## R Notebook library(ggplot2) library(plotly) ## 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 msleep conservation name genus vore order sleep\_total <chr> <chr> <|db|> <chr> <chr> <chr> lc 12.1 Cheetah Acinonyx Carnivora carni Owl monkey Primates NA 17.0 Aotus omni Mountain beaver Aplodontia herbi Rodentia nt 14.4 Greater short-tailed shrew Blarina omni Soricomorpha lc 14.9 Cow Bos herbi Artiodactyla domesticated 4.0 Three-toed sloth Pilosa NA Bradypus herbi 14.4 8.7 Northern fur seal Callorhinus carni Carnivora vu Vesper mouse Calomys NA Rodentia NA 7.0 10.1 Dog Canis carni Carnivora domesticated Roe deer Capreolus herbi Artiodactyla lc 3.0 1-10 of 83 rows | 1-6 of 11 columns Previous **1** 2 3 4 5 6 ... 9 Next cat(factor(msleep\$order)) ## 3 15 17 19 2 14 3 17 3 2 2 17 15 17 19 17 19 6 10 7 16 5 13 13 9 15 17 3 15 2 4 3 10 15 15 16 7 15 17 17 17 17 5 17 15 17 17 11 2 15 3 3 3 15 9 15 17 8 3 4 8 6 10 17 17 15 19 17 17 17 17 17 17 19 2 12 17 13 1 18 4 3 3 3 Pie-Chart df\_order = data.frame(table(msleep\$order)) print(df\_order) Var1 Freq Afrosoricida ## 2 Artiodactyla 6 ## 3 Carnivora 12 ## 4 Cetacea 3 2 Chiroptera ## 5 2 ## 6 Cingulata ## 7 Didelphimorphia 2 2 ## 8 Diprotodontia ## 9 Erinaceomorpha 2 Hyracoidea ## 10 3 Lagomorpha ## 11 1 ## 12 Monotremata 1 ## 13 Perissodactyla 3 Pilosa ## 14 1 ## 15 Primates 12 Proboscidea 2 ## 16 ## 17 Rodentia 22 ## 18 Scandentia 1 ## 19 Soricomorpha fig\_order = plot\_ly(type='pie', labels=df\_order\$Var1, values=df\_order\$Freq, textinfo='label+percent',insidetextorientation='radial') fig\_order ilii 0 Rodentia Carnivora Primates Artiodactyla Soricomorpha Cetacea Hyracoidea Perissodactyla Chiroptera Cingulata Primates Didelphimorphia 14.5% Diprotodontia Scar 1. Erinaceomorpha Pilosa Proboscidea 1.2% Afrosoricida Monot Lagomorpha 1. Lagom Monotremata 1.2 Pilosa Afrosorio Scandentia 1.2% Proboscidea 2.41% Erinaceomorpha 2.41% Diprotodontia df\_vore = data.frame(table(msleep\$vore)) df\_vore Var1 Freq <fct> <int> 19 carni 32 herbi 5 insecti 20 omni 4 rows fig\_vore = plot\_ly(type='pie', labels=df\_vore\$Var1, values=df\_vore\$Freq, textinfo='label+percent',insidetextorientation='radial') fig\_vore herbi omni carni insecti herbi 42.1% Scatter plot fig\_sp = plot\_ly(data = msleep, x=~brainwt, y=~bodywt, color = ~order) fig\_sp ## No trace type specified: Based on info supplied, a 'scatter' trace seems appropriate. Read more about this trace type -> https://plotly.com/r/reference/#scatter ## No scatter mode specifed: Setting the mode to markers Read more about this attribute -> https://plotly.com/r/reference/#scatter-mode ## 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 ## 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 7000 Afrosoricida Artiodactyla Carnivora 6000 Chiroptera Cingulata Didelphimorphia 5000 Diprotodontia Erinaceomorpha Hyracoidea 4000 bodywt 3000 Lagomorpha Monotremata Perissodactyla Primates Proboscidea 2000 Rodentia Scandentia Soricomorpha 1000 2 3 5 6 brainwt



Hu∰an

Chimoanzee Dontey

Gra**©**sea

2.0

1.5

1.0

2

sqrt(msleep\$brainwt)

