	14.4	2.2

6 rows · 1-7 of 11 columns

### 2) a) Regular Barchart

Hide

r\_barchart = plot\_ly(data=df, y=order, type="bar") %>%  
 layout(  
 title= list(text = "<b>Total sleep time of Animals based on Vore"),  
 legend = list(title = list(text= '<b>Vore'),  
 xaxis = list(title = list(text = "<b>sleep total", tickformat = "%"),  
 yaxis = list(title = list(text = "<b>Count"))  
 )  
 r\_barchart

### 2) b) Stacked Barchart

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r\_stack\_barchart = data.table::melt(df, id.vars="vore") %>%  
 plot\_ly(x = ~vore, y = ~value, type = 'bar', name = ~variable, color = ~variable) %>%  
 layout(  
 title= list(text = "<b>Total Distribution based on Vore"),  
 legend = list(title = list(text= '<b>Vores'),  
 xaxis = list(title = list(text = "<b>Vores"),  
 yaxis = list(title = list(text = "<b>Count"), barnode = 'stack')  
 )  
 r\_stack\_barchart

Warning in data.table::melt(df, id.vars = "vore") :  
The melt generic in data.table has been passed a tbl\_df and will attempt to redirect to the relevant reshape2 method; please note that reshape2 is deprecated, and this redirection is now deprecated as well. To continue using melt methods from reshape2 while both libraries are attached, e.g. melt.list, you can prepend the namespace like reshape2::melt(df). In the next version, this warning will become an error.

Hide

r\_stack\_barchart

Warning: Ignoring 184 observations  
Warning in RColorBrewer::brewer.pal(N, "Set2") :  
n too large, allowed maximum for palette Set2 is 8  
Returning the palette you asked for with that many colors  
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n too large, allowed maximum for palette Set2 is 8  
Returning the palette you asked for with that many colors

### 2) c) Grouped Barchart

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r\_group\_barchart = data.table::melt(df, id.vars="vore") %>%  
 plot\_ly(x = ~vore, y = ~value, type = 'bar', name = ~variable, color = ~variable) %>%  
 layout(  
 title= list(text = "<b>Total Distribution based on Vore"),  
 legend = list(title = list(text= '<b>Animal Feature'),  
 xaxis = list(title = list(text = "<b>Vores"),  
 yaxis = list(title = list(text = "<b>Count"), barnode = 'group')  
 )  
 r\_group\_barchart

Warning in data.table::melt(df, id.vars = "vore") :  
The melt generic in data.table has been passed a tbl\_df and will attempt to redirect to the relevant reshape2 method; please note that reshape2 is deprecated, and this redirection is now deprecated as well. To continue using melt methods from reshape2 while both libraries are attached, e.g. melt.list, you can prepend the namespace like reshape2::melt(df). In the next version, this warning will become an error.

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r\_group\_barchart

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Warning in RColorBrewer::brewer.pal(N, "Set2") :  
n too large, allowed maximum for palette Set2 is 8  
Returning the palette you asked for with that many colors  
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n too large, allowed maximum for palette Set2 is 8  
Returning the palette you asked for with that many colors

## 3) Histogram

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# Define labels for the bars  
labs = c('herbi'='Herbivore',  
 'carni'='Carnivore',  
 'omni'='Omnivore',  
 'insecti'='Insectivore')

Hide

histogram\_plot = plot\_ly(data = df, x = ~sleep\_total, name=~vore,type="histogram") %>%  
 layout(  
 title= list(text = "<b>Total sleep time of Animals based on Vore"),  
 legend = list(title = list(text= '<b>Vore'),  
 xaxis = list(title = list(text = "<b>sleep total"),  
 yaxis = list(title = list(text = "<b>Count"))  
 )  
 histogram\_plot

## 4) Pie-Chart

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df\_order = data.frame(table(msleep\$order))  
df\_order

Var1	Freq
<chr>	<int>
Afrosericida	1
Artiodactyla	6
Carnivora	12
Cetacea	3
Chiroptera	2
Cingulata	2
Didelphimorphia	2
Diprotodontia	2
Eumastomorphia	2
Hyracoida	3

1-10 of 19 rows

Previous 1 2 Next

Hide

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"),  
 legend = list(title = list(text= '<b>Order'))  
 )  
 pie\_chart

## 5) Donut Chart / Open Pie-Chart

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df\_vore = data.frame(table(msleep\$vore))  
df\_vore

Var1	Freq
<chr>	<int>
carni	19
herbi	32
insecti	5
omni	20

4 rows

Hide

donut\_chart = plot\_ly(labels=df\_vore\$Var1, values=df\_vore\$Freq, textinfo="label+percent") %>%  
 add\_pie(hole = 0.6) %>%  
 layout(  
 title= list(text = "<b>Order Distributions"),  
 legend = list(title = list(text= '<b>Order'))  
 )  
 donut\_chart

## 6) Box Plot

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box\_plot=plot\_ly(data=msleep, y=~sleep\_total, color=~vore, type='box') %>%  
 layout(  
 title= list(text = "<b>Total sleep time Distribution in Vore Basis"),  
 legend = list(title = list(text= '<b>Vore'),  
 xaxis = list(title = list(text = "<b>Vore"),  
 yaxis = list(title = list(text = "<b>Sleep Total Distribution"))  
 )  
 box\_plot