**Using Normalization** 

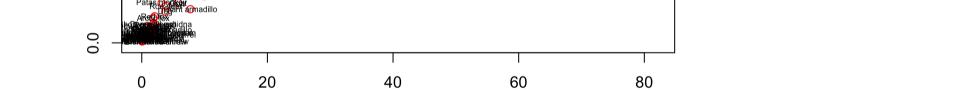
plot(sqrt(msleep\$bodywt), sqrt(msleep\$brainwt), col="red")

Нфве

plot(msleep\$bodywt^(1/100), msleep\$brainwt^(1/100), col="red")

 $text(msleep\$bodywt^{(1/100)}, msleep\$brainwt^{(1/100)}, msleep\$name, cex=0.5)$ 

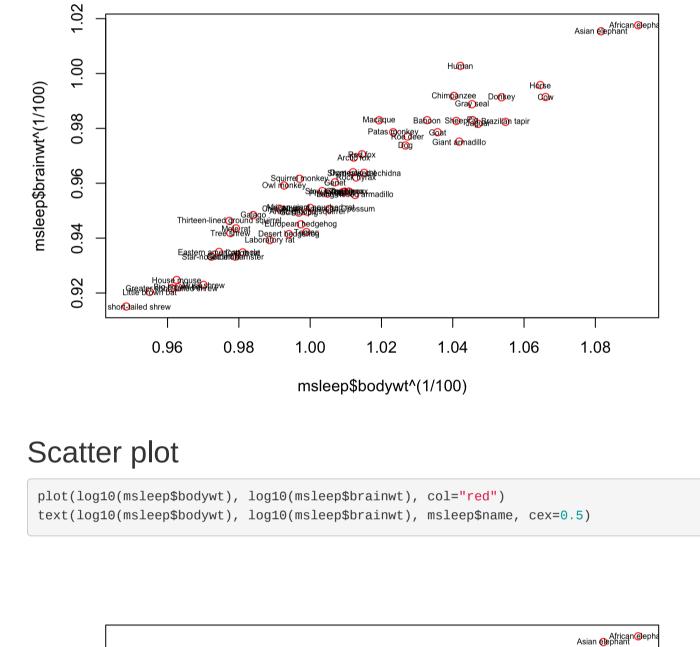
text(sqrt(msleep\$bodywt), sqrt(msleep\$brainwt), msleep\$name, cex=0.5)



sqrt(msleep\$bodywt)

African@eph

African@epl



## t <- list(family = "Helvetica", size = 14, color = "blue") t1 <- list(family = "Times New Roman", color = "red")</pre>

fig\_sp

1

ggplotly(bar\_plot)

0.3-

Percentage of Vore

0.1-

Histogram

Percentage of the quality of the Vore

0

7

-2

က

House house Halle be with the work of the Life be with t

-1

t2 <- list(family = "Courier New", size = 14, color = "green")

## Returning the palette you asked for with that many colors

## Returning the palette you asked for with that many colors

0

plot\_bgcolor='#e5ecf6')

log10(msleep\$bodywt)

-2

t3 <- list(family = 'Arial')

## Warning: Ignoring 27 observations

log10(msleep\$brainwt)

```
fig_sp = plot_ly(data = msleep, x = \sim log10(bodywt), y = \sim log10(brainwt), color = \sim name,
                  type = 'scatter', mode = 'markers')%>%
                           layout(title= list(text = "Body weight vs Brain weight", font = t1), font=t,
                           legend = list(title=list(text='Animals', font = t2)),
                           xaxis = list(title = list(text = 'Brain Weight', font = t3)),
```

yaxis = list(title = list(text = 'Body Weight', font = t3)),

## Warning in RColorBrewer::brewer.pal(N, "Set2"): n too large, allowed maximum for palette Set2 is 8

## Warning in RColorBrewer::brewer.pal(N, "Set2"): n too large, allowed maximum for palette Set2 is 8

Body weight vs Brainweight o 🛨 🖃 🐹 🍙 🕳 🚍 🟢

**Animals** 

African elephant

Arctic fox

African giant pouched rat

factor(vore) carni

herbi

NA

insecti

omni

Arctic ground squirrel

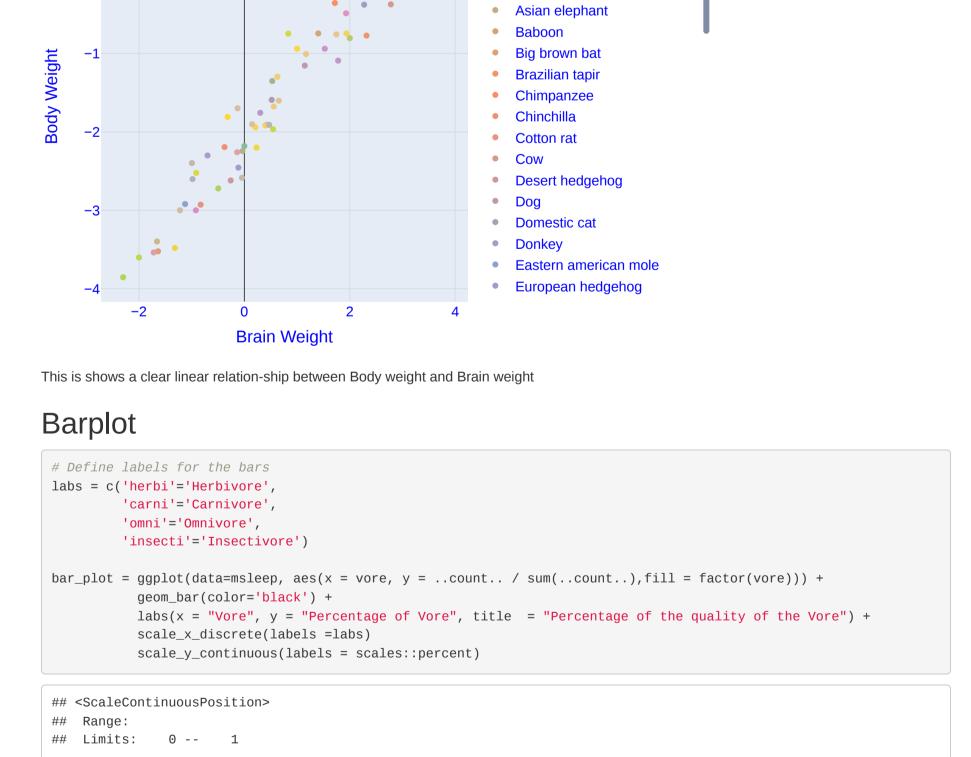
Humar

Patas monkey Coat
Roe deer Giant madillo

Batoon Sheep Bagazilon tapir

2

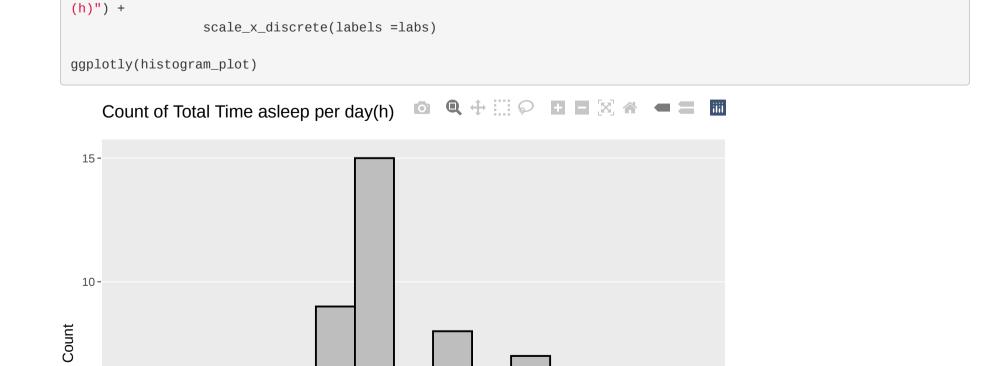
3



## 0.0 Herbivore Carnivore Insectivore Omnivore

 $histogram_plot = ggplot(data=msleep, aes(x = sleep_total)) +$ 

Vore



labs(x = "Total Time asleep per day(h)", y="Count", title="Count of Total Time asleep per day")

geom\_histogram(binwidth = 1.25, color = "black", fill = "grey") +

