Lab1

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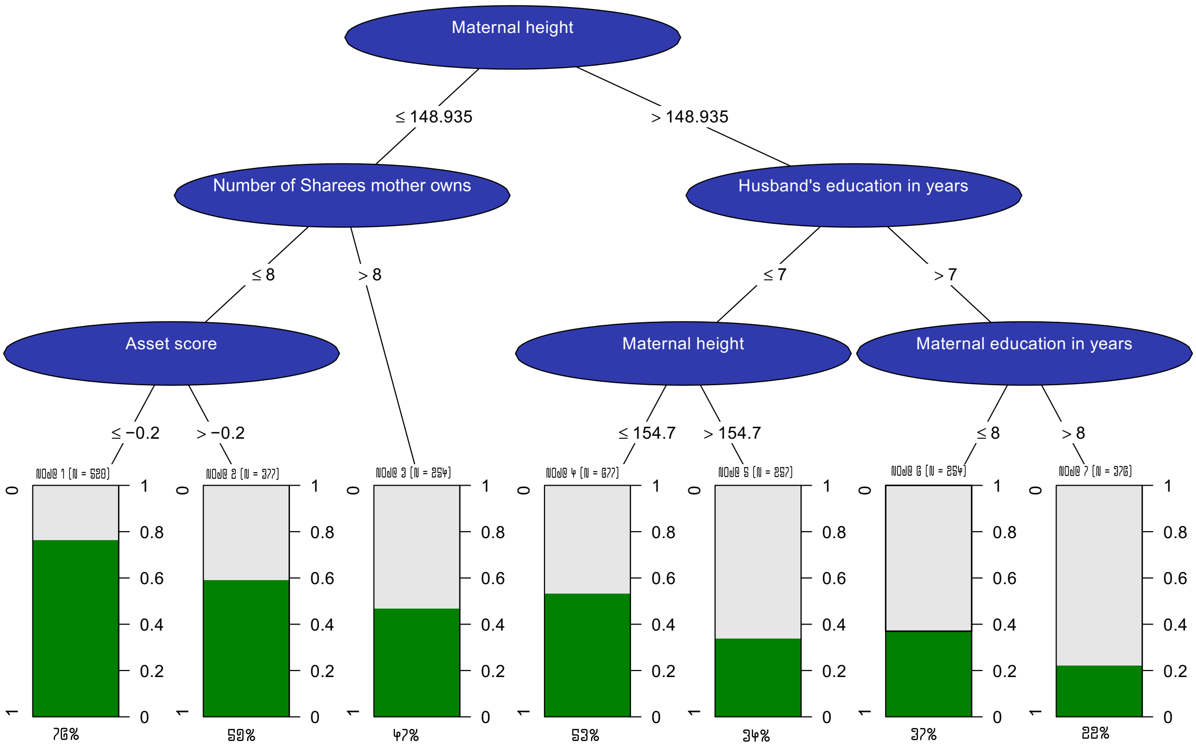
Assignment 1

Made the required changes to the tree.pdf The final one is tree_fixed.svg



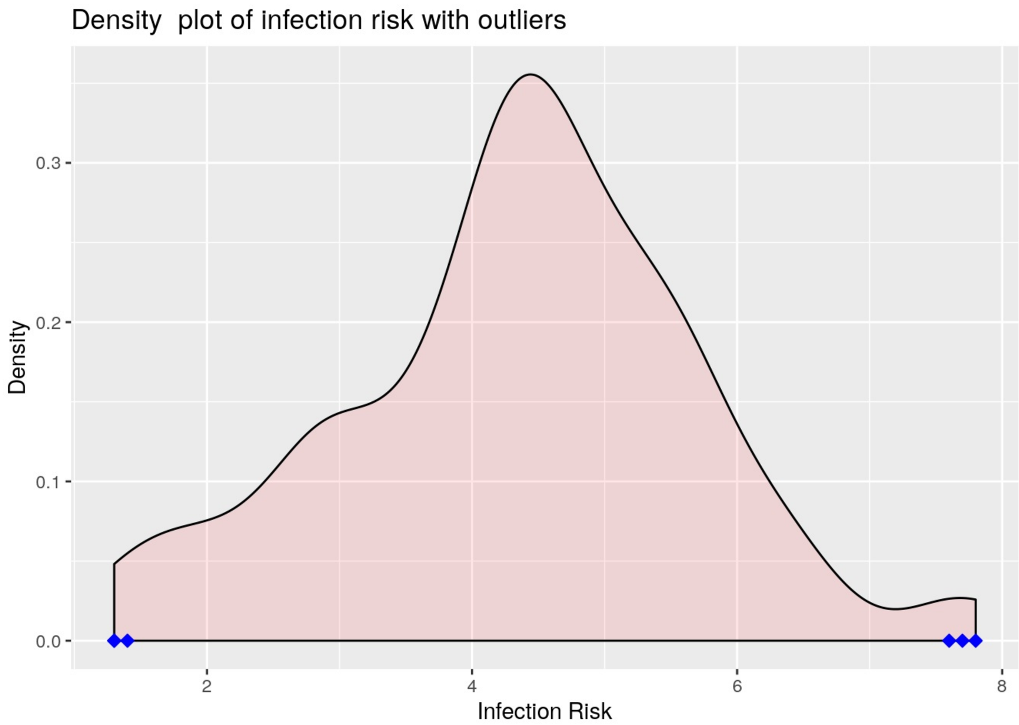
Assignment 2

Read Data from file and load libraries

creating function to return indices

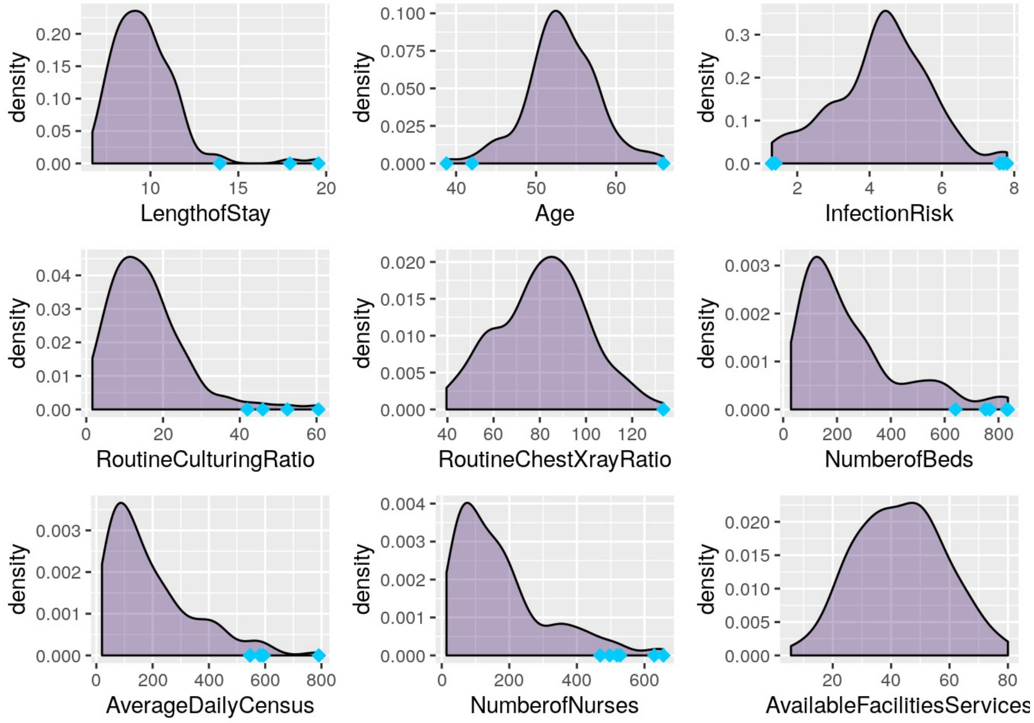
```
# Assignment 1 ------------------------------------------------------------

# 1 ------------------------------

senic=read.table("SENIC.txt")

# 2 ------------------------------

outlier_function=function(X){
  q1=as.numeric(quantile(X,0.25))
  q3=as.numeric(quantile(X,0.75))
  greater=q3+1.5*(q3-q1)
  smaller=q1-1.5*(q3-q1)
  indices=which(X>greater | X<smaller)
  return(indices)
}
```

Density Ploting of Infection Risk



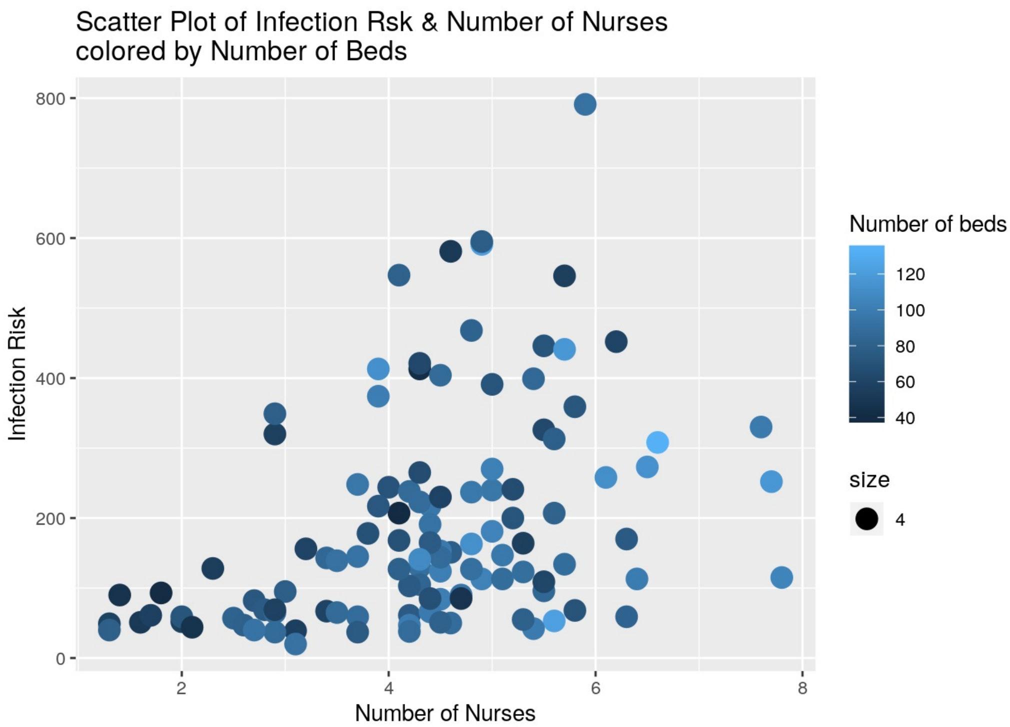
The density of infection rate has 5 outliers.the outliers are on either side of the graph. the probability of infection risk lies in a band of 2-6 and there is a very minimal probability for infection risk to cross the above mentioned limit.

Producce graphs for all other variables



We could see that all graphs exept AvailableFacilitiesServices have outliers. We feel that the graphs of Age,InfectionRisk,RoutineChestXrayRatio,AvailableFacilitiesServices follow a normal distribution. Also the LengthofStay,RoutineCulturingRatio,NumberofBeds,AverageDailyCensus,NumberofNurses follow a chi-square distribution. The outliers skews the data.

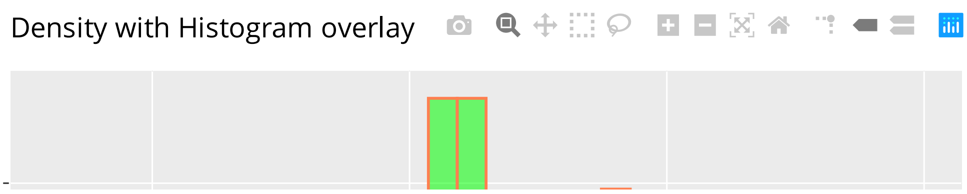
Scatter Plot

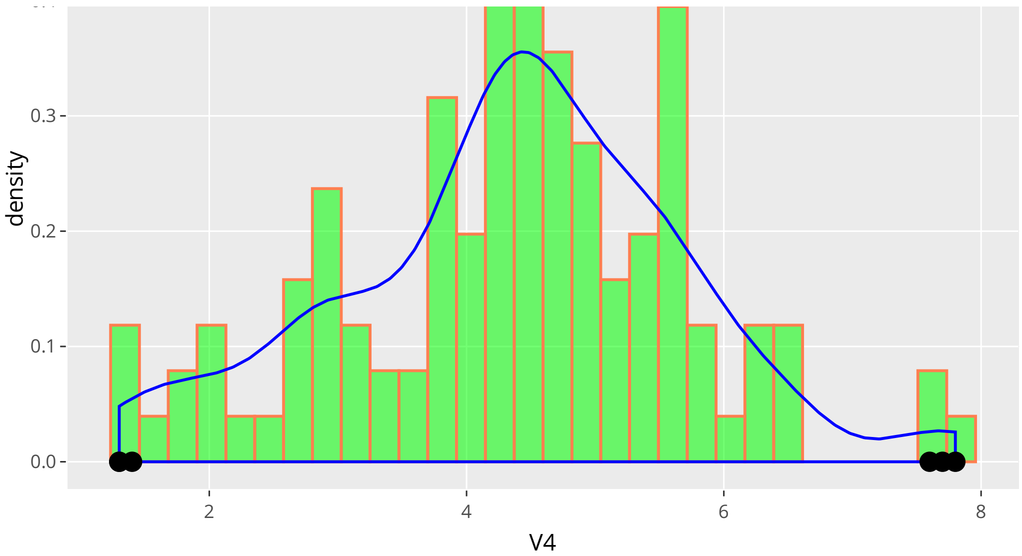


This scatter plot shows you the dependence of Infection Risk on the Number of Nurses where the points are colored by Number of Beds.Here the graph shows number of nurses and number of bed increases the infection rate.More number of beds means more number of patients can be accomadated.As the patients increases the infections also increases as the patients coming to hospital will be sick.The color scale itself is confusing as we usually think the light colours give a smaller value and dark a higher . Since the colours are very similar it is difficult to differentiate as well.

Plotly Graph

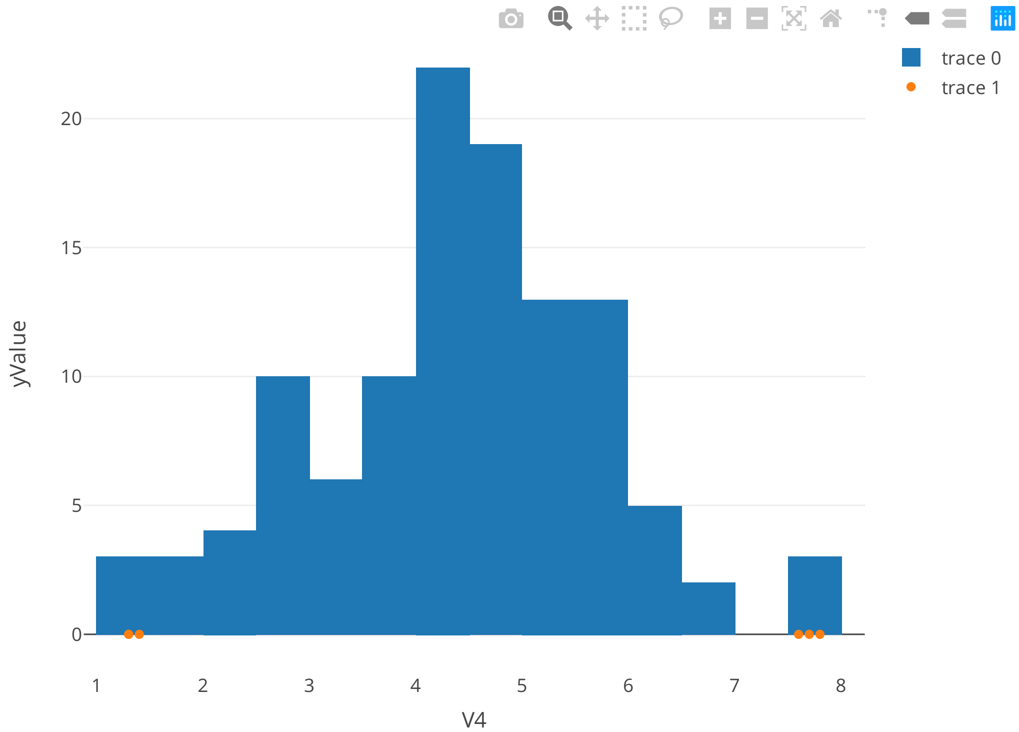
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```





THe plotly has features like zoom in,zoom out,reset the axis,autoscaling,box slection,lassso selection etc.As a whole we feel like there are lot more that we can do with plotly graphs when compared to ggplot.

Plolty Plot Made with Pipe operator



Shiny App

```r
library(shiny)
library(gridExtra)
df<-read.table("SENIC.txt")
quantile_function<-function(dat)
{
  Q1<-quantile(dat,0.25)
  Q3<-quantile(dat,0.75)
  greater<-Q3+1.5*(Q3-Q1)
  smaller<-Q1-1.5*(Q3-Q1)
  result<-subset(dat,dat > greater | dat < smaller)
  indices<-which(dat %in% result)
  return(result)
}



# Define UI for application that draws a histogram

ui <- fluidPage(

  # Application title
  titlePanel("Density Plots"),

  # Sidebar with checkbox of variables
  sidebarLayout(
    sidebarPanel(
      checkboxGroupInput(inputId = "input_value",
                         label = "Select Variables:",
                         choiceValues = paste("V", c(2:7,10,11), sep = ""),
                         choiceNames = c("LengthofStay", "Age", "InfectionRisk",
                                         "RoutineCulturingRatio", "Routine Chest X-ray Ratio",
                                         "Number of Beds", "Average Daily Census",
                                         "Number of Nurses"),
                         selected = "V4"),

      sliderInput(inputId = "bw_value", label = "Bandwidth", min = 0, max = 20, value = 1, step = .1)
    ),

    # Show a plot of the generated distribution
    mainPanel(
      plotOutput("output_val")
    )
  )
)


server <- function(input, output){

  output$output_val <- renderPlot({
    # Render plot
    p <- lapply(input$input_value, function(i){ggplot() +
        geom_density(aes(df[,i]), fill = "green", bw = input$bw_value) +
        geom_point(aes(x = df[quantile_function(df[,i]),i], y = 0), shape = 23, col = "black", fill = "black") +
        labs(x = "") +
        theme_minimal()})

    if(length(p) <= 4){
      n_col <- length(p)
      n_row = 1} else{
        n_col <- 4
        n_row <- 2
      }

    marrangeGrob(p, ncol = n_col, nrow = n_row)
  })
}

# Run the application
shinyApp(ui = ui, server = server)
```

Seems like a bandwidth of 4 is a good choice.

Appendix

```r
## ----echo=FALSE------------------------------------------------------------
knitr::opts_chunk$set(echo = F)
```

```r
## ----message=FALSE-----------------------------------------------------------

# libraries ---------------------------------------------------------------
library(ggplot2)
library(gridExtra)
library(plotly)
library(shiny)
library(gridExtra)
library(tidyverse)



## ----echo=TRUE---------------------------------------------------------------

# Assignment 1 ------------------------------------------------------------

# 1 ------------------------------

senic=read.table("SENIC.txt")

# 2 ------------------------------

outlier_function=function(X){
  q1=as.numeric(quantile(X,0.25))
  q3=as.numeric(quantile(X,0.75))
  greater=q3+1.5*(q3-q1)
  smaller=q1-1.5*(q3-q1)
  indices=which(X>greater | X<smaller)
  return(indices)
}


## ------------------------------------------------------------------------
# 3------------------------------

outliersInf=outlier_function(senic$V4)
infRisk=data.frame("outliers"=senic$V4[outliersInf],"rep"=0)

datfrm<-data.frame(senic$V4)
names(datfrm)<-c('InfectionRisk')
ggplot_value<-ggplot(datfrm,aes(x=InfectionRisk))+geom_density(color="black",fill="red",alpha=0.1)+
  geom_point(data=infRisk,aes(x=outliers,y=rep),shape=23,color="blue",size=2,fill="blue")+
  labs(x="Infection Risk",y="Density")+ggtitle("Density  plot of infection risk with outliers")
ggplot_value



## ------------------------------------------------------------------------
# 4 ------------------------------
dt<-senic[c(-1,-8,-9)]
names(dt)<-c('LengthofStay','Age','InfectionRisk','RoutineCulturingRatio',
             'RoutineChestXrayRatio','NumberofBeds','AverageDailyCensus',
             'NumberofNurses','AvailableFacilitiesServices')

my_plots=list()

for(name in names(dt)){
  indices=outlier_function(dt[[name]])
  outliers=dt[[name]][indices]
  outliers_names=tibble("x"=outliers,"y"=0)
  my_plots[[name]]=ggplot(dt, aes_string(x =name)) + geom_density(color="black",fill="#330066",alpha=0.3)+
    geom_point(data=outliers_names,aes(x,y),size=2,color="#00CCFF",pch=23,fill="#00CCFF")
}
grid.arrange(grobs=my_plots)



## ------------------------------------------------------------------------
# 5 ------------------------------
ggplot(senic,aes(V4,V10))+geom_point(aes(size=4,color=V6))+
  ggtitle("Scatter Plot of Infection Rsk & Number of Nurses \ncolored by Number of Beds")+
  labs(x="Number of Nurses",y="Infection Risk")+
  scale_colour_continuous("Number of beds")



## ------------------------------------------------------------------------
# 6 ------------------------------
```

```
indices_infection=outlier_function(senic$V4)
outliers_infection=senic$V4[indices_infection]
outliers = tibble(x = outliers_infection, y = 0)

plot<-ggplot(senic,aes(V4))+geom_histogram(aes(y=..density..,alpha=0.7),col="coral",fill="green")+
  geom_density(col="blue")+ggtitle("Density with Histogram overlay")+
  geom_point(data = outliers, aes(x,y),size=3)

ggplotly(plot)

# using the plot from 3
#p<-ggplot_value+geom_histogram(aes(y=..density..,alpha=0.5),col="gray",fill="blue",alpha=0.5)
#ggplotly(p)



## ------------------------------------------------------------------------
# 7 ------------------------------

Outlier_indices= outlier_function(senic$V4)
Outlier_values<-senic$V4[Outlier_indices]
yValue <- rep(0,length(Outlier_values))

hisPlot <- senic %>% select(V4) %>% plot_ly(x=~V4,type="histogram")  %>%
  add_markers(x=~Outlier_values, y=~yValue)

hisPlot


## ----eval=FALSE,echo=T---------------------------------------------------
##
## library(shiny)
## library(gridExtra)
## df<-read.table("SENIC.txt")
## quantile_function<-function(dat)
## {
##   Q1<-quantile(dat,0.25)
##   Q3<-quantile(dat,0.75)
##   greater<-Q3+1.5*(Q3-Q1)
##   smaller<-Q1-1.5*(Q3-Q1)
##   result<-subset(dat,dat > greater | dat < smaller)
##   indices<-which(dat %in% result)
##   return(result)
## }
##
##
##
## # Define UI for application that draws a histogram
##
## ui <- fluidPage(
##
##   # Application title
##   titlePanel("Density Plots"),
##
##   # Sidebar with checkbox of variables
##   sidebarLayout(
##     sidebarPanel(
##       checkboxGroupInput(inputId = "input_value",
##                          label = "Select Variables:",
##                          choiceValues = paste("V", c(2:7,10,11), sep = ""),
##                          choiceNames = c("LengthofStay", "Age", "InfectionRisk",
##                                          "RoutineCulturingRatio", "Routine Chest X-ray Ratio",
##                                          "Number of Beds", "Average Daily Census",
##                                          "Number of Nurses"),
##                          selected = "V4"),
##
##       sliderInput(inputId = "bw_value", label = "Bandwidth", min = 0, max = 20, value = 1, step = .1)
##     ),
##
##     # Show a plot of the generated distribution
##     mainPanel(
##       plotOutput("output_val")
##     )
##   )
## )
##
##
## server <- function(input, output){
```

```
##
##   output$output_val <- renderPlot({
##     # Render plot
##     p <- lapply(input$input_value, function(i){ggplot() +
##         geom_density(aes(df[,i]), fill = "green", bw = input$bw_value) +
##         geom_point(aes(x = df[quantile_function(df[,i]),i], y = 0), shape = 23, col = "black", fill = "black")
+
##         labs(x = "") +
##         theme_minimal()})
##
##     if(length(p) <= 4){
##       n_col <- length(p)
##       n_row = 1} else{
##         n_col <- 4
##         n_row <- 2
##       }
##
##     marrangeGrob(p, ncol = n_col, nrow = n_row)
##   })
## }
##
## # Run the application
## shinyApp(ui = ui, server = server)
##
##
##


## ----code = readLines(knitr::purl("~/Courses/Visualization_Group_labs/Group25_Lab1/Group25_lab1.Rmd",documentati
on = 1)), echo = T, eval = F----
## NA
```

Lab2

Priya(priku577) and Andreas(andch552)

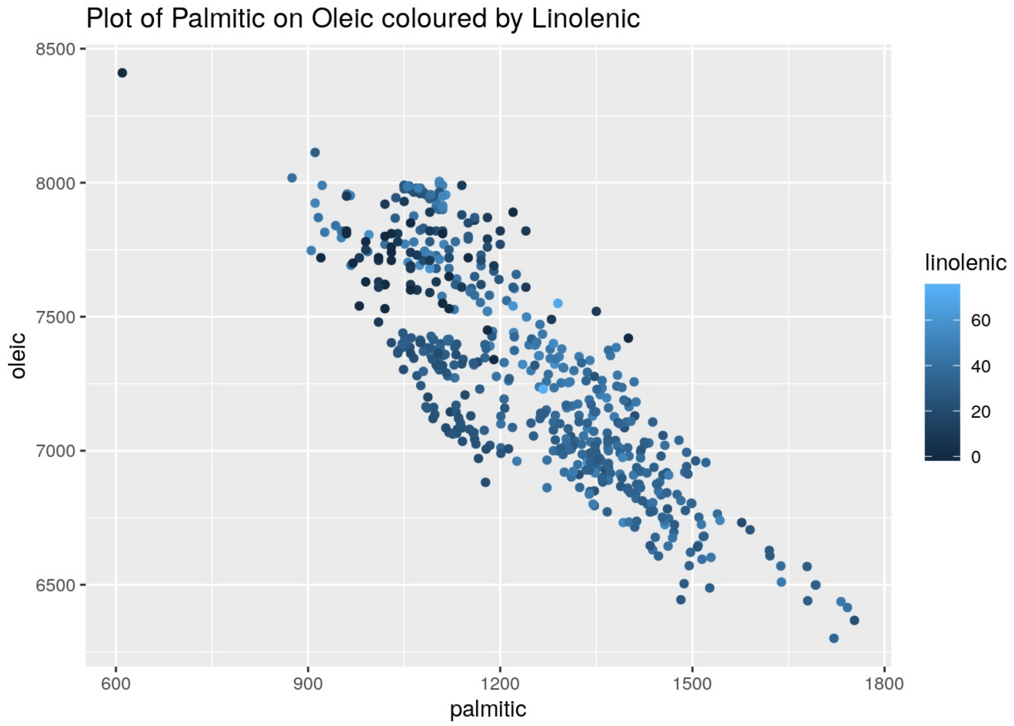
19 September 2018

###Assignment 1

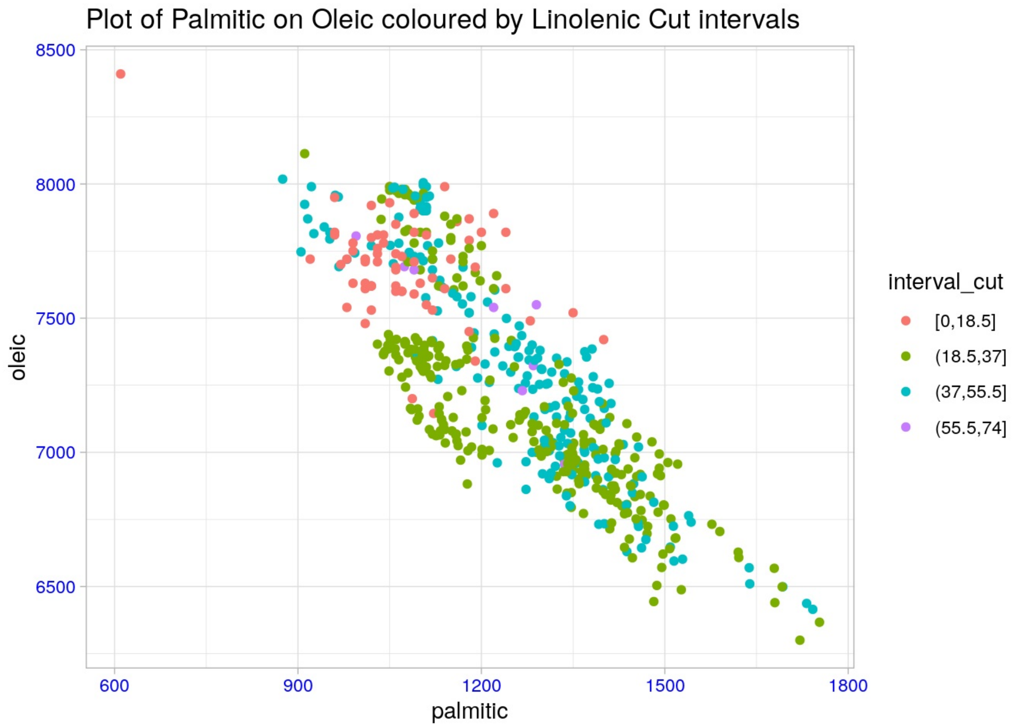
##1

scatterplot in Ggplot2 that shows dependence of Palmitic on Oleic in which observations are colored by Linolenic

```
library(ggplot2)
library(plotly)
library(MASS)

olive<-read.csv("olive.csv",header=TRUE, sep=",")

p1<-ggplot(olive,aes(palmitic,oleic,col=linolenic))+geom_point()+labs(x="palmitic",y="oleic")+ggtitle("Plot of Pal
mitic on Oleic coloured by Linolenic")
p1
```




```
interval_cut <- cut_interval(olive$linolenic, 4)
p2<-ggplot(olive,aes(palmitic,oleic,col=interval_cut))+geom_point()+theme_light()+labs(x="palmitic",y="oleic")+ggt
itle("Plot of Palmitic on Oleic coloured by Linolenic Cut intervals")+theme(axis.text = element_text(colour = "blu
e"))
p2
```



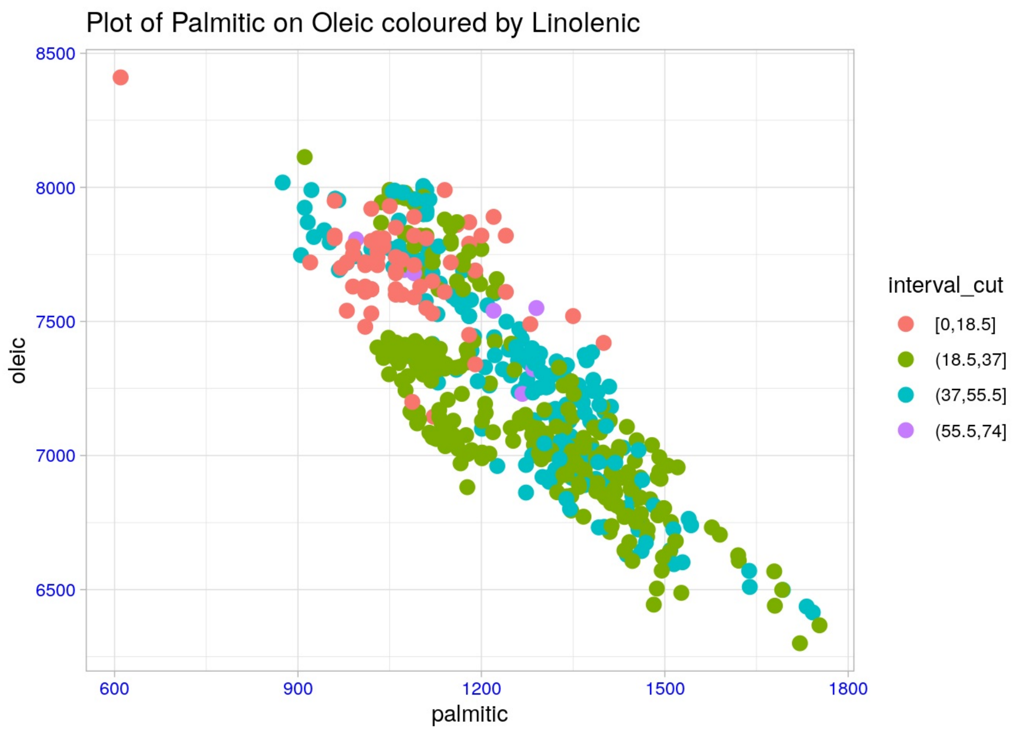
Channel capacity of the human perception is the perception problem told here.The perception consists of three steps: recognizing, organizing and interpreting.Grouping is hard to do in the first plot as different shades of same hue are used. THe groups can be easily identified by perception in the second plot.Its difficult to distinguish between different shades of same hue while its easier to distinguish between differnet hues (channel capacity is here).

##2

scatterplots of Palmitic vs Oleic in which you map the discretized Linolenic with four classes to:

a. Color

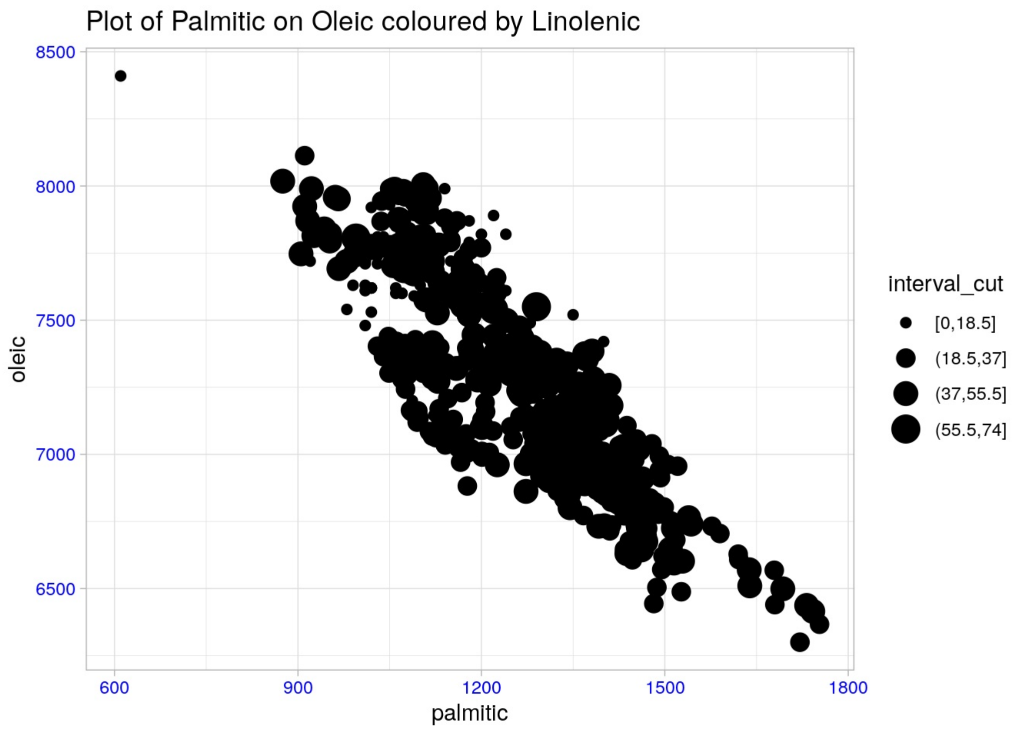
```
p3<-s2<-ggplot(olive,aes(palmitic,oleic,col=interval_cut))+geom_point()+theme_light()+labs(x="palmitic",y="oleic")
+geom_point(size=3)+ggtitle("Plot of Palmitic on Oleic coloured by Linolenic")+theme(axis.text = element_text(colo
ur = "blue"))
p3
```



b. Size

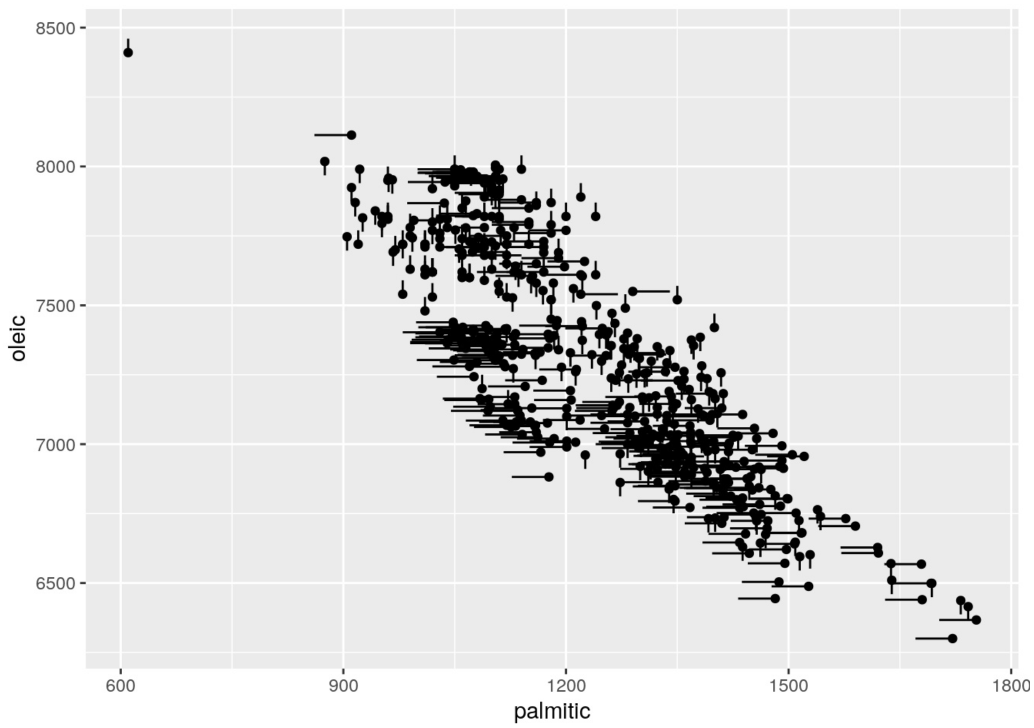
```
p4<-s2<-ggplot(olive,aes(palmitic,oleic))+geom_point(aes(size=interval_cut))+theme_light()+labs(x="palmitic",y="ol
eic")+geom_point()+ggtitle("Plot of Palmitic on Oleic coloured by Linolenic")+theme(axis.text = element_text(colou
r = "blue"))
p4
```

```
## Warning: Using size for a discrete variable is not advised.
```



c. Orientation angle

```
angleplot<-ggplot(olive,aes(x=palmitic,y=oleic)) +
  geom_point() +geom_spoke(aes(angle = as.numeric(cut_interval(linolenic, 4))*pi/2), radius = 50)
angleplot
```

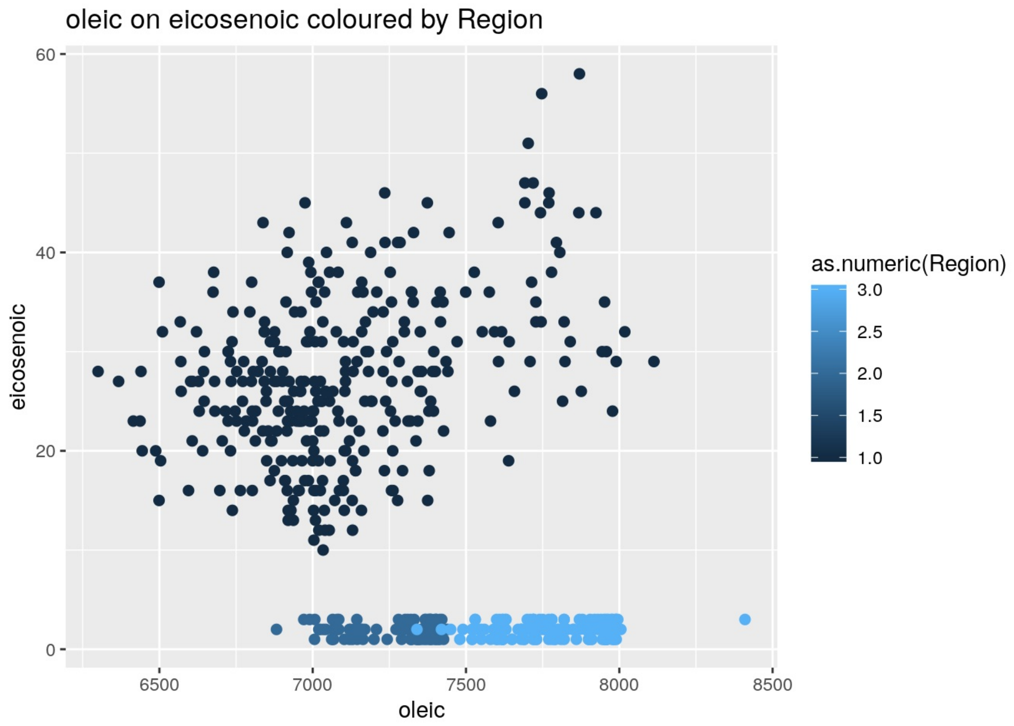


We feel it is very difficult to differenciate between categories in the second plot with size (b.size).The third plot is not good either.The first graph is obviously the best. The coloured graph is 3.1 bits the size plot 2.2 bits and the angle plot is 2.8 bits

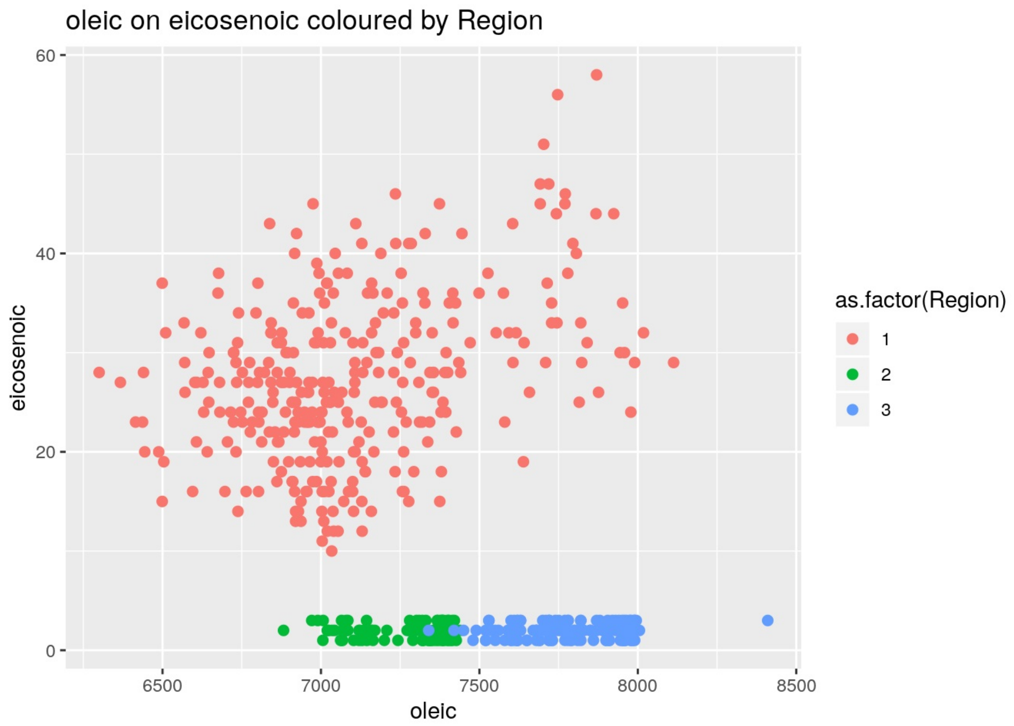
##3

Create a scatterplot of Oleic vs Eicosenoic in which color is defined by numeric values of Region.

```
p6<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=as.numeric(Region)))+labs(x="oleic",y="eicosenoic")+geom_point(siz
e=2)+ggtitle("oleic on eicosenoic coloured by Region")
p6
```




```
p7<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=as.factor(Region)))+labs(x="oleic",y="eicosenoic")+geom_point(size
=2)+ggtitle("oleic on eicosenoic coloured by Region")
p7
```



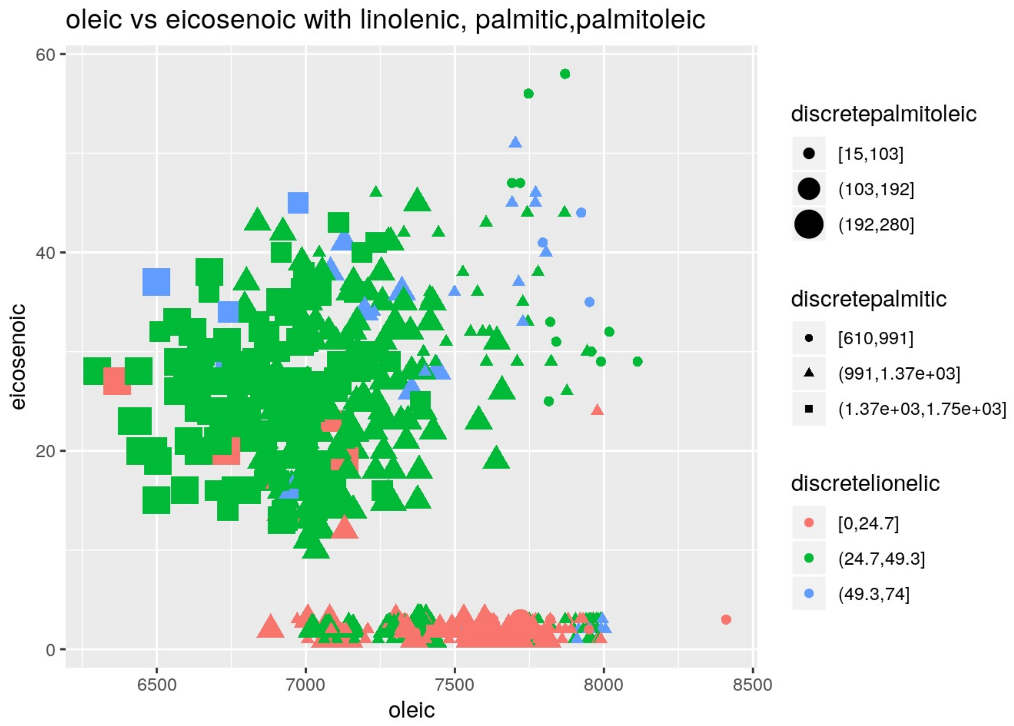
In the second plot it is very easy to find the decision boundaries as using discrete hues is a preattendive feature and identifying the boundaries take very less time.

##4

scatterplot of Oleic vs Eicosenoic in which color is defined by a discretized Linoleic (3 classes), shape is defined by a discretized Palmitic (3 classes) and size is defined by a discretized Palmitoleic (3 classes)

```
discretelionelic<-cut_interval(olive$linolenic, 3)
discretepalmitic<-cut_interval(olive$palmitic, 3)
discretepalmitoleic<-cut_interval(olive$palmitoleic, 3)

p8<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=discretelionelic,shape=discretepalmitic,size=discretepalmitoleic))
+geom_point()+ggtitle("oleic vs eicosenoic with linolenic, palmitic,palmitoleic")
p8
```

```
## Warning: Using size for a discrete variable is not advised.
```



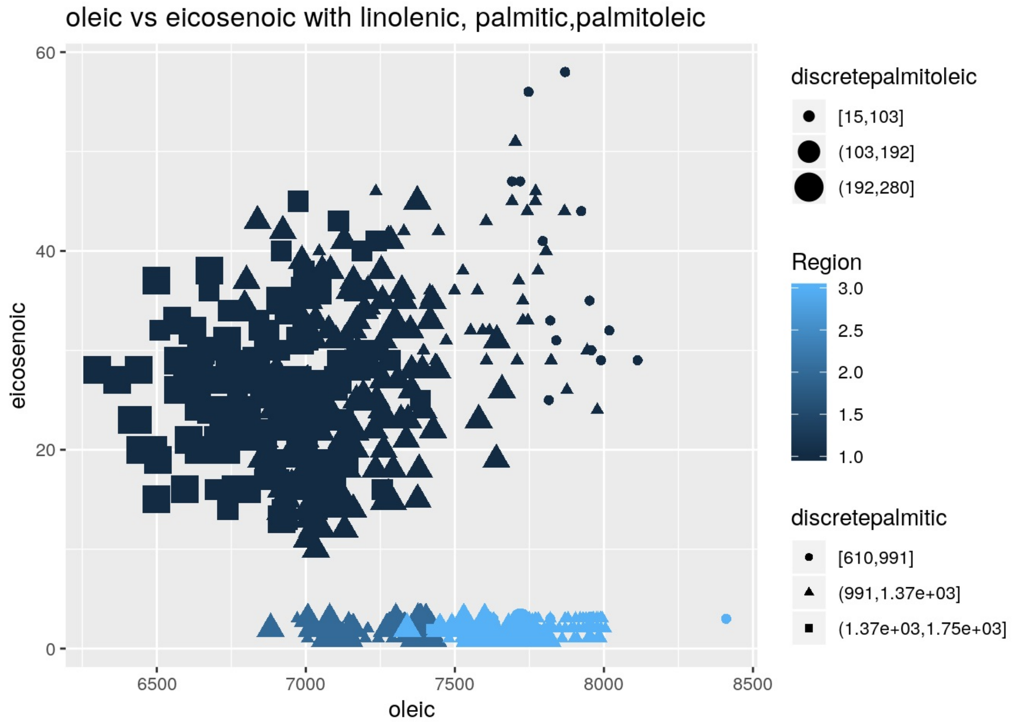
It is really difficult to differentiate between 27 different types of observations as there are no clear cut boundaries. Here there are three shades of colour and three types of shapes.Their summation is not the same as summation of the channel capacity of three shapes and three colours.

##5

scatterplot of Oleic vs Eicosenoic in which color is defined by Region,shape is defined by a discretized Palmitic (3 classes) and size is defined by a discretized Palmitoleic (3 classes)

```
p9<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=Region,shape=discretepalmitic,size=discretepalmitoleic))+geom_poin
t()+ggtitle("oleic vs eicosenoic with linolenic, palmitic,palmitoleic")
p9
```

```
## Warning: Using size for a discrete variable is not advised.
```

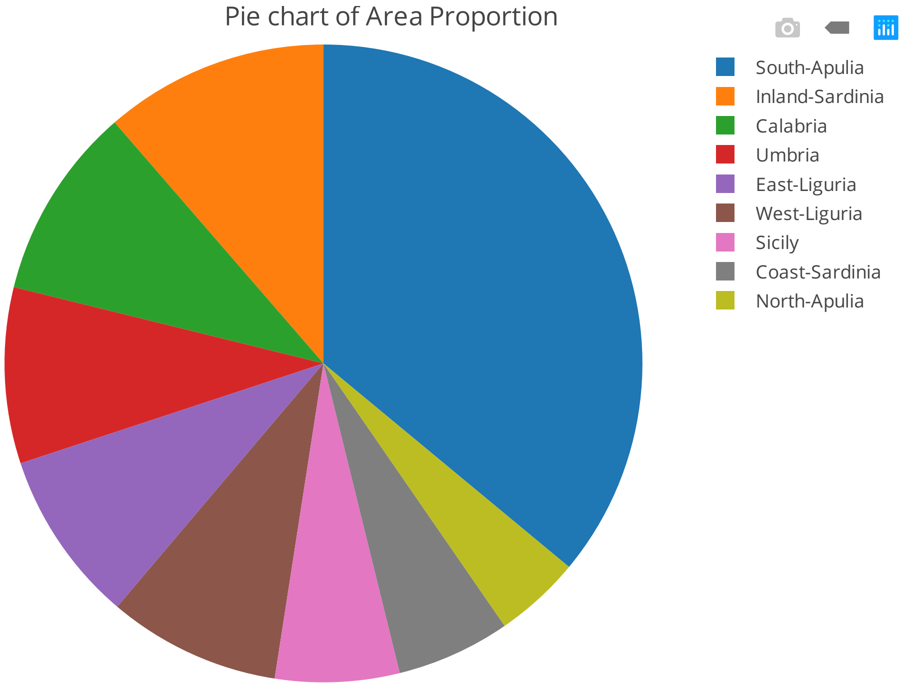


The boundary between the regions is easily identified as we have colour to distinguish the boundaries.Colour,orientation and intensity can be automatically percieved by human eye according to treistman theory of integration and the combination of thes may require time to distinguish as seen in the quetion 4.Here colour is the one that helps as distinguish faster.

##6

create a pie chart that shows the proportions of oils coming from different Areas using plotly

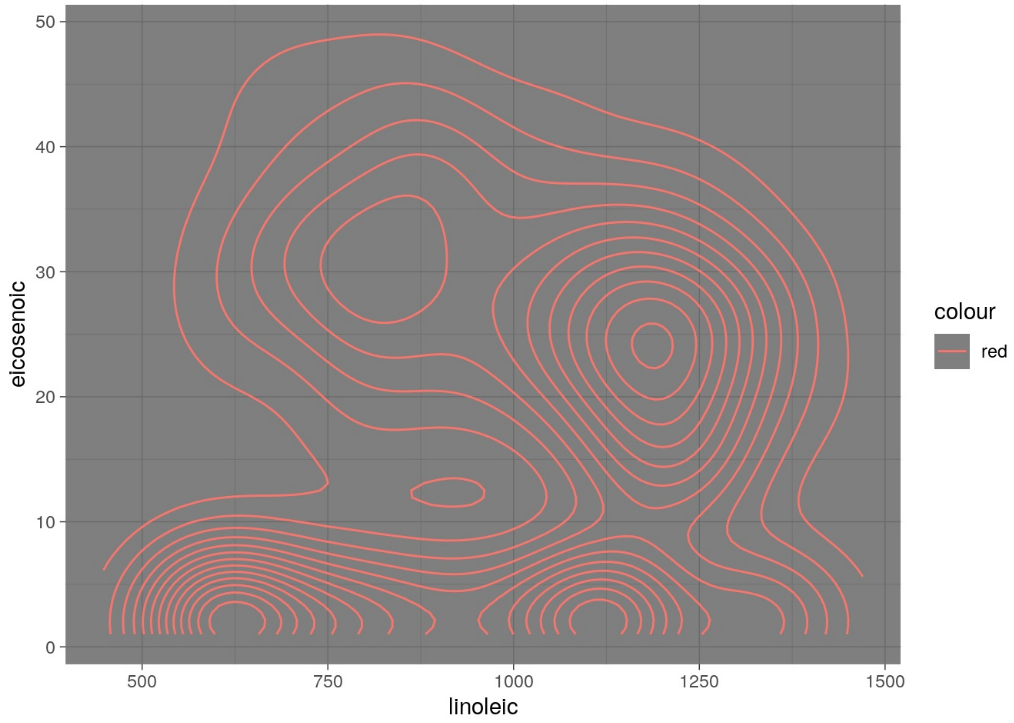
```
library(plotrix)
library(plotly)

mytable <- table(olive$Area)
dframe<-as.data.frame(mytable)

#pie3D(dframe$Freq,labels=dframe$Var1,explode=0.1,main="Pie Chart of Area Proportion ")

p10 <- plot_ly(dframe, labels = ~Var1, values = ~Freq, type = 'pie',textinfo = "none", hoverinfo = "text",text=~Va
r1) %>%
  layout(title = 'Pie chart of Area Proportion',
         xaxis = list(showgrid = FALSE, zeroline = FALSE, showticklabels = FALSE),
         yaxis = list(showgrid = FALSE, zeroline = FALSE, showticklabels = FALSE))

p10
```



THe pie chart is less effective than the bar chart.When the values differ by small number it is diffcult to predict which area's frequency was more without hovering and finding for the exact value.In barchart just looking at the lenght we can find this. ##7

2d-density contour plot

```
p11<-ggplot(olive, aes(x=linoleic, y=eicosenoic,col="red") ) +geom_density_2d(position="identity")+theme_dark()
p11
```



Outliers are missed in contour plots.

###Assignment 2

Load the baseball data in r

```
library(readxl)
library(ggplot2)
library(plotly)
library(MASS)


df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)
```

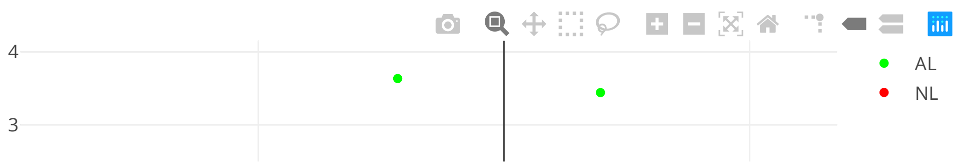
It is reasonable to scale the data because we have different range of features in the data.

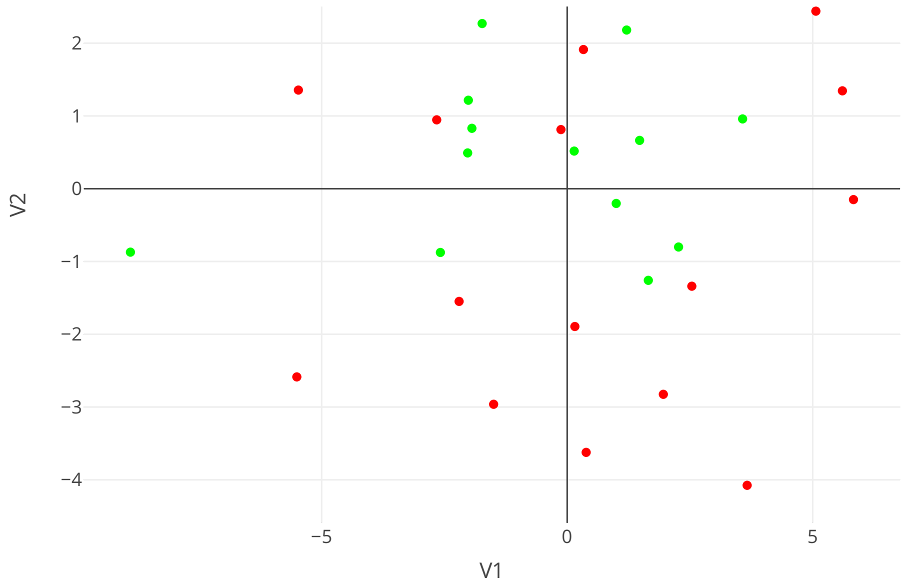
```
library(readxl)

df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)
df<-data.frame(df)

scaled_df<-scale(df[,-c(1,2)])
d<-dist(scaled_df)
mds<-isoMDS(d,k=2)
```

```
## initial  value 19.856833
## iter   5 value 16.319153
## iter  10 value 16.046215
## final  value 15.935476
## converged
```

```
dt<-(mds$points)
dt_new<-as.data.frame(dt)
dt_new$League<-df[,2]
dt_new$Team<-df[,1]



plot_ly(dt_new, x=~V1, y=~V2, type="scatter", hovertext=~Team, color=~League, colors=c("green", "red"))
```

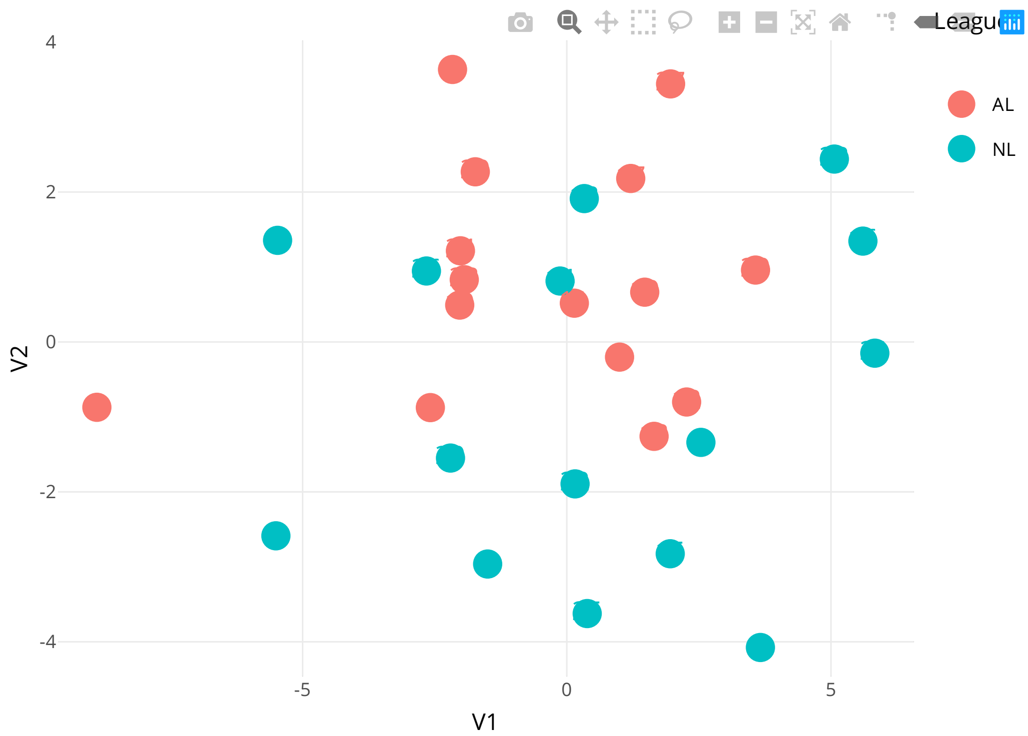
```
## No scatter mode specifed:
##   Setting the mode to markers
##   Read more about this attribute -> https://plot.ly/r/reference/#scatter-mode
```





Form the graph we can first observe that Boston Red Sox,Baltimore orles,philadelphia philles seems to be outliers.Theres seems to be some kind of diffrence between the Leagues.V2 seems to provide a better differenciation between leagues.ALso the NL is more scattered than AL.

```
p <- ggplot(data=dt_new,aes(x=V1,y=V2,col=League,size=5))+geom_point()+theme_minimal()+
  geom_text(aes(label=rownames(dt_new),size=5))
ggplotly(p)
```

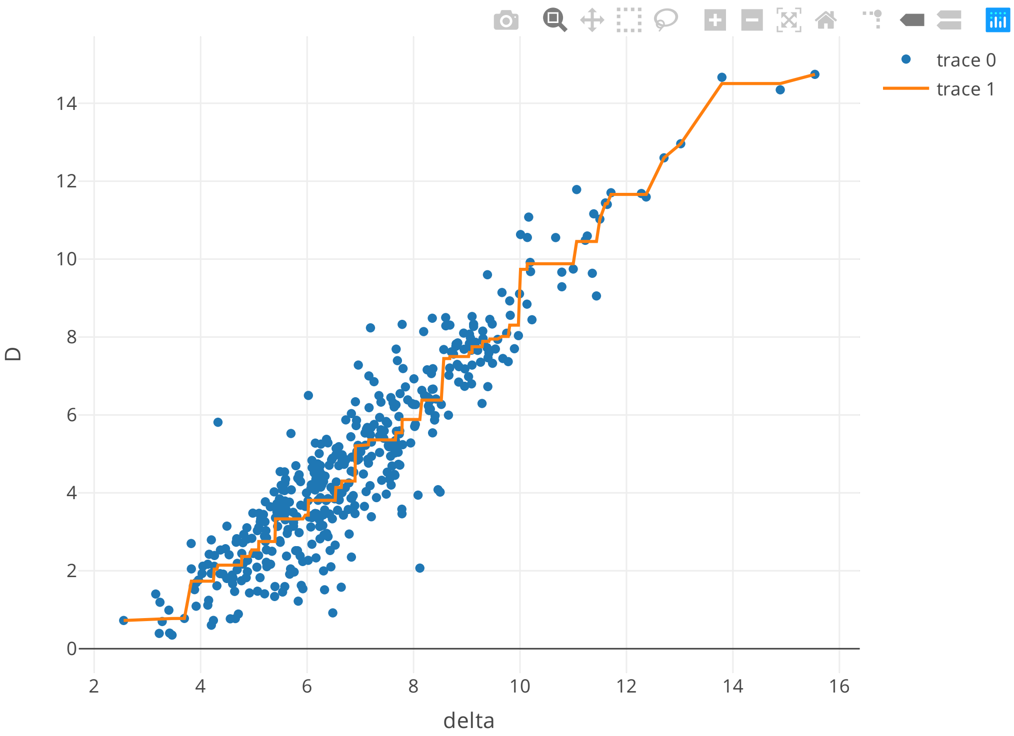


#3

```
library(readxl)
library(ggplot2)
library(plotly)
library(MASS)


df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)
scaled_df<-scale(df[,-c(1,2)])
d<-dist(scaled_df)
mds<-isoMDS(d,k=2)
```

```
## initial  value 19.856833
## iter   5 value 16.319153
## iter  10 value 16.046215
## final  value 15.935476
## converged
```

```
dt<-(mds$points)
dt_new<-as.data.frame(dt)
dt_new$League<-df$League
rownames(dt_new)<-df$Team


sh <- Shepard(d,dt)
delta <-as.numeric(d)
D<- as.numeric(dist(dt))

n=nrow(dt)
index=matrix(1:n, nrow=n, ncol=n)
index1=as.numeric(index[lower.tri(index)])

n=nrow(dt)
index=matrix(1:n, nrow=n, ncol=n, byrow = T)
index2=as.numeric(index[lower.tri(index)])



plot_ly()%>%
  add_markers(x=~delta, y=~D, hoverinfo ='text', text = ~paste('Obj1: ', df[index1,1],
                          '<br> Obj 2:', df[index2,1]))%>%add_lines(x=~sh$x, y=~sh$yf)
```

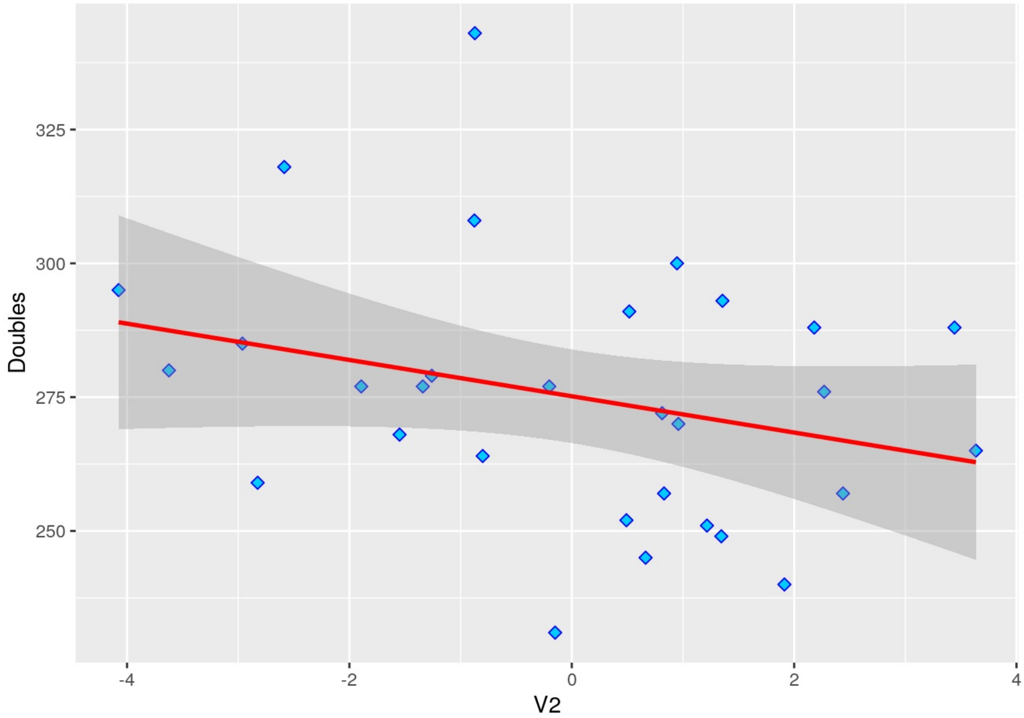


The data points away from the line are the ones that are problamatic.They are like Minnesota Twins and Arizona Diamondbacks, Oakland Athletics and Milwaukee Brewers) were hardest to plot from Shepard plot.

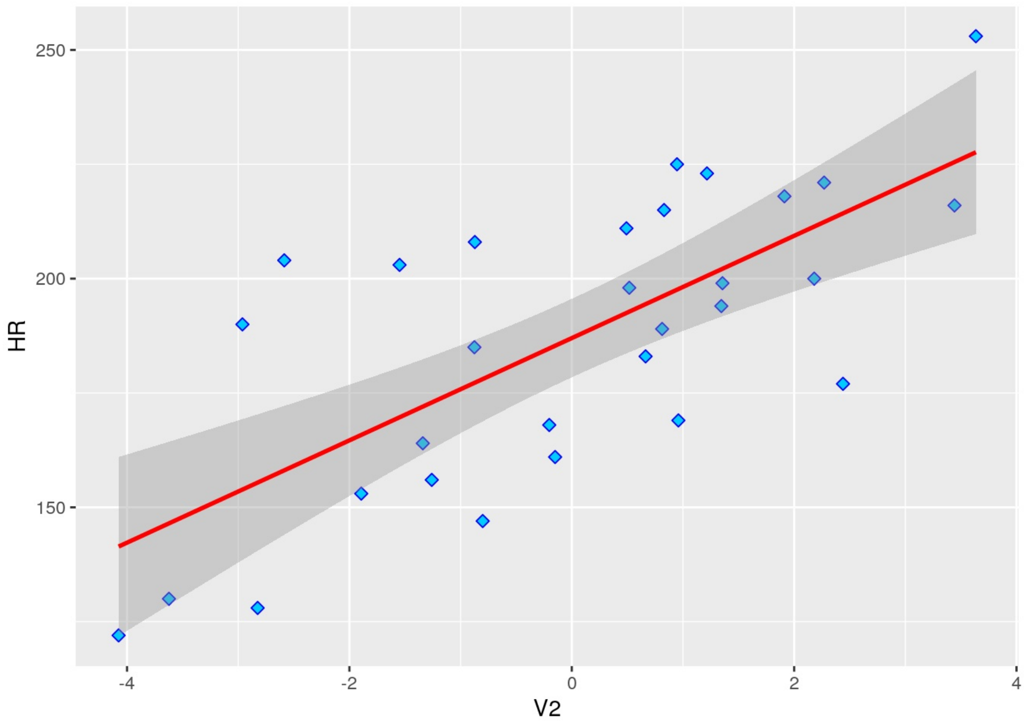
```
library(gridExtra)
num_df<-df[,-c(1,2)]
num_df$V2-dt_new$V2
```

```
## numeric(0)
```

```
num_df<-as.data.frame(num_df)
names(num_df)[8]<-"Doubles"
names(num_df)[9]<-"Triples"


ggplot(num_df,aes(x=dt_new$V2,y=Doubles))+geom_point(size=2,color="blue",pch=23,fill="#00CCFF")+stat_smooth(method
= "lm", col = "red")+xlab("V2")
```




```
ggplot(num_df,aes(x=dt_new$V2,y=HR))+geom_point(size=2,color="blue",pch=23,fill="#00CCFF")+stat_smooth(method = "l
m", col = "red")+xlab("V2")
```



Doubles and Home RUn could be observed as the two components that showed the strongest connection.This is true when considering the game itself especially for scoring. ###Appendix

```
## ----setup, include=FALSE,message=FALSE,warning=FALSE--------------------
knitr::opts_chunk$set(echo = TRUE)


## ----message=FALSE,warning=FALSE-----------------------------------------
library(ggplot2)
library(plotly)
library(MASS)



olive<-read.csv("olive.csv",header=TRUE, sep=",")



p1<-ggplot(olive,aes(palmitic,oleic,col=linolenic))+geom_point()+labs(x="palmitic",y="oleic")+ggtitle("Plot of Pal
mitic on Oleic coloured by Linolenic")
```

```
p1

interval_cut <- cut_interval(olive$linolenic, 4)
p2<-ggplot(olive,aes(palmitic,oleic,col=interval_cut))+geom_point()+theme_light()+labs(x="palmitic",y="oleic")+ggt
itle("Plot of Palmitic on Oleic coloured by Linolenic Cut intervals")+theme(axis.text = element_text(colour = "blu
e"))
p2



## ---------------------------------------------------------------------------
p3<-s2<-ggplot(olive,aes(palmitic,oleic,col=interval_cut))+geom_point()+theme_light()+labs(x="palmitic",y="oleic")
+geom_point(size=3)+ggtitle("Plot of Palmitic on Oleic coloured by Linolenic")+theme(axis.text = element_text(colo
ur = "blue"))
p3



## ---------------------------------------------------------------------------
p4<-s2<-ggplot(olive,aes(palmitic,oleic))+geom_point(aes(size=interval_cut))+theme_light()+labs(x="palmitic",y="ol
eic")+geom_point()+ggtitle("Plot of Palmitic on Oleic coloured by Linolenic")+theme(axis.text = element_text(colou
r = "blue"))
p4


## ---------------------------------------------------------------------------
angleplot<-ggplot(olive,aes(x=palmitic,y=oleic)) +
  geom_point() +geom_spoke(aes(angle = as.numeric(cut_interval(linolenic, 4))*pi/2), radius = 50)
angleplot


## ---------------------------------------------------------------------------
p6<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=as.numeric(Region)))+labs(x="oleic",y="eicosenoic")+geom_point(siz
e=2)+ggtitle("oleic on eicosenoic coloured by Region")
p6


## ---------------------------------------------------------------------------
p7<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=as.factor(Region)))+labs(x="oleic",y="eicosenoic")+geom_point(size
=2)+ggtitle("oleic on eicosenoic coloured by Region")
p7


## ---------------------------------------------------------------------------
discretelionelic<-cut_interval(olive$linolenic, 3)
discretepalmitic<-cut_interval(olive$palmitic, 3)
discretepalmitoleic<-cut_interval(olive$palmitoleic, 3)

p8<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=discretelionelic,shape=discretepalmitic,size=discretepalmitoleic))
+geom_point()+ggtitle("oleic vs eicosenoic with linolenic, palmitic,palmitoleic")
p8


## ---------------------------------------------------------------------------
p9<-ggplot(olive,aes(x=oleic,y=eicosenoic,color=Region,shape=discretepalmitic,size=discretepalmitoleic))+geom_poin
t()+ggtitle("oleic vs eicosenoic with linolenic, palmitic,palmitoleic")
p9


## ----message=FALSE,warning=FALSE---------------------------------------------
library(plotrix)
library(plotly)

mytable <- table(olive$Area)
dframe<-as.data.frame(mytable)

#pie3D(dframe$Freq,labels=dframe$Var1,explode=0.1,main="Pie Chart of Area Proportion ")

p10 <- plot_ly(dframe, labels = ~Var1, values = ~Freq, type = 'pie',textinfo = "none", hoverinfo = "text",text=~Va
r1) %>%
  layout(title = 'Pie chart of Area Proportion',
         xaxis = list(showgrid = FALSE, zeroline = FALSE, showticklabels = FALSE),
         yaxis = list(showgrid = FALSE, zeroline = FALSE, showticklabels = FALSE))

p10


## ---------------------------------------------------------------------------
```

```
p11<-ggplot(olive, aes(x=linoleic, y=eicosenoic,col="red") ) +geom_density_2d(position="identity")+theme_dark()
p11


## ----message=FALSE,warning=FALSE----------------------------------------
library(readxl)
library(ggplot2)
library(plotly)
library(MASS)


df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)


## --------------------------------------------------------------------------
library(readxl)

df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)
df<-data.frame(df)

scaled_df<-scale(df[,-c(1,2)])
d<-dist(scaled_df)
mds<-isoMDS(d,k=2)

dt<-(mds$points)
dt_new<-as.data.frame(dt)
dt_new$League<-df[,2]
dt_new$Team<-df[,1]



plot_ly(dt_new, x=~V1, y=~V2, type="scatter", hovertext=~Team, color=~League, colors=c("green", "red"))


## ----message=FALSE,warning=FALSE----------------------------------------
library(readxl)
library(ggplot2)
library(plotly)
library(MASS)


df<-read_xlsx("baseball-2016.xlsx",col_names=TRUE)
scaled_df<-scale(df[,-c(1,2)])
d<-dist(scaled_df)
mds<-isoMDS(d,k=2)

dt<-(mds$points)
dt_new<-as.data.frame(dt)
dt_new$League<-df$League
rownames(dt_new)<-df$Team


sh <- Shepard(d,dt)
delta <-as.numeric(d)
D<- as.numeric(dist(dt))

n=nrow(dt)
index=matrix(1:n, nrow=n, ncol=n)
index1=as.numeric(index[lower.tri(index)])

n=nrow(dt)
index=matrix(1:n, nrow=n, ncol=n, byrow = T)
index2=as.numeric(index[lower.tri(index)])



plot_ly()%>%
  add_markers(x=~delta, y=~D, hoverinfo ='text', text = ~paste('Obj1: ', df[index1,1],
                    '<br> Obj 2:', df[index2,1]))%>%add_lines(x=~sh$x, y=~sh$yf)


## ----message=FALSE,warning=FALSE----------------------------------------
library(gridExtra)
num_df<-df[,-c(1,2)]
num_df$V2-dt_new$V2
num_df<-as.data.frame(num_df)
names(num_df)[8]<-"Doubles"
names(num_df)[9]<-"Triples"
```

```
ggplot(num_df,aes(x=dt_new$V2,y=Doubles))+geom_point(size=2,color="blue",pch=23,fill="#00CCFF")+stat_smooth(method
= "lm", col = "red")+xlab("V2")
```

```
## ------------------------------------------------------------------------
```

```
ggplot(num_df,aes(x=dt_new$V2,y=HR))+geom_point(size=2,color="blue",pch=23,fill="#00CCFF")+stat_smooth(method = "l
m", col = "red")+xlab("V2")
```

Lab3

Priya (priku577) and Andreas(andch552)

26 September 2018

Assignment 1

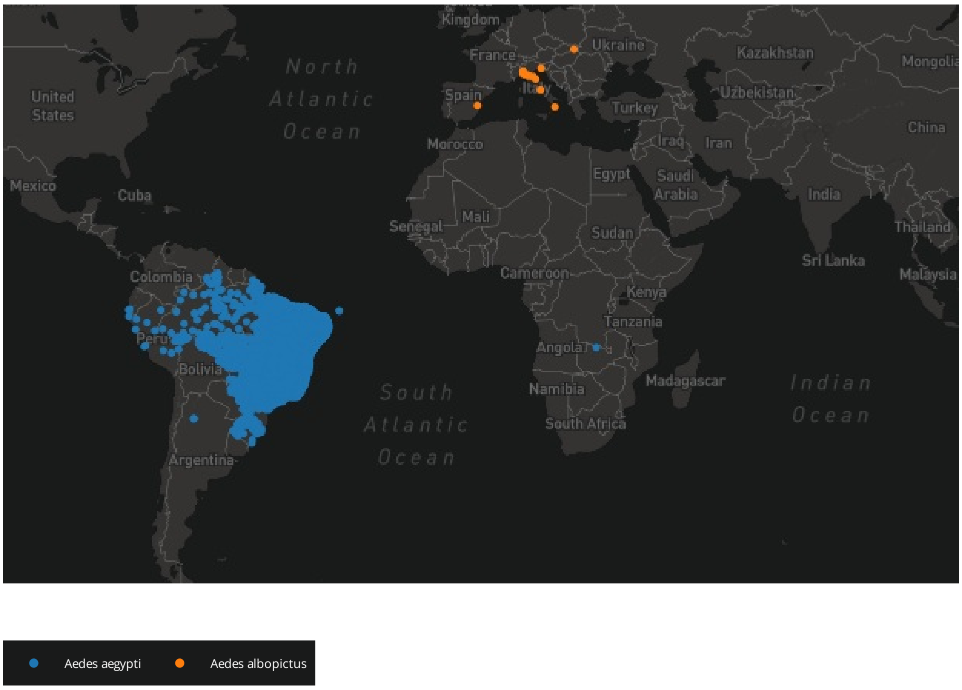
1.Mapbox plotly

MAPBOX PLOT FOR YEAR 2004

```
library(tidyverse)
library(plotly)
library(RCurl)
library(gridExtra)
library(RColorBrewer)


Sys.setenv('MAPBOX_TOKEN'='pk.eyJ1IjoicXVhcnRlcm1haW5lIiwiYSI6ImNqbWJucjh4MjA2dm0zd25xMmp4ejZzMnQifQ.-FXHcA1t8b_YZ
kdRSUXuGw')

mosquitos<-read.csv('aegypti_albopictus.csv',header=TRUE)
p_2004<-mosquitos%>%filter(YEAR=='2004')%>%plot_mapbox(lat = ~Y, lon = ~X,
                                                         split=~VECTOR,colors = 'Set3',
                                                         mode = 'scattermapbox', hoverinfo='name')%>%
  layout(title = 'MOSQUITOS PLOTS FOR YEAR 2004',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))
p_2004
```

MAPBOX PLOT FOR YEAR 2013

```
p_2013<-mosquitos %>%filter(YEAR=='2013')%>%plot_mapbox(lat = ~Y, lon = ~X,
                                                        split=~VECTOR,colors = 'Set3',mode = 'scattermapbox', hove
rinfo='name')%>%
  layout(title = 'MOSQUITOS PLOTS FOR YEAR 2013',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',
                       font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))
p_2013
```



Comparing the two plots we can come to conclusions like

1.The amount of Aedes aegypti in Brazil has increased from 2004 to 2013.Brazil had one of the highest number of Aedes aegypti in 2013 as wellThe regions of rio di Janeiro had more cases.

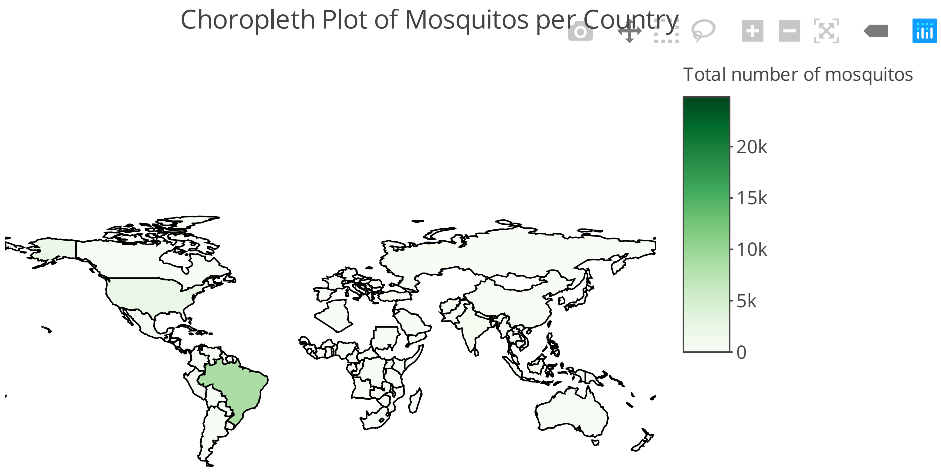
2.The amount of aedes albopictus was high in the US and Taiwan during the yer 2004.The regions most affected were mississippi in US and kaohsiung,Tainam in vietnam.Seems like US could eradicate the aedes albopictus from the missippi area completey but taiwan on other hand in taiwan their number increased.

The perception problems are overplotting,comparison on the poplulation of mosquitoes in each region is difficult.

2.Choropleth Map

CHOROPLETH MAP Equirectangular Projection

```
d<-mosquitos%>%select(c("VECTOR","COUNTRY_ID"))
x<-group_by(d,COUNTRY_ID)%>%count()
s<-as.data.frame(x)

g1 <- list(
  showframe = FALSE,
  showcoastlines = FALSE,
  projection = list(type = 'equirectangular')
)


p1 <- s%>% plot_geo()  %>%
  add_trace(
    z = ~n, color=~n,colors = 'Greens',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country',
    geo = g1
  )

p1
```

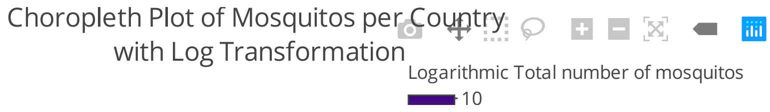


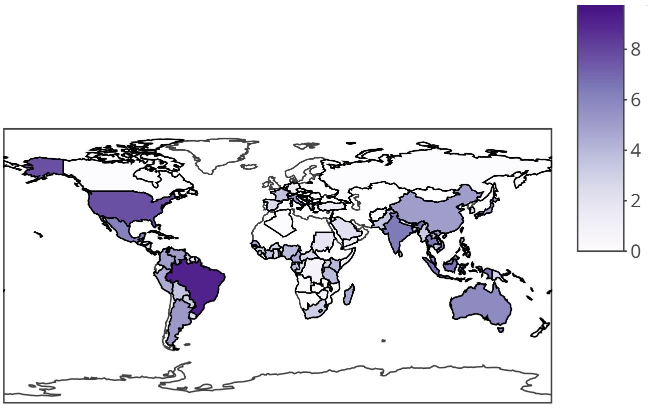
Here the colour scale is from 0-20k .It is very difficult to percieve the data based on this colous scale as instead of different hues intensity varies.

3.Choropleth Map with LOG(Z) transformation

a.Equidistant projection log(z)

```
s$log_n<-log(s$n)

g2 <- list(
  projection = list(type = "equirectangular")
)


p2 <- s%>% plot_geo()  %>%
  add_trace(
    z = ~log_n, color=~log_n,colors = 'Purples',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Logarithmic Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country \n with Log Transformation',
         geo = g2
  )

p2
```

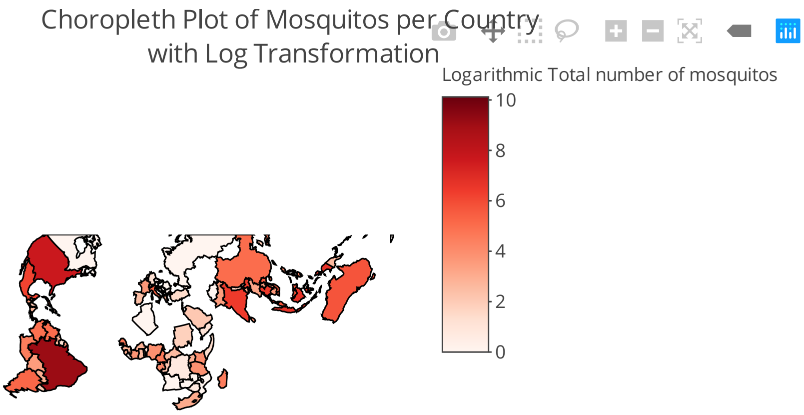




Here we can see the colour scale is from 0-10 instead of 0-20K.The changes can be noted in a better way.A point to be noted here is Russia had a mosquito count of 1 earlier and now it log(1) and hence 0.Countries like India,USA can be diffetniated better now.

b.Conic Equal Projection log(Z)

```
s$log_n<-log(s$n)

g3 <- list(
  showframe = FALSE,
  showcoastlines = FALSE,
  projection = list(type = "conic equal area")
)


p3 <- s%>% plot_geo()  %>%
  add_trace(
    z = ~log_n, color=~log_n,colors = 'Reds',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Logarithmic Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country \n with Log Transformation',
         geo = g3
  )

p3
```



comparing both the map it is clear that the map 3.a is better.The map 3b leads to misinterpretations.In conical projections as we move away from regions where cone intersects the globe the distortions become more.

Mapbox of Brazil

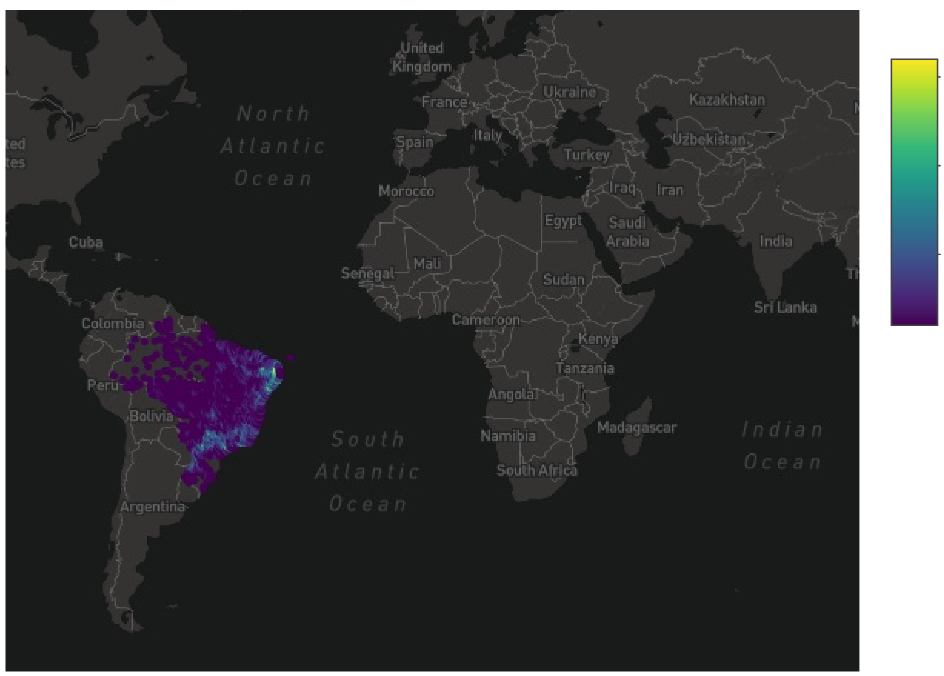
```r
mosquitos_brazil<-mosquitos[(mosquitos$COUNTRY == "Brazil" & mosquitos$YEAR =="2013" ), ]

mosquitos_brazil$X1<-cut_interval(mosquitos_brazil$X,100)
mosquitos_brazil$Y1<-cut_interval(mosquitos_brazil$Y,100)


#mos_group_X1<-as.data.frame(mosquitos_brazil%>%group_by(X1)%>%summarise(mean_group_X=mean(X),n_group_X=n()))
#mos_group_Y1<-as.data.frame(mosquitos_brazil%>%group_by(Y1)%>%summarise(mean_group_Y=mean(Y),n_group_Y=n()))


mos<-as.data.frame(mosquitos_brazil)%>%group_by(X1,Y1)%>%summarise(m1=mean(X),m2=mean(Y),N=n())
```

```
## Warning: Factor `X1` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```
## Warning: Factor `Y1` contains implicit NA, consider using
## `forcats::fct_explicit_na`
```

```r
mos<-as.data.frame(mos)

br <-mos %>%plot_mapbox(lat = ~m2, lon = ~m1,color = ~N ,mode = 'scattermapbox', hoverinfo='name')%>%
  layout(title = 'Mean values of X and Y per group (X1,Y1) and amount of obs per group (X1,Y1) ',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',
                       font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))

br
```

```
## Warning: Ignoring 1 observations
```



As we can observe from the plot Nova Cruz,Guarabira and Sao Paulo are some cities with high levels of Mosquitos. This discretization defenetly help in analyzing the distribution of mosquitoes accross Brazil.

Assignment 2

1.Young,Adult and senior of the swedish counties are grouped.

```
library(RCurl)
library(tidyverse)

swedish<-read.csv("kd.csv", header=TRUE,encoding = "latin1")

swedish_wide <- spread(swedish, age,X2016)
swedish_wide =swedish_wide[,-2]

names(swedish_wide)<-c("Region","Young","Adult","Senior")
```

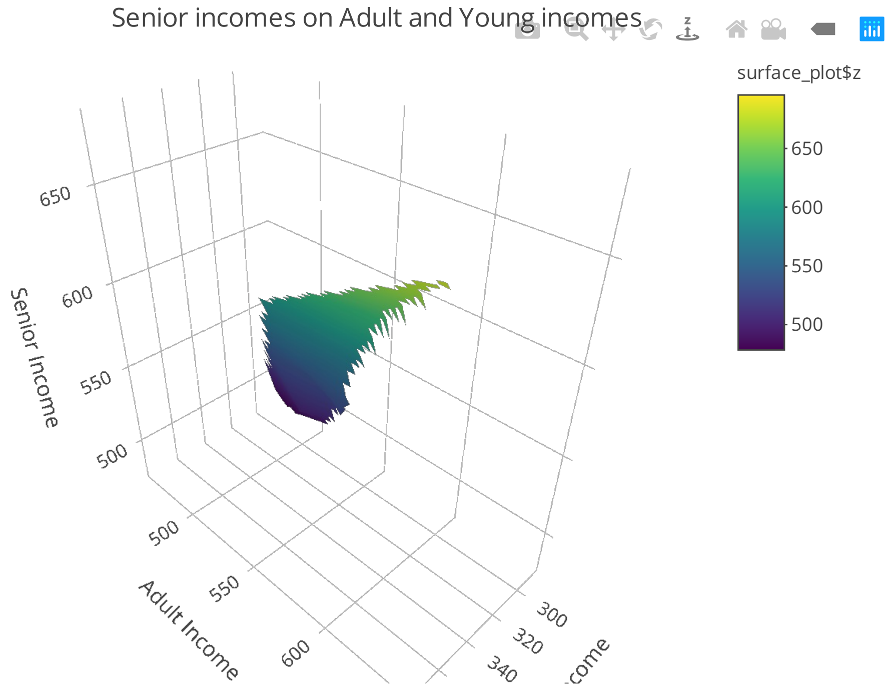
2.Violin plot

```
ee <- swedish_wide %>%
  plot_ly(type = 'violin') %>%
  add_trace(y = ~Young,name = 'Young',box = list(visible = T),
    meanline = list(visible = T),line = list(color = 'pink')
  )%>%
  add_trace(y = ~Adult,name = 'Adults',box = list(visible = T),
            meanline = list(visible = T),line = list(color = 'blue')) %>%
  add_trace(
    y = ~Senior,name = 'Senior',box = list(visible = T),
    meanline = list(visible = T),line = list(color = 'green')
  )%>%
  layout(yaxis = list(title = "income ",
                      zeroline = F), xaxis = list(title = "Age Group"), title = "Income vs  Age Group"
  )


ee
```

The mean income is lowest for age 18-24.This is true may be coz they just start working. All three groups have a small group of people having very high income range (outliers). The age groups of 30-49 and 50-64 have almost similar mean and distribution, with majority having income in range 500 K SEK.

3.Surface plot

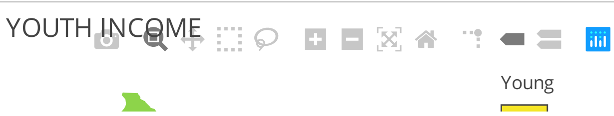
```
library(akima)

surface_plot=interp(swedish_wide$Young, swedish_wide$Adult, swedish_wide$Senior, duplicate = "mean")

plot_ly(x=~surface_plot$x, y=~surface_plot$y, z=~surface_plot$z, type="surface") %>%  layout(
  title = "Senior incomes on Adult and Young incomes",
  scene = list(
    xaxis = list(title = "Young Income"),
    yaxis = list(title = "Adult Income"),
    zaxis = list(title = "Senior Income")
  ))
```

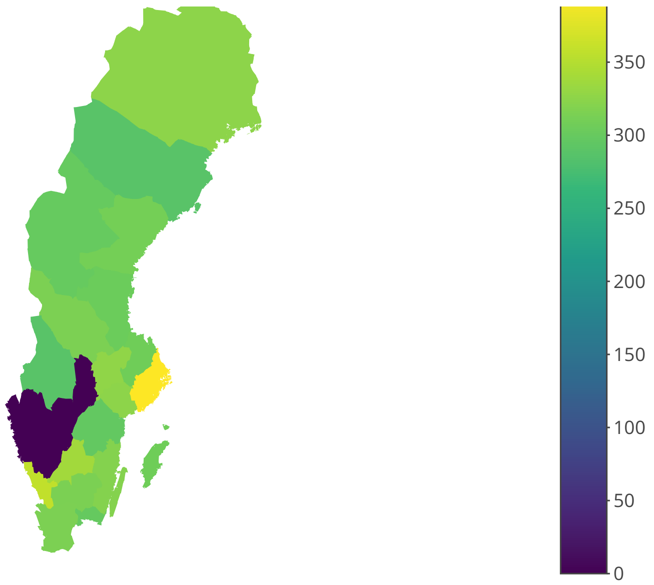


There is linear relationship and hence linear model fits well.

4.Choropleth Plots of Adults and Youngs

```
library(RCurl)
library(tidyverse)
#ibrary(sf)
library(plotly)
library(RCurl)
library(tidyverse)
library(sf)
library(plotly)

swedish<-read.csv("kd.csv", header=TRUE,encoding = "latin1")

swedish_wide <- spread(swedish, age,X2016)
swedish_wide =swedish_wide[,-2]

names(swedish_wide)<-c("Region","Young","Adult","Senior")
map<-readRDS("gadm36_SWE_1_sf.rds")


swedish <- swedish_wide %>% separate(Region,c("Num","Region","County"),extra = 'drop')%>%select("Region","Young","
Adult","Senior")

rownames(swedish)=swedish$Region
map$Young=swedish[map$NAME_1, "Young"]
map$Young[is.na(map$Young)]=0
map$Adult=swedish[map$NAME_1, "Adult"]
map$Adult[is.na(map$Adult)]=0
Young_value <- plot_ly() %>% add_sf(data=map, split=~NAME_1, color=~Young, showlegend=F, alpha=1) %>%
  layout(title="YOUTH INCOME")
Young_value
```

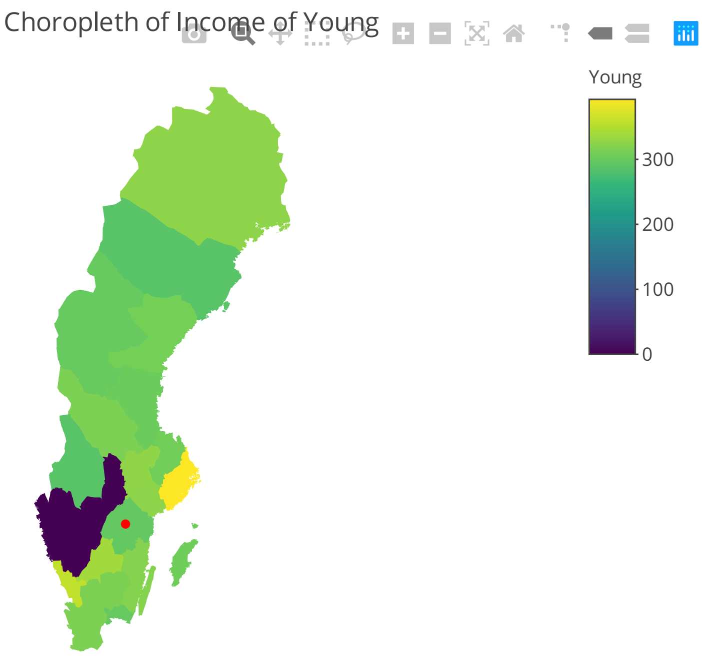




As we can observe from both Choropleth Plots both Young and Adults in Stockhom have higher income regarding rest of Sweden.This seems to be reasonable as stockholm is the capital city and there would be lot of job oppertunities there.It is easier to compare between regions.BUt when we look the country map it is difficult to say about the inome distribution because of the continous colour scale of colour blue.

5.Choropleth Plots of Adults and Youngs with Linkoping coords

```
library(sf)
lat= 58.409814
longitude = 15.624525
name = "Linkoping"
desc = "Linköping, Östergötlands län, SE"

data_point <- data.frame(lat, longitude, name, desc)
plot_ly() %>% add_sf(data=map, split=~NAME_1, color=~Young, showlegend=F, alpha=1,
                     type = "scatter") %>% layout(title = "Choropleth of Income of Young") %>% add_markers(data =
data_point,
                                                                                                    y = ~la
t, x = ~longitude, color = I("red"), text='Linkoping')
```



APPENDIX

```
Appendix Code
GROUP_25
```

```r
# Assignment 1 ------------------------------------------------------------


# 1 --------------
library(tidyverse)
library(plotly)
library(RCurl)
library(gridExtra)
library(RColorBrewer)


Sys.setenv('MAPBOX_TOKEN'='pk.eyJ1IjoicXVhcnRlcm1haW5lIiwiYSI6ImNqbWJucjh4MjA2dm0zd25xMmp4ejZzMnQifQ.-FXHcA1t8b_YZ
kdRSUXuGw')

mosquitos<-read.csv('aegypti_albopictus.csv',header=TRUE)
p_2004<-mosquitos%>%filter(YEAR=='2004')%>%plot_mapbox(lat = ~Y, lon = ~X,
                                                       split=~VECTOR,colors = 'Set3',
                                                       mode = 'scattermapbox', hoverinfo='name')%>%
  layout(title = 'MOSQUITOS PLOTS FOR YEAR 2004',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))
p_2004

p_2013<-mosquitos %>%filter(YEAR=='2013')%>%plot_mapbox(lat = ~Y, lon = ~X,
                                                        split=~VECTOR,colors = 'Set3',mode = 'scattermapbox', hove
rinfo='name')%>%
  layout(title = 'MOSQUITOS PLOTS FOR YEAR 2013',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',
                       font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))
p_2013

# 2 --------------

d<-mosquitos%>%select(c("VECTOR","COUNTRY_ID"))
x<-group_by(d,COUNTRY_ID)%>%count()
s<-as.data.frame(x)

g1 <- list(
  showframe = FALSE,
  showcoastlines = FALSE,
  projection = list(type = 'equirectangular')
)


p1 <- s%>% plot_geo()  %>%
  add_trace(
    z = ~n, color=~n,colors = 'Greens',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country',
         geo = g1
  )

p1

# 3 --------------

s$log_n<-log(s$n)

g2 <- list(
  projection = list(type = "equirectangular")
)


p2 <- s%>% plot_geo()  %>%
  add_trace(
```

```
    z = ~log_n, color=~log_n,colors = 'Purples',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Logarithmic Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country \n with Log Transformation',
         geo = g2
  )

p2


s$log_n<-log(s$n)

g3 <- list(
  showframe = FALSE,
  showcoastlines = FALSE,
  projection = list(type = "conic equal area")
)


p3 <- s%>% plot_geo()  %>%
  add_trace(
    z = ~log_n, color=~log_n,colors = 'Reds',
    text = ~COUNTRY_ID,locations=~COUNTRY_ID
  ) %>% colorbar(title = 'Logarithmic Total number of mosquitos')%>%
  layout(title = 'Choropleth Plot of Mosquitos per Country \n with Log Transformation',
         geo = g3
  )

p3

# 4 --------------

mosquitos_brazil<-mosquitos[(mosquitos$COUNTRY == "Brazil" & mosquitos$YEAR =="2013" ), ]

mosquitos_brazil$X1<-cut_interval(mosquitos_brazil$X,100)
mosquitos_brazil$Y1<-cut_interval(mosquitos_brazil$Y,100)


#mos_group_X1<-as.data.frame(mosquitos_brazil%>%group_by(X1)%>%summarise(mean_group_X=mean(X),n_group_X=n()))
#mos_group_Y1<-as.data.frame(mosquitos_brazil%>%group_by(Y1)%>%summarise(mean_group_Y=mean(Y),n_group_Y=n()))


mos<-as.data.frame(mosquitos_brazil)%>%group_by(X1,Y1)%>%summarise(m1=mean(X),m2=mean(Y),N=n())
mos<-as.data.frame(mos)

br <-mos %>%plot_mapbox(lat = ~m2, lon = ~m1,color = ~N ,mode = 'scattermapbox', hoverinfo='name')%>%
  layout(title = 'Mean values of X and Y per group (X1,Y1) and amount of obs per group (X1,Y1) ',
         font = list(color='white'),
         plot_bgcolor = '#191A1A', paper_bgcolor = '#191A1A',
         mapbox = list(style = 'dark'),
         legend = list(orientation = 'h',
                       font = list(size = 8)),
         margin = list(l = 25, r = 25,
                       b = 25, t = 25,
                       pad = 2))

br

# Assignment 2 ------------------------------------------------------------

# 1 --------------
library(RCurl)
library(tidyverse)

swedish<-read.csv("kd.csv", header=TRUE,encoding = "latin1")

swedish_wide <- spread(swedish, age,X2016)
swedish_wide =swedish_wide[,-2]

names(swedish_wide)<-c("Region","Young","Adult","Senior")

# 2 --------------
ee <- swedish_wide %>%
  plot_ly(type = 'violin') %>%
  add_trace(y = ~Young,name = 'Young',box = list(visible = T),
            meanline = list(visible = T),line = list(color = 'pink')
  )%>%
  add_trace(y = ~Adult,name = 'Adults',box = list(visible = T),
            meanline = list(visible = T),line = list(color = 'blue')) %>%
```

```
  add_trace(
    y = ~Senior,name = 'Senior',box = list(visible = T),
    meanline = list(visible = T),line = list(color = 'green')
  )%>%
  layout(yaxis = list(title = "income ",
                      zeroline = F), xaxis = list(title = "Age Group"), title = "Income vs  Age Group"
  )


ee

# 3 --------------

library(akima)

surface_plot=interp(swedish_wide$Young, swedish_wide$Adult, swedish_wide$Senior, duplicate = "mean")

plot_ly(x=~surface_plot$x, y=~surface_plot$y, z=~surface_plot$z, type="surface") %>%  layout(
  title = "Senior incomes on Adult and Young incomes",
  scene = list(
    xaxis = list(title = "Young Income"),
    yaxis = list(title = "Adult Income"),
    zaxis = list(title = "Senior Income")
  ))

# 4 --------------

library(RCurl)
library(tidyverse)
#ibrary(sf)
library(plotly)
library(RCurl)
library(tidyverse)
library(sf)
library(plotly)

swedish<-read.csv("kd.csv", header=TRUE,encoding = "latin1")

swedish_wide <- spread(swedish, age,X2016)
swedish_wide =swedish_wide[,-2]

names(swedish_wide)<-c("Region","Young","Adult","Senior")
map<-readRDS("gadm36_SWE_1_sf.rds")


swedish <- swedish_wide %>% separate(Region,c("Num","Region","County"),extra = 'drop')%>%select("Region","Young","
Adult","Senior")

rownames(swedish)=swedish$Region
map$Young=swedish[map$NAME_1, "Young"]
map$Young[is.na(map$Young)]=0
map$Adult=swedish[map$NAME_1, "Adult"]
map$Adult[is.na(map$Adult)]=0
Young_value <- plot_ly() %>% add_sf(data=map, split=~NAME_1, color=~Young, showlegend=F, alpha=1) %>%
  layout(title="YOUTH INCOME")
Young_value

# 4 --------------
library(sf)
lat= 58.409814
longitude = 15.624525
name = "Linkoping"
desc = "Linköping, Östergötlands län, SE"

data_point <- data.frame(lat, longitude, name, desc)
plot_ly() %>% add_sf(data=map, split=~NAME_1, color=~Young, showlegend=F, alpha=1,
                     type = "scatter") %>% layout(title = "Choropleth of Income of Young") %>% add_markers(data =
data_point,
                                                                                                          y = ~la
t, x = ~longitude, color = I("red"), text='Linkoping')
```

Lab4

Priya(priku577) and Andreas(andch552)

October 3, 2018

Assignment1

1.Importing the data and filtering it

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------------------------------------
---------------------------------- tidyverse 1.2.1 --
```

```
## <U+221A> ggplot2 3.0.0     <U+221A> purrr   0.2.5
## <U+221A> tibble  1.4.2     <U+221A> dplyr   0.7.6
## <U+221A> tidyr   0.8.1     <U+221A> stringr 1.3.1
## <U+221A> readr   1.1.1     <U+221A> forcats 0.3.0
```

```
## -- Conflicts ------------------------------------------------------------------------------------
---------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(RColorBrewer)
library(plotly)
```

```
##
## Attaching package: 'plotly'
```

```
## The following object is masked from 'package:ggplot2':
##
##     last_plot
```

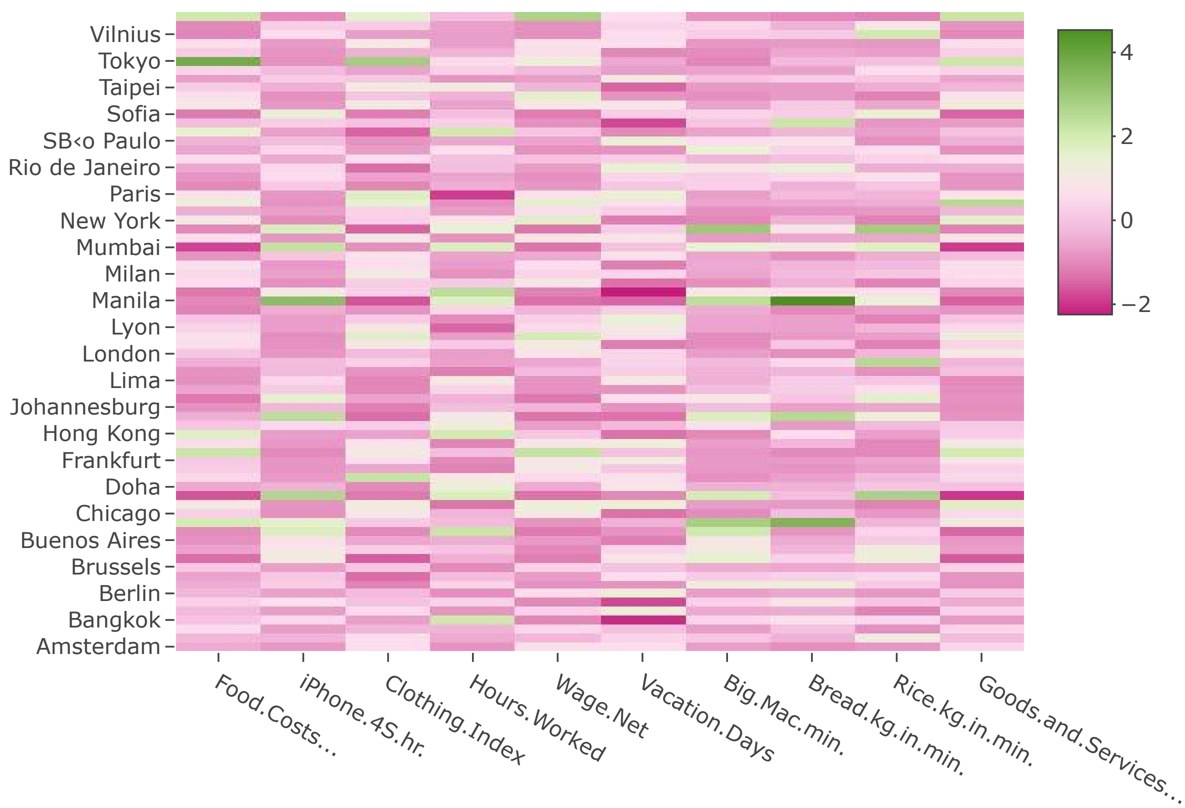
```
## The following object is masked from 'package:stats':
##
##     filter
```

```
## The following object is masked from 'package:graphics':
##
##     layout
```

```
library(seriation)
df<-read.csv("prices-and-earnings.csv")
adults<-df[c(1,2,5,6,7,9,10,16,17,18,19)]

rownames(adults)<-df[,1]
adults<-adults[,-c(1)]
```

2.Heat map of the data

```
coul = colorRampPalette(brewer.pal(8, "PiYG"))(25)
adscaled=scale(adults)
p2<-plot_ly(x=colnames(adscaled), y=rownames(adscaled), z=adscaled, type="heatmap", colors = cou
l)
p2
```

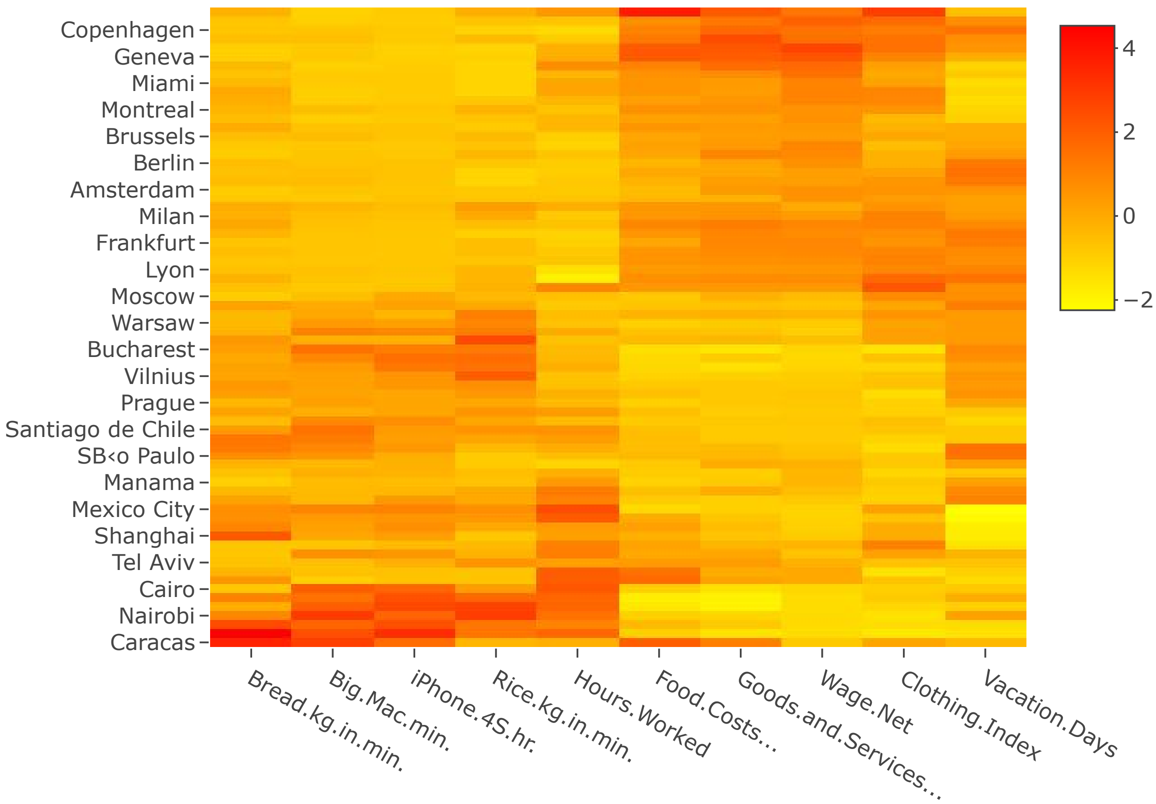


some outliers can be spotted.But it is very difficult to plot clusters since the data is unordered.

3.Heatmaps

Heat map using eucledian distance

```
rowdist_e<-dist(adscaled,method = "minkowski", p=2)
coldist_e<-dist(t(adscaled),method = "minkowski", p=2)
order1_e<-seriate(rowdist_e, "GW")
order2_e<-seriate(coldist_e, "GW")
ord1_e<-get_order(order1_e)
ord2_e<-get_order(order2_e)
reordmatr_euc<-adscaled[rev(ord1_e),ord2_e]
plot_ly(x=colnames(reordmatr_euc), y=rownames(reordmatr_euc),
        z=as.matrix(reordmatr_euc), type="heatmap", colors =colorRamp(c("yellow", "red")))
```



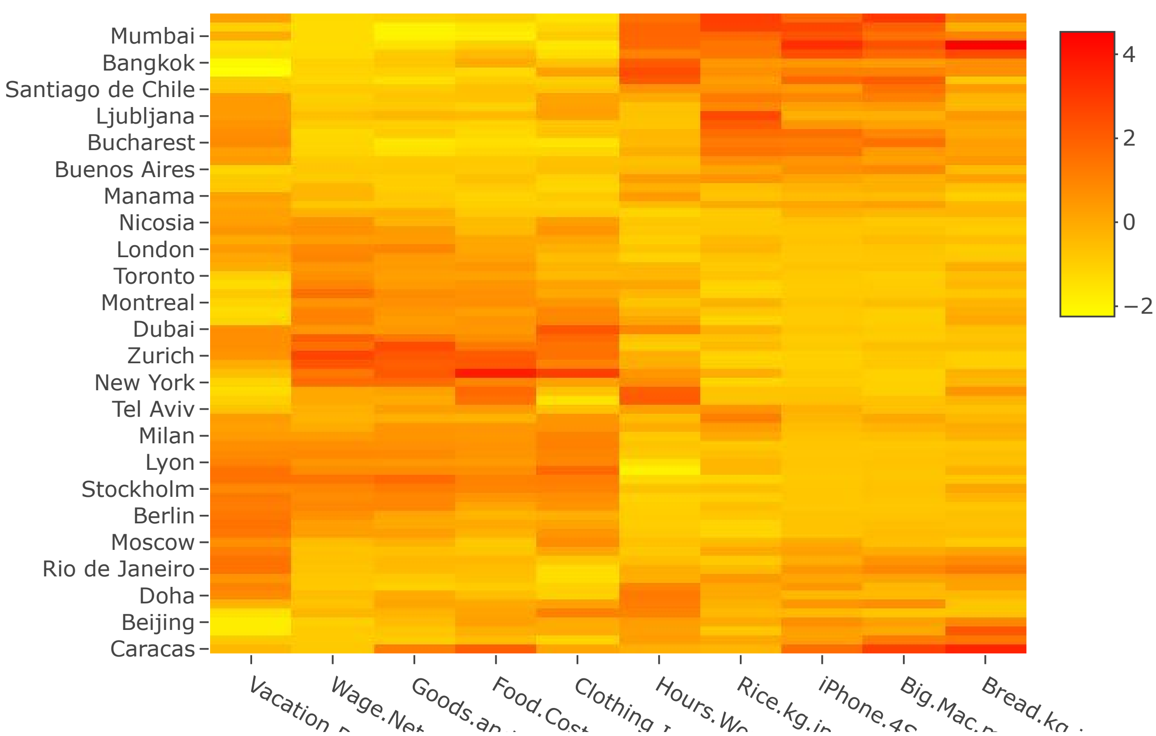
Heat Map with 1-Correlation HC

```
coldist_c<-as.dist(1-cor(adscaled))
rowdist_c<-as.dist(1-cor(t(adscaled)))
order1_c<-seriate(rowdist_c, "GW")
order2_c<-seriate(coldist_c, "GW")
ord1_c<-get_order(order1_c)
ord2_c<-get_order(order2_c)
reordmatr_c<-adscaled[rev(ord1_c),ord2_c]
plot_ly(x=colnames(reordmatr_c), y=rownames(reordmatr_c),
        z=as.matrix(reordmatr_c), type="heatmap", colors =colorRamp(c("yellow", "red")))
```

THe two plots arrive at same conclusions as both of the plots are related.

4.Heat Map with Euclidean Distance TSP

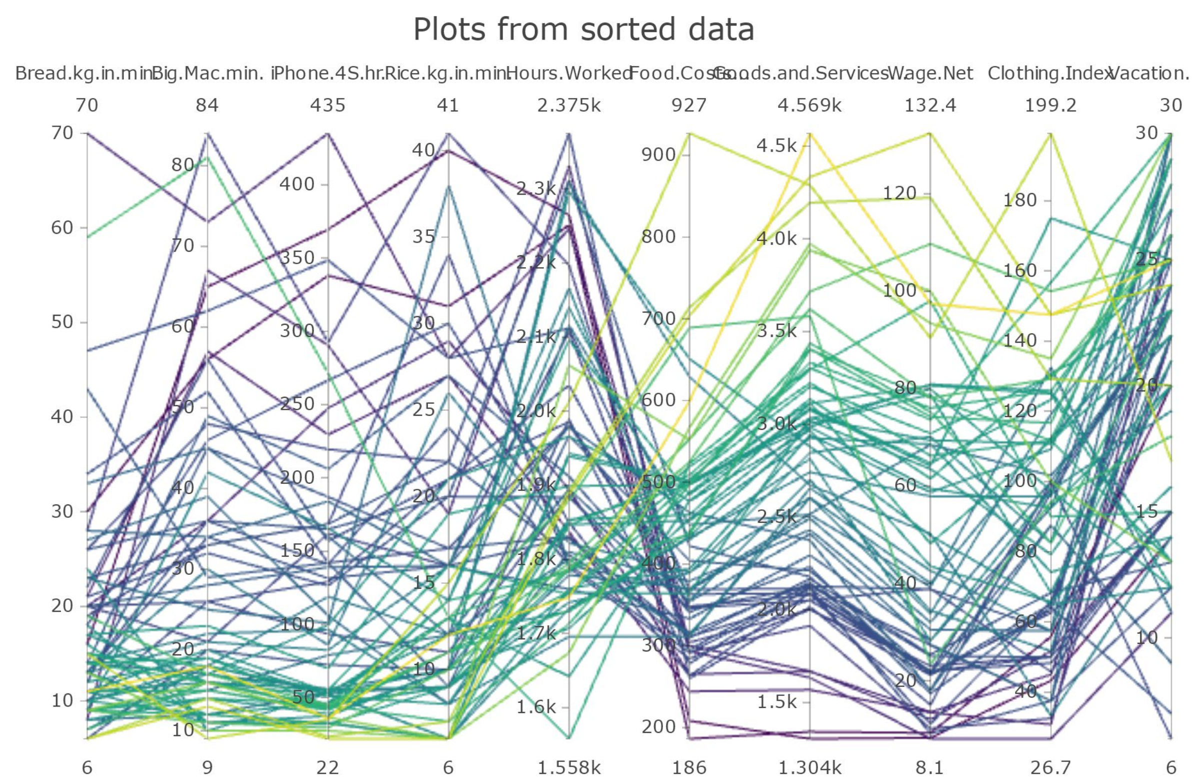
```
rowdist_tsp<-dist(adscaled,method = "minkowski", p=2)
coldist_tsp<-dist(t(adscaled),method = "minkowski", p=2)
order1_tsp<-seriate(rowdist_tsp, "TSP")
order2_tsp<-seriate(coldist_tsp, "TSP")
ord1_tsp<-get_order(order1_tsp)
ord2_tsp<-get_order(order2_tsp)
reordmatr_tsp<-adscaled[rev(ord1_tsp),ord2_tsp]
plot_ly(x=colnames(reordmatr_tsp), y=rownames(reordmatr_tsp),
        z=as.matrix(reordmatr_tsp), type="heatmap", colors =colorRamp(c("yellow", "red")))
```



TSP during each run produce a different result due to the randomness.

5. Parallel Coordinate Plot for Unsorted data

```
v<-1:11
ord=sample(v)
#ord=ord2

dims0=list()
for( i in 1:ncol(adults)){
  dims0[[i]]=list( label=colnames(adults)[ord2_e[i]],
                   values=as.formula(paste("~",colnames(adults)[ord2_e[i]])))
}
p <-adults %>%
  plot_ly(type = 'parcoords',
          line = list(color = ~as.numeric(Goods.and.Services...)),
          dimensions = dims0
  )%>%layout(title = "Plots from sorted data")

p
```



6. Radar plot

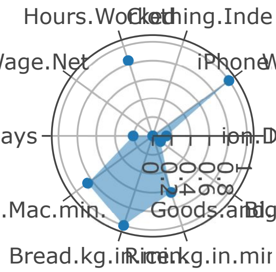
```
library(scales)
Ps=list()
nPlot=72

ad<-as.data.frame(adscaled)
ad[rev(ord1_e),]%>%
  add_rownames( var = "group" ) %>%
  mutate_each(funs(rescale), -group) -> pe_radar
```

```
## Warning: Deprecated, use tibble::rownames_to_column() instead.
```

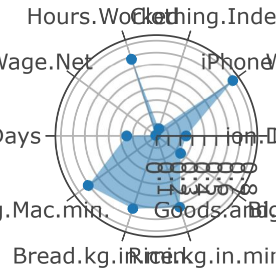
```
for (i in 1:nPlot){
  Ps[[i]] <- htmltools::tags$div(
    plot_ly(type = 'scatterpolar',
            r=as.numeric(pe_radar[i,-1]),
            theta= colnames(pe_radar)[-1],
            fill="toself")%>%
      layout(title=pe_radar$group[i]), style="width: 20%;")  # 4 plots per row
}

h <-htmltools::tags$div(style = "display: flex; flex-wrap: wrap", Ps)
p <- htmltools::browsable(h)
p
```

Caracas

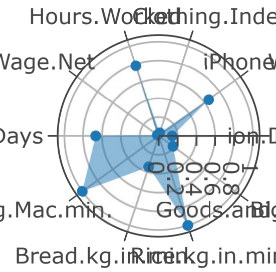
Manila



Jakarta

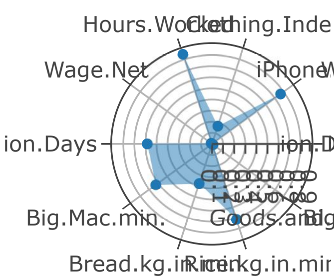


Nairobi

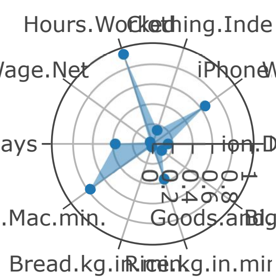


Delhi

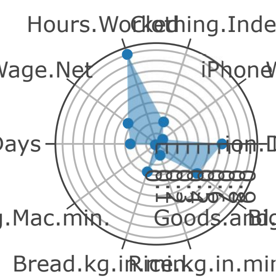
Mumbai



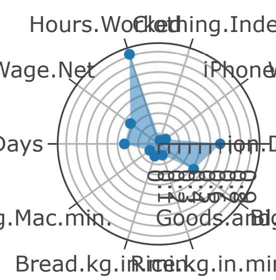
Cairo



Hong Kong



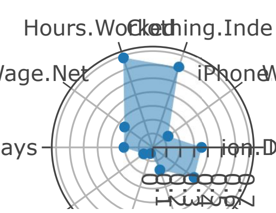
Seoul



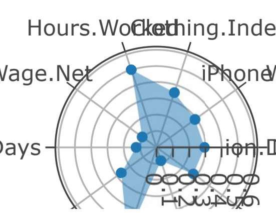
Tel Aviv

Istanbul

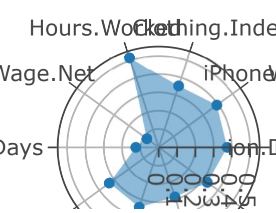
Taipei



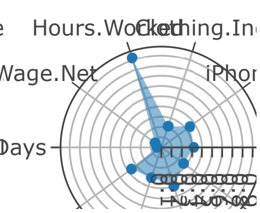
Shanghai



Beijing



Bangkok



```
#Using Juxtaposed and set scale to True
# stars(adults[rev(ord1_e),],
#       key.loc=c(23,2),
#       col.stars =rep("lightblue", nrow(df)),
#       cex = 0.5, lwd = 0.25, lty = par("lty"),
#       scale = TRUE)
```

7.Best one

We think radarchart is good.Radar charts are best when we need to compare small amount of observations.Plotting one over the other we can come to conclusions.BUt if the data is dissimilar then it is hard to compare.

Assignment 2

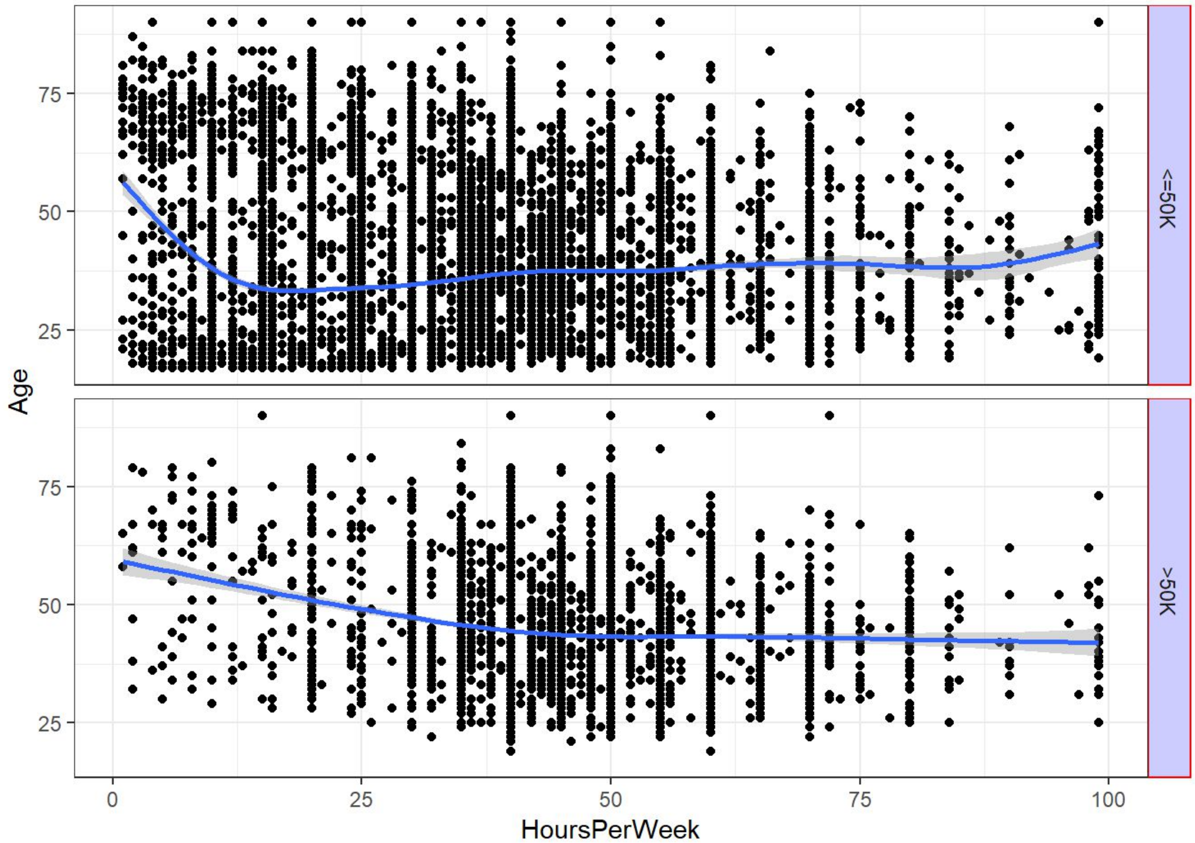
1.Scatterplot

```
library(tidyverse)
library(RColorBrewer)
library(plotly)
library(ggplot2)


adults<-read.csv("adult.csv",sep=",")
names(adults)<-c("Age","Workclass","PolpulationIndex","Education","EducationNum","MaritalStatus"
,"Occupation","Relationship",
                 "Race","Sex","CapitalGain","CapitalLoss","HoursPerWeek","NativeCountry","Income
Level")


sc1<-ggplot(adults,aes(x=HoursPerWeek,y=Age,col=IncomeLevel))+geom_point()
sc1
```

trillis plot

```
tr1<-ggplot(adults,aes(x=HoursPerWeek,y=Age))+geom_point()+facet_grid(IncomeLevel~.)+theme_bw()+
theme(strip.background = element_rect(colour="red", fill="#CCCCFF"))+geom_smooth()
tr1
```

```
## `geom_smooth()` using method = 'gam' and formula 'y ~ s(x, bs = "cs")'
```

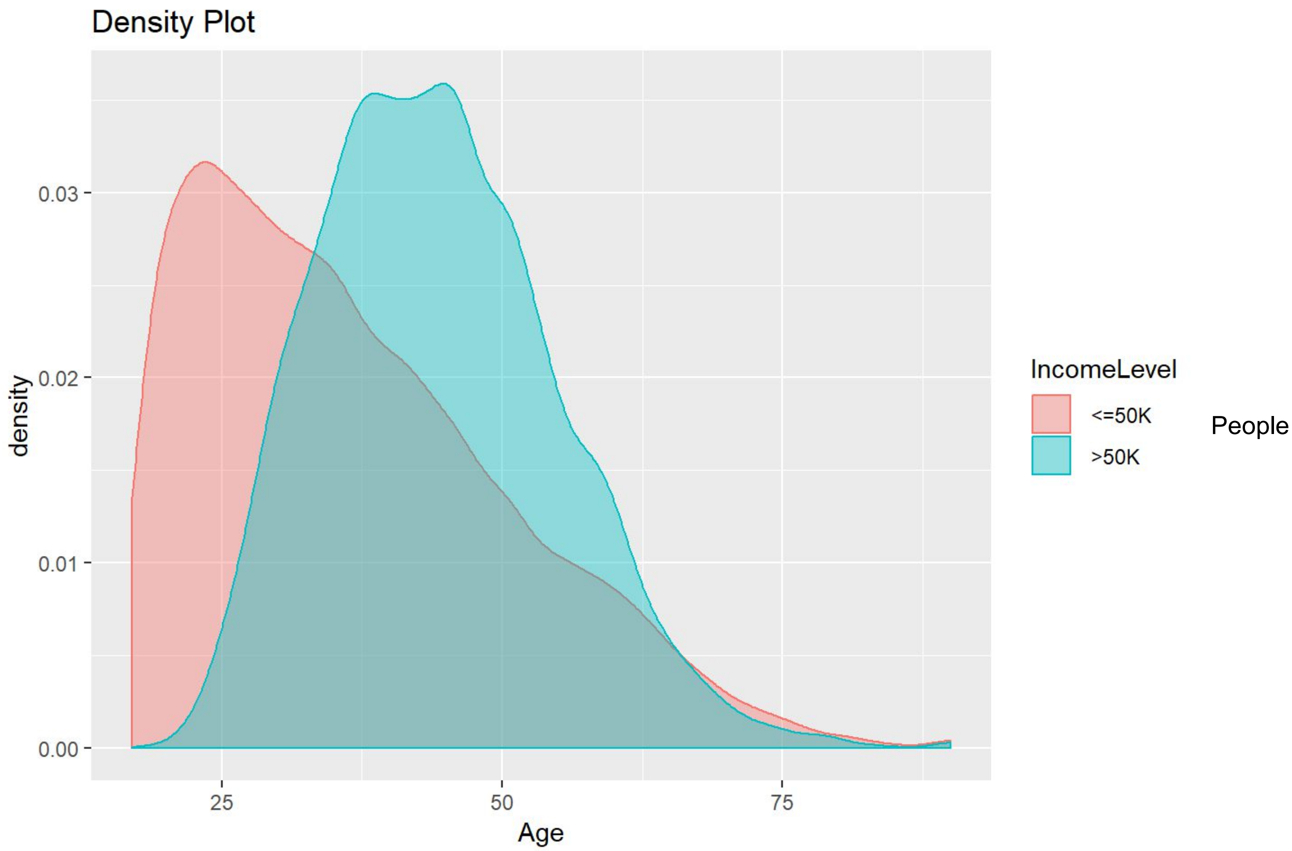


THe first plot is clear case of overplotting and hence difficult to make conclusions.People having less income work more hours per week.The people having less income also seems to work for a longer age.We can make this conclusion easily using trillis plot.

2.

Use ggplot2 to create a density plot of age grouped by the Income level.

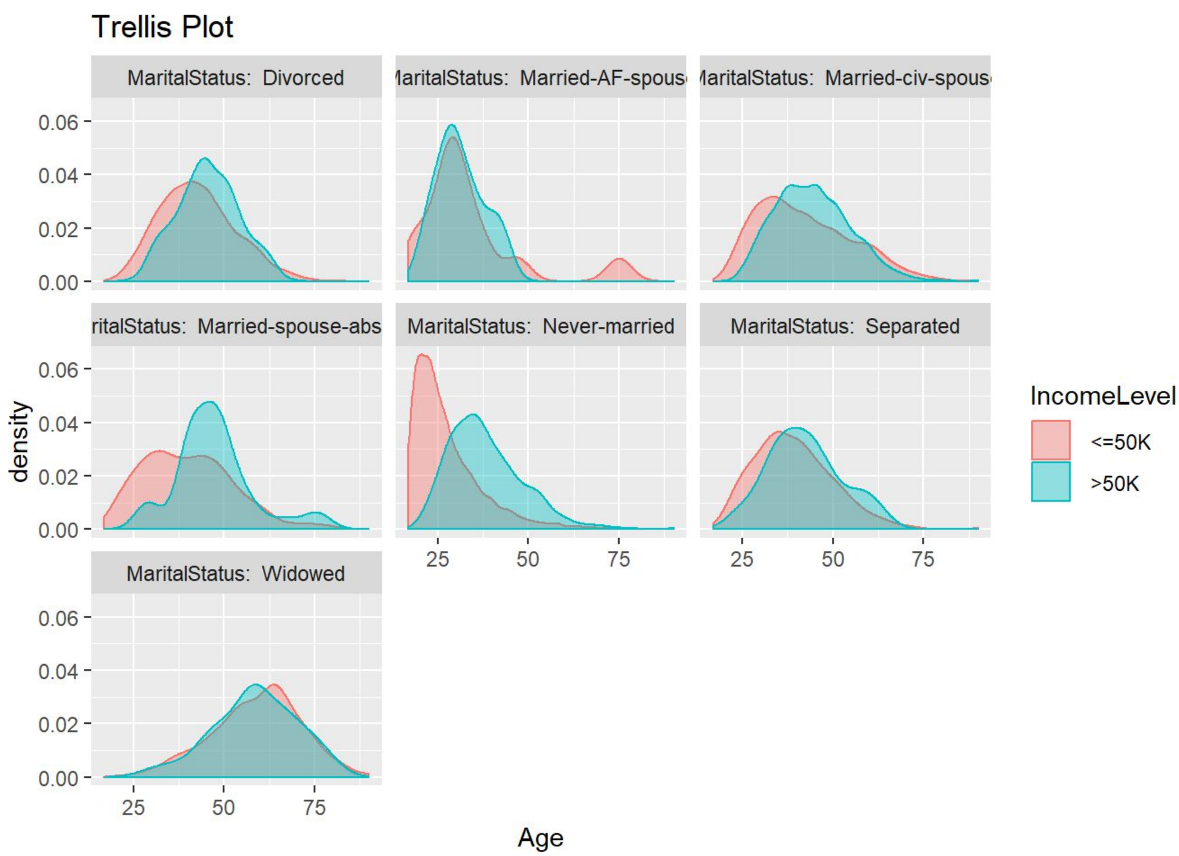
```
d1<-ggplot(adults,aes(x=Age))+geom_density(aes(fill=IncomeLevel,color=IncomeLevel),alpha=0.4)+gg
title("Density Plot")
d1
```



earning less than 50k are younger age group mostly between 20 and 35 and those with income level greater than 50k are in range of age group 30-50

Create a trellis plot of the same kind where you condition on Marital Status

```
d2<-ggplot(adults,aes(x=Age))+
  geom_density(aes(col=IncomeLevel,fill=IncomeLevel),alpha=0.4)+facet_wrap(~MaritalStatus, label
ler = "label_both")+ggtitle("Trellis Plot ")
d2
```

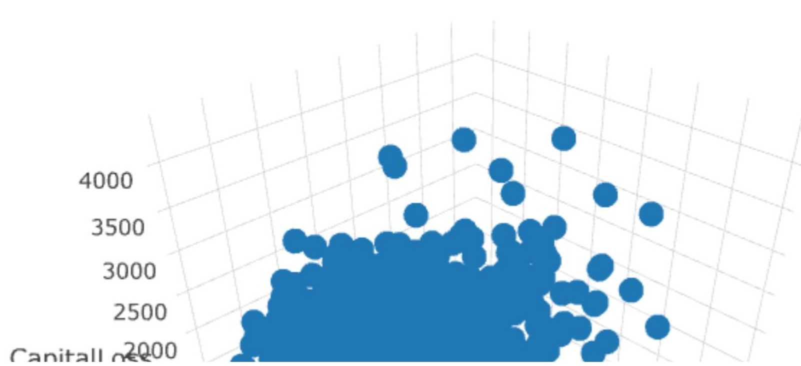


There are 7 different plots for different married status.Never married and Married AF spouse have the same pattern.Rest five plots follow another same pattern of income distribution for different age group and also these plots are similar to the normal density plot of income vs age group.

2.3

3 d scatter plot

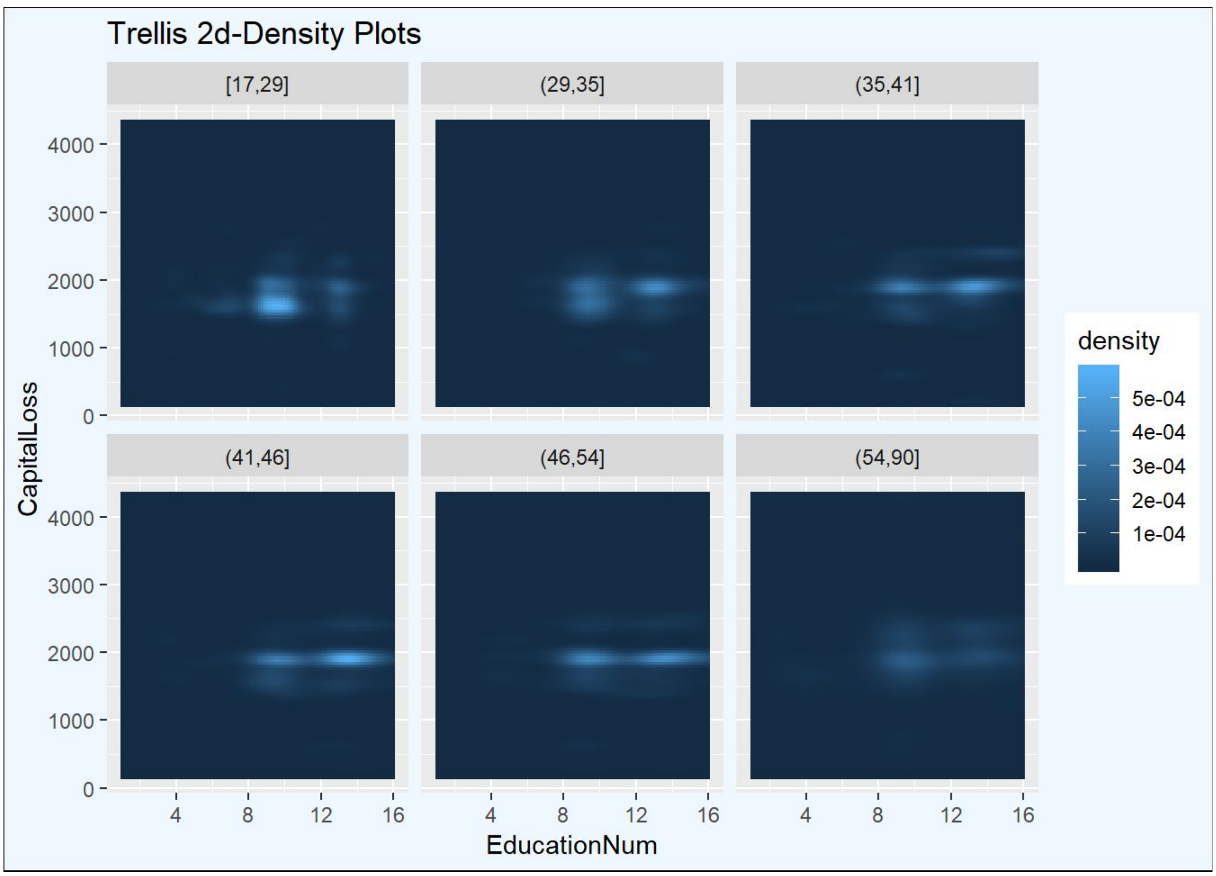
```
pp <- adults%>%filter(CapitalLoss!=0)%>%plot_ly( x = ~EducationNum, y = ~Age, z = ~CapitalLoss)
%>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'EducationNum'),
                      yaxis = list(title = 'Age'),
                      zaxis = list(title = 'CapitalLoss')))
pp
```



The above plot is a clear example of overplotting.Hence we cannot get a clear understanding of the data.

Create a trellis plot with 6 panels in ggplot2 in which each panel shows a raster-type 2d-density plot of Capital Loss versus Education-num conditioned on values of Age (use cut_number())

```
tr2<-adults[which(adults$CapitalLoss!=0),]%>%ggplot(aes(y=CapitalLoss,x=EducationNum))+stat_dens
ity2d(aes(fill = stat(density)), geom = "raster",contour = FALSE)+facet_wrap(~cut_number(Age,n=6
))
tr2+ggtitle("Trellis 2d-Density Plots")+theme_gray()%+replace%theme(plot.background = element_re
ct(fill = "aliceblue"))
```



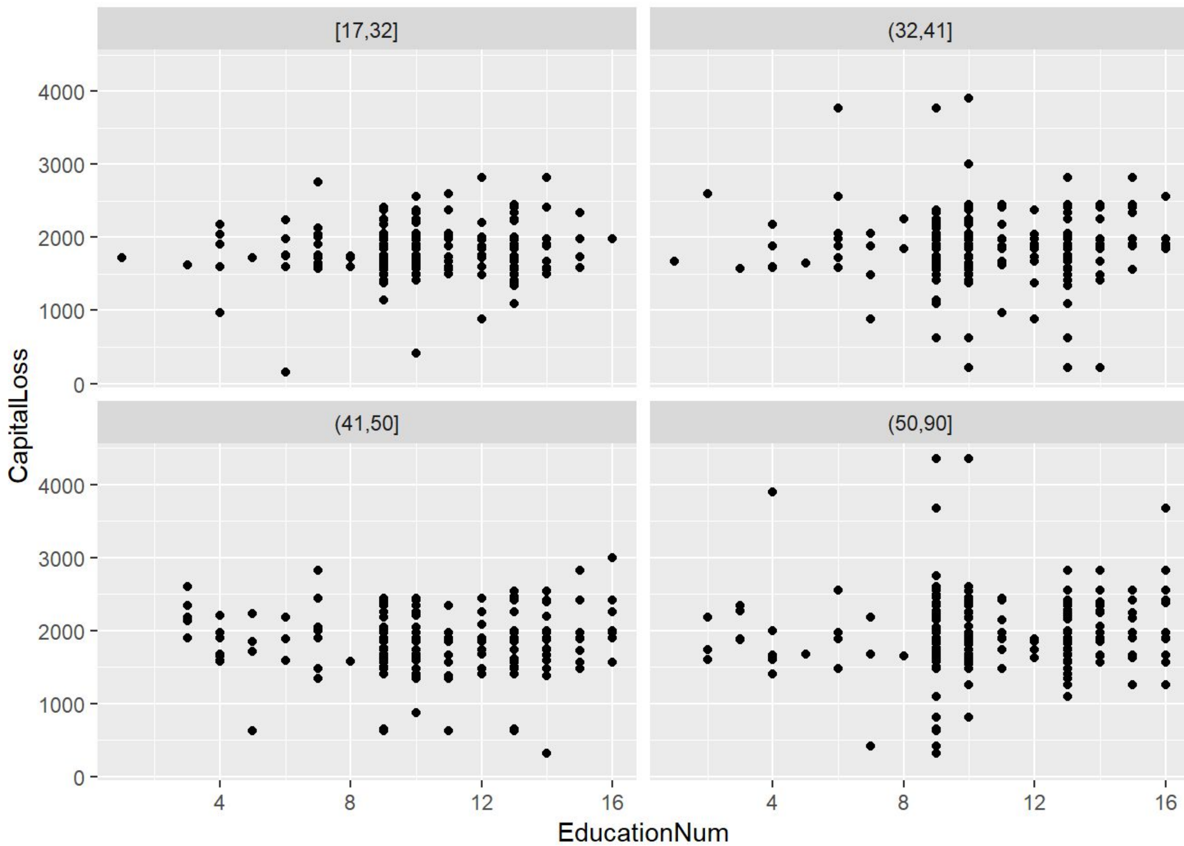
The data is better understandable in this plot when compared to the 3 d plot.We can say there is high density of capital loss around 2000 for age groups [17,29],(46,54].

2.4

Make a trellis plot containing 4 panels where each panel should show a scatter plot of Capital Loss versus Education-num conditioned on the values of Age by

a. using cut_number()

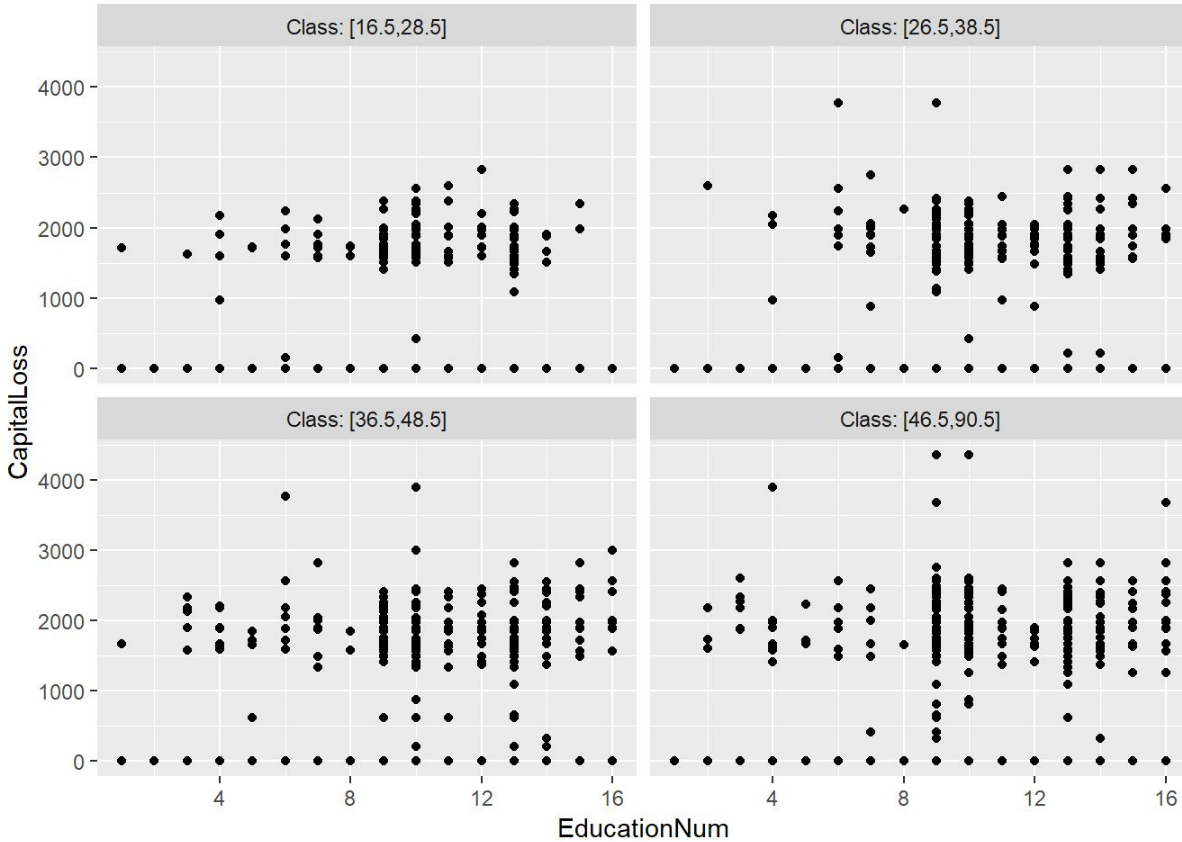
```
adults%>%filter(CapitalLoss!=0)%>%ggplot(aes(x=EducationNum,y=CapitalLoss))+geom_point()+facet_w
rap(~cut_number(Age,n=4))
```



b) using

Shingles with 10% overlap.

```
Agerange<-lattice::equal.count(adults$Age, number=4, overlap=0.10) #overlap is 10%
L<-matrix(unlist(levels(Agerange)), ncol=2, byrow = T)
L1<-data.frame(Lower=L[,1],Upper=L[,2], Interval=factor(1:nrow(L)))
index=c()
Class=c()
for(i in 1:nrow(L)){
  Cl=paste("[", L1$Lower[i], ",", L1$Upper[i], "]", sep="")
  ind=which(adults$Age>=L1$Lower[i] & adults$Age<=L1$Upper[i])
  index=c(index,ind)
  Class=c(Class, rep(Cl, length(ind))) }

df4<-adults[index,]
df4$Class<-as.factor(Class)
h1<-ggplot(df4, aes(x=EducationNum,y=CapitalLoss))+ geom_point()+ facet_wrap(~Class, labeller =
"label_both")
h1
```



Advantage of the shingles is that sudden jumps in data would not be missed if it occured in the transition period .One disadvantage is that amount of coding is high and the next is that sometimes the data will be overalpped and hence be present in both plots and can lead to misleading calculations.

Appendix

```
library(tidyverse)
library(RColorBrewer)
library(plotly)
library(seriation)

df<-read.csv("prices-and-earnings.csv")
adults<-df[c(1,2,5,6,7,9,10,16,17,18,19)+1]

rownames(adults)<-df[,1]
coul = colorRampPalette(brewer.pal(8, "PiYG"))(25)
adscaled=scale(as.matrix(adults))
p2<-plot_ly(x=colnames(adscaled), y=rownames(adscaled), z=adscaled, type="heatmap", colors = cou
l)
p2


rowdist<-dist(adscaled,method = "minkowski", p=2)
coldist<-dist(t(adscaled),method = "minkowski", p=2)
order1<-seriate(rowdist, "HC")
order2<-seriate(coldist, "HC")
ord1<-get_order(order1)
ord2<-get_order(order2)
reordmatr_euc<-adscaled[rev(ord1),ord2]
plot_ly(x=colnames(reordmatr_euc), y=rownames(reordmatr_euc),
        z=as.matrix(reordmatr_euc), type="heatmap", colors =colorRamp(c("yellow", "red")))

v<-1:11
ord=sample(v)
#ord=ord2
dims0=list()
for( i in 1:ncol(adults)){
  dims0[[i]]=list( label=colnames(adults)[ord[i]],
                   values=as.formula(paste("~",colnames(adults)[ord[i]])))
}
p <-adults%>%
  plot_ly(type = 'parcoords',
          line = list(color = ~as.numeric(Hours.Worked)),dimensions = dims0)
p


radar_value <- reordmatr_euc%>%
  as.tibble(rownames = "name")%>%
  tidyr::gather(variable, value, -name, factor_key=T)%>%
  mutate(name = factor(name,levels = rownames(reordmatr_euc)))

radar_value %>%
  ggplot(aes(x=variable, y=value, group=name)) +
  coord_polar() + theme_bw() + facet_wrap(~name, ncol=13) +
  theme(axis.text.x = element_text(size = rel(.5)))
Ps<-list()
for (i in 1:12){
  Ps[[i]] <- htmltools::tags$div(
    plot_ly(type = 'scatterpolar',
            r=as.numeric(reordmatr_euc[i,-1]),
            theta= colnames(reordmatr_euc)[-1],
            fill="toself")%>%
```

```
      layout(title=rownames(reordmatr_euc)[i]), style="width: 25%;")
}

h <-htmltools::tags$div(style = "display: flex; flex-wrap: wrap", Ps)

htmltools::browsable(h)

library(tidyverse)
library(RColorBrewer)
library(plotly)


adults<-read.csv("adult.csv",sep=",")
names(adults)<-c("Age","Workclass","PolpulationIndex","Education","EducationNum","MaritalStatus"
,"Occupation","Relationship",
                 "Race","Sex","CapitalGain","CapitalLoss","HoursPerWeek","NativeCountry","Income
Level")

### scatter plot of Hours per Week versus age where observations are colored by Income level.
# Make a trellis plot of the same kind where you condition on Income Level

sc1<-ggplot(adults,aes(x=HoursPerWeek,y=Age,col=IncomeLevel))+geom_point()
sc1

tr1<-ggplot(adults,aes(x=HoursPerWeek,y=Age))+geom_point()+facet_grid(IncomeLevel~.)+theme_bw()+
theme(strip.background = element_rect(colour="red", fill="#CCCCFF"))+geom_smooth()
tr1

##Use ggplot2 to create a density plot of age grouped by the Income level.
##Create a trellis plot of the same kind where you condition on Marital Status


d1<-ggplot(adults,aes(x=Age))+geom_density(aes(fill=IncomeLevel,color=IncomeLevel),alpha=0.4)+gg
title("Density Plot")
d1


d2<-ggplot(adults,aes(x=Age))+
  geom_density(aes(col=IncomeLevel,fill=IncomeLevel),alpha=0.4)+facet_wrap(~MaritalStatus, label
ler = "label_both")+ggtitle("Trellis Plot ")
d2


##Filter out all observations having Capital loss equal to zero. For the remaining data,
##use Plotly to create a 3D-scatter plot of Education-num vs Age vs Captial Loss

pp <- adults%>%filter(CapitalLoss!=0)%>%plot_ly( x = ~EducationNum, y = ~Age, z = ~CapitalLoss,c
olor=~EducationNum) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'EducationNum'),
                      yaxis = list(title = 'Age'),
                      zaxis = list(title = 'CapitalLoss')))
pp

###Create a trellis plot with 6 panels in ggplot2 in which each panel shows a raster-type 2d-den
sity plot of Capital Loss
```

```
####versus Education-num conditioned on values of Age (use cut_number())


tr2<-adults[which(adults$CapitalLoss!=0),]%>%ggplot(aes(x=CapitalLoss,y=EducationNum))+geom_dens
ity_2d()+facet_wrap(~cut_number(Age,n=6))
tr2+ggtitle("Trellis 2d-Density Plots")+theme_gray()%+replace%theme(plot.background = element_re
ct(fill = "aliceblue"))





###Make a trellis plot containing 4 panels where each panel should show a scatter plot of Capita
l Loss versus Education-num
###conditioned on the values of Age by a) using cut_number() b) using Shingles with 10% overlap.


#a)
adults%>%filter(CapitalLoss!=0)%>%ggplot(aes(x=CapitalLoss,y=EducationNum))+geom_point()+facet_w
rap(~cut_number(Age,n=4))


#b)

#cap_adults<-adults[which(adults$CapitalLoss!=0),]
Agerange<-lattice::equal.count(adults$Age, number=4, overlap=0.10) #overlap is 10%
L<-matrix(unlist(levels(Agerange)), ncol=2, byrow = T)

index=c()
Class=c()
for(i in 1:nrow(L)){
  Cl=paste("[", L1$Lower[i], ",", L1$Upper[i], "]", sep="")
  ind=which(df3$age>=L1$Lower[i] &df3$age<=L1$Upper[i])
  index=c(index,ind)
  Class=c(Class, rep(Cl, length(ind))) }


df4<-adults[index,]
df4$Class<-as.factor(Class)
h1<-ggplot(df4, aes(x=CapitalLoss,y=EducationNum))+ geom_point()+ facet_wrap(~Class, labeller =
"label_both")
h1
```

lab5

Andreas and Priya

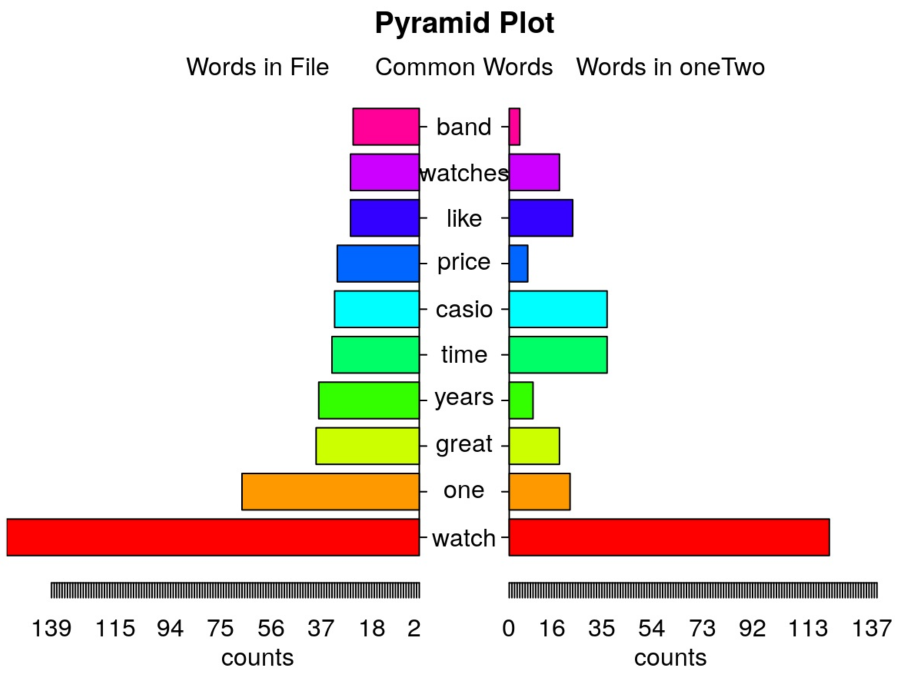
11 October 2018

##Assignment 1

###Word Cloud Plot for five

###Word Cloud Plot for One Two

###Pyramid Plot




```
## [1] 5.1 4.1 4.1 2.1
```

The word cloud for five.txt which is the good feedback has more frequent words like watch,great,one,price,casio,years,battery etc.This makes sense as words watch and casio will be often coming in the words as this is the product.As it is a positive feedback,people are happy with the price.Great is a posisive word and may be telling it last for long with word years.

THe oneTwo.txt is the negative feedback and the frequesnt words are amazon,one,back,watch,casio,battery etc.casio and watch comes frequent like before as this is the product.Amazon ,may be because they are not happy with the amazon more than product(may be the deal,return policy,shipping etc).They would like to return back the product and hence **back** has come multiple times.

###Phrasenets

Phrase nets of five.text

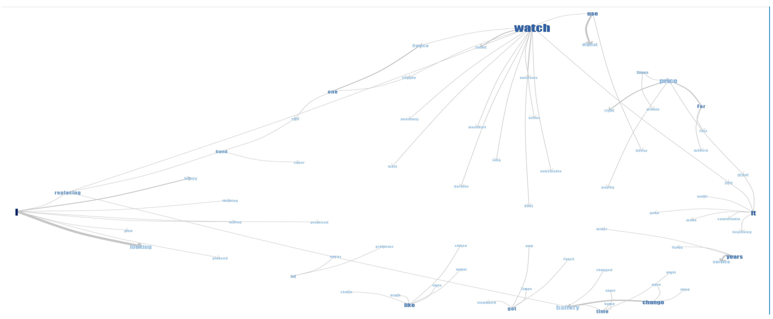


Figure 1. positive.

phrase nets of negative words

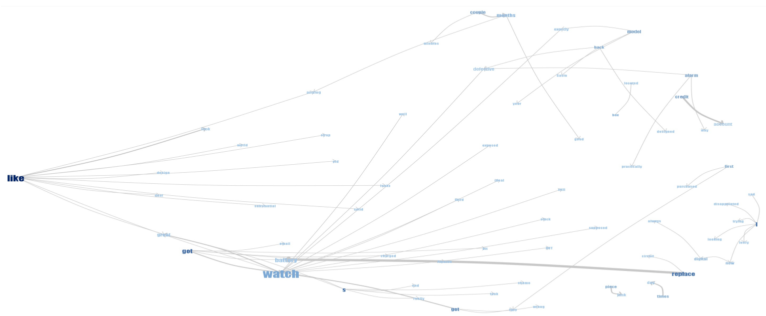


Figure 2. negative

word trees

word tree of battery with the positive feedback

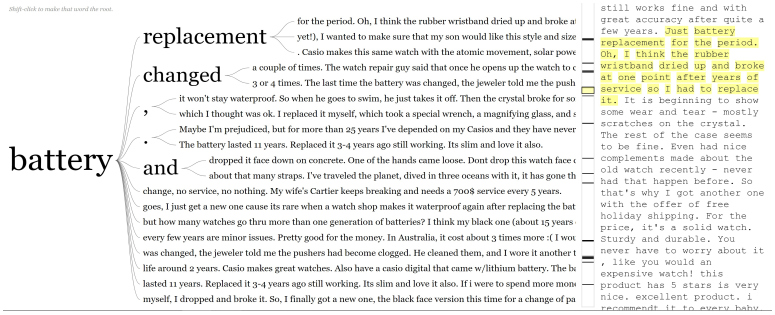


Figure 4. wordtree battery pos feedback

word tree with the word battery in negative feedback

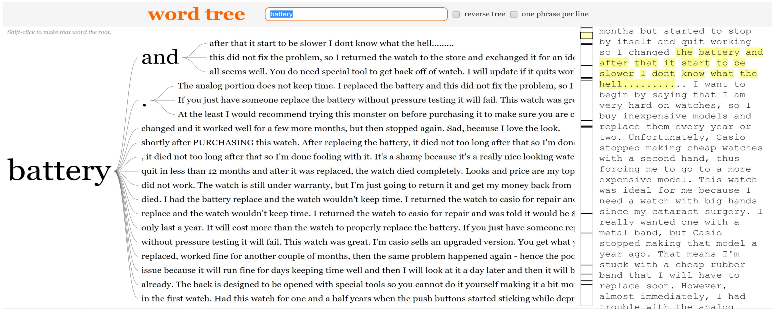


Figure 4. wordtree battery neg feedback

###Analysis

Looking at the above graphs we come to conclusions like

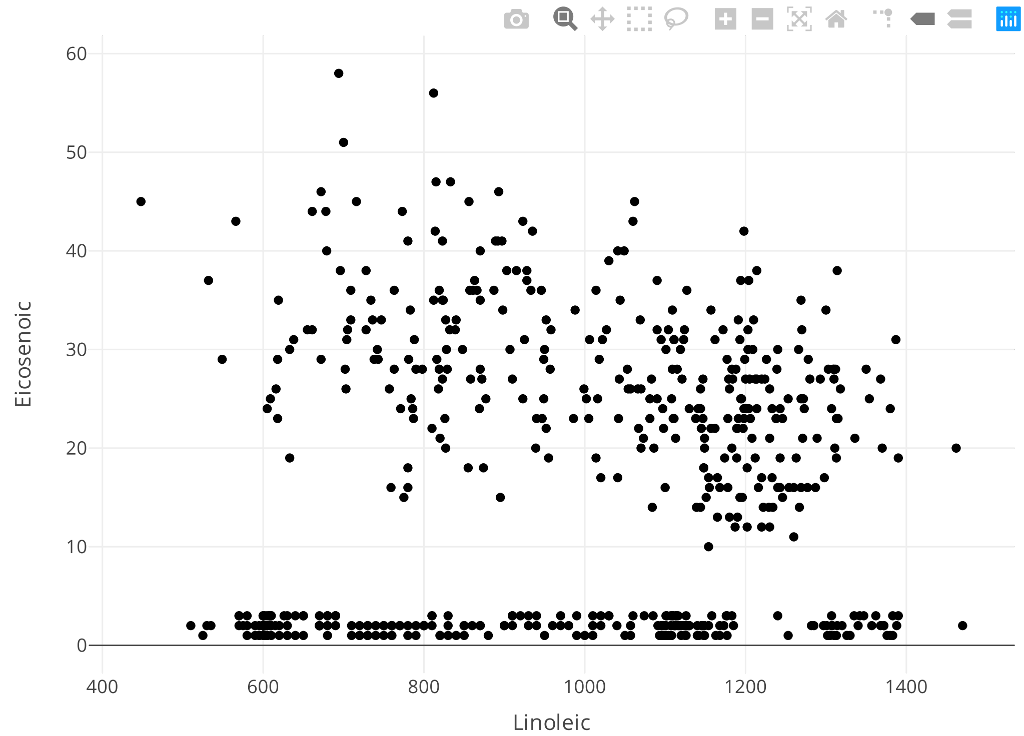
THe watch has analog and dgital display and it appears in black,gold and white.It has sporty look,rubbery band and waterprrof and good value for money.The satisfied customers are talking about modern look,water resistance,some of them say the battery last long and it is good priced.Dis statisfied customers talk about the defective alrams,battery once changed the watch does not work well,The analog portions becomes defective etc.Also Replacing battery is costly .

Seems like the customers are satisfied with the look and feel and price of the watch .With some changesin the battery and all it can be a good product.

##Assignment 2

###1.Scatter Plot eicoseinoic vs linoleic

Choose region



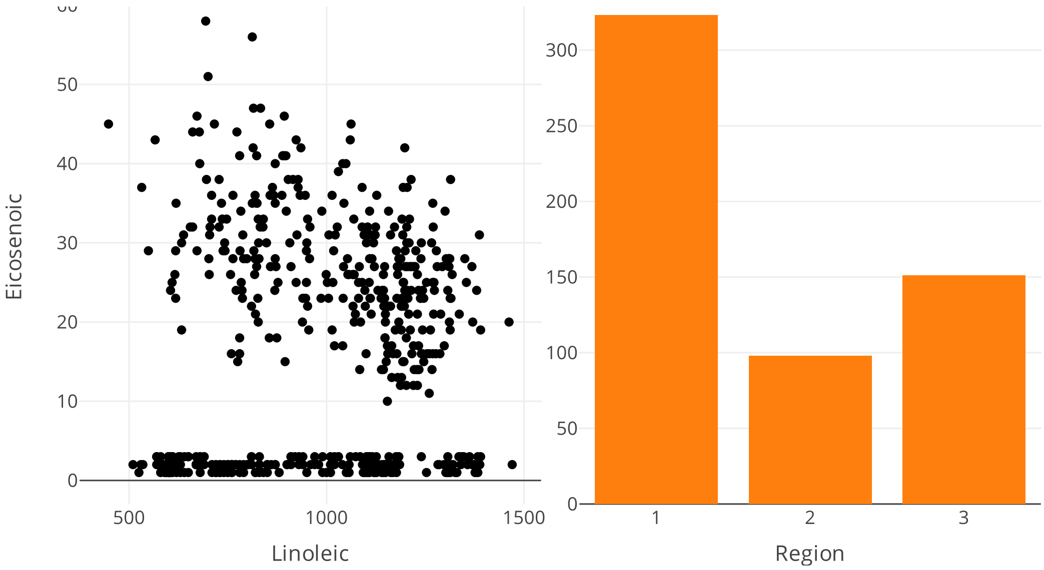
The value of eicosenoic is between one and three. ###2.Linked Scatterplot and Bar chart

values of stearic **Brush color**

152 375

rgba(228,2

152 248 344



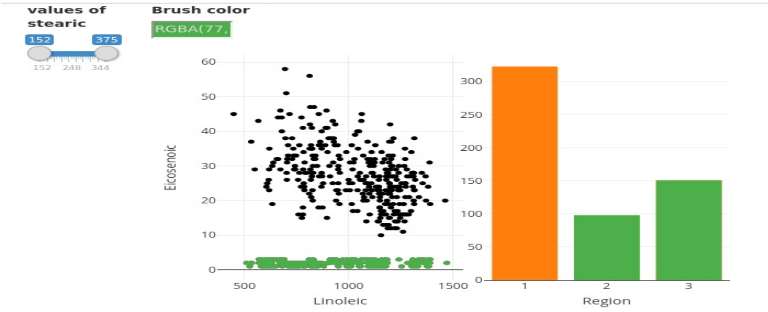


Figure 1. coloured

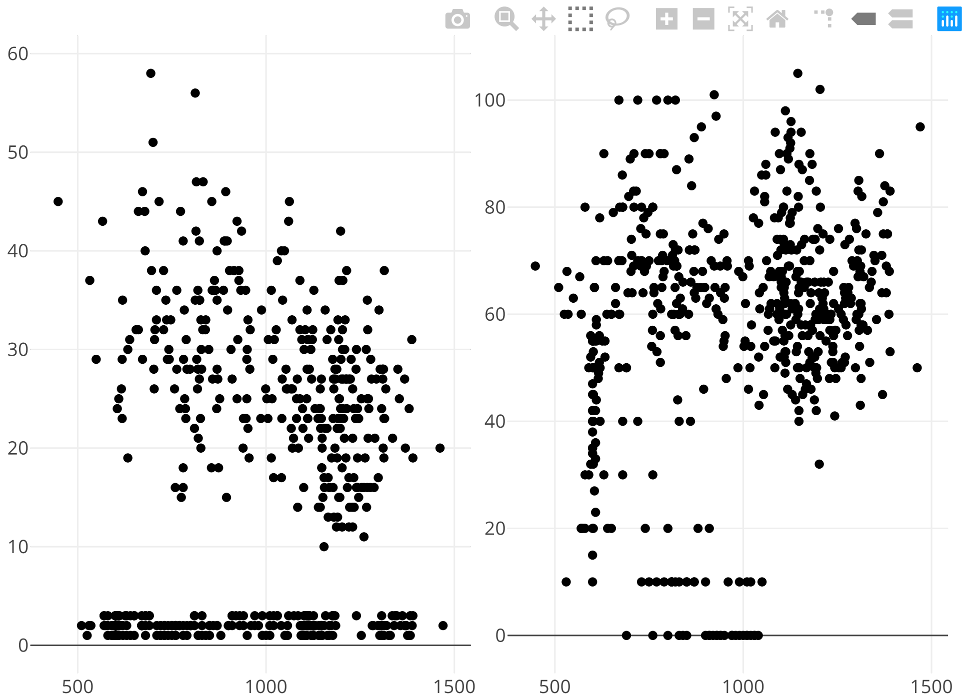
Using brushing when we take out the lower values of eicosenoic(between 1 and 3),we can see they correspond to region south and sardinia Island.In south region the amount of stearic acid is between 190 and 270.

The operators used here are seelction operators for brushing,Connection operator for connecting the plots and Filtering operator for filtering stearic values

###3.Linked Scatter Plots

Brush color

rgba(228,2



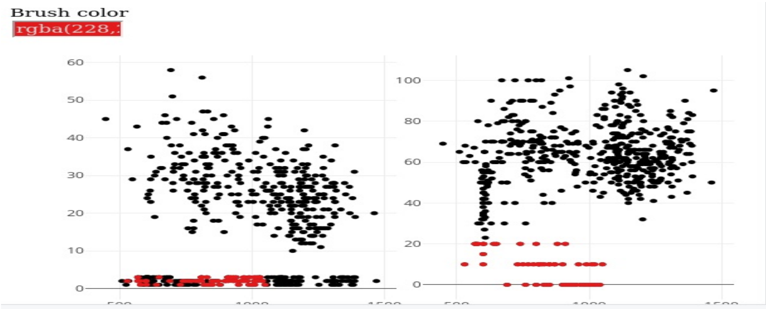


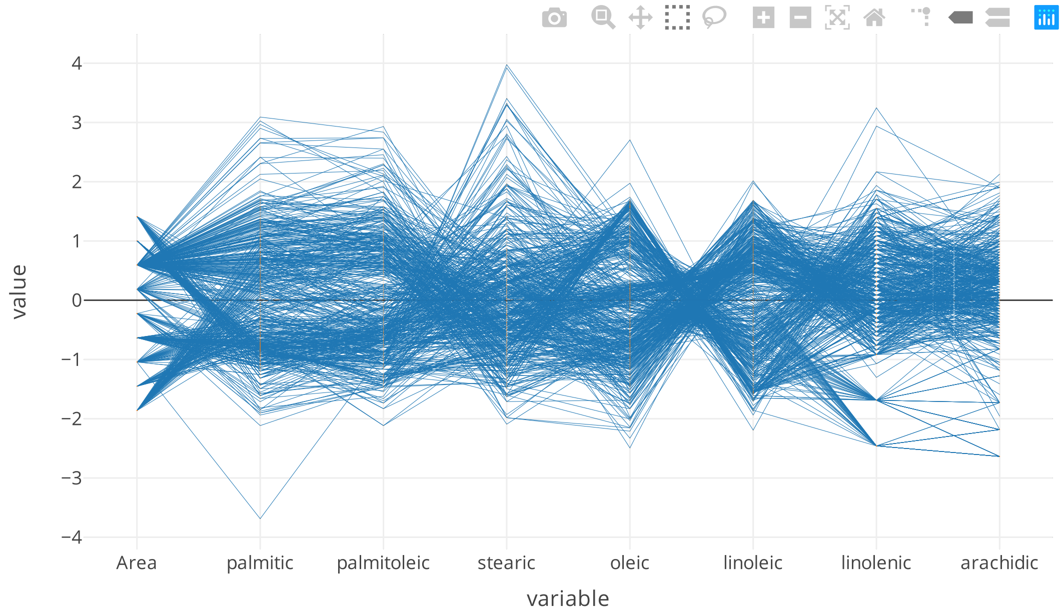
Figure 1. linked scatter

The values of arachidic below 40 are outliers in the plot2 are also oultiers in plot 1.IN plot one their eicosenoic values are between 1 and 3.

###4.Parallel Coordinate Plot linked Barplot and Scatterplot

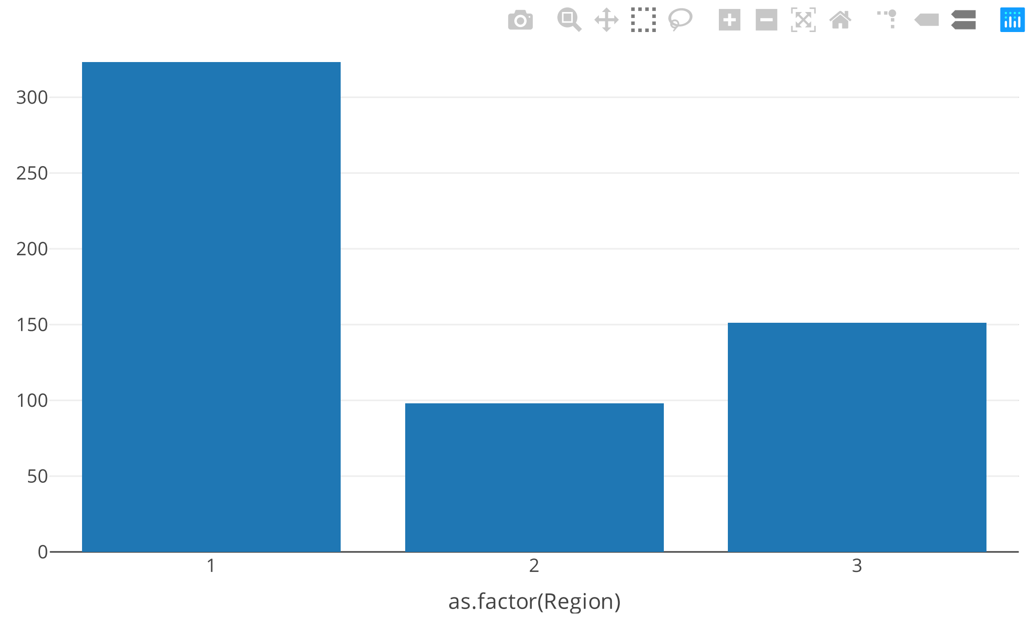
Brush color

rgba(228,2



Brush color

rgba(228,2



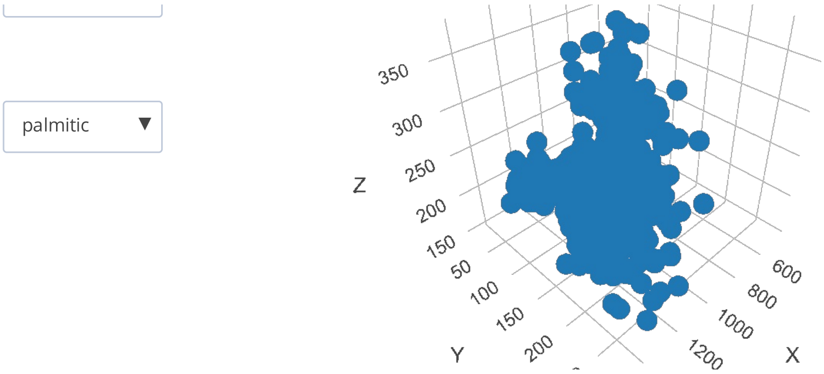
Brush color

rgba(228,2

palmitic ▼

Distribution of Oil

palmitic ▼



When we analysed the parallel coordinate plot, linolenic, oleic and palmitonic seemed to have more clusters hence they are influentional variables to differentiate regions.

In South region we can observe multiple clusters. linolenic, oleic and linoleic forms cluster, steraric, oleic, linoleic forms another cluster.

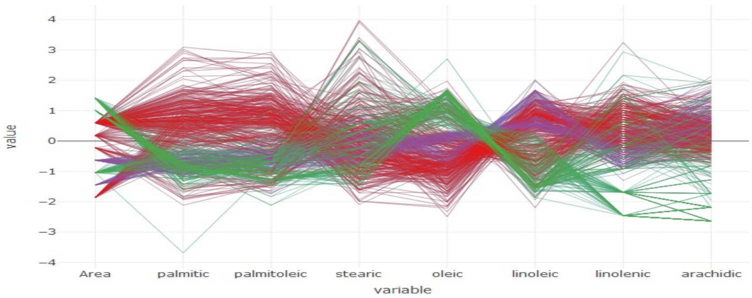


Figure 1. plot_123

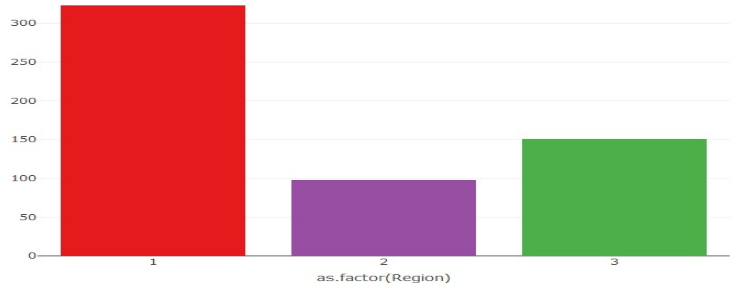


Figure 1. plot_123

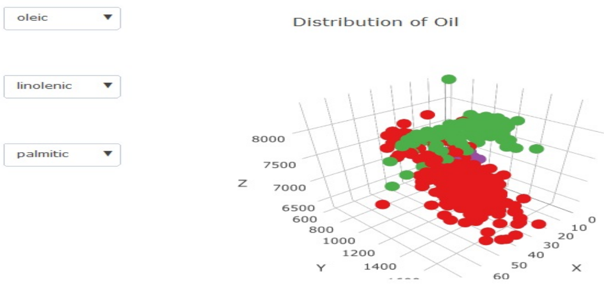


Figure 1. plot_123

As seen in the above screenshots, when we select the 3 variables and brush the regions with 3 different colours, the plot is almost clusterd in 3 seperate groups.

###5.Analysis

In step 4 we have used:

selection operator while brushing the plots ,connection operator to connect plots, Reconfiguring operator dynamically selectiong axix variables in 3D plot on data value space operand

An additional interaction operator which can be used is Filtering operator.This operator can be used to filter based on regions and analyse the concentration of acids in oil from each region. This data can be used for analysing the region of origin of an oil given the concentration of acids in that oil.s

##Appendix

```
## ----message=FALSE,echo=FALSE--------------------------------------------
library(tm)
library(wordcloud)
```

```r
library(RColorBrewer)
#library(viridisLite)
library(plotrix)
library(tidyverse)


## ----message=FALSE,echo=F---------------------------------------------------
five<-read.table("Five.txt",header=F, sep='\n',encoding="latin1")#Read file
five$doc_id=1:nrow(five)
colnames(five)[1]<-"text"
mycorpus <- Corpus(DataframeSource(five)) #Creating corpus (collection of text data)

clean_corpus <- function(corpus){
  corpus <- tm_map(corpus, removePunctuation)
  corpus <- tm_map(corpus, content_transformer(tolower))
  corpus <- tm_map(corpus, stripWhitespace)
  corpus <- tm_map(corpus,function(x) removeWords(x,stopwords("english")))
  return(corpus)
}


mycorpus <- clean_corpus(mycorpus)
tdm <- TermDocumentMatrix(mycorpus) #Creating term-document matrix
m <- as.matrix(tdm)

#here we merge all rows
v <- sort(rowSums(m),decreasing=TRUE) #Sum up the frequencies of each word
d <- data.frame(word = names(v),freq=v) #Create one column=names, second=frequences

pal<-brewer.pal(6,"PRGn") #Create palette of colors
#color_pal <- cividis(n = 8)


#wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=col_pal, vfo
nt=c("sans #serif","plain"))

wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal, vfont=c(
"sans serif","plain"))



## ----message=F,echo=F-------------------------------------------------------
oneTwo<-read.table("OneTwo.txt",header=F,sep="\n")
oneTwo$doc_id=1:nrow(oneTwo)
colnames(oneTwo)[1]<-"text"

mycor <- Corpus(DataframeSource(oneTwo))

mycor <- clean_corpus(mycor)
tdm1<- TermDocumentMatrix(mycor) #Creating term-document matrix
m1 <- as.matrix(tdm1)

#here we merge all rows
v1 <- sort(rowSums(m1),decreasing=TRUE) #Sum up the frequencies of each word
d1<- data.frame(word = names(v1),freq=v1)
pal<-brewer.pal(8,"Dark2")

wordcloud(d1$word,d1$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal, vfont=
c("sans serif","plain"))


## ----message=FALSE,warning=FALSE,echo=F-------------------------------------
j<-left_join(d,d1,by="word")

pyramid.plot(
  j$freq.x[1:10],j$freq.y[1:10],
  # Words
  labels = j$word[1:10],
  top.labels = c("Words in File", "Common Words", "Words in oneTwo"),
  main = "Pyramid Plot",gap=17,unit="counts")



## ----message=FALSE,echo=FALSE-----------------------------------------------
library(tidyverse)
library(plotly)
library(plyr)
library(crosstalk)
library(GGally)
```

```r
olive<-read.csv("olive.csv")
olive$Region<-as.factor(olive$Region)
levels(olive$Region)<-c("1","2","3")
o<-SharedData$new(olive)
oo<-SharedData$new(olive,~Region,group = "Choose region")


## ----set-options,message=F,echo=F----------------------------------------

scatterolive <- plot_ly(oo, y = ~eicosenoic, x = ~ linoleic)%>%group_by(Region)%>%
  add_markers(color = I("black"),name="hollow")%>%highlight(on="plotly_hover",persistent = F,selectize = T) %>%  l
ayout(xaxis = list(title = "Linoleic"),
      yaxis = list(title = "Eicosenoic"))

scatterolive


## ----message=FALSE,warning=FALSE,echo=F----------------------------------



barolive <- plot_ly(oo, x=~as.factor(Region))%>%add_histogram()%>%layout(barmode="overlay",xaxis=list(title="Regio
n"))

bscols(widths=c(2, NA),filter_slider("stearic", "values of stearic", oo, ~stearic),subplot(scatterolive,barolive,t
itleY = TRUE,  titleX = TRUE)%>%highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%hide
_legend())





## ----message=FALSE,echo=F------------------------------------------------

scatter1 <- plot_ly(o, x = ~linoleic, y = ~eicosenoic) %>%
  add_markers(color = I("black"))  %>% layout(xaxis = list(title = "linoleic"),
                                         yaxis = list(title = "Eicosenoic"))
scatter2 <- plot_ly(o, x = ~linoleic, y = ~arachidic) %>%
  add_markers(color = I("black"))%>% layout(xaxis = list(title = "linoleic"),
                                            yaxis = list(title = "arachidic"))


subplot(scatter1,scatter2)%>%
  highlight(on="plotly_select", dynamic=T, persistent=T, opacityDim = I(1))%>%hide_legend()




## ----message=FALSE,fig.width=20, fig.height=18,echo=F--------------------
oliveparralelcord<-ggparcoord(olive, columns = c(3:10))


d<-plotly_data(ggplotly(oliveparralelcord))%>%group_by(.ID)
d1<-SharedData$new(d, ~.ID, group="olive")

p1<-plot_ly(d1, x=~variable, y=~value)%>%
  add_lines(line=list(width=0.3))%>%
  add_markers(marker=list(size=0.3),
              text=~.ID, hoverinfo="text")


oildata <- olive
oildata$.ID=1:nrow(oildata)
d2<-SharedData$new(oildata, ~.ID, group="olive")
p2 <- plot_ly(d2, x=~as.factor(Region))%>%add_histogram()%>%layout(barmode="overlay")


ButtonsX=list()
for (i in 4:10){
  ButtonsX[[i-3]]= list(method = "restyle",
                        args = list( "x", list(olive[[i]])),
                        label = colnames(olive)[i])
}


ButtonsY=list()
for (i in 4:10){
  ButtonsY[[i-3]]= list(method = "restyle",
```

```
                        args = list( "y", list(olive[[i]])),
                        label = colnames(olive)[i])
}

ButtonsZ=list()
for (i in 4:10){
  ButtonsZ[[i-3]]= list(method = "restyle",
                        args = list( "z", list(olive[[i]])),
                        label = colnames(olive)[i])
}


axx <- list(
  title = "X"
)

axy <- list(
  title = "Y"
)

axz <- list(
  title = "Z"
)
 p3 <- plot_ly(d2,x= ~linoleic,y = ~palmitoleic, z = ~stearic)%>%add_markers()%>%
  layout(xaxis=list(title=""), yaxis=list(title=""),
         title = "Distribution of Oil",
         updatemenus = list(
           list(y=0.9, buttons = ButtonsX),
           list(y=0.6, buttons = ButtonsY),
           list(y=1.2, buttons = ButtonsZ)
         )  )%>%layout(scene = list(xaxis=axx,yaxis=axy,zaxis=axz))




ps<-htmltools::tagList(p1%>%
                         highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
                         hide_legend(),
                       p2%>%
                         highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
                         hide_legend(),
                       p3%>%
                         highlight(on="plotly_click", dynamic=T, persistent = T, opacityDim = I(1))%>%
                         hide_legend()
)
htmltools::browsable(ps)
```

Lab6

Andreas

29 Οκτωβρίου 2018

Assignment 1

This assignment is all about network visualsation of the terrorist connections.

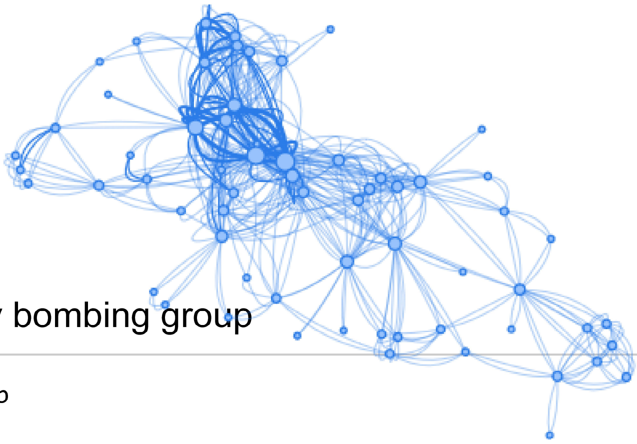
The files given are *trainData.dat* and *trainMeta.dat*.The files have the data about thenetwork of people involved in Madrid bombing.

We plot a graph using the *visNetwork* package

The basic graph is as below

```
library(ggraph)
library(igraph)
library(visNetwork)
library(seriation)
library(plotly)

#setwd("C:/Users/quartermaine/Documents/Visualization/lab_6")
edges <- read.delim("trainData.dat", header = FALSE, sep  = " ")
nodes <- read.delim("trainMeta.dat", header = FALSE, sep = " ")
set.seed(12345)

nodes$id <- rownames(nodes)
colnames(nodes) <- c("bombers", "b_group", "id")
colnames(edges) <- c("temp", "from", "to", "value")
edges$temp <- NULL
graph <- graph.data.frame(edges, directed = T)
degree_value <- degree(graph)
nodes$value <- degree_value[match(nodes$id, names(degree_value))]
nodes <- na.omit(nodes)
nodes$label<-nodes$bombers
#### a.Basic
visNetwork(nodes=nodes,edges=edges,main = "Madrid bombing people network")
```

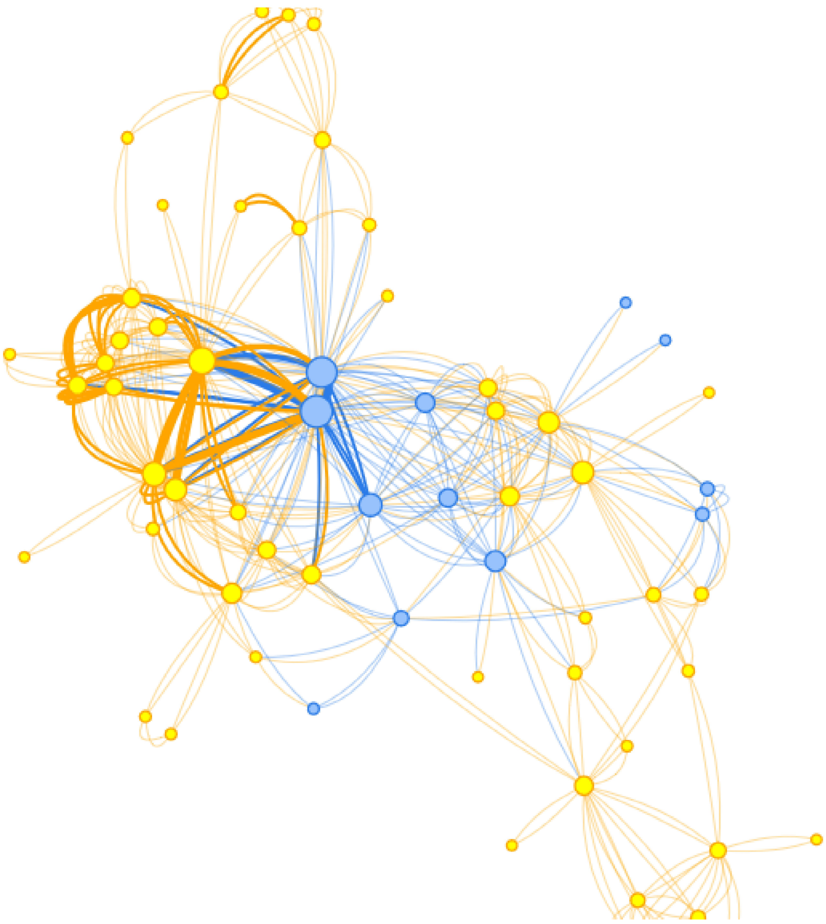
Madrid bombing people network



b.nodes are coloured by bombing group

```
nodes$group<-nodes$b_group

visNetwork(nodes=nodes,edges=edges,main = "Madrid bombing people network")
```

Madrid bombing people network



c. Strength

Strength can be also showed by degree

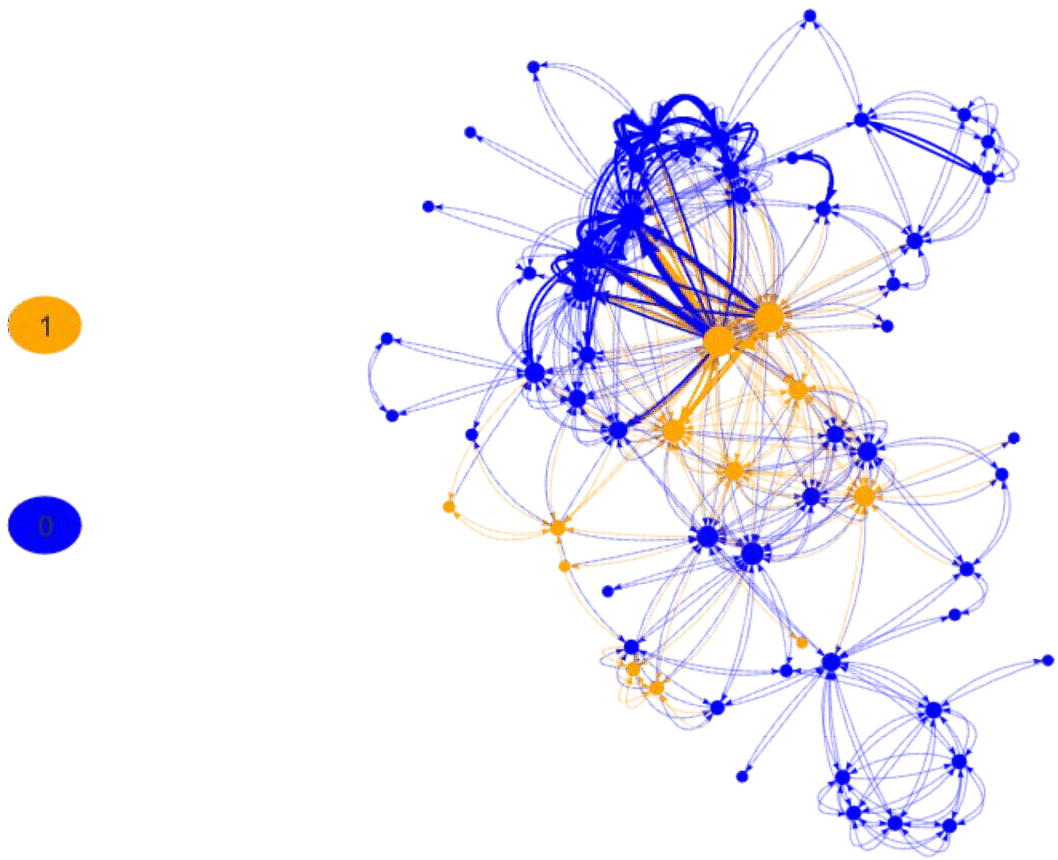
```
graph <- graph.data.frame(edges, directed = T)
degree_value <- degree(graph)
```

d.replusion

```
visNetwork(nodes = nodes, edges = edges, main = "Madrid bombing people network") %>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "from") %>%
  visOptions(collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()
```

Madrid bombing people network

Select by group

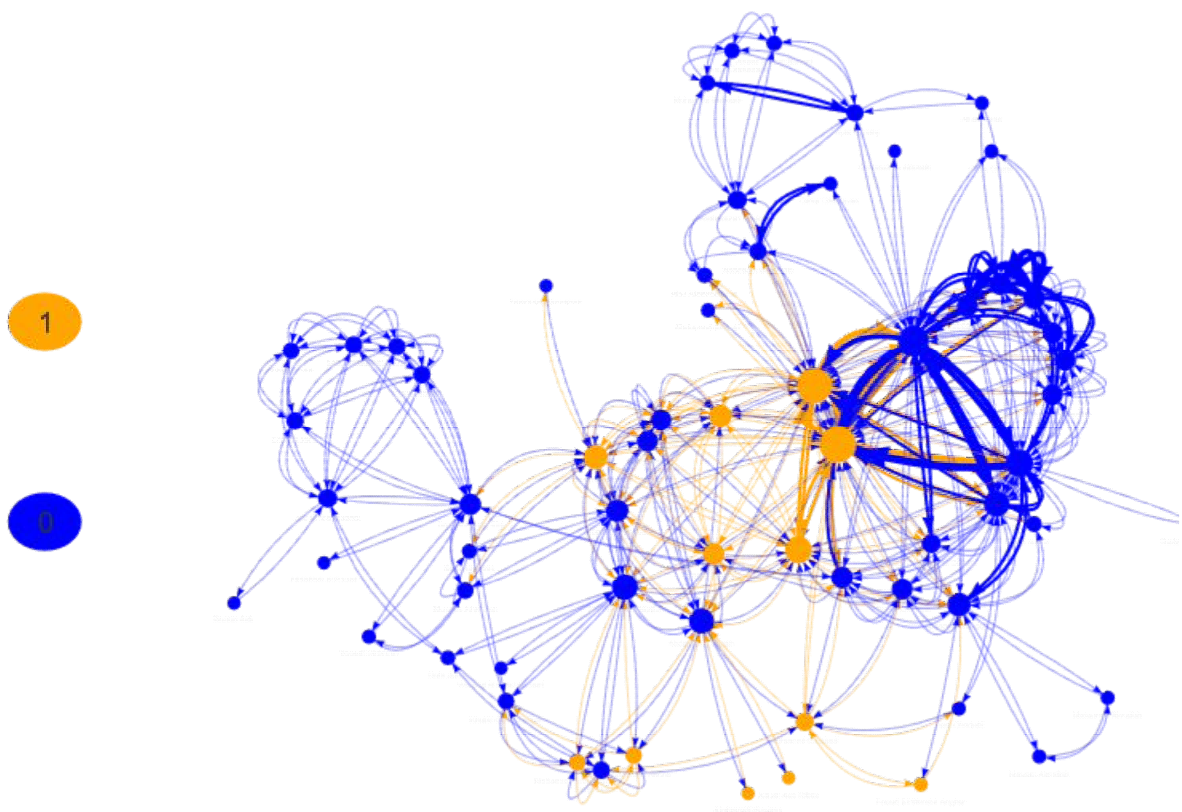


e.Highlighted nodes ans the end graph

```
visNetwork(nodes = nodes, edges = edges,main = "Madrid bombing people network") %
>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "to") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
                                    degree = 1),
             collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()
```

Madrid bombing people network

Select by group



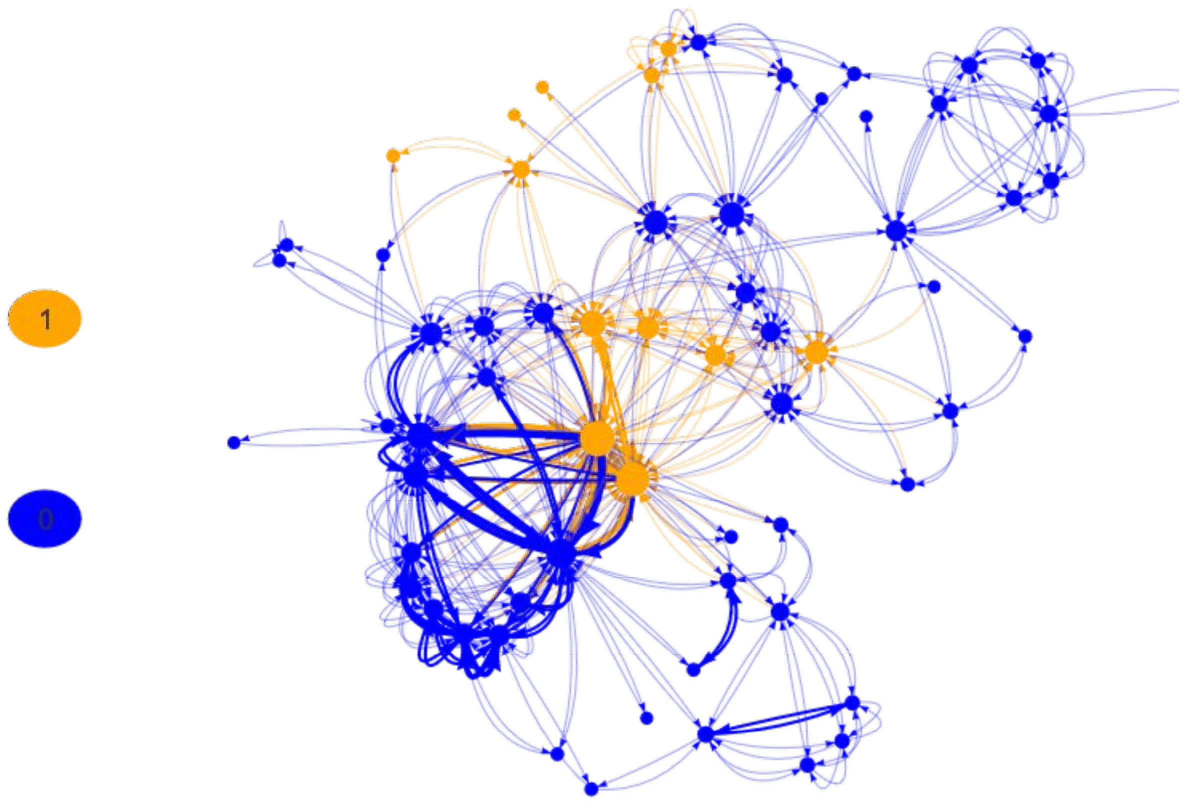
Group 1 is for those involved in blasting and 0 for others.We could see one main cluster centered around Mohamed chaoui,Jamal Zougam,Basel chayoun ,SB abdelmajid Fakher.They are the people actievely involved in bombing.Also there are three other small clusters of family members one with abdel karim,Tayser,mohamed bekkali etc.another with seeman gaby eid,el gitano etc and last one with mohamed chedadi,mohamed oulat akcha etc.

2.

degree = list(from = 1, to = 2)) gives the highlight required

```
visNetwork(nodes = nodes, edges = edges) %>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "from") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
                                    degree = list(from = 1, to = 2)),
             collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()
```

Select by group



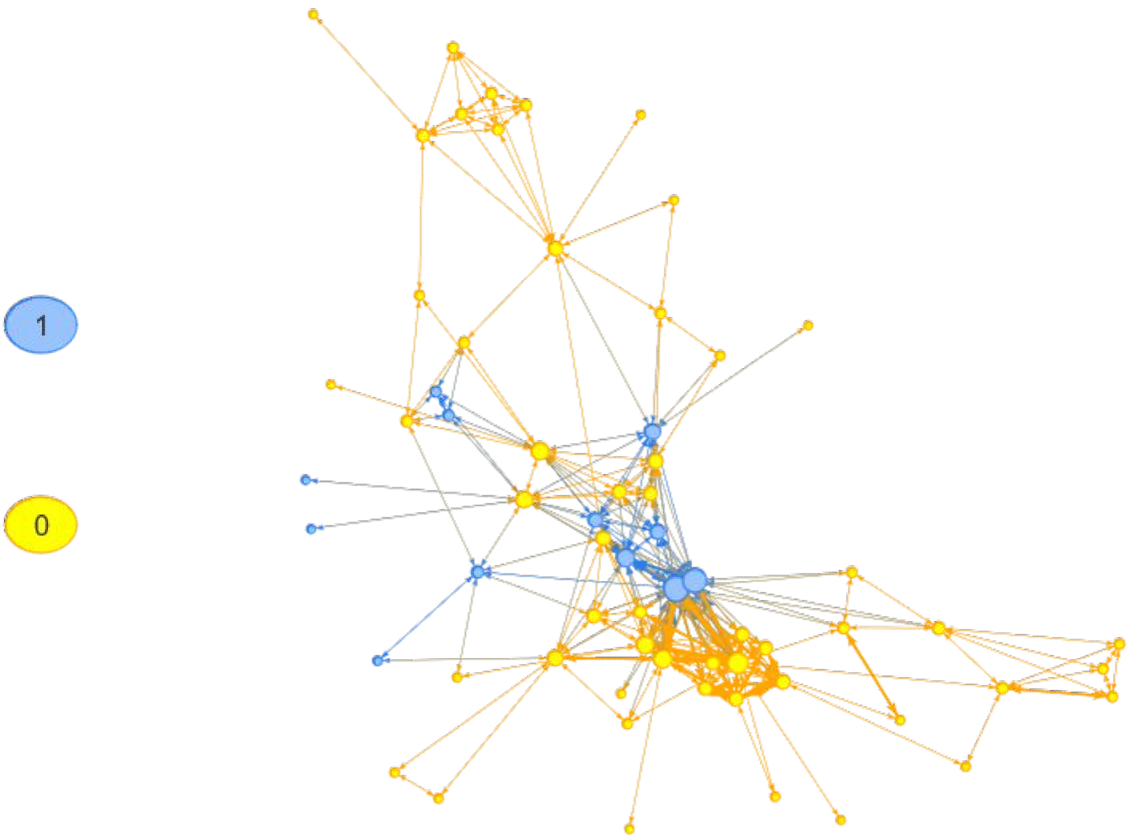
We couls see jamal Zougam and mohamed chaoui were best in spreading news.The BBC 18-4-2014 (http://news.bbc.co.uk/2/hi/europe/3515790.stm) shows him as an early suspect of the attack and he oowned a mobile shop so he could be the point of contact to get all the fake sim cards that connected the people.

3.

```
graph_data_frame <- graph.data.frame(edges, directed = FALSE)
clusters <- cluster_edge_betweenness(graph_data_frame, directed = T)
nodes$clusters <- clusters$membership

visNetwork(nodes = nodes, edges = edges, main = "Madrid Bombing") %>%
  visEdges(arrows = "from") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
                                     degree = list(from = 1, to = 2)),
             collapse = TRUE,
             selectedBy = "group")  %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome() %>%visIgraphLayout()
```

Madrid Bombing

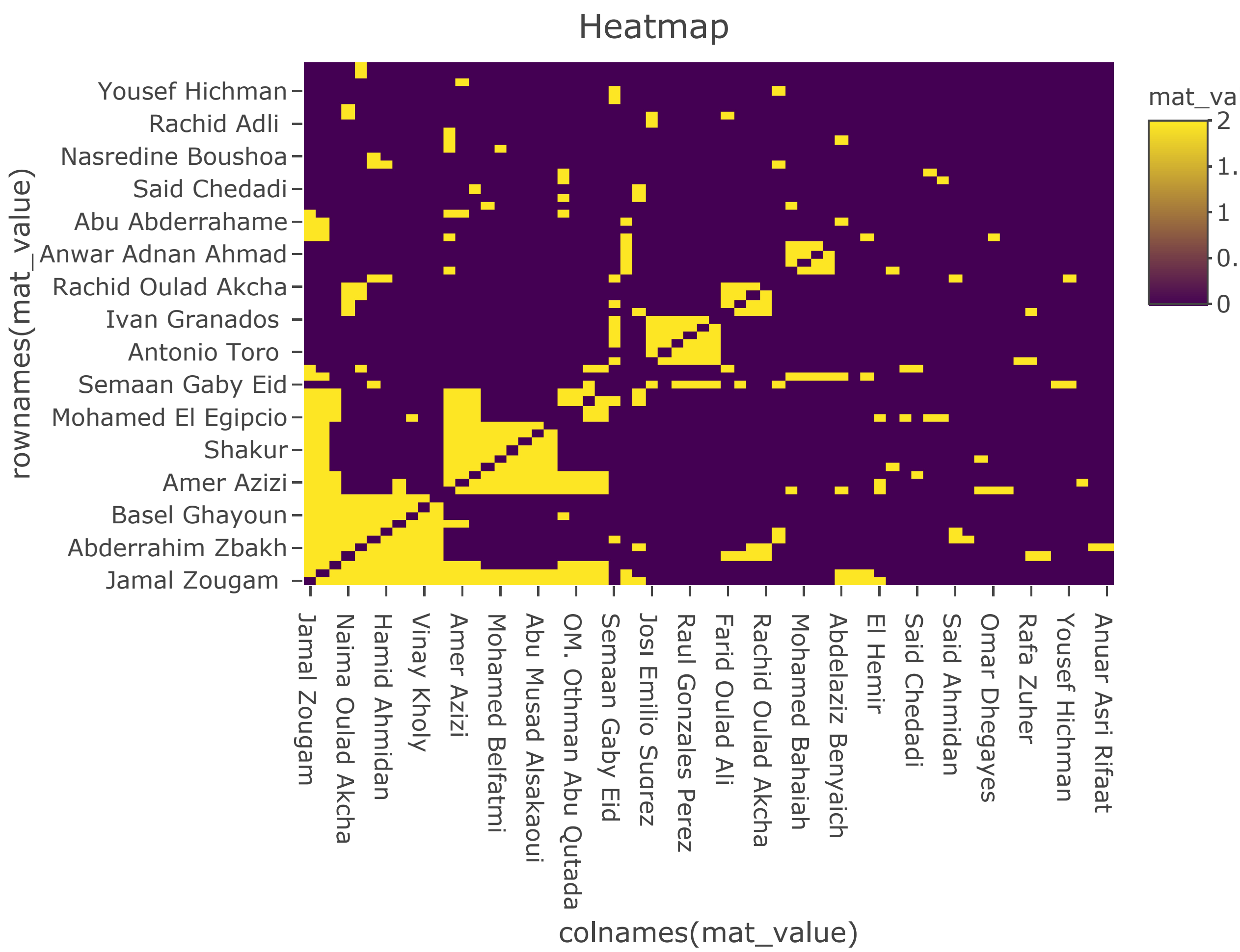
Select by group



The main cluster with Jamal Zougam is clearly evident in both the graphs.The two other clusters can be also seen one with seeman gaby eid and other with mohamed chedadi,mohamed oulat akcha the third small cluster is not so visible.In conclusion the promintent cluster of Jamal Zougm can be defenetly seen in both the clusters.

4.

```
adjecency <- get.adjacency(graph_data_frame, sparse=F)
colnames(adjecency) <- nodes$label
rownames(adjecency) <- nodes$label
rowdist<-dist(adjecency)


reord<-get_order(seriate(rowdist, "HC"))
mat_value<-adjecency[reord,reord]

##SInce using ubuntu system using the below line of code.



plot_ly(z=~mat_value, x=~colnames(mat_value),
        y=~rownames(mat_value), type="heatmap") %>% layout(title = "Heatmap")
```



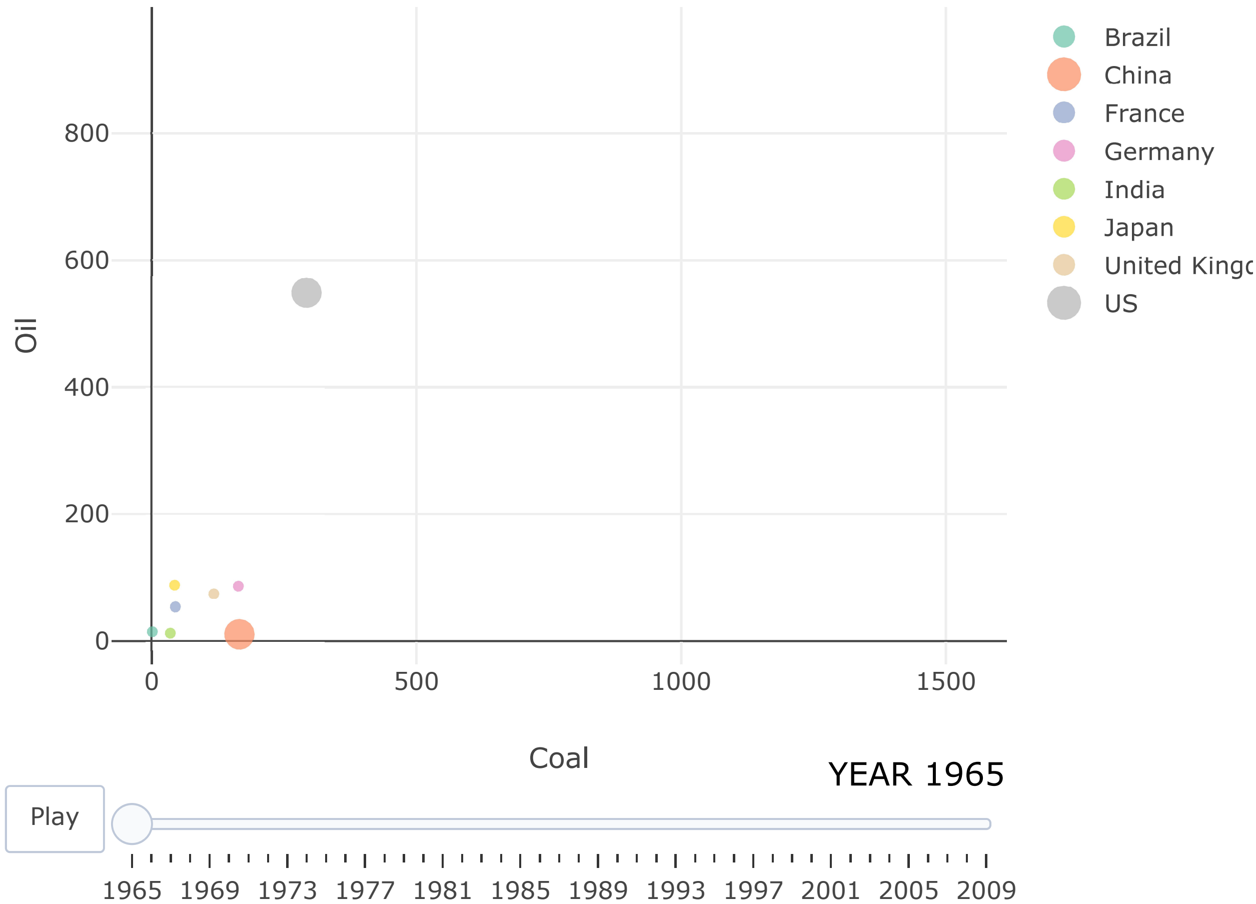
The cluster that is most prominent identified here is same identified in step 1 and step 3.That is the one containing Jamal zougham,Mohamed chaoui etc.

Assignment 2

The consumption of oil and coal in many countries within a time period is given in the oilcoal.csv.

1.plotly visualisation

```
library(tidyr)
library(tourr)
oilcoal<-read.csv("Oilcoal.csv",header=T,sep=";",stringsAsFactors = F)
oilcoal<-oilcoal[,c(1:5)]
oilcoal$Coal<-as.numeric(gsub(",",".",oilcoal$Coal))
oilcoal$Oil<-as.numeric(gsub(",",".",oilcoal$Oil))
oilcoal$Marker.size<-as.numeric(gsub(",",".",oilcoal$Marker.size))
#Visualize data in Plotly as an animated bubble chart of Coal versus Oil
#in which the bubble size corresponds to the country size.
#List several noteworthy features of the investigated animation.

###1

base<-oilcoal%>%plot_ly(x=~Coal,y=~Oil,size=~Marker.size,text=~Country,hoverinfo="t
ext")%>%
  add_markers(color=~Country,frame=~Year,ids=~Country)%>%
  animation_opts(8,redraw = F)%>%animation_slider(
    currentvalue = list(prefix = "YEAR ", font = list(color="black")))
base
```

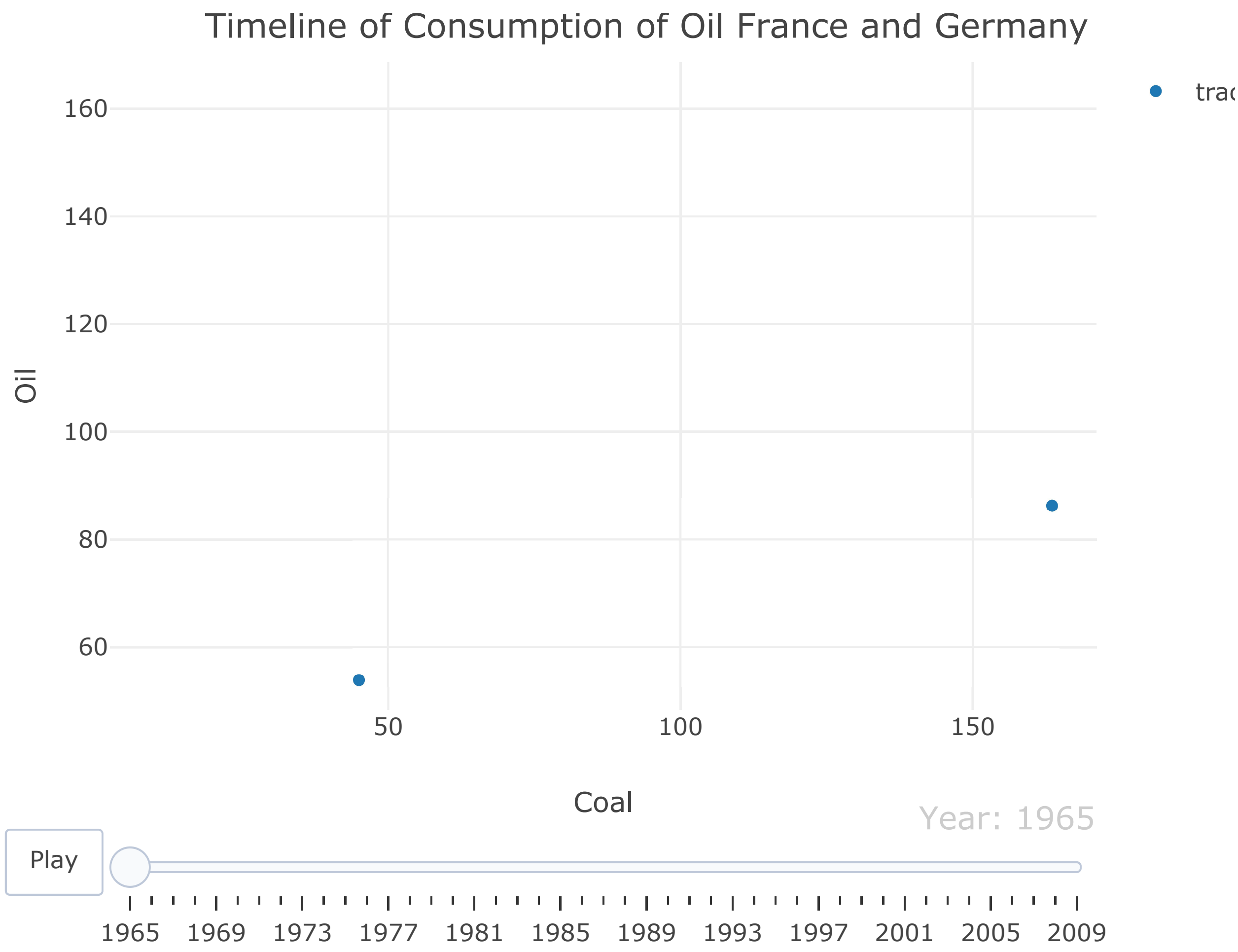


We can say like three countries grab our attention in the animation mostly.US,China and India.We could see that in the start of the animation,that is year 1965,the US had the highest oil and coal consumption ,then germany,uk,britain and china.Coal is a dwindling resource.May be the europen countries and US have started coal mining earlier and over a period of time they would have found it is a bad souce of energy becuase of the bad working condition of miners,price increased as the coal resource decreases and the pollution.SO they might have opted other cleaner source of energy, Us has a high consumtion of oil may be because the population has tripled or so by 2007 and hence domestic consumption increases.

We think the increased consumption of oil and coal and oil in India and china are related to the decreased consumption in other countries.As time progressed India,china,Japan etc became industrialised and other countries have outsourced everyhting to these countries.We can say that producton is very less in the europe and US now.They import a lot from India and China.As Industries increases the consumption becomes high.Ofcourse the domestic need in India and china has increased is another thing because their polpulation is way up the ladder when compared to 1968.

2.Motion chart

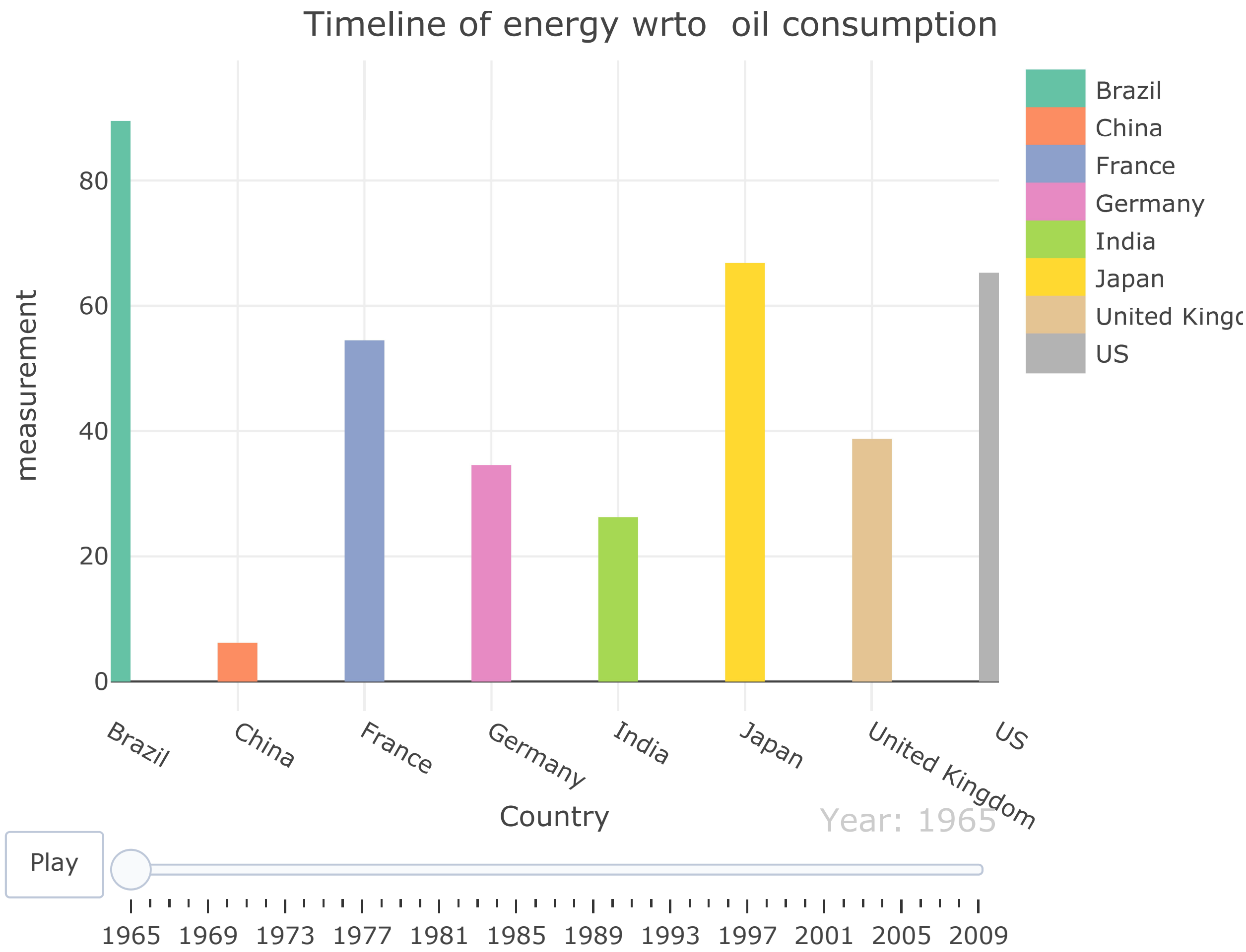
```
oilcoal %>% filter(Country %in% c("France", "Germany")) %>% plot_ly(x=~Coal, y=~Oi
l, frame =~Year, type = 'scatter', text = ~Country, mode = 'markers') %>%
  animation_opts(100, easing = "cubic", redraw = F) %>% layout(title="Timeline of C
onsumption of Oil France and Germany")
```



ONe reason could be that they understood they need to focus on renewable sources of energy and another would be the industires were shifted to the developing countries like china and India.

3.

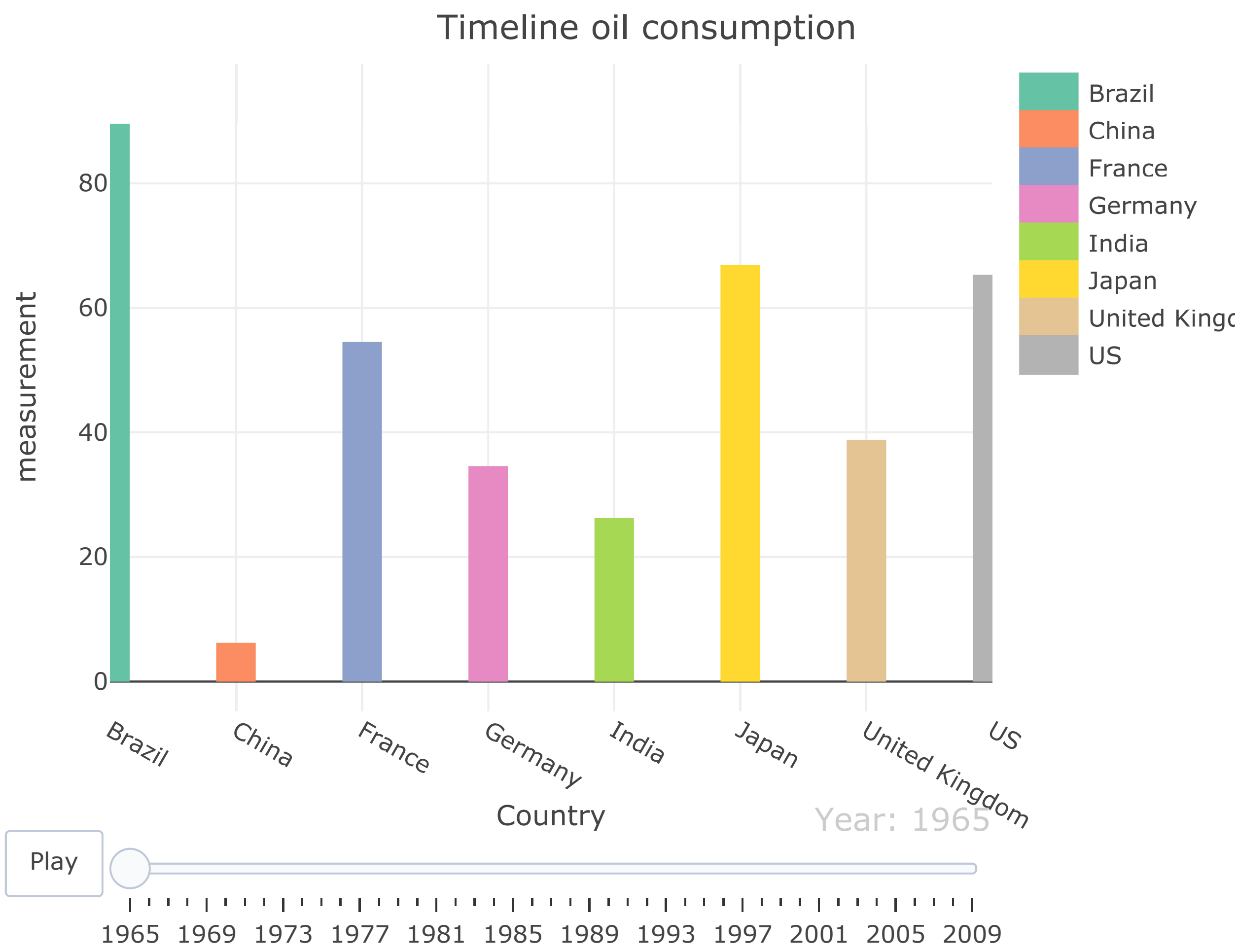
```
oilcoal$oilprop<-100*oilcoal$Oil/(oilcoal$Oil+oilcoal$Coal)

oilcoal$oilprop_0<-0

melt_oil<-gather(oilcoal, condition, measurement,oilprop,oilprop_0)


melt_oil %>%  plot_ly(x=~Country, y=~measurement, frame =~Year, type = 'scatter', m
ode='lines', text = ~Country,  color = ~Country, line = list(width = 20)) %>%
  animation_opts(300, easing = "cubic", redraw = F) %>% layout(title="Timeline of e
nergy wrto  oil consumption")
```



When we use the line plot it is easier to comapre because the length will help as to visualize easier.So the variations can also be visualised better using this plot.But it does not take into account the oilconsumption and the coalconsumption seperately.Or in bubble chart the x and y axis had oil and coal consumption respectively.But in the line plot together of the oil and coal is given as measurement in the y axis.

4.

```
melt_oil %>%  plot_ly(x=~Country, y=~measurement, frame =~Year, type = 'scatter', m
ode='lines', text = ~Country,  color = ~Country, line = list(width = 20)) %>%
  animation_opts(300, easing = "elastic", redraw = F) %>% layout(title="Timeline oi
l consumption")
```

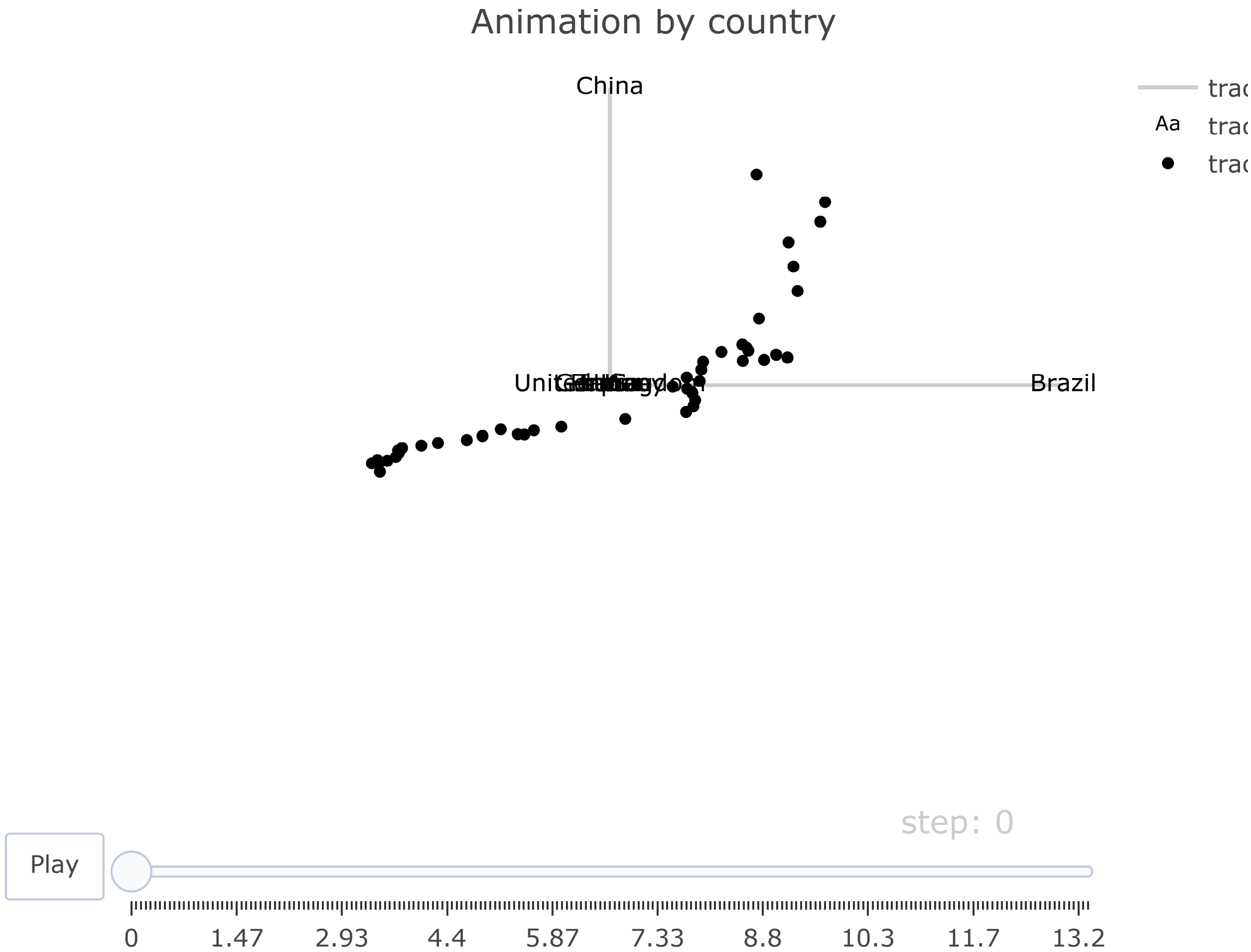


The transitions are visible more clerly here we think.

5.

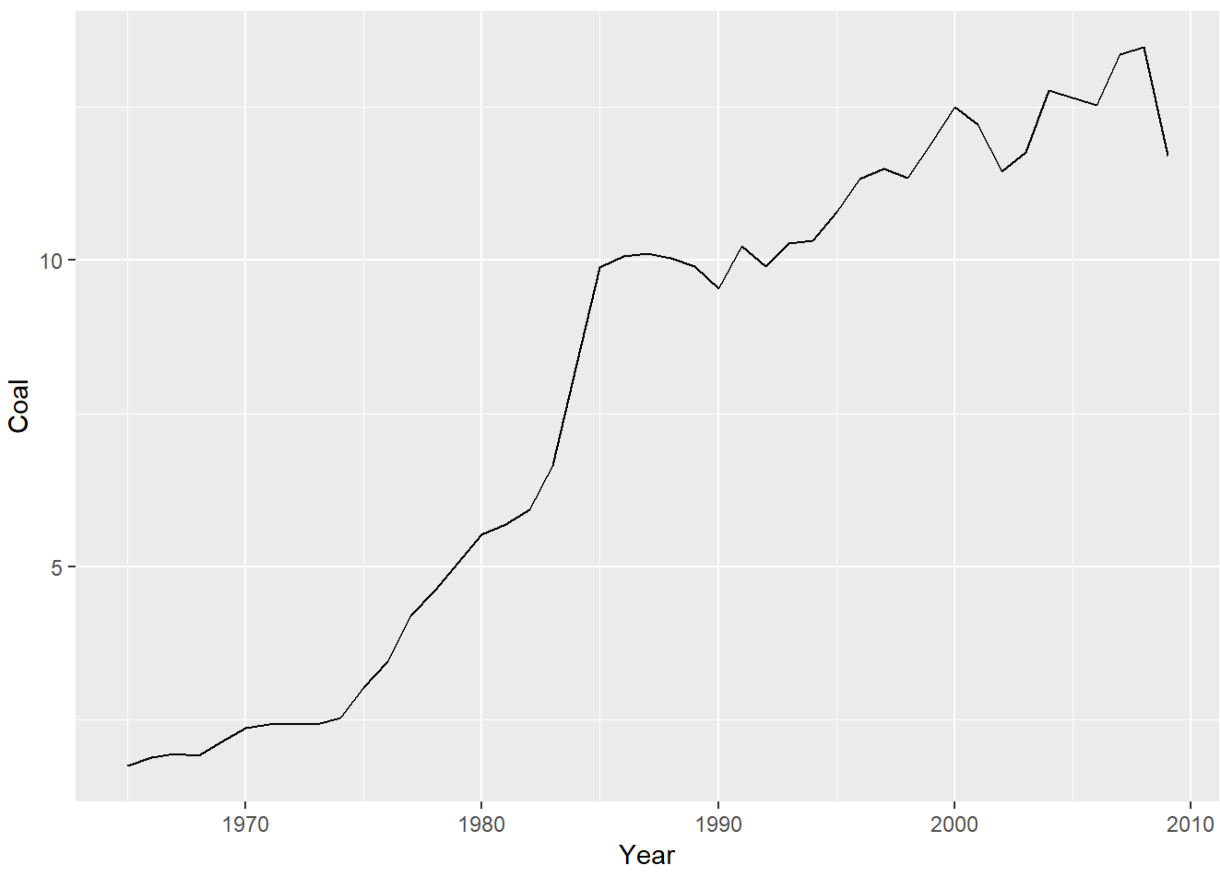
```r
oilcoal_c <- oilcoal[, c("Country", "Year", "Coal")]
oilcoal_tour <- oilcoal_c %>%spread(Country, Coal)
oilcoal_scale <- rescale(oilcoal_tour[, 2:9])

rownames(oilcoal_scale) <- oilcoal_tour$Year
colnames(oilcoal_scale) <- names(oilcoal_tour)[-1]

set.seed(12345)
tour <- new_tour(oilcoal_scale, grand_tour(), NULL)
#tour<- new_tour(mat, guided_tour(cmass), NULL)

steps <- c(0, rep(1/15, 200))


Projs<-lapply(steps, function(step_size){
  step <- tour(step_size)
  if(is.null(step)) {
    .GlobalEnv$tour<- new_tour(oilcoal_scale, guided_tour(cmass), NULL)
    step <- tour(step_size)
  }
  step
}
)

# projection of each observation
tour_dat <- function(i) {
  step <- Projs[[i]]
  proj <- center(oilcoal_scale %*% step$proj)
  data.frame(x = proj[,1], y = proj[,2], state = rownames(oilcoal_scale))
}
# projection of each variable's axis
proj_dat <- function(i) {
  step <- Projs[[i]]
  data.frame(
    x = step$proj[,1], y = step$proj[,2], variable = colnames(oilcoal_scale)
  )
}
stepz <- cumsum(steps)
# tidy version of tour data
tour_dats <- lapply(1:length(steps), tour_dat)
tour_datz <- Map(function(x, y) cbind(x, step = y), tour_dats, stepz)
tour_dat <- dplyr::bind_rows(tour_datz)

# tidy version of tour projection data
proj_dats <- lapply(1:length(steps), proj_dat)
proj_datz <- Map(function(x, y) cbind(x, step = y), proj_dats, stepz)
proj_dat <- dplyr::bind_rows(proj_datz)

ax <- list(
  title = "", showticklabels = FALSE,
  zeroline = FALSE, showgrid = FALSE,
  range = c(-1.1, 1.1)
```

```
)
# for nicely formatted slider labels
options(digits = 3)
tour_dat <- highlight_key(tour_dat, ~state, group = "A")
tour <- proj_dat %>%
  plot_ly(x = ~x, y = ~y, frame = ~step, color = I("black")) %>%
  add_segments(xend = 0, yend = 0, color = I("gray80")) %>%
  add_text(text = ~variable) %>%
  add_markers(data = tour_dat, text = ~state, ids = ~state, hoverinfo = "text") %>%
  layout(xaxis = ax, yaxis = ax, title = "Animation by country")
tour
```



Yes the clusters correspond to different year ranges.We think brazil has the largest contribution to this projection

```
oilcoal%>%filter(Country=="Brazil")%>%ggplot(aes(y=Coal,x=Year))+geom_line()
```


Coal
10
5
1970
1980
1990
2000
2010
Year

Appendix

```r
library(ggraph)
library(igraph)
library(visNetwork)
library(seriation)
library(plotly)

#setwd("C:/Users/quartermaine/Documents/Visualization/lab_6")
edges <- read.delim("trainData.dat", header = FALSE, sep  = " ")
nodes <- read.delim("trainMeta.dat", header = FALSE, sep = " ")
set.seed(12345)

nodes$id <- rownames(nodes)
colnames(nodes) <- c("bombers", "b_group", "id")
colnames(edges) <- c("temp", "from", "to", "value")
edges$temp <- NULL
graph <- graph.data.frame(edges, directed = T)
degree_value <- degree(graph)
nodes$value <- degree_value[match(nodes$id, names(degree_value))]
nodes <- na.omit(nodes)
nodes$label<-nodes$bombers
#### a.Basic
visNetwork(nodes=nodes,edges=edges,main = "Madrid bombing people network")
nodes$group<-nodes$b_group

visNetwork(nodes=nodes,edges=edges,main = "Madrid bombing people network")
visNetwork(nodes = nodes, edges = edges, main = "Madrid bombing people network") %
>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "from") %>%
  visOptions(collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()
visNetwork(nodes = nodes, edges = edges,main = "Madrid bombing people network") %
>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "to") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
                                     degree = 1),
             collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()



visNetwork(nodes = nodes, edges = edges) %>%
  visGroups(groupname = "0", color = "blue") %>%
  visGroups(groupname = "1", color = "orange") %>%
  visEdges(arrows = "from") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
```

```
                                          degree = list(from = 1, to = 2)),
             collapse = TRUE,
             selectedBy = "group") %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome()

graph_data_frame <- graph.data.frame(edges, directed = FALSE)
clusters <- cluster_edge_betweenness(graph_data_frame, directed = T)
nodes$clusters <- clusters$membership

visNetwork(nodes = nodes, edges = edges, main = "Madrid Bombing") %>%
  visEdges(arrows = "from") %>%
  visOptions(highlightNearest = list(enabled =TRUE,
                                     degree = list(from = 1, to = 2)),
             collapse = TRUE,
             selectedBy = "group")  %>%
  visPhysics(solver= "repulsion") %>%
  visLegend() %>% addFontAwesome() %>%visIgraphLayout()

adjecency <- get.adjacency(graph_data_frame, sparse=F)
colnames(adjecency) <- nodes$label
rownames(adjecency) <- nodes$label
rowdist<-dist(adjecency)


reord<-get_order(seriate(rowdist, "HC"))
mat_value<-adjecency[reord,reord]

##SInce using ubuntu system using the below line of code.




plot_ly(z=~mat_value, x=~colnames(mat_value),
        y=~rownames(mat_value), type="heatmap") %>% layout(title = "Heatmap")
library(tidyr)
library(tourr)
oilcoal<-read.csv("Oilcoal.csv",header=T,sep=";",stringsAsFactors = F)
oilcoal<-oilcoal[,c(1:5)]
oilcoal$Coal<-as.numeric(gsub(",",".",oilcoal$Coal))
oilcoal$Oil<-as.numeric(gsub(",",".",oilcoal$Oil))
oilcoal$Marker.size<-as.numeric(gsub(",",".",oilcoal$Marker.size))
#Visualize data in Plotly as an animated bubble chart of Coal versus Oil
#in which the bubble size corresponds to the country size.
#List several noteworthy features of the investigated animation.

###1

base<-oilcoal%>%plot_ly(x=~Coal,y=~Oil,size=~Marker.size,text=~Country,hoverinfo="t
ext")%>%
  add_markers(color=~Country,frame=~Year,ids=~Country)%>%
  animation_opts(8,redraw = F)%>%animation_slider(
    currentvalue = list(prefix = "YEAR ", font = list(color="black")))
```

```
base

oilcoal %>% filter(Country %in% c("France", "Germany")) %>% plot_ly(x=~Coal, y=~Oi
l, frame =~Year, type = 'scatter', text = ~Country, mode = 'markers') %>%
  animation_opts(100, easing = "cubic", redraw = F) %>% layout(title="Timeline of C
onsumption of Oil France and Germany")

oilcoal$oilprop<-100*oilcoal$Oil/(oilcoal$Oil+oilcoal$Coal)

oilcoal$oilprop_0<-0

melt_oil<-gather(oilcoal, condition, measurement,oilprop,oilprop_0)


melt_oil %>%  plot_ly(x=~Country, y=~measurement, frame =~Year, type = 'scatter', m
ode='lines', text = ~Country,  color = ~Country, line = list(width = 20)) %>%
  animation_opts(300, easing = "cubic", redraw = F) %>% layout(title="Timeline of e
nergy wrto  oil consumption")

melt_oil %>%  plot_ly(x=~Country, y=~measurement, frame =~Year, type = 'scatter', m
ode='lines', text = ~Country,  color = ~Country, line = list(width = 20)) %>%
  animation_opts(300, easing = "elastic", redraw = F) %>% layout(title="Timeline o
f wrto and oil consumption")
oilcoal_c <- oilcoal[, c("Country", "Year", "Coal")]
oilcoal_tour <- oilcoal_c %>%spread(Country, Coal)
oilcoal_scale <- rescale(oilcoal_tour[, 2:9])

rownames(oilcoal_scale) <- oilcoal_tour$Year
colnames(oilcoal_scale) <- names(oilcoal_tour)[-1]

set.seed(12345)
tour <- new_tour(oilcoal_scale, grand_tour(), NULL)
#tour<- new_tour(mat, guided_tour(cmass), NULL)

steps <- c(0, rep(1/15, 200))


Projs<-lapply(steps, function(step_size){
  step <- tour(step_size)
  if(is.null(step)) {
    .GlobalEnv$tour<- new_tour(oilcoal_scale, guided_tour(cmass), NULL)
    step <- tour(step_size)
  }
  step
}
)

# projection of each observation
tour_dat <- function(i) {
  step <- Projs[[i]]
  proj <- center(oilcoal_scale %*% step$proj)
  data.frame(x = proj[,1], y = proj[,2], state = rownames(oilcoal_scale))
```

```
}
# projection of each variable's axis
proj_dat <- function(i) {
  step <- Projs[[i]]
  data.frame(
    x = step$proj[,1], y = step$proj[,2], variable = colnames(oilcoal_scale)
  )
}
stepz <- cumsum(steps)
# tidy version of tour data
tour_dats <- lapply(1:length(steps), tour_dat)
tour_datz <- Map(function(x, y) cbind(x, step = y), tour_dats, stepz)
tour_dat <- dplyr::bind_rows(tour_datz)

# tidy version of tour projection data
proj_dats <- lapply(1:length(steps), proj_dat)
proj_datz <- Map(function(x, y) cbind(x, step = y), proj_dats, stepz)
proj_dat <- dplyr::bind_rows(proj_datz)

ax <- list(
  title = "", showticklabels = FALSE,
  zeroline = FALSE, showgrid = FALSE,
  range = c(-1.1, 1.1)
)
# for nicely formatted slider labels
options(digits = 3)
tour_dat <- highlight_key(tour_dat, ~state, group = "A")
tour <- proj_dat %>%
  plot_ly(x = ~x, y = ~y, frame = ~step, color = I("black")) %>%
  add_segments(xend = 0, yend = 0, color = I("gray80")) %>%
  add_text(text = ~variable) %>%
  add_markers(data = tour_dat, text = ~state, ids = ~state, hoverinfo = "text") %>%
  layout(xaxis = ax, yaxis = ax, title = "Animation by country")
tour


 oilcoal%>%filter(Country=="Brazil")%>%ggplot(aes(y=Coal,x=Year))+geom_line()
```

Data Transformation with dplyr : : CHEAT SHEET

dplyr

dplyr functions work with pipes and expect **tidy data**. In tidy data:

Each **variable** is in its own **column** & Each **observation**, or **case**, is in its own **row**

pipes

x %>% f(y) becomes **f(x, y)**

Summarise Cases

These apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

summary function

summarise(.data, …)
Compute table of summaries.
summarise(mtcars, avg = mean(mpg))

count(x, ..., wt = NULL, sort = FALSE)
Count number of rows in each group defined by the variables in … Also **tally**().
count(iris, Species)

VARIATIONS

summarise_all() - Apply funs to every column.
summarise_at() - Apply funs to specific columns.
summarise_if() - Apply funs to all cols of one type.

Group Cases

Use **group_by()** to create a "grouped" copy of a table. dplyr functions will manipulate each "group" separately and then combine the results.

```
mtcars %>%
group_by(cyl) %>%
summarise(avg = mean(mpg))
```

group_by(.data, ..., add = FALSE**)**
Returns copy of table grouped by …
g_iris <- group_by(iris, Species)

ungroup(x, …**)**
Returns ungrouped copy of table.
ungroup(g_iris)

Manipulate Cases

EXTRACT CASES

Row functions return a subset of rows as a new table.

filter(.data, …**)** Extract rows that meet logical criteria. *filter(iris, Sepal.Length > 7)*

distinct(.data, ..., .keep_all = FALSE**)** Remove rows with duplicate values.
distinct(iris, Species)

sample_frac(tbl, size = 1, replace = FALSE, weight = NULL, .env = parent.frame()**)** Randomly select fraction of rows.
sample_frac(iris, 0.5, replace = TRUE)

sample_n(tbl, size, replace = FALSE, weight = NULL, .env = parent.frame()**)** Randomly select size rows. *sample_n(iris, 10, replace = TRUE)*

slice(.data, …**)** Select rows by position.
slice(iris, 10:15)

top_n(x, n, wt**)** Select and order top n entries (by group if grouped data). *top_n(iris, 5, Sepal.Width)*

Logical and boolean operators to use with filter()

<	<=	is.na()	%in%	|	xor()
>	>=	!is.na()	!	&	

See **?base::logic** and **?Comparison** for help.

ARRANGE CASES

arrange(.data, …**)** Order rows by values of a column or columns (low to high), use with **desc()** to order from high to low.
arrange(mtcars, mpg)
arrange(mtcars, desc(mpg))

ADD CASES

add_row(.data, ..., .before = NULL, .after = NULL**)** Add one or more rows to a table.
add_row(faithful, eruptions = 1, waiting = 1)

Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.

pull(.data, var = -1**)** Extract column values as a vector. Choose by name or index.
pull(iris, Sepal.Length)

select(.data, …**)**
Extract columns as a table. Also **select_if()**.
select(iris, Sepal.Length, Species)

Use these helpers with select (),
e.g. select(iris, starts_with("Sepal"))

contains(match)	**num_range**(prefix, range)	:, e.g. mpg:cyl
ends_with(match)	**one_of**(…)	-, e.g, -Species
matches(match)	**starts_with**(match)	

MAKE NEW VARIABLES

These apply **vectorized functions** to columns. Vectorized funs take vectors as input and return vectors of the same length as output (see back).

vectorized function

mutate(.data, …)
Compute new column(s).
mutate(mtcars, gpm = 1/mpg)

transmute(.data, …)
Compute new column(s), drop others.
transmute(mtcars, gpm = 1/mpg)

mutate_all(.tbl, .funs, …**)** Apply funs to every column. Use with **funs()**. Also **mutate_if()**.
mutate_all(faithful, funs(log(.), log2(.)))
mutate_if(iris, is.numeric, funs(log(.)))

mutate_at(.tbl, .cols, .funs, …**)** Apply funs to specific columns. Use with **funs()**, **vars()** and the helper functions for select().
mutate_at(iris, vars(-Species), funs(log(.)))

add_column(.data, ..., .before = NULL, .after = NULL**)** Add new column(s). Also **add_count()**, **add_tally()**. *add_column(mtcars, new = 1:32)*

rename(.data, …**)** Rename columns.
rename(iris, Length = Sepal.Length)

RStudio

Vector Functions

TO USE WITH MUTATE ()

mutate() and **transmute()** apply vectorized functions to columns to create new columns. Vectorized functions take vectors as input and return vectors of the same length as output.

vectorized function

OFFSETS

dplyr::**lag()** - Offset elements by 1
dplyr::**lead()** - Offset elements by -1

CUMULATIVE AGGREGATES

dplyr::**cumall()** - Cumulative all()
dplyr::**cumany()** - Cumulative any()
cummax() - Cumulative max()
dplyr::**cummean()** - Cumulative mean()
cummin() - Cumulative min()
cumprod() - Cumulative prod()
cumsum() - Cumulative sum()

RANKINGS

dplyr::**cume_dist()** - Proportion of all values <=
dplyr::**dense_rank()** - rank with ties = min, no gaps
dplyr::**min_rank()** - rank with ties = min
dplyr::**ntile()** - bins into n bins
dplyr::**percent_rank()** - min_rank scaled to [0,1]
dplyr::**row_number()** - rank with ties = "first"

MATH

+, - , *, /, ^, %/%, %% - arithmetic ops
log(), log2(), log10() - logs
<, <=, >, >=, !=, == - logical comparisons
dplyr::**between()** - x >= left & x <= right
dplyr::**near()** - safe == for floating point numbers

MISC

dplyr::**case_when()** - multi-case if_else()
dplyr::**coalesce()** - first non-NA values by element across a set of vectors
dplyr::**if_else()** - element-wise if() + else()
dplyr::**na_if()** - replace specific values with NA
pmax() - element-wise max()
pmin() - element-wise min()
dplyr::**recode()** - Vectorized switch()
dplyr::**recode_factor()** - Vectorized switch() for factors

Summary Functions

TO USE WITH SUMMARISE ()

summarise() applies summary functions to columns to create a new table. Summary functions take vectors as input and return single values as output.

summary function

COUNTS

dplyr::**n()** - number of values/rows
dplyr::**n_distinct()** - # of uniques
sum(!is.na()) - # of non-NA's

LOCATION

mean() - mean, also **mean(!is.na())**
median() - median

LOGICALS

mean() - Proportion of TRUE's
sum() - # of TRUE's

POSITION/ORDER

dplyr::**first()** - first value
dplyr::**last()** - last value
dplyr::**nth()** - value in nth location of vector

RANK

quantile() - nth quantile
min() - minimum value
max() - maximum value

SPREAD

IQR() - Inter-Quartile Range
mad() - median absolute deviation
sd() - standard deviation
var() - variance

Row Names

Tidy data does not use rownames, which store a variable outside of the columns. To work with the rownames, first move them into a column.

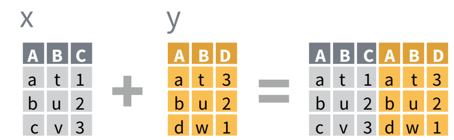
rownames_to_column()
Move row names into col.
a <- rownames_to_column(iris, var = "C")

column_to_rownames()
Move col in row names.
column_to_rownames(a, var = "C")

Also **has_rownames()**, **remove_rownames()**

Combine Tables

COMBINE VARIABLES



Use **bind_cols()** to paste tables beside each other as they are.

bind_cols(...) Returns tables placed side by side as a single table.
BE SURE THAT ROWS ALIGN.

Use a "**Mutating Join**" to join one table to columns from another, matching values with the rows that they correspond to. Each join retains a different combination of values from the tables.

left_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),...)
Join matching values from y to x.

right_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),...)
Join matching values from x to y.

inner_join(x, y, by = NULL, copy = FALSE, suffix=c(".x",".y"),...)
Join data. Retain only rows with matches.

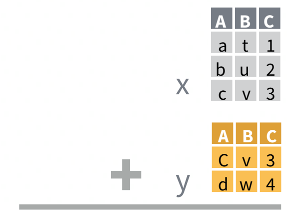
full_join(x, y, by = NULL, copy=FALSE, suffix=c(".x",".y"),...)
Join data. Retain all values, all rows.

Use **by = c("col1", "col2", ...)** to specify one or more common columns to match on.
left_join(x, y, by = "A")

Use a named vector, **by = c("col1" = "col2")**, to match on columns that have different names in each table.
left_join(x, y, by = c("C" = "D"))

Use **suffix** to specify the suffix to give to unmatched columns that have the same name in both tables.
left_join(x, y, by = c("C" = "D"), suffix = c("1", "2"))

COMBINE CASES



Use **bind_rows()** to paste tables below each other as they are.

bind_rows(..., .id = NULL)
Returns tables one on top of the other as a single table. Set .id to a column name to add a column of the original table names (as pictured)

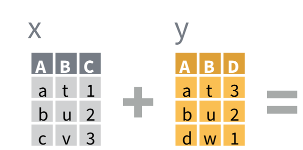
intersect(x, y, ...)
Rows that appear in both x and y.

setdiff(x, y, ...)
Rows that appear in x but not y.

union(x, y, ...)
Rows that appear in x or y. (Duplicates removed). union_all() retains duplicates.

Use **setequal()** to test whether two data sets contain the exact same rows (in any order).

EXTRACT ROWS



Use a "**Filtering Join**" to filter one table against the rows of another.

semi_join(x, y, by = NULL, ...)
Return rows of x that have a match in y.
USEFUL TO SEE WHAT WILL BE JOINED.

anti_join(x, y, by = NULL, ...)
Return rows of x that do not have a match in y. USEFUL TO SEE WHAT WILL NOT BE JOINED.

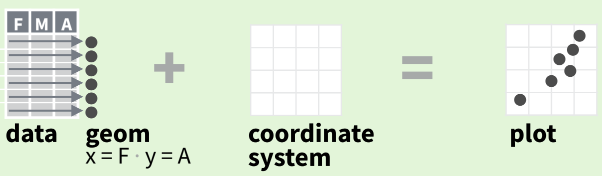
dplyr

RStudio

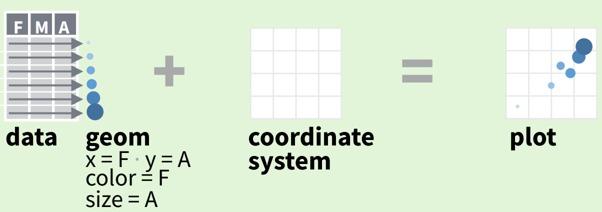
Data Visualization with ggplot2 : : CHEAT SHEET

Basics

ggplot2 is based on the **grammar of graphics**, the idea that you can build every graph from the same components: a **data** set, a **coordinate system**, and geoms—visual marks that represent data points.



To display values, map variables in the data to visual properties of the geom (**aesthetics**) like **size**, **color**, and **x** and **y** locations.



Complete the template below to build a graph.

```
ggplot (data = <DATA>) +
  <GEOM_FUNCTION>(mapping = aes(<MAPPINGS>),
  stat = <STAT>, position = <POSITION>) +
  <COORDINATE_FUNCTION> +
  <FACET_FUNCTION> +
  <SCALE_FUNCTION> +
  <THEME_FUNCTION>
```

required (first two lines); Not required, sensible defaults supplied (remaining lines)

ggplot(data = mpg, **aes**(x = cty, y = hwy)) Begins a plot that you finish by adding layers to. Add one geom function per layer.

aesthetic mappings — data — geom

qplot(x = cty, y = hwy, data = mpg, geom = "point") Creates a complete plot with given data, geom, and mappings. Supplies many useful defaults.

last_plot() Returns the last plot

ggsave("plot.png", width = 5, height = 5) Saves last plot as 5' x 5' file named "plot.png" in working directory. Matches file type to file extension.

Geoms

Use a geom function to represent data points, use the geom's aesthetic properties to represent variables. Each function returns a layer.

GRAPHICAL PRIMITIVES

a <- ggplot(economics, aes(date, unemploy))
b <- ggplot(seals, aes(x = long, y = lat))

a + geom_blank()
(Useful for expanding limits)

b + geom_curve(aes(yend = lat + 1, xend=long+1,curvature=z)**)** - x, xend, y, yend, alpha, angle, color, curvature, linetype, size

a + geom_path(lineend="butt", linejoin="round", linemitre=1**)**
x, y, alpha, color, group, linetype, size

a + geom_polygon(aes(group = group)**)**
x, y, alpha, color, fill, group, linetype, size

b + geom_rect(aes(xmin = long, ymin=lat, xmax= long + 1, ymax = lat + 1)**)** - xmax, xmin, ymax, ymin, alpha, color, fill, linetype, size

a + geom_ribbon(aes(ymin=unemploy - 900, ymax=unemploy + 900)**)** - x, ymax, ymin, alpha, color, fill, group, linetype, size

LINE SEGMENTS

common aesthetics: x, y, alpha, color, linetype, size

b + geom_abline(aes(intercept=0, slope=1)**)**
b + geom_hline(aes(yintercept = lat)**)**
b + geom_vline(aes(xintercept = long)**)**

b + geom_segment(aes(yend=lat+1, xend=long+1)**)**
b + geom_spoke(aes(angle = 1:1155, radius = 1)**)**

ONE VARIABLE continuous

c <- ggplot(mpg, aes(hwy)); c2 <- ggplot(mpg)

c + geom_area(stat = "bin")
x, y, alpha, color, fill, linetype, size

c + geom_density(kernel = "gaussian"**)**
x, y, alpha, color, fill, group, linetype, size, weight

c + geom_dotplot()
x, y, alpha, color, fill

c + geom_freqpoly() x, y, alpha, color, group, linetype, size

c + geom_histogram(binwidth = 5**)** x, y, alpha, color, fill, linetype, size, weight

c2 + geom_qq(aes(sample = hwy)**)** x, y, alpha, color, fill, linetype, size, weight

discrete

d <- ggplot(mpg, aes(fl))

d + geom_bar()
x, alpha, color, fill, linetype, size, weight

TWO VARIABLES

continuous x , continuous y

e <- ggplot(mpg, aes(cty, hwy))

e + geom_label(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)** x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

e + geom_jitter(height = 2, width = 2**)**
x, y, alpha, color, fill, shape, size

e + geom_point(), x, y, alpha, color, fill, shape, size, stroke

e + geom_quantile(), x, y, alpha, color, group, linetype, size, weight

e + geom_rug(sides = "bl"**)**, x, y, alpha, color, linetype, size

e + geom_smooth(method = lm**)**, x, y, alpha, color, fill, group, linetype, size, weight

e + geom_text(aes(label = cty), nudge_x = 1, nudge_y = 1, check_overlap = TRUE**)**, x, y, label, alpha, angle, color, family, fontface, hjust, lineheight, size, vjust

discrete x , continuous y

f <- ggplot(mpg, aes(class, hwy))

f + geom_col(), x, y, alpha, color, fill, group, linetype, size

f + geom_boxplot(), x, y, lower, middle, upper, ymax, ymin, alpha, color, fill, group, linetype, shape, size, weight

f + geom_dotplot(binaxis = "y", stackdir = "center"**)**, x, y, alpha, color, fill, group

f + geom_violin(scale = "area"**)**, x, y, alpha, color, fill, group, linetype, size, weight

discrete x , discrete y

g <- ggplot(diamonds, aes(cut, color))

g + geom_count(), x, y, alpha, color, fill, shape, size, stroke

continuous bivariate distribution

h <- ggplot(diamonds, aes(carat, price))

h + geom_bin2d(binwidth = c(0.25, 500)**)**
x, y, alpha, color, fill, linetype, size, weight

h + geom_density2d()
x, y, alpha, colour, group, linetype, size

h + geom_hex()
x, y, alpha, colour, fill, size

continuous function

i <- ggplot(economics, aes(date, unemploy))

i + geom_area()
x, y, alpha, color, fill, linetype, size

i + geom_line()
x, y, alpha, color, group, linetype, size

i + geom_step(direction = "hv")
x, y, alpha, color, group, linetype, size

visualizing error

df <- data.frame(grp = c("A", "B"), fit = 4:5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit-se, ymax = fit+se))

j + geom_crossbar(fatten = 2**)**
x, y, ymax, ymin, alpha, color, fill, group, linetype, size

j + geom_errorbar(), x, ymax, ymin, alpha, color, group, linetype, size, width (also **geom_errorbarh()**)

j + geom_linerange()
x, ymin, ymax, alpha, color, group, linetype, size

j + geom_pointrange()
x, y, ymin, ymax, alpha, color, fill, group, linetype, shape, size

maps

data <- data.frame(murder = USArrests$Murder,
state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))

k + geom_map(aes(map_id = state), map = map**)**
+ expand_limits(x = map$long, y = map$lat**)**,
map_id, alpha, color, fill, linetype, size

THREE VARIABLES

seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2))l <- ggplot(seals, aes(long, lat))

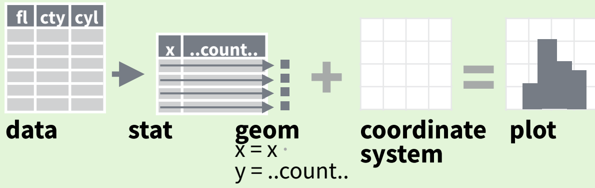
l + geom_contour(aes(z = z))
x, y, z, alpha, colour, group, linetype, size, weight

l + geom_raster(aes(fill = z)**)**, hjust=0.5, vjust=0.5, interpolate=FALSE)
x, y, alpha, fill

l + geom_tile(aes(fill = z)**)**, x, y, alpha, color, fill, linetype, size, width

Stats An alternative way to build a layer

A stat builds new variables to plot (e.g., count, prop).



Visualize a stat by changing the default stat of a geom function, **geom_bar(stat="count")** or by using a stat function, **stat_count(geom="bar")**, which calls a default geom to make a layer (equivalent to a geom function). Use **..name..** syntax to map stat variables to aesthetics.

geom to use | stat function | geommappings

i + stat_density2d(aes(fill = ..level..), geom = "polygon")

variable created by stat

c + stat_bin(binwidth = 1, origin = 10)
x, y | ..count.., ..ncount.., ..density.., ..ndensity..

c + stat_count(width = 1) **x, y,** | ..count.., ..prop..

c + stat_density(adjust = 1, kernel = "gaussian")
x, y, | ..count.., ..density.., ..scaled..

e + stat_bin_2d(bins = 30, drop = T)
x, y, fill | ..count.., ..density..

e + stat_bin_hex(bins=30) **x, y, fill** | ..count.., ..density..

e + stat_density_2d(contour = TRUE, n = 100)
x, y, color, size | ..level..

e + stat_ellipse(level = 0.95, segments = 51, type = "t")

l + stat_contour(aes(z = z)) **x, y, z, order** | ..level..

l + stat_summary_hex(aes(z = z), bins = 30, fun = max)
x, y, z, fill | ..value..

l + stat_summary_2d(aes(z = z), bins = 30, fun = mean)
x, y, z, fill | ..value..

f + stat_boxplot(coef = 1.5) **x, y** | ..lower.., ..middle.., ..upper.., ..width.. , ..ymin.., ..ymax..

f + stat_ydensity(kernel = "gaussian", scale = "area") **x, y** | ..density.., ..scaled.., ..count.., ..n.., ..violinwidth.., ..width..

e + stat_ecdf(n = 40) **x, y** | ..x.., ..y..

e + stat_quantile(quantiles = c(0.1, 0.9), formula = y ~ log(x), method = "rq") **x, y** | ..quantile..

e + stat_smooth(method = "lm", formula = y ~ x, se=T, level=0.95) **x, y** | ..se.., ..x.., ..y.., ..ymin.., ..ymax..

ggplot() + stat_function(aes(x = -3:3), n = 99, fun = dnorm, args = list(sd=0.5)) **x** | ..x.., ..y..

e + stat_identity(na.rm = TRUE)

ggplot() + stat_qq(aes(sample=1:100), dist = qt, dparam=list(df=5)) **sample, x, y** | ..sample.., ..theoretical..

e + stat_sum() x, y, size | ..n.., ..prop..

e + stat_summary(fun.data = "mean_cl_boot")

h + stat_summary_bin(fun.y = "mean", geom = "bar")

e + stat_unique()

Scales

Scales map data values to the visual values of an aesthetic. To change a mapping, add a new scale.

(n <- d + geom_bar(aes(fill = fl)))

scale_ | aesthetic to adjust | prepackaged scale to use | scale-specific arguments

n + scale_fill_manual(
values = c("skyblue", "royalblue", "blue", "navy"),
limits = c("d", "e", "p", "r"), breaks =c("d", "e", "p", "r"),
name = "fuel", labels = c("D", "E", "P", "R"))

range of values to include in mapping | title to use in legend/axis | labels to use in legend/axis | breaks to use in legend/axis

GENERAL PURPOSE SCALES

Use with most aesthetics

scale_*_continuous() - map cont' values to visual ones
scale_*_discrete() - map discrete values to visual ones
scale_*_identity() - use data values **as** visual ones
scale_*_manual(values = c()) - map discrete values to manually chosen visual ones
scale_*_date(date_labels = "%m/%d"), date_breaks = "2 weeks") - treat data values as dates.
scale_*_datetime() - treat data x values as date times. Use same arguments as scale_x_date(). See ?strptime for label formats.

X & Y LOCATION SCALES

Use with x or y aesthetics (x shown here)

scale_x_log10() - Plot x on log10 scale
scale_x_reverse() - Reverse direction of x axis
scale_x_sqrt() - Plot x on square root scale

COLOR AND FILL SCALES (DISCRETE)

n <- d + geom_bar(aes(fill = fl))

n + scale_fill_brewer(palette = "Blues")
For palette choices:
RColorBrewer::display.brewer.all()

n + scale_fill_grey(start = 0.2, end = 0.8, na.value = "red")

COLOR AND FILL SCALES (CONTINUOUS)

o <- c + geom_dotplot(aes(fill = ..x..))

o + scale_fill_distiller(palette = "Blues")

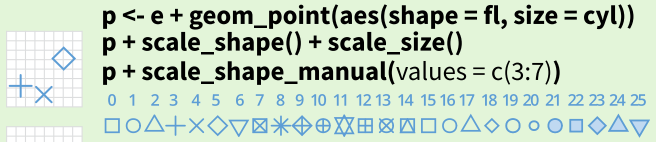
o + scale_fill_gradient(low="red", high="yellow")

o + scale_fill_gradient2(low="red", high="blue", mid = "white", midpoint = 25)

o + scale_fill_gradientn(colours=topo.colors(6))
Also: rainbow(), heat.colors(), terrain.colors(), cm.colors(), RColorBrewer::brewer.pal()

SHAPE AND SIZE SCALES

p <- e + geom_point(aes(shape = fl, size = cyl))
p + scale_shape() + scale_size()
p + scale_shape_manual(values = c(3:7))



p + scale_radius(range = c(1,6))
p + scale_size_area(max_size = 6)

Coordinate Systems

r <- d + geom_bar()

r + coord_cartesian(xlim = c(0, 5))
xlim, ylim
The default cartesian coordinate system

r + coord_fixed(ratio = 1/2)
ratio, xlim, ylim
Cartesian coordinates with fixed aspect ratio between x and y units

r + coord_flip()
xlim, ylim
Flipped Cartesian coordinates

r + coord_polar(theta = "x", direction=1)
theta, start, direction
Polar coordinates

r + coord_trans(ytrans = "sqrt")
xtrans, ytrans, limx, limy
Transformed cartesian coordinates. Set xtrans and ytrans to the name of a window function.

π + coord_quickmap()
π + coord_map(projection = "ortho", orientation=c(41, -74, 0))projection, orienztation, xlim, ylim
Map projections from the mapproj package (mercator (default), azequalarea, lagrange, etc.)

Position Adjustments

Position adjustments determine how to arrange geoms that would otherwise occupy the same space.

s <- ggplot(mpg, aes(fl, fill = drv))

s + geom_bar(position = "dodge")
Arrange elements side by side

s + geom_bar(position = "fill")
Stack elements on top of one another, normalize height

e + geom_point(position = "jitter")
Add random noise to X and Y position of each element to avoid overplotting

e + geom_label(position = "nudge")
Nudge labels away from points

s + geom_bar(position = "stack")
Stack elements on top of one another

Each position adjustment can be recast as a function with manual **width** and **height** arguments
s + geom_bar(position = position_dodge(width = 1))

Themes

r + theme_bw()
White background with grid lines

r + theme_gray()
Grey background (default theme)

r + theme_dark()
dark for contrast

r + theme_classic()

r + theme_light()

r + theme_linedraw()

r + theme_minimal()
Minimal themes

r + theme_void()
Empty theme

Faceting

Facets divide a plot into subplots based on the values of one or more discrete variables.

t <- ggplot(mpg, aes(cty, hwy)) + geom_point()

t + facet_grid(. ~ fl)
facet into columns based on fl

t + facet_grid(year ~ .)
facet into rows based on year

t + facet_grid(year ~ fl)
facet into both rows and columns

t + facet_wrap(~ fl)
wrap facets into a rectangular layout

Set **scales** to let axis limits vary across facets

t + facet_grid(drv ~ fl, scales = "free")
x and y axis limits adjust to individual facets
"free_x" - x axis limits adjust
"free_y" - y axis limits adjust

Set **labeller** to adjust facet labels

t + facet_grid(. ~ fl, labeller = label_both)

fl: c	fl: d	fl: e	fl: p	fl: r

t + facet_grid(fl ~ ., labeller = label_bquote(alpha ^ .(fl)))

α^c	α^d	α^e	α^p	α^r

t + facet_grid(. ~ fl, labeller = label_parsed)

c	d	e	p	r

Labels

t + labs(**x** = "New x axis label", **y** = "New y axis label",
title ="Add a title above the plot",
subtitle = "Add a subtitle below title",
caption = "Add a caption below plot",
<AES> = "New <AES> legend title")

Use scale functions to update legend labels

t + annotate(geom = "text", x = 8, y = 9, label = "A")

geom to place | manual values for geom's aesthetics

Legends

n + theme(legend.position = "bottom")
Place legend at "bottom", "top", "left", or "right"

n + guides(fill = "none")
Set legend type for each aesthetic: colorbar, legend, or none (no legend)

n + scale_fill_discrete(name = "Title", labels = c("A", "B", "C", "D", "E"))
Set legend title and labels with a scale function.

Zooming

Without clipping (preferred)
t + coord_cartesian(
xlim = c(0, 100), ylim = c(10, 20))

With clipping (removes unseen data points)
t + xlim(0, 100) **+ ylim**(10, 20)

t + scale_x_continuous(limits = c(0, 100)) **+ scale_y_continuous**(limits = c(0, 100))

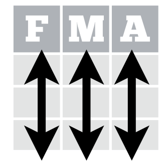
RStudio

Data Wrangling
with dplyr and tidyr
Cheat Sheet

RStudio®

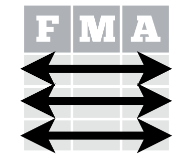
Tidy Data - A foundation for wrangling in R

In a tidy data set:



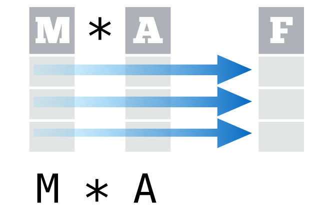
Each **variable** is saved in its own **column**

&



Each **observation** is saved in its own **row**

Tidy data complements R's **vectorized operations**. R will automatically preserve observations as you manipulate variables. No other format works as intuitively with R.



Syntax - Helpful conventions for wrangling

dplyr::**tbl_df(iris)**

Converts data to tbl class. tbl's are easier to examine than data frames. R displays only the data that fits onscreen:

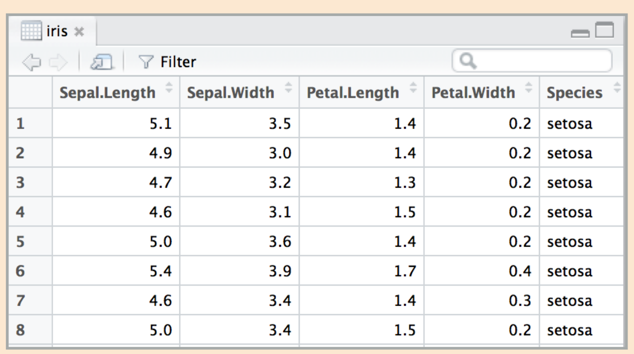
```
Source: local data frame [150 x 5]

  Sepal.Length Sepal.Width Petal.Length
1          5.1         3.5          1.4
2          4.9         3.0          1.4
3          4.7         3.2          1.3
4          4.6         3.1          1.5
5          5.0         3.6          1.4
..         ...         ...          ...
Variables not shown: Petal.Width (dbl),
  Species (fctr)
```

dplyr::**glimpse(iris)**

Information dense summary of tbl data.

utils::**View(iris)**

View data set in spreadsheet-like display (note capital V).



	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
7	4.6	3.4	1.4	0.3	setosa
8	5.0	3.4	1.5	0.2	setosa

dplyr::**%>%**

Passes object on left hand side as first argument (or . argument) of function on righthand side.

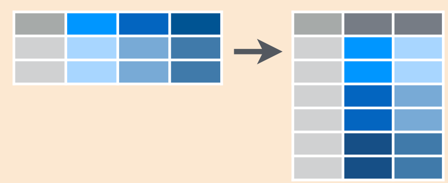
`x %>% f(y)` *is the same as* `f(x, y)`

`y %>% f(x, ., z)` *is the same as* `f(x, y, z )`

"Piping" with %>% makes code more readable, e.g.

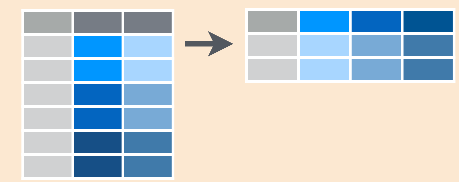
```
iris %>%
  group_by(Species) %>%
  summarise(avg = mean(Sepal.Width)) %>%
  arrange(avg)
```

Reshaping Data - Change the layout of a data set



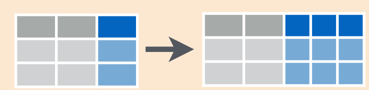
tidyr::**gather(cases, "year", "n", 2:4)**

Gather columns into rows.



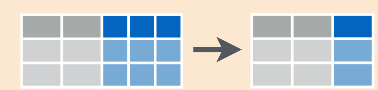
tidyr::**spread(pollution, size, amount)**

Spread rows into columns.



tidyr::**separate(storms, date, c("y", "m", "d"))**

Separate one column into several.



tidyr::**unite(data, col, ..., sep)**

Unite several columns into one.

dplyr::**data_frame(a = 1:3, b = 4:6)**

Combine vectors into data frame (optimized).

dplyr::**arrange(mtcars, mpg)**

Order rows by values of a column (low to high).

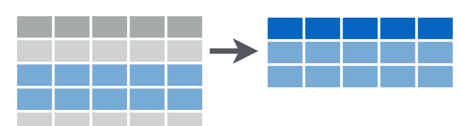
dplyr::**arrange(mtcars, desc(mpg))**

Order rows by values of a column (high to low).

dplyr::**rename(tb, y = year)**

Rename the columns of a data frame.

Subset Observations (Rows)



dplyr::**filter(iris, Sepal.Length > 7)**

Extract rows that meet logical criteria.

dplyr::**distinct(iris)**

Remove duplicate rows.

dplyr::**sample_frac(iris, 0.5, replace = TRUE)**

Randomly select fraction of rows.

dplyr::**sample_n(iris, 10, replace = TRUE)**

Randomly select n rows.

dplyr::**slice(iris, 10:15)**

Select rows by position.

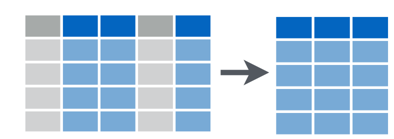
dplyr::**top_n(storms, 2, date)**

Select and order top n entries (by group if grouped data).

Logic in R - ?Comparison, ?base::Logic

<	Less than	!=	Not equal to
>	Greater than	%in%	Group membership
==	Equal to	is.na	Is NA
<=	Less than or equal to	!is.na	Is not NA
>=	Greater than or equal to	&,|,!,xor,any,all	Boolean operators

Subset Variables (Columns)



dplyr::**select(iris, Sepal.Width, Petal.Length, Species)**

Select columns by name or helper function.

Helper functions for select - ?select

select(iris, **contains(".")**)

Select columns whose name contains a character string.

select(iris, **ends_with("Length")**)

Select columns whose name ends with a character string.

select(iris, **everything()**)

Select every column.

select(iris, **matches(".t.")**)

Select columns whose name matches a regular expression.

select(iris, **num_range("x", 1:5)**)

Select columns named x1, x2, x3, x4, x5.

select(iris, **one_of(c("Species", "Genus"))**)

Select columns whose names are in a group of names.

select(iris, **starts_with("Sepal")**)

Select columns whose name starts with a character string.

select(iris, **Sepal.Length:Petal.Width**)

Select all columns between Sepal.Length and Petal.Width (inclusive).

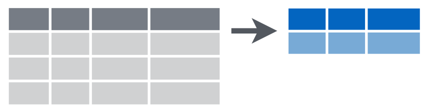
select(iris, **-Species**)

Select all columns except Species.

devtools::install_github("rstudio/EDAWR") for data sets

Learn more with browseVignettes(package = c("dplyr", "tidyr")) • dplyr 0.4.0• tidyr 0.2.0 • Updated: 1/15

Summarise Data



dplyr::**summarise(iris, avg = mean(Sepal.Length))**
Summarise data into single row of values.

dplyr::**summarise_each(iris, funs(mean))**
Apply summary function to each column.

dplyr::**count(iris, Species, wt = Sepal.Length)**
Count number of rows with each unique value of variable (with or without weights).

Summarise uses **summary functions**, functions that take a vector of values and return a single value, such as:

dplyr::**first**
First value of a vector.

dplyr::**last**
Last value of a vector.

dplyr::**nth**
Nth value of a vector.

dplyr::**n**
\# of values in a vector.

dplyr::**n_distinct**
\# of distinct values in a vector.

IQR
IQR of a vector.

min
Minimum value in a vector.

max
Maximum value in a vector.

mean
Mean value of a vector.

median
Median value of a vector.

var
Variance of a vector.

sd
Standard deviation of a vector.

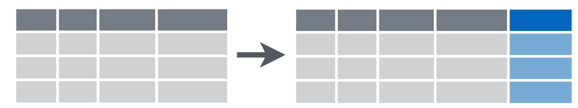
Group Data

dplyr::**group_by(iris, Species)**
Group data into rows with the same value of Species.

dplyr::**ungroup(iris)**
Remove grouping information from data frame.

iris %>% group_by(Species) %>% summarise(…)
Compute separate summary row for each group.

Make New Variables



dplyr::**mutate(iris, sepal = Sepal.Length + Sepal. Width)**
Compute and append one or more new columns.

dplyr::**mutate_each(iris, funs(min_rank))**
Apply window function to each column.

dplyr::**transmute(iris, sepal = Sepal.Length + Sepal. Width)**
Compute one or more new columns. Drop original columns.

Mutate uses **window functions**, functions that take a vector of values and return another vector of values, such as:

dplyr::**lead**
Copy with values shifted by 1.

dplyr::**lag**
Copy with values lagged by 1.

dplyr::**dense_rank**
Ranks with no gaps.

dplyr::**min_rank**
Ranks. Ties get min rank.

dplyr::**percent_rank**
Ranks rescaled to [0, 1].

dplyr::**row_number**
Ranks. Ties got to first value.

dplyr::**ntile**
Bin vector into n buckets.

dplyr::**between**
Are values between a and b?

dplyr::**cume_dist**
Cumulative distribution.

dplyr::**cumall**
Cumulative `all`

dplyr::**cumany**
Cumulative `any`

dplyr::**cummean**
Cumulative `mean`

cumsum
Cumulative `sum`

cummax
Cumulative `max`

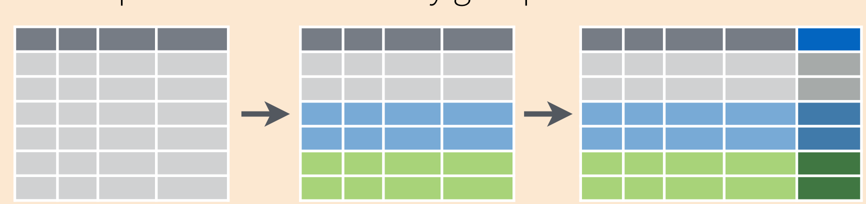
cummin
Cumulative `min`

cumprod
Cumulative `prod`

pmax
Element-wise `max`

pmin
Element-wise `min`

iris %>% group_by(Species) %>% mutate(…)
Compute new variables by group.



Combine Data Sets

a

x1	x2
A	1
B	2
C	3

\+

b

x1	x3
A	T
B	F
D	T

=

Mutating Joins

x1	x2	x3
A	1	T
B	2	F
C	3	NA

dplyr::**left_join(a, b, by = "x1")**
Join matching rows from b to a.

x1	x3	x2
A	T	1
B	F	2
D	T	NA

dplyr::**right_join(a, b, by = "x1")**
Join matching rows from a to b.

x1	x2	x3
A	1	T
B	2	F

dplyr::**inner_join(a, b, by = "x1")**
Join data. Retain only rows in both sets.

x1	x2	x3
A	1	T
B	2	F
C	3	NA
D	NA	T

dplyr::**full_join(a, b, by = "x1")**
Join data. Retain all values, all rows.

Filtering Joins

x1	x2
A	1
B	2

dplyr::**semi_join(a, b, by = "x1")**
All rows in a that have a match in b.

x1	x2
C	3

dplyr::**anti_join(a, b, by = "x1")**
All rows in a that do not have a match in b.

y

x1	x2
A	1
B	2
C	3

\+

z

x1	x2
B	2
C	3
D	4

=

Set Operations

x1	x2
B	2
C	3

dplyr::**intersect(y, z)**
Rows that appear in both y and z.

x1	x2
A	1
B	2
C	3
D	4

dplyr::**union(y, z)**
Rows that appear in either or both y and z.

x1	x2
A	1

dplyr::**setdiff(y, z)**
Rows that appear in y but not z.

Binding

x1	x2
A	1
B	2
C	3
B	2
C	3
D	4

dplyr::**bind_rows(y, z)**
Append z to y as new rows.

x1	x2	x1	x2
A	1	B	2
B	2	C	3
C	3	D	4

dplyr::**bind_cols(y, z)**
Append z to y as new columns.
Caution: matches rows by position.

Basic Regular Expressions in R
Cheat Sheet

Character Classes

[[:digit:]] or \\d	Digits; `[0-9]`
\\D	Non-digits; `[^0-9]`
[[:lower:]]	Lower-case letters; `[a-z]`
[[:upper:]]	Upper-case letters; `[A-Z]`
[[:alpha:]]	Alphabetic characters; `[A-z]`
[[:alnum:]]	Alphanumeric characters `[A-z0-9]`
\\w	Word characters; `[A-z0-9_]`
\\W	Non-word characters
[[:xdigit:]] or \\x	Hexadec. digits; `[0-9A-Fa-f]`
[[:blank:]]	Space and tab
[[:space:]] or \\s	Space, tab, vertical tab, newline, form feed, carriage return
\\S	Not space; `[^[:space:]]`
[[:punct:]]	Punctuation characters; `!"#$%&'()*+,-./:;<=>?@[]^_`{|}~`
[[:graph:]]	Graphical characters; `[[:alnum:][:punct:]]`
[[:print:]]	Printable characters; `[[:alnum:][:punct:]\\s]`
[[:cntrl:]] or \\c	Control characters; `\n`, `\r` etc.

Special Metacharacters

\n	New line
\r	Carriage return
\t	Tab
\v	Vertical tab
\f	Form feed

Lookaraounds and Conditionals*

(?=)	Lookahead (requires PERL = TRUE), e.g. `(?=yx)`: position followed by `'xy'`
(?!)	Negative lookahead (PERL = TRUE); position NOT followed by pattern
(?<=)	Lookbehind (PERL = TRUE), e.g. `(?<=yx)`: position following `'xy'`
(?<!)	Negative lookbehind (PERL = TRUE); position NOT following pattern
?(if)then	If-then-condition (PERL = TRUE); use lookaheads, optional char. etc in if-clause
?(if)then|else	If-then-else-condition (PERL = TRUE)

*see, e.g. http://www.regular-expressions.info/lookaround.html
http://www.regular-expressions.info/conditional.html

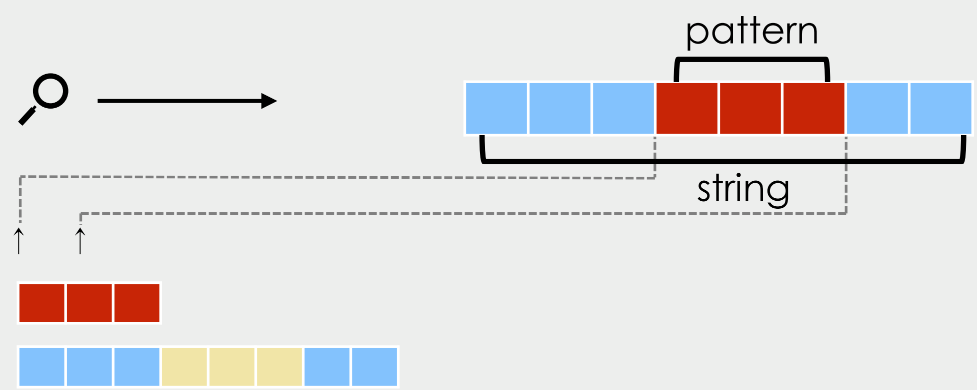
Functions for Pattern Matching

Detect pattern

Locate pattern

Extract pattern

Replace pattern




```
> string <- c("Hiphopopotamus", "Rhymenoceros", "time for bottomless lyrics")
> pattern <- "t.m"
```

Detect Patterns

grep(pattern, string)
`[1] 1 3`

grep(pattern, string, value = TRUE)
`[1] "Hiphopopotamus"`
`[2] "time for bottomless lyrics"`

grepl(pattern, string)
`[1]  TRUE FALSE  TRUE`

stringr::str_detect(string, pattern)
`[1]  TRUE FALSE  TRUE`

Locate Patterns

regexpr(pattern, string)
find starting position and length of first match

gregexpr(pattern, string)
find starting position and length of all matches

stringr::**str_locate(string, pattern)**
find starting and end position of first match

stringr::**str_locate_all(string, pattern)**
find starting and end position of all matches

Split a String using a Pattern

strsplit(string, pattern) or stringr::**str_split(string, pattern)**

Extract Patterns

regmatches(string, regexpr(pattern, string))
extract first match `[1] "tam" "tim"`

regmatches(string, gregexpr(pattern, string))
extract all matches, outputs a list
`[[1]] "tam" [[2]] character(0) [[3]] "tim" "tom"`

stringr::**str_extract(string, pattern)**
extract first match `[1] "tam" NA  "tim"`

stringr::**str_extract_all(string, pattern)**
extract all matches, outputs a list

stringr::**str_extract_all(string, pattern, simplify = TRUE)**
extract all matches, outputs a matrix

stringr::**str_match(string, pattern)**
extract first match + individual character groups

stringr::**str_match_all(string, pattern)**
extract all matches + individual character groups

Replace Patterns

sub(pattern, replacement, string)
replace first match

gsub(pattern, replacement, string)
replace all matches

stringr::**str_replace(string, pattern, replacement)**
replace first match

stringr::**str_replace_all(string, pattern, replacement)**
replace all matches

Character Classes and Groups

.	Any character except `\n`
|	Or, e.g. `(a|b)`
[...]	List permitted characters, e.g. `[abc]`
[a-z]	Specify character ranges
[^...]	List excluded characters
(...)	Grouping, enables back referencing using `\\N` where `N` is an integer

Anchors

^	Start of the string
$	End of the string
\\b	Empty string at either edge of a word
\\B	NOT the edge of a word
\\<	Beginning of a word
\\>	End of a word

Quantifiers

*	Matches at least 0 times
+	Matches at least 1 time
?	Matches at most 1 time; optional string
{n}	Matches exactly n times
{n,}	Matches at least n times
{n,m}	Matches between n and m times

General Modes

By default R uses *extended* regular expressions. You can switch to *PCRE regular expressions* using `PERL = TRUE` for base or by wrapping patterns with `perl()` for stringr.

All functions can be used with literal searches using `fixed = TRUE` for base or by wrapping patterns with `fixed()` for stringr.

All base functions can be made case insensitive by specifying `ignore.cases = TRUE`.

Escaping Characters

Metacharacters (`. * +` etc.) can be used as literal characters by escaping them. Characters can be escaped using `\\` or by enclosing them in `\\Q...\\E`.

Case Conversions

Regular expressions can be made case insensitive using `(?i)`. In backreferences, the strings can be converted to lower or upper case using `\\L` or `\\U` (e.g. `\\L\\1`). This requires `PERL = TRUE`.

Greedy Matching

By default the asterisk `*` is greedy, i.e. it always matches the longest possible string. It can be used in lazy mode by adding `?`, i.e. `*?`.

Greedy mode can be turned off using `(?U)`. This switches the syntax, so that `(?U)a*` is lazy and `(?U)a*?` is greedy.

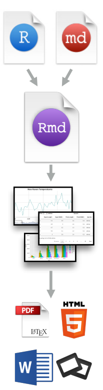
Note

Regular expressions can conveniently be created using e.g. the packages rex or rebus.

Updated: 10/18

R Markdown : : CHEAT SHEET

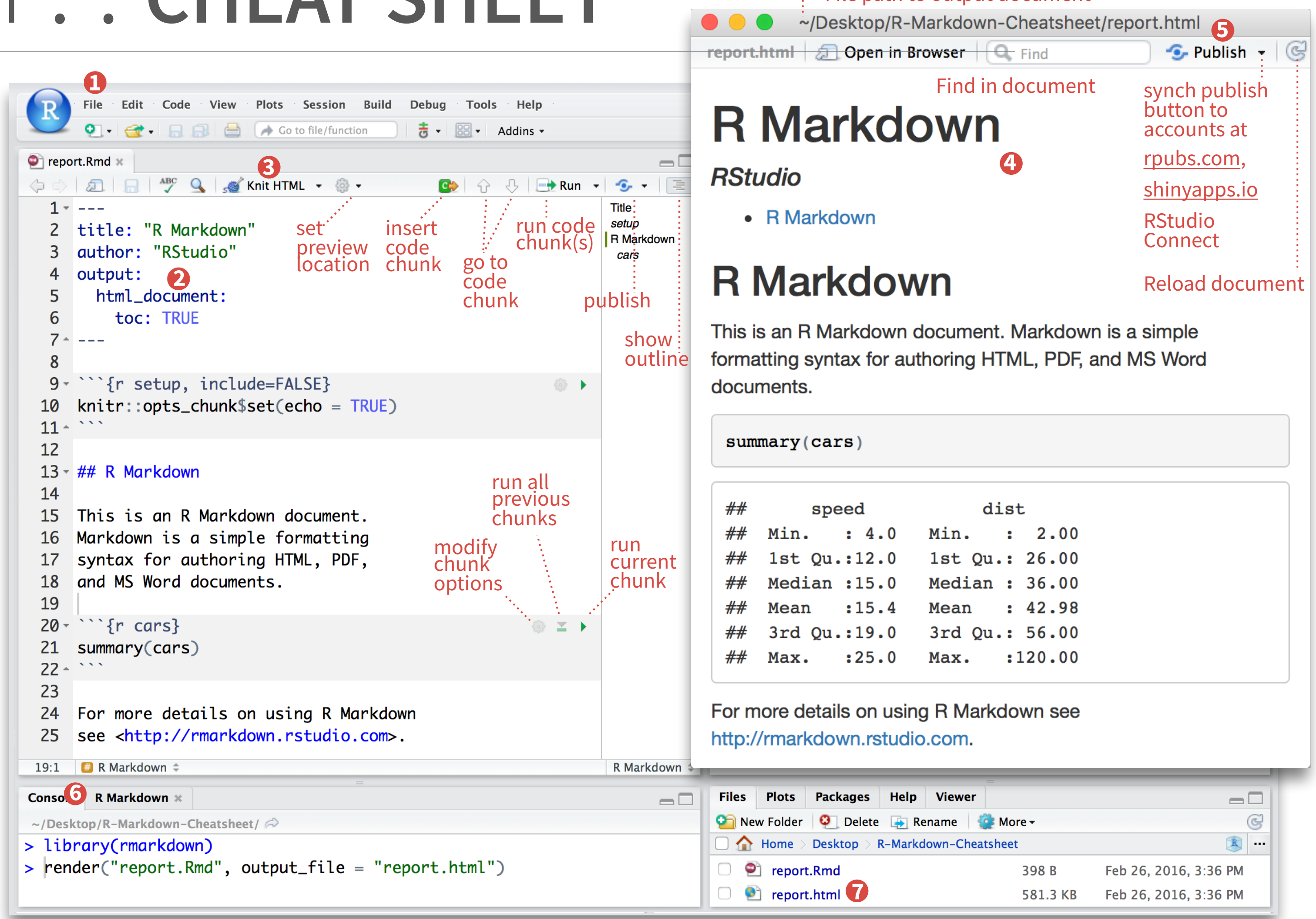
What is R Markdown?



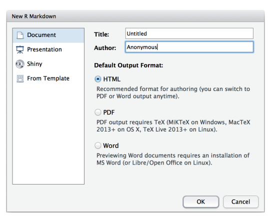
.Rmd files · An R Markdown (.Rmd) file is a record of your research. It contains the code that a scientist needs to reproduce your work along with the narration that a reader needs to understand your work.

Reproducible Research · At the click of a button, or the type of a command, you can rerun the code in an R Markdown file to reproduce your work and export the results as a finished report.

Dynamic Documents · You can choose to export the finished report in a variety of formats, including html, pdf, MS Word, or RTF documents; html or pdf based slides, Notebooks, and more.



Workflow



1. **Open a new .Rmd file** at File ▶ New File ▶ R Markdown. Use the wizard that opens to pre-populate the file with a template
2. **Write document** by editing template
3. **Knit document to create report**; use knit button or **render()** to knit
4. **Preview Output** in IDE window
5. **Publish** (optional) to web server
6. **Examine build log** in R Markdown console
7. **Use output file** that is saved along side .Rmd

.rmd Structure

YAML Header
Optional section of render (e.g. pandoc) options written as key:value pairs (YAML).

At start of file

Between lines of - - -

Text
Narration formatted with markdown, mixed with:

Code Chunks
Chunks of embedded code. Each chunk:

Begins with ```{r}

ends with ```

R Markdown will run the code and append the results to the doc.

It will use the location of the .Rmd file as the **working directory**

Parameters

Parameterize your documents to reuse with different inputs (e.g., data, values, etc.)

1. **Add parameters** · Create and set parameters in the header as sub-values of params

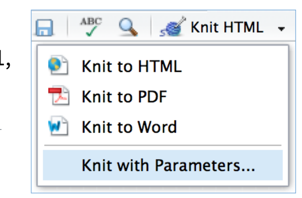
```
---
params:
  n: 100
  d: !r Sys.Date()
---
```

2. **Call parameters** · Call parameter values in code as params$<name>

```
Today's date
is `r params$d`
```

3. **Set parameters** · Set values with Knit with parameters or the params argument of render():

render("doc.Rmd", params = list(n = 1, d = as.Date("2015-01-01"))



render

Use rmarkdown::**render()** to render/knit at cmd line. Important args:

input - file to render

output_format

output_options - List of render options (as in YAML)

output_file

output_dir

params - list of params to use

envir - environment to evaluate code chunks in

encoding - of input file

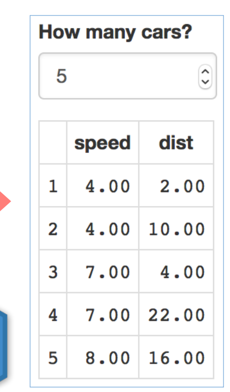
Interactive Documents

Turn your report into an interactive Shiny document in 4 steps

1. Add runtime: shiny to the YAML header.
2. Call Shiny input functions to embed input objects.
3. Call Shiny render functions to embed reactive output.
4. Render with rmarkdown::run or click Run Document in RStudio IDE

~~~~
---
output: html_document
runtime: shiny
---

```{r, echo = FALSE}
numericInput("n",
  "How many cars?", 5)

renderTable({
  head(cars, input$n)
})
```
~~~~



Embed a complete app into your document with shiny::**shinyAppDir()**

NOTE: *Your report will rendered as a Shiny app, which means you must choose an html output format, like* ***html_document****, and serve it with an active R Session.*

Embed code with knitr syntax

INLINE CODE

Insert with `r <code>`. Results appear as text without code.

Built with `r getRversion()` ➔ Built with 3.2.3

CODE CHUNKS

One or more lines surrounded with ```{r} and ```. Place chunk options within curly braces, after **r**. Insert with

~~~~
```{r echo=TRUE}
getRversion()
```
~~~~

➔

```
getRversion()
## [1] '3.2.3'
```

GLOBAL OPTIONS

Set with knitr::**opts_chunk$set()**, e.g.

~~~~
```{r include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```
~~~~

IMPORTANT CHUNK OPTIONS

cache - cache results for future knits (default = FALSE)

cache.path - directory to save cached results in (default = "cache/")

child - file(s) to knit and then include (default = NULL)

collapse - collapse all output into single block (default = FALSE)

comment - prefix for each line of results (default = '##')

dependson - chunk dependencies for caching (default = NULL)

echo - Display code in output document (default = TRUE)

engine - code language used in chunk (default = 'R')

error - Display error messages in doc (TRUE) or stop render when errors occur (FALSE) (default = FALSE)

eval - Run code in chunk (default = TRUE)

fig.align - 'left', 'right', or 'center' (default = 'default')

fig.cap - figure caption as character string (default = NULL)

fig.height, fig.width - Dimensions of plots in inches

highlight - highlight source code (default = TRUE)

include - Include chunk in doc after running (default = TRUE)

message - display code messages in document (default = TRUE)

results (default = 'markup')
'asis' - passthrough results
'hide' - do not display results
'hold' - put all results below all code

tidy - tidy code for display (default = FALSE)

warning - display code warnings in document (default = TRUE)

Options not listed above: R.options, aniopts, autodep, background, cache.comments, cache.lazy, cache.rebuild, cache.vars, dev, dev.args, dpi, engine.opts, engine.path, fig.asp, fig.env, fig.ext, fig.keep, fig.lp, fig.path, fig.pos, fig.process, fig.retina, fig.scap, fig.show, fig.showtext, fig.subcap, interval, out.extra, out.height, out.width, prompt, purl, ref.label, render, size, split, tidy.opts

Pandoc's Markdown

Write with syntax on the left to create effect on right (after render)

```
Plain text
End a line with two spaces
to start a new paragraph.
*italics* and **bold**
`verbatim code`
sub/superscript^2^~2~
~~strikethrough~~
escaped: \* \_ \\
endash: --, emdash: ---
equation: $A = \pi*r^{2}$
equation block:

$$E = mc^{2}$$

> block quote

# Header1 {#anchor}

## Header 2 {#css_id}

### Header 3 {.css_class}

#### Header 4

##### Header 5

###### Header 6

<!--Text comment-->

\textbf{Tex ignored in HTML}
<em>HTML ignored in pdfs</em>

<http://www.rstudio.com>
[link](www.rstudio.com)
Jump to [Header 1](#anchor)
image:

![Caption](smallorb.png)

* unordered list
    + sub-item 1
    + sub-item 2
        - sub-sub-item 1

* item 2

    Continued (indent 4 spaces)

1. ordered list
2. item 2
    i) sub-item 1
         A.  sub-sub-item 1

(@)  A list whose numbering

continues after

(@)  an interruption

Term 1

:   Definition 1

| Right | Left | Default | Center |
|------:|:-----|---------|:------:|
|   12  |  12  |    12   |    12  |
|  123  |  123 |   123   |   123  |
|    1  |    1 |     1   |     1  |

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

***

A footnote [^1]

[^1]: Here is the footnote.
```

Plain text
End a line with two spaces
to start a new paragraph.
italics and **bold**
`verbatim code`
sub/superscript^2$_2$
~~strikethrough~~
escaped: * _ \
endash: –, emdash: —
equation: $A = \pi * r^2$
equation block:

$$E = mc^2$$

> block quote

Header1

Header 2

Header 3

Header 4

Header 5

Header 6

HTML ignored in pdfs

http://www.rstudio.com
link
Jump to Header 1
image:

Caption

- unordered list
  - sub-item 1
  - sub-item 2
    - sub-sub-item 1
- item 2

  Continued (indent 4 spaces)

1. ordered list
2. item 2
   i. sub-item 1
      A. sub-sub-item 1

1. A list whose numbering

continues after

2. an interruption

Term 1

Definition 1

Right	Left	Default	Center
12	12	12	12
123	123	123	123
1	1	1	1

- slide bullet 1
- slide bullet 2

(>- to have bullets appear on click)

horizontal rule/slide break:

A footnote [1]

1. Here is the footnote. ↩

Set render options with YAML

When you render, R Markdown
1. runs the R code, embeds results and text into .md file with knitr
2. then converts the .md file into the finished format with pandoc

Set a document's default output format in the YAML header:

```
---
output: html_document
---
# Body
```

output value	creates
html_document	html
pdf_document	pdf (requires Tex)
word_document	Microsoft Word (.docx)
odt_document	OpenDocument Text
rtf_document	Rich Text Format
md_document	Markdown
github_document	Github compatible markdown
ioslides_presentation	ioslides HTML slides
slidy_presentation	slidy HTML slides
beamer_presentation	Beamer pdf slides (requires Tex)

Customize output with sub-options (listed to the right):

Indent 2 spaces — Indent 4 spaces

```
---
output: html_document:
  code_folding: hide
  toc_float: TRUE
---
# Body
```

html tabsets

Use tablet css class to place sub-headers into tabs

```
# Tabset {.tabset .tabset-fade .tabset-pills}
## Tab 1
text 1
## Tab 2
text 2
### End tabset
```

Tabset

Tab 1 Tab 2

text 1
End tabset

sub-option	description	html	pdf	word	odt	rtf	md	gituhb	ioslides	slidy	beamer
citation_package	The LaTeX package to process citations, natbib, biblatex or none		X				X				X
code_folding	Let readers to toggle the display of R code, "none", "hide", or "show"	X									
colortheme	Beamer color theme to use										X
css	CSS file to use to style document	X							X	X	
dev	Graphics device to use for figure output (e.g. "png")	X	X				X	X	X	X	X
duration	Add a countdown timer (in minutes) to footer of slides									X	
fig_caption	Should figures be rendered with captions?	X	X	X	X				X	X	X
fig_height, fig_width	Default figure height and width (in inches) for document	X	X	X	X	X	X	X	X	X	X
highlight	Syntax highlighting: "tango", "pygments", "kate","zenburn", "textmate"	X	X	X						X	X
includes	File of content to place in document (in_header, before_body, after_body)	X	X		X		X	X	X	X	X
incremental	Should bullets appear one at a time (on presenter mouse clicks)?								X	X	X
keep_md	Save a copy of .md file that contains knitr output	X		X	X	X			X	X	
keep_tex	Save a copy of .tex file that contains knitr output		X								X
latex_engine	Engine to render latex, "pdflatex", "xelatex", or "lualatex"		X								X
lib_dir	Directory of dependency files to use (Bootstrap, MathJax, etc.)	X							X	X	
mathjax	Set to local or a URL to use a local/URL version of MathJax to render equations	X							X	X	
md_extensions	Markdown extensions to add to default definition or R Markdown	X	X	X	X	X	X	X	X	X	X
number_sections	Add section numbering to headers	X	X								
pandoc_args	Additional arguments to pass to Pandoc	X	X	X	X	X	X	X	X	X	X
preserve_yaml	Preserve YAML front matter in final document?						X				
reference_docx	docx file whose styles should be copied when producing docx output			X							
self_contained	Embed dependencies into the doc	X							X	X	
slide_level	The lowest heading level that defines individual slides										X
smaller	Use the smaller font size in the presentation?								X		
smart	Convert straight quotes to curly, dashes to em-dashes, … to ellipses, etc.	X							X	X	
template	Pandoc template to use when rendering file quarterly_report.html).	X	X		X					X	X
theme	Bootswatch or Beamer theme to use for page	X									X
toc	Add a table of contents at start of document	X	X	X		X	X	X			X
toc_depth	The lowest level of headings to add to table of contents	X	X	X		X	X	X			
toc_float	Float the table of contents to the left of the main content	X									

Create a Reusable Template

1. **Create a new package** with a inst/rmarkdown/templates directory
2. In the directory, **Place a folder** that contains:
template.yaml (see below)
skeleton.Rmd (contents of the template)
any supporting files
3. **Install the package**
4. **Access template** in wizard at File ▶ New File ▶ R Markdown

template.yaml

```
---
name: My Template
—
```

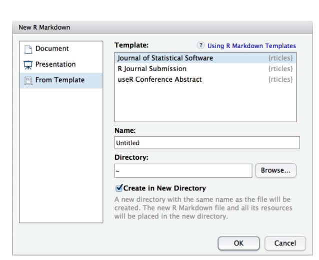


Table Suggestions

Several functions format R data into tables

Table with kable

eruptions	waiting
3.600	79
1.800	54
3.333	74
2.283	62

	eruptions	waiting
1	3.60	79.00
2	1.80	54.00
3	3.33	74.00
4	2.28	62.00

Table with xtable

Table with stargazer

	eruptions	waiting
1	3.600	79
2	1.800	54
3	3.333	74
4	2.283	62

```
data <- faithful[1:4, ]
```{r results = 'asis'}
knitr::kable(data, caption = "Table with kable")
```
```{r results = "asis"}
print(xtable::xtable(data, caption = "Table with xtable"),
      type = "html", html.table.attributes = "border=0"))
```
```{r results = "asis"}
stargazer::stargazer(data, type = "html", title = "Table
                     with stargazer")
```
```

Learn more in **the stargazer, xtable, and knitr** packages.

Citations and Bibliographies

Create citations with .bib, .bibtex, .copac, .enl, .json, .medline, .mods, .ris, .wos, and .xml files

1. **Set bibliography file** and CSL 1.0 Style file (optional) in the YAML header
2. **Use citation keys in text**

```
---
bibliography: refs.bib
csl: style.csl
---
```

```
Smith cited [@smith04].
Smith cited without author [-@smith04].
@smith04 cited in line.
```

3. **Render.** Bibliography will be added to end of document

Smith cited (Joe Smith 2004).
Smith cited without author (2004).
Joe Smith (2004) cited in line.

RStudio

R Markdown Reference Guide

Learn more about R Markdown at rmarkdown.rstudio.com
Learn more about Interactive Docs at shiny.rstudio.com/articles

Contents:

Syntax

```
Plain text

End a line with two spaces
to start a new paragraph.

*italics* and _italics_

**bold** and __bold__

superscript^2^

~~strikethrough~~

[link](www.rstudio.com)

# Header 1

## Header 2

### Header 3

#### Header 4

##### Header 5

###### Header 6

endash: --

emdash: ---

ellipsis: ...

inline equation: $A = \pi*r^{2}$

image: ![](path/to/smallorb.png)

horizontal rule (or slide break):

***

> block quote

* unordered list
* item 2
    + sub-item 1
    + sub-item 2

1. ordered list
2. item 2
    + sub-item 1
    + sub-item 2

Table Header  | Second Header
------------- | -------------
Table Cell    | Cell 2
Cell 3        | Cell 4
```

Becomes

Plain text

End a line with two spaces to start a new paragraph.

italics and *italics*

bold and **bold**

superscript^2

~~strikethrough~~

link

Header 1

Header 2

Header 3

Header 4

Header 5

Header 6

endash: –

emdash: —

ellipsis: …

inline equation: $A = \pi * r^2$

image:

horizontal rule (or slide break):

> block quote

- unordered list
- item 2
    - sub-item 1
    - sub-item 2

1. ordered list
2. item 2
    - sub-item 1
    - sub-item 2

Table Header	Second Header
Table Cell	Cell 2
Cell 3	Cell 4

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Contents:

Syntax	Becomes
Make a code chunk with three back ticks followed by an r in braces. End the chunk with three back ticks: ` ```{r} ` `paste("Hello", "World!")` ` ``` `	Make a code chunk with three back ticks followed by an r in braces. End the chunk with three back ticks: `paste("Hello", "World!")` `## [1] "Hello World!"`
Place code inline with a single back ticks. The first back tick must be followed by an R, like this `` `r paste("Hello", "World!")` ``.	Place code inline with a single back ticks. The first back tick must be followed by an R, like this Hello World!.
Add chunk options within braces. For example, `` `echo=FALSE` `` will prevent source code from being displayed: ` ```{r eval=TRUE, echo=FALSE} ` `paste("Hello", "World!")` ` ``` `	Add chunk options within braces. For example, `echo=FALSE` will prevent source code from being displayed: `## [1] "Hello World!"`

Learn more about chunk options at http://yihui.name/knitr/options

Chunk options

option	default value	description
Code evaluation		
child	NULL	A character vector of filenames. Knitr will knit the files and place them into the main document.
code	NULL	Set to R code. Knitr will replace the code in the chunk with the code in the code option.
engine	'R'	Knitr will evaluate the chunk in the named language, e.g. **engine = 'python'.** Run **names(knitr::knit_engines$get())** to see supported languages.
eval	TRUE	If **FALSE**, knitr will not run the code in the code chunk.
include	TRUE	If **FALSE**, knitr will run the chunk but not include the chunk in the final document.
purl	TRUE	If **FALSE**, knitr will not include the chunk when running **purl()** to extract the source code.
Results		
collapse	FALSE	If **TRUE**, knitr will collapse all the source and output blocks created by the chunk into a single block.
echo	TRUE	If **FALSE**, knitr will not display the code in the code chunk above it's results in the final document.
results	'markup'	If **'hide'**, knitr will not display the code's results in the final document. If **'hold'**, knitr will delay displaying all output pieces until the end of the chunk. If **'asis'**, knitr will pass through results without reformatting them (useful if results return raw HTML, etc.)
error	TRUE	If **FALSE**, knitr will not display any error messages generated by the code.
message	TRUE	If **FALSE**, knitr will not display any messages generated by the code.
warning	TRUE	If **FALSE**, knitr will not display any warning messages generated by the code.
Code Decoration		
comment	'##'	A character string. Knitr will append the string to the start of each line of results in the final document.
highlight	TRUE	If **TRUE**, knitr will highlight the source code in the final output.
prompt	FALSE	If **TRUE**, knitr will add > to the start of each line of code displayed in the final document.
strip.white	TRUE	If **TRUE**, knitr will remove white spaces that appear at the beginning or end of a code chunk.
tidy	FALSE	If **TRUE**, knitr will tidy code chunks for display with the **tidy_source()** function in the **formatR** package.

Contents:

Chunk options (Continued)

option	default value	description
Chunks		
opts.label	NULL	The label of options set in **knitr:: opts_template()** to use with the chunk.
R.options	NULL	Local R options to use with the chunk. Options are set with **options()** at start of chunk. Defaults are restored at end.
ref.label	NULL	A character vector of labels of the chunks from which the code of the current chunk is inherited.
Cache		
autodep	FALSE	If **TRUE**, knitr will attempt to figure out dependencies between chunks automatically by analyzing object names.
cache	FALSE	If **TRUE**, knitr will cache the results to reuse in future knits. Knitr will reuse the results until the code chunk is altered.
cache.comments	NULL	If **FALSE**, knitr will not rerun the chunk if only a code comment has changed.
cache.lazy	TRUE	If **TRUE**, knitr will use **lazyload()** to load objects in chunk. If **FALSE**, knitr will use **load()** to load objects in chunk.
cache.path	'cache/'	A file path to the directory to store cached results in. Path should begin in the directory that the .Rmd file is saved in.
cache.vars	NULL	A character vector of object names to cache if you do not wish to cache each object in the chunk.
dependson	NULL	A character vector of chunk labels to specify which other chunks a chunk depends on. Knitr will update a cached chunk if its dependencies change.
Animation		
anipots	'controls,loop'	Extra options for animations (see the **animate** package).
interval	1	The number of seconds to pause between animation frames.
Plots		
dev	'png'	The R function name that will be used as a graphical device to record plots, e.g. **dev='CairoPDF'**.
dev.args	NULL	Arguments to be passed to the device, e.g. **dev.args=list(bg='yellow', pointsize=10)**.
dpi	72	A number for knitr to use as the dots per inch (dpi) in graphics (when applicable).
external	TRUE	If **TRUE**, knitr will externalize tikz graphics to save LaTex compilation time (only for the **tikzDevice::tikz()** device).
fig.align	'default'	How to align graphics in the final document. One of 'left', 'right', or 'center'.
fig.cap	NULL	A character string to be used as a figure caption in LaTex.
fig.env	'figure'	The Latex environment for figures.
fig.ext	NULL	The file extension for figure output, e.g. **fig.ext='png'**.
fig.height, fig.width	7	The width and height to use in R for plots created by the chunk (in inches).
fig.keep	'high'	If **'high'**, knitr will merge low-level changes into high level plots. If **'all'**, knitr will keep all plots (low-level changes may produce new plots). If **'first'**, knitr will keep the first plot only. If **'last'**, knitr will keep the last plot only. If **'none'**, knitr will discard all plots.
fig.lp	'fig:'	A prefix to be used for figure labels in latex.
fig.path	'figure/'	A file path to the directory where knitr should store the graphics files created by the chunk.
fig.pos	''	A character string to be used as the figure position arrangement in LaTex.
fig.process	NULL	A function to post-process a figure file. Should take a filename and return a filename of a new figure source.
fig.retina	1	Dpi multiplier for displaying HTML output on retina screens.
fig.scap	NULL	A character string to be used as a short figure caption.
fig.subcap	NULL	A character string to be used as captions in sub-figures in LaTex.
fig.show	'asis'	If **'hide'**, knitr will generate the plots created in the chunk, but not include them in the final document. If **'hold'**, knitr will delay displaying the plots created by the chunk until the end of the chunk. If **'animate'**, knitr will combine all of the plots created by the chunk into an animation.
fig.showtext	NULL	If **TRUE**, knitr will call **showtext::showtext.begin**() before drawing plots.
out.extra	NULL	A character string of extra options for figures to be passed to LaTex or HTML.
out.height, out.width	NULL	The width and height to scale plots to in the final output. Can be in units recognized by output, e.g. **8\\linewidth, 50px**
resize.height, resize.width	NULL	The width and height to resize tike graphics in LaTex, passed to **\resizebox{}{}.**
sanitize	FALSE	If **TRUE**, knitr will sanitize tike graphics for LaTex.

R Markdown Reference Guide

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Learn more about Interactive Docs at shiny.rstudio.com/articles

Contents:

Templates

html_document
pdf_document
word_document
md_document
ioslides_presentation
slidy_presentation
beamer_presentation

Basic YAML

```
---
title: "A Web Doc"
author: "John Doe"
date: "May 1, 2015"
output: md_document
---
```

Template options

```
---
title: "Chapters"
output:
  html_document:
    toc: true
    toc_depth: 2
---
```

Latex options

```
---
title: "My PDF"
output: pdf_document
fontsize: 11pt
geometry: margin=1in
---
```

Interactive Docs

```
---
title: "Slides"
output:
  slidy_presentation:
    incremental: true
runtime: shiny
---
```

Syntax for slide formats (ioslides, slidy, beamer)

```
# Dividing slides 1

Pandoc will start a new slide at each first level header

## Header 2

… as well as each second level header

***

You can start a new slide with a horizontal rule`***` if you do not want
a header.

## Bullets

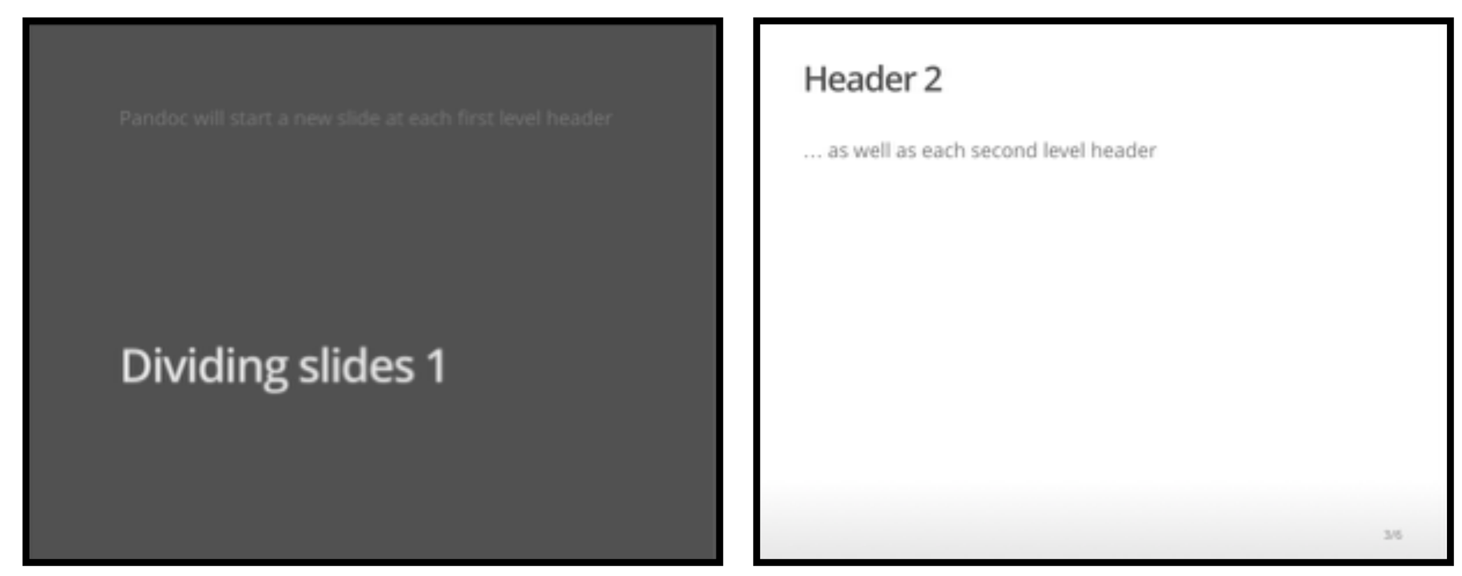
Render bullets with

- a dash
- another dash

## Incremental bullets

>- Use this format
>- to have bullets appear
>- one at a time (incrementally)
```

becomes



Slide display modes

*Press a key below during presentation to enter display mode. Press **esc** to exit display mode.*

ioslides

f - enable fullscreen mode
w - toggle widescreen mode
o - enable overview mode
h - enable code highlight mode
p - show presenter notes

slidy

C - show table of contents
F - toggle display of the footer
A - toggle display of current vs all slides
S - make fonts smaller
B - make fonts bigger

Top level options to customize LaTex (pdf) output

option	description
lang	Document language code
fontsize	Font size (e.g. 10pt, 11pt, 12 pt)
documentclass	Latex document class (e.g. article)
classoption	Option for document class (e.g. oneside); may be repeated
geometry	Options for geometry class (e.g. margin=1in); may be repeated
mainfont, sansfont, monofont, mathfont	Document fonts (works only with xelatex and lualatex, see the latex_engine option)
linkcolor, urlcolor, citecolor	Color for internal, external, and citation links (red, green, magenta, cyan, blue, black)

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Contents:

option	html	pdf	word	md	ioslides	slidy	beamer	description
colortheme							X	Beamer color theme to use (e.g., `colortheme: "dolphin"`).
css	X				X	X		Filepath to CSS style to use to style document (e.g., `css: styles.css`).
duration						X		Add a countdown timer (in minutes) to footer of slides (e.g., `duration: 45`).
fig_caption	X	X	X		X	X	X	Should figures be rendered with captions?
fig_crop		X					X	Should pdfcrop utility be automatically applied to figures (when available)?
fig_height	X	X	X	X	X	X	X	Default figure height (in inches) for document.
fig_retina	X			X	X	X		Scaling to perform for retina displays (e.g., `fig_retina: 2`).
fig_width	X	X	X	X	X	X	X	Default figure width (in inches) for document.
font_adjustmen						X		Increase or decrease font size for entire presentation (e.g., `font_adjustment: -1`).
fonttheme							X	Beamer font theme to use (e.g., `fonttheme: "structurebold"`).
footer						X		Text to add to footer of each slide (e.g., `footer: "Copyright (c) 2014 RStudio"`).
highlight	X	X				X	X	Syntax highlighting style (e.g. `"tango"`, `"pygments"`, `"kate"`, `"zenburn"`, and
includes	X	X		X	X	X	X	See below
-in_header	X	X			X	X	X	File of content to place in document header (e.g., `in_header: header.html`).
-before_body	X	X			X	X	X	File of content to place before document body (e.g., `before_body:`
-after_body	X	X			X	X	X	File of content to place after document body (e.g., `after_body: doc_suffix.html`).
incremental					X	X	X	Should bullets appear one at a time (on presenter mouse clicks)?
keep_md	X				X	X		Save a copy of .md file that contains knitr output (in addition to the .Rmd and HTML files)?
keep_tex		X					X	Save a copy of .tex file that contains knitr output (in addition to the .Rmd and PDF files)?
latex_engine		X						Engine to render latex. Should be one of `"pdflatex"`, `"xelatex"`, and `"lualatex"`.
lib_dir	X				X	X		Directory of dependency files to use (Bootstrap, MathJax, etc.) (e.g., `lib_dir: libs`).
logo					X			File path to a logo (at least 128 x 128) to add to presentation (e.g., `logo: logo.png`).
mathjax	X				X	X		Set to `local` or a URL to use a local/URL version of MathJax to render equations
number_section	X	X						Add section numbering to headers (e.g., `number_sections: true`).
pandoc_args	X	X	X	X	X	X	X	Arguments to pass to Pandoc (e.g., `pandoc_args: ["--title-prefix", "Foo"]`).
preserve_yaml				X				Preserve YAML front matter in final document?
reference_docx			X					A .docx file whose styles should be copied to use (e.g., `reference_docx:`
self_contained	X				X	X		Embed dependencies into the doc? Set to `false` to keep dependencies in external files.
slide_level							X	The lowest heading level that defines individual slides (e.g., `slide_level: 2`).
smaller					X			Use the smaller font size in the presentation?
smart	X				X	X		Convert straight quotes to curly, dashes to em-dashes, … to ellipses, and so on?
template	X	X				X	X	Pandoc template to use when rendering file (e.g., `template:`
theme	X						X	Bootswatch or Beamer theme to use for page. Valid bootswatch themes include `"cerulean"`, `"journal"`, `"flatly"`, `"readable"`, `"spacelab"`, `"united"`, and `"cosmo"`.
toc	X	X		X			X	Add a table of contents at start of document? (e.g., `toc: true`).
toc_depth	X	X		X				The lowest level of headings to add to table of contents (e.g., `toc_depth: 2`).
transition					X			Speed of slide transitions should be `"slower"`, `"faster"` or a number in seconds.
variant				X				The flavor of markdown to use; one of `"markdown"`, `"markdown_strict"`, `"markdown_github"`, `"markdown_mmd"`, and `"markdown_phpextra"`
widescreen					X			Display presentation in widescreen format?

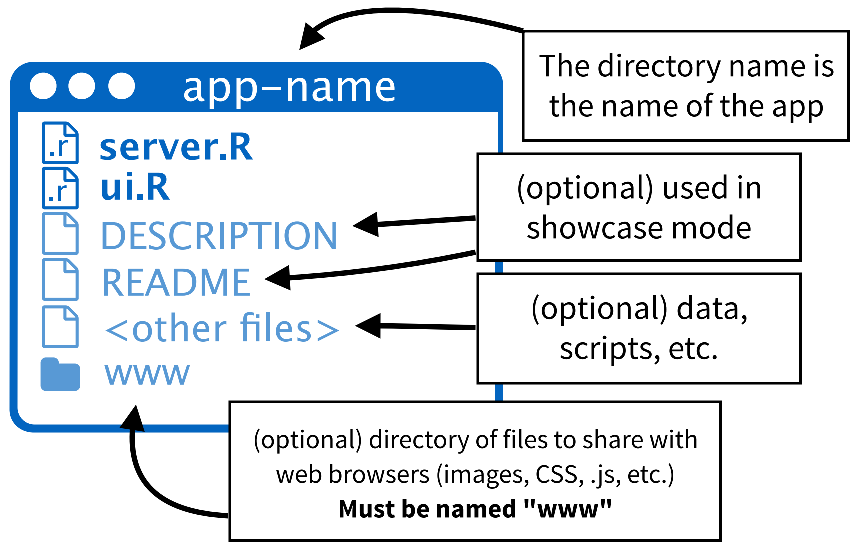
Shiny Cheat Sheet

learn more at shiny.rstudio.com

Shiny 0.10.0 Updated: 6/14

RStudio

1. Structure
Each app is a directory that contains a **server.R** file and usually a **ui.R** file (plus optional extra files)



render* functions

function	expects	creates
renderDataTable	any table-like object	DataTables.js table
renderImage	list of image attributes	HTML image
renderPlot	plot	plot
renderPrint	any printed output	text
renderTable	any table-like object	plain table
renderText	character string	text
renderUI	Shiny tag object or	UI element (HTML)

input values are reactive.
They must be surrounded with one of:

render* - creates a shiny UI component
reactive - creates a reactive expression
observe - creates a reactive observer
isolate - creates a non-reactive copy of a reactive object

2. server.R
A set of instructions that build the R components of your app. To write server.R:

- **A** Provide server.R with the minimum necessary code, **shinyServer(function(input, output) {})**
- **B** Define the R components for your app between the braces that follow **function(input, output)**
- **C** Save each R component in your UI as **output$<component name>**
- **D** Create each output component with a render* function.
- **E** Give each render* function the R code the server needs to build the component. The server will note any reactive values that appear in the code and will rebuild the component whenever these values change.
- **F** Refer to widget values with **input$<widget name>**

server.R

```
# load libraries, scripts, data

A shinyServer(function(input, output) { B

  # make user specific variables

    output$text <- renderText({
      input$title
    })

  C output$plot <- renderPlot({ D
      x <- mtcars[ , input$x] F
  E   y <- mtcars[ , input$y]
      plot(x, y, pch = 16)
    })

})
```

3. Execution
Place code where it will be run the minimum necessary number of times

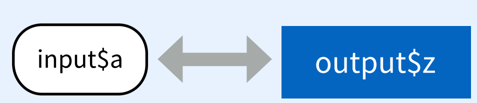
Run once - code placed *outside of shinyServer* will be run once, when you first launch your app. Use this code to set up the tools that your server will only need one copy of.

Run once per user - code placed *inside shinyServer* will be run once each time a user visits your app (or refreshes his or her browser). Use this code to set up the tools that your server will need a unique copy of for each user.

Run often - code placed within a render*, reactive, or observe function will be run many times. Place here only the code that the server needs to rebuild a UI component after a widget changes.

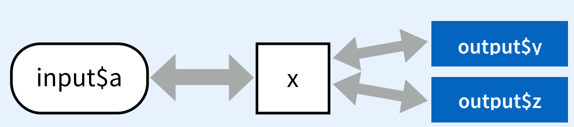
4. Reactivity
When an input changes, the server will rebuild each output that depends on it (even if the dependence is indirect). You can control this behavior by shaping the chain of dependence.

render* - An output will automatically update whenever an input in its render* function changes.




```
output$z <- renderText({
  input$a
})
```

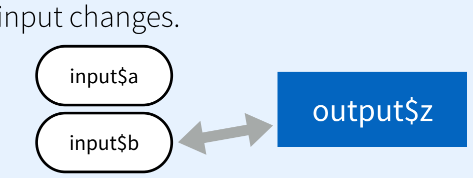
Reactive expression - use reactive to create objects that will be used in multiple outputs.




```
x <- reactive({
  input$a
})

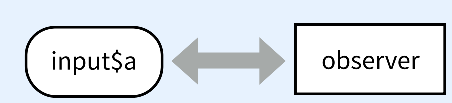
output$y <- renderText({
  x()
})
output$z <- renderText({
  x()
})
```

isolate - use use isolate to use an input without depending on it. Shiny will not rebuild the output when the isolated input changes.




```
output$z <- renderText({
  paste(
    isolate(input$a),
    input$b
  )
)
```

observe - use observe to create code that runs when an input changes, but does not create an output object.




```
observe({
  input$a
  # code to run
})
```

ui.R

```
Ⓐ shinyUI(fluidPage(

    titlePanel("mtcars data"),
  Ⓑ sidebarLayout(
      sidebarPanel(

    Ⓒ   textInput("title", "Plot title:",
          value = "x v y"),

        selectInput("x", "Choose an x var:",
          choices = names(mtcars),
          selected = "disp"),

        selectInput("y", "Choose a y var:",
          choices = names(mtcars),
          selected = "mpg")
      ),

      mainPanel(
        h3(textOutput("text")),
        plotOutput("plot")
      )
    )
))
```

5. ui.R A description of your app's User Interface (UI), the web page that displays your app.

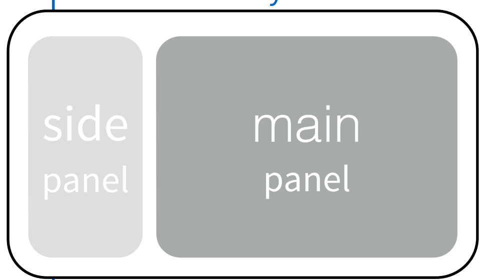
To write ui.R:

A Include the minimum necessary code for ui.R, **shinyUI(fluidPage())**

* note: use `navbarPage` instead of `fluidPage` if you'd like your app to have multiple pages connected by a navbar

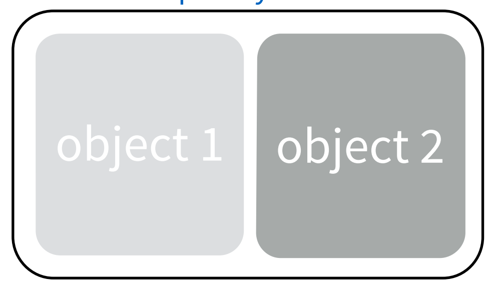
B Build a layout for your UI. **sidebarLayout** provides a default layout when used with **sidebarPanel** and **mainPanel.** **splitLayout**, **flowLayout**, and **inputLayout** divide the page into equally spaced regions. **fluidRow** and **column** work together to create a grid-based layout, which you can use to layout a page or a panel.

sidebarLayout



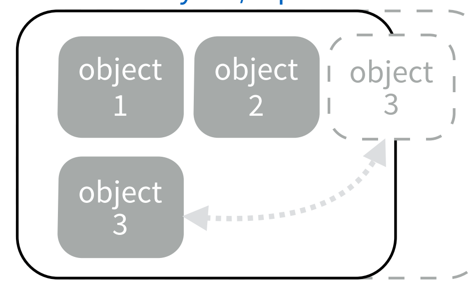

```
shinyUI(fluidPage(
  sidebarLayout(
    sidebarPanel(…),
    mainPanel(…)
  )
))
```

splitLayout



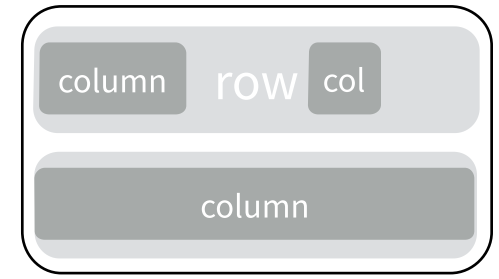

```
shinyUI(fluidPage(
  splitLayout(
    numericInput(…),
    selectInput(…)
  )
))
```

flowLayout/inputPanel




```
shinyUI(fluidPage(
  flowLayout(
    numericInput(…),
    selectInput(…),
    sliderInput(…)
  )
))
```

fluidRow




```
shinyUI(fluidPage(
  fluidRow(
    column(width = 4, …),
    column(width = 2,
      offset = 3, …),
  ),
  fluidRow(
    column(width = 12, …)
  )
))
```

C In each panel or column, place…

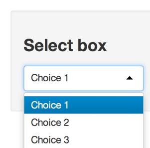
R components - These are the output objects that you defined in **server.R**. To place a component:

1. Select the ***Output** function that builds the type of object you want to place in the UI.
2. Pass the ***Output** function a character string that corresponds to the name you assigned the object in **server.R**, e.g.

output$plot <- renderPlot({ … }) ⟷ plotOutput("plot")

*Output functions

dataTableOutput	tableOutput
htmlOutput	textOutput
imageOutput	uiOutput
plotOutput	verbatimTextOutput



Widgets - The first argument of each widget function is the **<name>** for the widget. You can access a widget's current value in **server.R** with **input$<name>**

widget	function	common arguments
Action button	`actionButton`	inputId, label
checkbox	`checkboxInput`	inputId, label, value
checkbox group	`checkboxGroupInput`	inputId, label, choices, selected
date selector	`dateInput`	inputId, label, value, min, max, format
date range selector	`dateRangeInput`	inputId, label, start, end, min, max, format
file uploader	`fileInput`	inputId, label, multiple
Number field	`numericInput`	inputId, label, value, min, max, step
Radio buttons	`radioButtons`	inputId, label, choices, selected
select box	`selectInput`	inputId, label, choices, selected, multiple
slider	`sliderInput`	inputId, label, min, max, value, step
submit button	`submitButton`	text
text field	`textInput`	inputId, label, value

HTML elements - Add html elements with shiny functions that parallel common HTML tags.

a
tags$abbr
tags$address
tags$area
tags$article
tags$aside
tags$audio
tags$b
tags$base
tags$bdi
tags$bdo
tags$blockquote
tags$body
br
tags$button
tags$canvas
tags$caption
tags$cite
code
tags$col
tags$colgroup
tags$command
tags$data
tags$datalist
tags$dd
tags$del
tags$details
tags$dfn
div
tags$dl
tags$dt
em
tags$embed
tags$eventsource
tags$fieldset
tags$figcaption
tags$figure
tags$footer
tags$form
h1
h2
h3
h4
h5
h6
tags$head
tags$header
tags$hgroup
hr
HTML
tags$i
tags$iframe
img
includeCSS
includeMarkdo
wn
includeScript
tags$input
tags$ins
tags$kbd
tags$keygen
tags$label
tags$legend
tags$li
tags$link
tags$mark
tags$map
tags$menu
tags$meta
tags$meter
tags$nav
tags$noscript
tags$object
tags$ol
tags$optgroup
tags$option
tags$output
p
tags$param
pre
tags$progress
tags$q
tags$ruby
tags$rp
tags$rt
tags$s
tags$samp
tags$script
tags$section
tags$select
tags$small
tags$source
span
strong
tags$style
tags$sub
tags$summary
tags$sup
tags$table
tags$tbody
tags$td
tags$textarea
tags$tfoot
tags$th
tags$thead
tags$time
tags$title
tags$tr
tags$track
tags$u
tags$ul
tags$var
tags$video
tags$wbr

6. Run your app

runApp - run from local files
runGitHub - run from files hosted on www.GitHub.com
runGist - run from files saved as a gist (gist.github.com)
runURL - run from files saved at any URL

7. Share your app Launch your app as a live web page that users can visit online.

ShinyApps.io

Host your apps on RStudio's server. Free and paid options
www.shinyapps.io

Shiny Server

Build your own linux server to host apps. Free and open source.
shiny.rstudio.com/deploy

Shiny Server Pro

Build a commercial server with authentication, resource management, and more.
shiny.rstudio.com/deploy

Rcookbook

Andreas

29 OCT 2018

Cookbook for R

Manipulating Data Converting data between wide and long format

Converting data between wide and long format

Problem Solution Sample data tidyr From wide to long From long to wide reshape2 From wide to long From long to wide

Problem

You want to do convert data from a wide format to a long format.

Many functions in R expect data to be in a long format rather than a wide format. Programs like SPSS, however, often use wide-formatted data. Solution

There are two sets of methods that are explained below: gather() and spread() from the tidyr package. This is a newer interface to the reshape2 package. melt() and dcast() from the reshape2 package.

There are a number of other methods which aren't covered here, since they are not as easy to use: The reshape() function, which is confusingly not part of the reshape2 package; it is part of the base install of R. stack() and unstack()

Sample data

These data frames hold the same data, but in wide and long formats. They will each be converted to the other format below.

```
#Wide data
olddata_wide <- read.table(header=TRUE, text='
                           subject sex control cond1 cond2
                           1   M     7.9  12.3  10.7
                           2   F     6.3  10.6  11.1
                           3   F     9.5  13.1  13.8
                           4   M    11.5  13.4  12.9
                           ')
# Make sure the subject column is a factor
olddata_wide$subject <- factor(olddata_wide$subject)
```

```
#Long data
olddata_long <- read.table(header=TRUE, text='
                           subject sex condition measurement
                           1   M   control         7.9
                           1   M     cond1        12.3
                           1   M     cond2        10.7
                           2   F   control         6.3
                           2   F     cond1        10.6
                           2   F     cond2        11.1
                           3   F   control         9.5
                           3   F     cond1        13.1
                           3   F     cond2        13.8
                           4   M   control        11.5
                           4   M     cond1        13.4
```

```
                           4   M     cond2        12.9
                           ')
# Make sure the subject column is a factor
olddata_long$subject <- factor(olddata_long$subject)
```

tidyr

From wide to long

Use gather:

```
# olddata_wide
#>   subject sex control cond1 cond2
#> 1       1   M     7.9  12.3  10.7
#> 2       2   F     6.3  10.6  11.1
#> 3       3   F     9.5  13.1  13.8
#> 4       4   M    11.5  13.4  12.9

library(tidyr)

# The arguments to gather():
# - data: Data object
# - key: Name of new key column (made from names of data columns)
# - value: Name of new value column
# - ...: Names of source columns that contain values
# - factor_key: Treat the new key column as a factor (instead of character vector)
data_long <- gather(olddata_wide, condition, measurement, control:cond2, factor_key=TRUE)
data_long
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 2        2   F   control         6.3
#> 3        3   F   control         9.5
#> 4        4   M   control        11.5
#> 5        1   M     cond1        12.3
#> 6        2   F     cond1        10.6
#> 7        3   F     cond1        13.1
#> 8        4   M     cond1        13.4
#> 9        1   M     cond2        10.7
#> 10       2   F     cond2        11.1
#> 11       3   F     cond2        13.8
#> 12       4   M     cond2        12.9
```

In this example, the source columns that are gathered are specified with control:cond2. This means to use all the columns, positionally, between control and cond2. Another way of doing it is to name the columns individually, as in: gather(olddata_wide, condition, measurement, control, cond1, cond2)

If you need to use gather() programmatically, you may need to use variables containing column names. To do this, you should use the gather_() function instead, which takes strings instead of bare (unquoted) column names.

```
keycol <- "condition"
valuecol <- "measurement"
gathercols <- c("control", "cond1", "cond2")

gather_(olddata_wide, keycol, valuecol, gathercols)
```

Optional: Rename the factor levels of the variable column, and sort.

```
# Rename factor names from "cond1" and "cond2" to "first" and "second"

levels(data_long$condition)[levels(data_long$condition)=="cond1"] <- "first"
levels(data_long$condition)[levels(data_long$condition)=="cond2"] <- "second"


# Sort by subject first, then by condition
data_long <- data_long[order(data_long$subject, data_long$condition), ]
data_long
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 5        1   M     first        12.3
#> 9        1   M    second        10.7
#> 2        2   F   control         6.3
#> 6        2   F     first        10.6
#> 10       2   F    second        11.1
#> 3        3   F   control         9.5
#> 7        3   F     first        13.1
#> 11       3   F    second        13.8
#> 4        4   M   control        11.5
#> 8        4   M     first        13.4
#> 12       4   M    second        12.9
```

From long to wide

Use spread:

```
#olddata_long
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 2        1   M     cond1        12.3
#> 3        1   M     cond2        10.7
#> 4        2   F   control         6.3
#> 5        2   F     cond1        10.6
#> 6        2   F     cond2        11.1
#> 7        3   F   control         9.5
#> 8        3   F     cond1        13.1
#> 9        3   F     cond2        13.8
#> 10       4   M   control        11.5
#> 11       4   M     cond1        13.4
#> 12       4   M     cond2        12.9
```

```
library(tidyr)

# The arguments to spread():
# - data: Data object
# - key: Name of column containing the new column names
# - value: Name of column containing values
data_wide <- spread(olddata_long, condition, measurement)
data_wide
#>   subject sex cond1 cond2 control
#> 1       1   M  12.3  10.7     7.9
```

```
#> 2       2   F  10.6  11.1     6.3
#> 3       3   F  13.1  13.8     9.5
#> 4       4   M  13.4  12.9    11.5
```

Optional: A few things to make the data look nicer.

```
# Rename cond1 to first, and cond2 to second
names(data_wide)[names(data_wide)=="cond1"] <- "first"
names(data_wide)[names(data_wide)=="cond2"] <- "second"

# Reorder the columns
data_wide <- data_wide[, c(1,2,5,3,4)]
data_wide
#>   subject sex control first second
#> 1       1   M     7.9  12.3   10.7
#> 2       2   F     6.3  10.6   11.1
#> 3       3   F     9.5  13.1   13.8
#> 4       4   M    11.5  13.4   12.9
```

The order of factor levels determines the order of the columns. The level order can be changed before reshaping, or the columns can be re-ordered afterward.

reshape2

From wide to long

Use melt:

```
#olddata_wide
#>   subject sex control cond1 cond2
#> 1       1   M     7.9  12.3  10.7
#> 2       2   F     6.3  10.6  11.1
#> 3       3   F     9.5  13.1  13.8
#> 4       4   M    11.5  13.4  12.9

library(reshape2)

# Specify id.vars: the variables to keep but not split apart on
melt(olddata_wide, id.vars=c("subject", "sex"))
#>    subject sex variable value
#> 1        1   M  control   7.9
#> 2        2   F  control   6.3
#> 3        3   F  control   9.5
#> 4        4   M  control  11.5
#> 5        1   M    cond1  12.3
#> 6        2   F    cond1  10.6
#> 7        3   F    cond1  13.1
#> 8        4   M    cond1  13.4
#> 9        1   M    cond2  10.7
#> 10       2   F    cond2  11.1
#> 11       3   F    cond2  13.8
#> 12       4   M    cond2  12.9
```

There are options for melt that can make the output a little easier to work with:

```
data_long <- melt(olddata_wide,
                  # ID variables - all the variables to keep but not split apart on
```

```
                  id.vars=c("subject", "sex"),
                  # The source columns
                  measure.vars=c("control", "cond1", "cond2" ),
                  # Name of the destination column that will identify the original
                  # column that the measurement came from
                  variable.name="condition",
                  value.name="measurement")
data_long
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 2        2   F   control         6.3
#> 3        3   F   control         9.5
#> 4        4   M   control        11.5
#> 5        1   M     cond1        12.3
#> 6        2   F     cond1        10.6
#> 7        3   F     cond1        13.1
#> 8        4   M     cond1        13.4
#> 9        1   M     cond2        10.7
#> 10       2   F     cond2        11.1
#> 11       3   F     cond2        13.8
#> 12       4   M     cond2        12.9
```

If you leave out the measure.vars, melt will automatically use all the other variables as the id.vars. The reverse is true if you leave out id.vars.

If you don't specify variable.name, it will name that column "variable", and if you leave out value.name, it will name that column "measurement".

Optional: Rename the factor levels of the variable column.

```
# Rename factor names from "cond1" and "cond2" to "first" and "second"
levels(data_long$condition)[levels(data_long$condition)=="cond1"] <- "first"
levels(data_long$condition)[levels(data_long$condition)=="cond2"] <- "second"

# Sort by subject first, then by condition
data_long <- data_long[ order(data_long$subject, data_long$condition), ]
data_long
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 5        1   M     first        12.3
#> 9        1   M    second        10.7
#> 2        2   F   control         6.3
#> 6        2   F     first        10.6
#> 10       2   F    second        11.1
#> 3        3   F   control         9.5
#> 7        3   F     first        13.1
#> 11       3   F    second        13.8
#> 4        4   M   control        11.5
#> 8        4   M     first        13.4
#> 12       4   M    second        12.9
```

From long to wide

The following code uses dcast to reshape the data. This function is meant for data frames; if you are working with arrays or matrices, use acast instead.

```
#olddata_long
```

```
#>    subject sex condition measurement
#> 1        1   M   control         7.9
#> 2        1   M     cond1        12.3
#> 3        1   M     cond2        10.7
#> 4        2   F   control         6.3
#> 5        2   F     cond1        10.6
#> 6        2   F     cond2        11.1
#> 7        3   F   control         9.5
#> 8        3   F     cond1        13.1
#> 9        3   F     cond2        13.8
#> 10       4   M   control        11.5
#> 11       4   M     cond1        13.4
#> 12       4   M     cond2        12.9

# From the source:
# "subject" and "sex" are columns we want to keep the same
# "condition" is the column that contains the names of the new column to put things in
# "measurement" holds the measurements
library(reshape2)

data_wide <- dcast(olddata_long, subject + sex ~ condition, value.var="measurement")
data_wide
#>   subject sex cond1 cond2 control
#> 1       1   M  12.3  10.7     7.9
#> 2       2   F  10.6  11.1     6.3
#> 3       3   F  13.1  13.8     9.5
#> 4       4   M  13.4  12.9    11.5
```

Optional: A few things to make the data look nicer.

```
# Rename cond1 to first, and cond2 to second
names(data_wide)[names(data_wide)=="cond1"] <- "first"
names(data_wide)[names(data_wide)=="cond2"] <- "second"

# Reorder the columns
data_wide <- data_wide[, c(1,2,5,3,4)]
data_wide
#>   subject sex control first second
#> 1       1   M     7.9  12.3   10.7
#> 2       2   F     6.3  10.6   11.1
#> 3       3   F     9.5  13.1   13.8
#> 4       4   M    11.5  13.4   12.9
```

The order of factor levels determines the order of the columns. The level order can be changed before reshaping, or the columns can be re-ordered afterward.

lab5

Andreas and Priya

11 Οκτωβρίου 2018

Assignment 1

```
library(tm)
library(wordcloud)
library(RColorBrewer)
library(viridisLite)
library(plotrix)
library(tidyverse)
```

Word Cloud Plot for five

```
five<-read.table("Five.txt",header=F, sep='\n')#Read file
five$doc_id=1:nrow(five)
colnames(five)[1]<-"text"
mycorpus <- Corpus(DataframeSource(five)) #Creating corpus (collection of text data)

clean_corpus <- function(corpus){
  corpus <- tm_map(corpus, removePunctuation)
  corpus <- tm_map(corpus, content_transformer(tolower))
  corpus <- tm_map(corpus, stripWhitespace)
  corpus <- tm_map(corpus,function(x) removeWords(x,stopwords("english")))
   return(corpus)
}


mycorpus <- clean_corpus(mycorpus)
tdm <- TermDocumentMatrix(mycorpus) #Creating term-document matrix
m <- as.matrix(tdm)

#here we merge all rows
v <- sort(rowSums(m),decreasing=TRUE) #Sum up the frequencies of each word
d <- data.frame(word = names(v),freq=v) #Create one column=names, second=frequences

pal<-brewer.pal(6,"PRGn") #Create palette of colors
#color_pal <- cividis(n = 8)


#wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=col_pal, vfon
t=c("sans #serif","plain"))

wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100,
          random.order=F, rot.per=.15, colors=pal, vfont=c("sans serif","plain"))
```

Word Cloud Plot for One Two

```
oneTwo<-read.table("oneTwo.txt",header=F,sep="\n")
oneTwo$doc_id=1:nrow(oneTwo)
colnames(oneTwo)[1]<-"text"

mycor <- Corpus(DataframeSource(oneTwo))

mycor <- clean_corpus(mycor)
tdm1<- TermDocumentMatrix(mycor) #Creating term-document matrix
m1 <- as.matrix(tdm1)

#here we merge all rows
v1 <- sort(rowSums(m1),decreasing=TRUE) #Sum up the frequencies of each word
d1<- data.frame(word = names(v1),freq=v1)
pal<-brewer.pal(8,"Dark2")

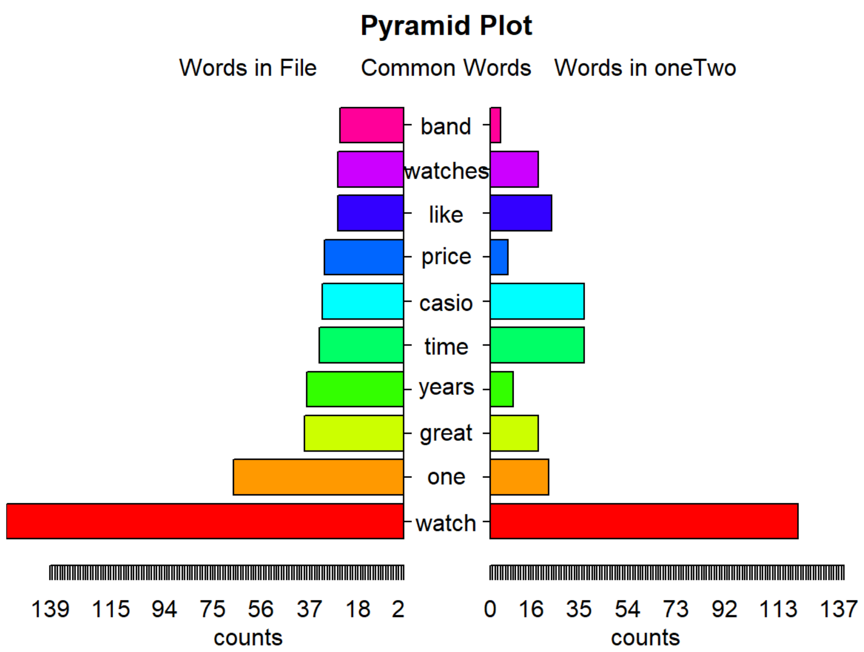
wordcloud(d1$word,d1$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal, vfont=c
("sans serif","plain"))
```

Pyramid Plot

```
j<-left_join(d,d1,by="word")
```

```
## Warning: Column `word` joining factors with different levels, coercing to
## character vector
```

```
pyramid.plot(
  j$freq.x[1:10],j$freq.y[1:10],
  # Words
  labels = j$word[1:10],
  top.labels = c("Words in File", "Common Words", "Words in oneTwo"),
  main = "Pyramid Plot",gap=17,unit="counts")
```



```
## [1] 5.1 4.1 4.1 2.1
```

The word cloud for five.txt which is the good feedback has more frequent words like watch,great,one,price,casio,years,battery etc.This makes sense as words watch and casio will be often coming in the words as this is the product.As it is a positive feedback,people are happy with the price.Great is a posisive word and may be telling it last for long with word years.

THe oneTwo.txt is the negative feedback and the frequesnt words are amazon,one,back,watch,casio,battery etc.casio and watch comes frequent like before as this is the product.Amazon ,may be because they are not happy with the amazon more than product(may be the deal,return policy,shipping etc).They would like to return back the product and hence **back** has come multiple times.

Phrasenets

Phrase nets of five.text

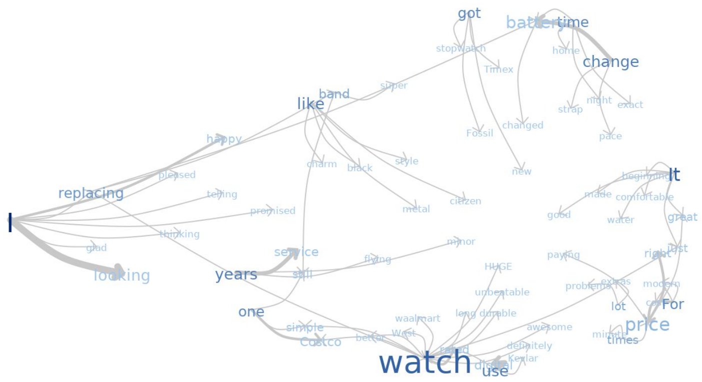


Figure 1. positive.

phrase nets of negative words

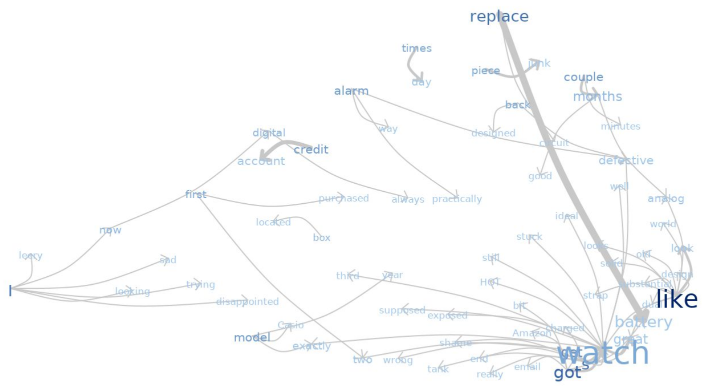


Figure 2. negative

word trees

word tree of not with the positive feedback

Figure 4. wordtree not pos feedback

word tree with the word amazon in negative feedback

Figure 4. wordtree amazon neg feedback

Assignment 2

```
library(tidyverse)
library(plotly)
library(plyr)
library(crosstalk)
library(GGally)

olive<-read.csv("olive.csv")
olive$Region<-as.factor(olive$Region)
levels(olive$Region)<-c("North","South","Sardinia island")
o<-SharedData$new(olive)
oo<-SharedData$new(olive,~Region,group = "Choose region")
```

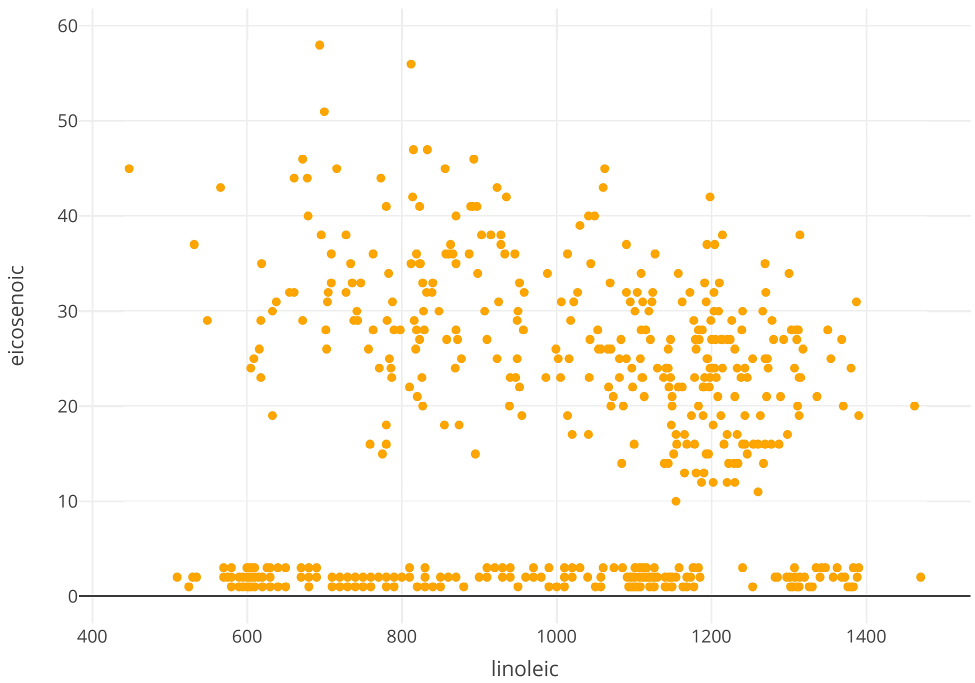
1.Scatter Plot eicoseinoic vs linoleic

```
scatterolive <- plot_ly(oo, y = ~eicosenoic, x = ~ linoleic)%>%group_by(Region)%>%
  add_markers(color = I("orange"),name="hollow")%>%highlight(on="plotly_hover",persistent = F,selectize = T)

scatterolive
```

```
## Setting the `off` event (i.e., 'plotly_doubleclick') to match the `on` event (i.e., 'plotly_hover'). You can cha
nge this default via the `highlight()` function.
```

Choose region

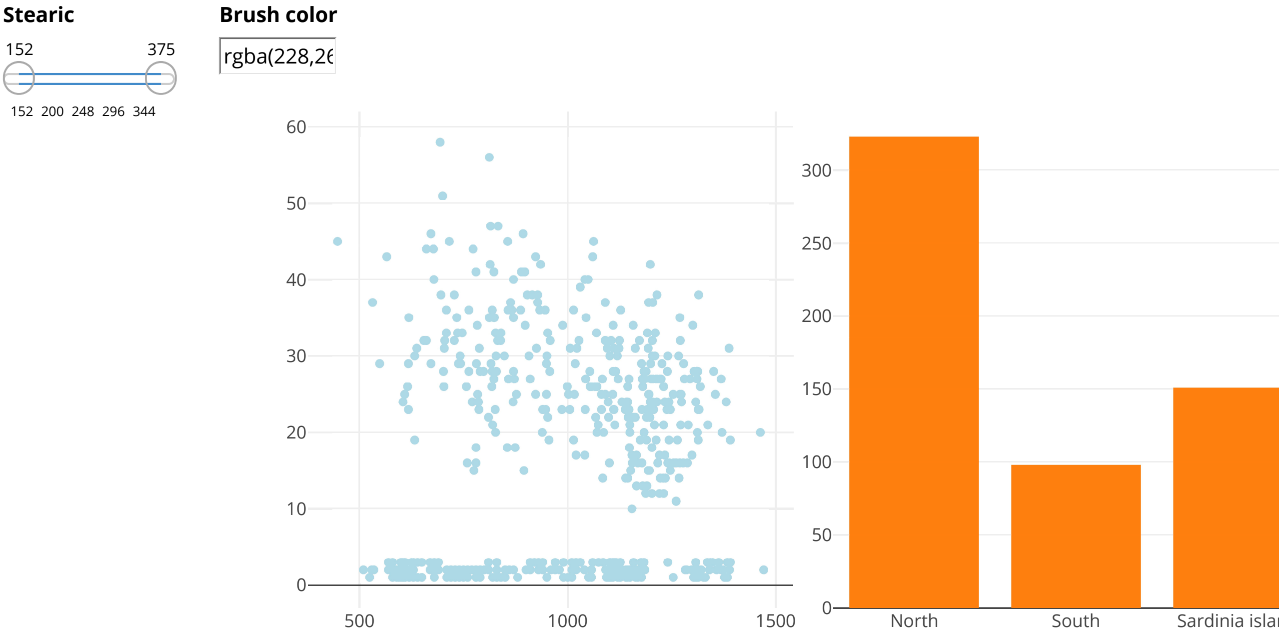


The value of eicosenoic is between one and three. ###2.Linked Scatterplot and Bar chart

```
scatterolive2 <- plot_ly(o, y = ~eicosenoic, x = ~ linoleic) %>%
  add_markers(color = I("lightblue"))
barolive <-plot_ly(o, x=~Region,group="Select your region")%>%add_histogram()%>%layout(barmode="overlay")
```

```
## Warning in plot_ly(o, x = ~Region, group = "Select your region"): The group argument has been deprecated. Use `g
roup_by()` or split instead.
## See `help('plotly_data')` for examples
```

```
bscols(widths=c(2, NA),filter_slider("Slider", "Stearic", o, ~stearic)
       ,subplot(scatterolive2,barolive)%>%
         highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%hide_legend())
```



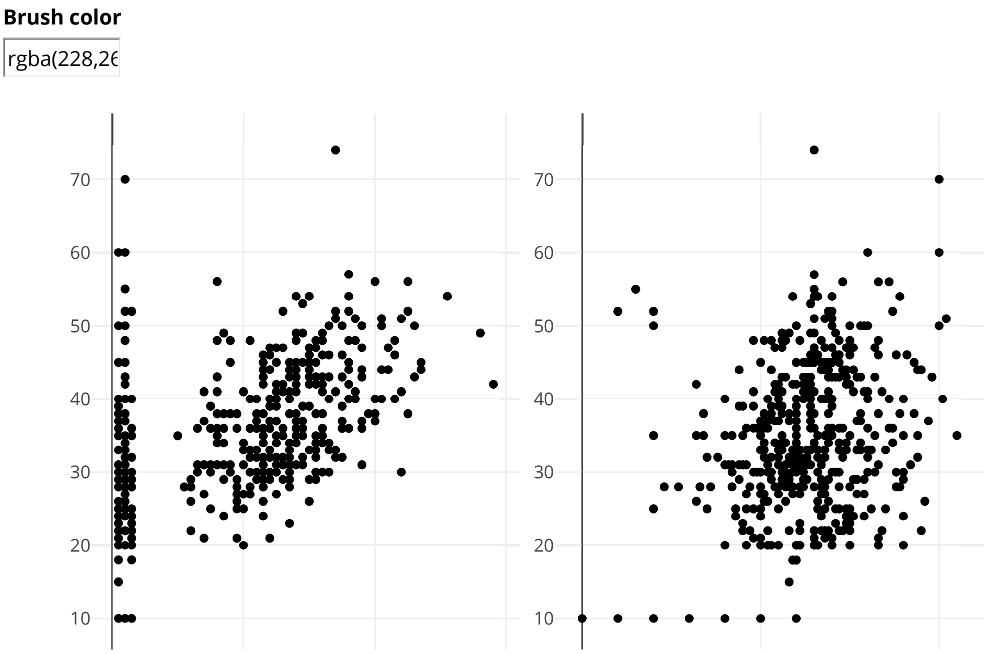
The brush colour and the slider,filter were the interaction operators used in this step.

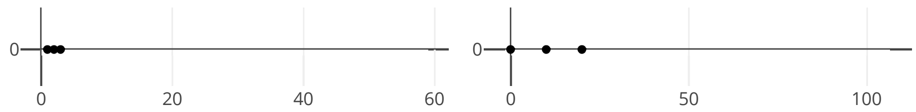
Using brushing when we take out the lower values of eicosenoic(between 1 and 3),we can see they correspond to region south and sardinia Island.Now when we use slider to find the higher values of stearic we can see that they correspond to the region of north and Sardinia Island

3.Linked Scatter Plots

```
scatter1 <- plot_ly(o, x = ~eicosenoic, y = ~linolenic) %>%
  add_markers(color = I("black"))
scatter2 <- plot_ly(o, x = ~arachidic, y = ~linolenic) %>%
  add_markers(color = I("black"))


subplot(scatter1,scatter2)%>%
  highlight(on="plotly_select", dynamic=T, persistent=T, opacityDim = I(1))%>%hide_legend()
```





The values of arachidic below 40 are outliers in the plot2 are also oultiers in plot 1.IN plot one their eicosenoic values are between 1 and 3.

4.Parallel Coordinate Plot linked Barplot and Scatterplot

```
p<-ggparcoord(olive,columns = c(4:11))

d<-plotly_data(ggplotly(p))%>%group_by(.ID)
d1<-SharedData$new(d, ~.ID, group="olive")
p1<-plot_ly(d1, x=~variable, y=~value)%>%
  add_lines(line=list(width=0.3))%>%
  add_markers(marker=list(size=0.3),
              text=~.ID, hoverinfo="text")

ButtonsX=list()
for (i in 4:11){
  ButtonsX[[i-3]]= list(method = "restyle",
                        args = list( "x", list(olive[[i]])),
                        label = colnames(olive)[i])
}

ButtonsY=list()
for (i in 4:11){
  ButtonsY[[i-3]]= list(method = "restyle",
                        args = list( "y", list(olive[[i]])),
                        label = colnames(olive)[i])
}

ButtonsZ=list()
for (i in 4:11){
  ButtonsZ[[i-3]]= list(method = "restyle",
                        args = list( "z", list(olive[[i]])),
                        label = colnames(olive)[i])
}

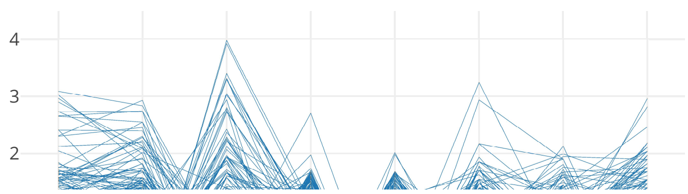
p3<-plot_ly(o,x=~palmitic,y=~stearic,z=~oleic)%>%add_markers() %>%
  layout(xaxis=list(title=""), yaxis=list(title=""),
         title = "Select variable:",
         updatemenus = list(
           list(y=0.9, buttons = ButtonsX),
           list(y=0.7, buttons = ButtonsY),
           list(y=0.5, buttons = ButtonsZ)
         )  )

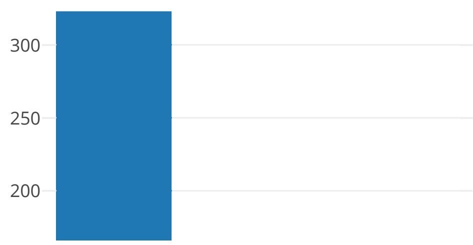

bscols(p1%>%highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
         hide_legend(),barolive,
       p3%>%highlight(on="plotly_click", dynamic=T, persistent = T)%>%hide_legend(),
       widths = c(7,5,9))
```

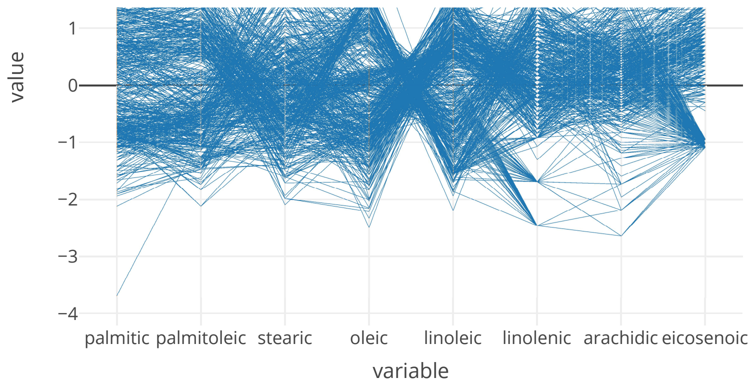
```
## Warning in bscols(p1 %>% highlight(on = "plotly_select", dynamic = T,
## persistent = T, : Sum of bscol width units is greater than 12
```

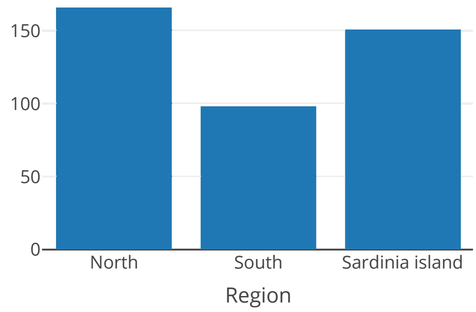
Brush color

rgba(228,26









Brush color

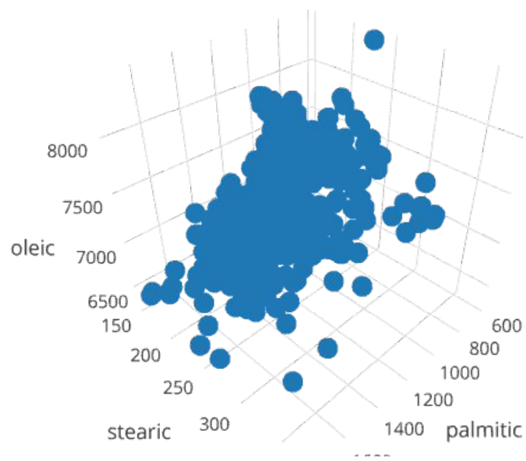
rgba(228,26

Select variable:

palmitic ▼

palmitic ▼

palmitic ▼



The parallel coordinate plot demonstrate clusters among observations that belong to the same region. i think oleic,lieoneic,Eicosenoic are three influential variables.while using this three variable we think we can differentiate regions.

Appendix

```
library(tm)
library(wordcloud)
library(RColorBrewer)
library(viridisLite)
library(plotrix)
library(tidyverse)
five<-read.table("Five.txt",header=F, sep='\n')#Read file
five$doc_id=1:nrow(five)
colnames(five)[1]<-"text"
mycorpus <- Corpus(DataframeSource(five)) #Creating corpus (collection of text data)

clean_corpus <- function(corpus){
  corpus <- tm_map(corpus, removePunctuation)
  corpus <- tm_map(corpus, content_transformer(tolower))
  corpus <- tm_map(corpus, stripWhitespace)
  corpus <- tm_map(corpus,function(x) removeWords(x,stopwords("english")))
  return(corpus)
}


mycorpus <- clean_corpus(mycorpus)
tdm <- TermDocumentMatrix(mycorpus) #Creating term-document matrix
m <- as.matrix(tdm)

#here we merge all rows
v <- sort(rowSums(m),decreasing=TRUE) #Sum up the frequencies of each word
d <- data.frame(word = names(v),freq=v) #Create one column=names, second=frequences

pal<-brewer.pal(6,"PRGn") #Create palette of colors
#color_pal <- cividis(n = 8)


#wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=col_pal, vfon
t=c("sans #serif","plain"))

wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal, vfont=c
("sans serif","plain"))

oneTwo<-read.table("oneTwo.txt",header=F,sep="\n")
oneTwo$doc_id=1:nrow(oneTwo)
colnames(oneTwo)[1]<-"text"

mycor <- Corpus(DataframeSource(oneTwo))

mycor <- clean_corpus(mycor)
tdm1<- TermDocumentMatrix(mycor) #Creating term-document matrix
m1 <- as.matrix(tdm1)

#here we merge all rows
v1 <- sort(rowSums(m1),decreasing=TRUE) #Sum up the frequencies of each word
d1<- data.frame(word = names(v1),freq=v1)
pal<-brewer.pal(8,"Dark2")

wordcloud(d1$word,d1$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal, vfont=c
("sans serif","plain"))

j<-left_join(d,d1,by="word")

pyramid.plot(
  j$freq.x[1:10],j$freq.y[1:10],
  # Words
  labels = j$word[1:10],
  top.labels = c("Words in File", "Common Words", "Words in oneTwo"),
  main = "Pyramid Plot",gap=17,unit="counts")


library(tidyverse)
library(plotly)
library(plyr)
library(crosstalk)
```

```r
library(GGally)

olive<-read.csv("olive.csv")
olive$Region<-as.factor(olive$Region)
levels(olive$Region)<-c("North","South","Sardinia island")
o<-SharedData$new(olive)
oo<-SharedData$new(olive,~Region,group = "Choose region")

scatterolive <- plot_ly(oo, y = ~eicosenoic, x = ~ linoleic)%>%group_by(Region)%>%
  add_markers(color = I("orange"),name="hollow")%>%highlight(on="plotly_hover",persistent = F,selectize = T)

scatterolive

scatterolive2 <- plot_ly(o, y = ~eicosenoic, x = ~ linoleic) %>%
  add_markers(color = I("lightblue"))
barolive <-plot_ly(o, x=~Region,group="Select your region")%>%add_histogram()%>%layout(barmode="overlay")
bscols(widths=c(2, NA),filter_slider("Slider", "Stearic", o, ~stearic)
       ,subplot(scatterolive2,barolive)%>%
         highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%hide_legend())


scatter1 <- plot_ly(o, y = ~eicosenoic, x = ~linolenic) %>%
  add_markers(color = I("black"))
scatter2 <- plot_ly(o, y = ~arachidic, x = ~linolenic) %>%
  add_markers(color = I("black"))


subplot(scatter1,scatter2)%>%
  highlight(on="plotly_select", dynamic=T, persistent=T, opacityDim = I(1))%>%hide_legend()

p<-ggparcoord(olive,columns = c(4:11))

d<-plotly_data(ggplotly(p))%>%group_by(.ID)
d1<-SharedData$new(d, ~.ID, group="olive")
p1<-plot_ly(d1, x=~variable, y=~value)%>%
  add_lines(line=list(width=0.3))%>%
  add_markers(marker=list(size=0.3),
              text=~.ID, hoverinfo="text")

ButtonsX=list()
for (i in 4:11){
  ButtonsX[[i-3]]= list(method = "restyle",
                        args = list( "x", list(olive[[i]])),
                        label = colnames(olive)[i])
}

ButtonsY=list()
for (i in 4:11){
  ButtonsY[[i-3]]= list(method = "restyle",
                        args = list( "y", list(olive[[i]])),
                        label = colnames(olive)[i])
}
```

Teachers code

Andreas C Charitos[andch552]

10/26/2019

Topic 1

Topic 2

```r
# Metric MDS ------------------------------------------------------------
library(plotly)

music = read.csv("music-sub.csv", row.names=1)
head(music)
music.numeric= scale(music[,4:7])
d=dist(music.numeric)
coords=cmdscale(d,2)
coordsMDS=as.data.frame(coords)
coordsMDS$name=rownames(coordsMDS)

plot_ly(coordsMDS, x=~V1, y=~V2, type="scatter", hovertext=~name)

# nonMetric MDS ---------------------------------------------------------
library(plotly)
library(MASS)

music = read.csv("music-sub.csv", row.names=1)
music.numeric= scale(music[,4:7])
d=dist(music.numeric)
res=isoMDS(d,k=3)
coords=res$points

coordsMDS=as.data.frame(coords)
coordsMDS$name=rownames(coordsMDS)
coordsMDS$artist=music$artist

plot_ly(coordsMDS, x=~V1, y=~V2, z=~V3, type="scatter3d", hovertext=~name, color= ~artist)

# shephard ----------------------------------------------------------------
sh <- Shepard(d, coords)
delta <-as.numeric(d)
D<- as.numeric(dist(coords))

n=nrow(coords)
index=matrix(1:n, nrow=n, ncol=n)
index1=as.numeric(index[lower.tri(index)])

n=nrow(coords)
index=matrix(1:n, nrow=n, ncol=n, byrow = T)
index2=as.numeric(index[lower.tri(index)])
```

```
plot_ly()%>%
  add_markers(x=~delta, y=~D, hoverinfo = 'text',
        text = ~paste('Obj1: ', rownames(music)[index1],
                      '<br> Obj 2: ', rownames(music)[index2]))%>%
  #if nonmetric MDS inolved
  add_lines(x=~sh$x, y=~sh$yf)
```

Topic 3

```
# cholopleth Map -------------------------------------------------------
library(plotly)

df <- read.csv('https://raw.githubusercontent.com/plotly/datasets/master/2014_world_gdp_with_codes.csv')



# WORLD MAP
g <- list(
  projection = list(type = 'Mercator')
)

p <- plot_geo(df) %>%
  add_trace(
    z = ~GDP..BILLIONS., color = ~GDP..BILLIONS., colors = 'Blues',
    text = ~COUNTRY, locations = ~CODE
  ) %>%
    layout(
    geo = g
  )

p

####Other country maps

rds<-readRDS("gadm36_GBR_2_sf.rds")
df<-read.csv("GBcities.csv")

rownames(df)=df$name
rds$Price=df[rds$NAME_2, "Price"]
#Data for some regions absent, setting to 0
rds$Price[is.na(rds$Price)]=0

#plotly
p<-plot_ly()%>%add_sf(data=rds, split=~NAME_2, color=~Price, showlegend=F, alpha=1)
p
#ggplot2
p<-ggplot(rds) +  geom_sf(aes(fill = Price))
ggplotly(p)

#mapbox
```

```r
p<-plot_mapbox(rds, split=~NAME_2, color=~Price, showlegend=F, alpha=0.5)
p

# densityPlot ----------------------------------------------------------------
library(dplyr)
library(ggplot2)
library(plotly)

#Ggplot2: histogram, density and violin plot

p1<-ggplot(mtcars, aes(mpg, fill=factor(am)))+geom_density(alpha=0.2)
p1

p2<-ggplot(mtcars, aes(mpg, fill=factor(am)))+geom_histogram(bins = 5)
p2

p3<-ggplot(mtcars, aes( y=mpg, x=factor(am)))+geom_violin(fill="orange")
p3

#Plotly: histogram, density and violin plot

p1<-plot_ly(mtcars, x=~mpg, color=~factor(am), alpha=0.6)%>%
  add_histogram()%>%
  layout(barmode = "overlay")

p1


#easiest from ggplot2:
p2<-ggplot(mtcars, aes(mpg, fill=factor(am)))+geom_density(alpha=0.6)
ggplotly(p2)

# Violin plot

p3<-plot_ly(mtcars, x=~factor(am), y=~mpg, split=~factor(am),
            type="violin", box=list(visible=T))
p3

# lineMaps ----------------------------------------------------------

library(plotly)
library(dplyr)
# airport locations
air <- read.csv('https://raw.githubusercontent.com/plotly/datasets/master/2011_february_us_airport_traf
# flights between airports
flights <- read.csv('https://raw.githubusercontent.com/plotly/datasets/master/2011_february_aa_flight_pa
flights$id <- seq_len(nrow(flights))

# map projection
geo <- list(
  scope = 'north america'
)
```

```r
p <- plot_geo(locationmode = 'USA-states', color = I("red")) %>%
  add_markers(
    data = air, x = ~long, y = ~lat, text = ~airport,
    size = ~cnt, hoverinfo = "text", alpha = 0.5
  ) %>%
  add_segments(
    data = group_by(flights, id),
    x = ~start_lon, xend = ~end_lon,
    y = ~start_lat, yend = ~end_lat,
    alpha = 0.3, size = I(1) , hoverinfo = "none"
  ) %>%
  layout(
    geo = geo
  )

p
# splom ----------------------------------------------------------------------
library(dplyr)
library(ggplot2)

library(plotly)

#plotly

mtcars %>% plot_ly()%>%
  add_trace(type='splom',     dimensions = list(
    list(label='MPG', values=~mpg),
    list(label='Displacement', values=~disp),
    list(label='#Horse Power', values=~hp),
    list(label='weight', values=~wt)),
    marker = list(
      color = as.integer(mtcars$cyl),
      size = ~qsec

    )

)

#ggplot2

library(GGally)
ggpairs(mtcars, columns=c(1,3,4,6),
        mapping =aes(color=factor(cyl), size=qsec))

# surfacecontour ---------------------------------------------------------------

library(dplyr)
library(ggplot2)
library(MASS)

library(plotly)

mtcars %>%plot_ly(x=~mpg, y=~disp, z=~wt, type="scatter3d")
```

```r
mtcars %>%plot_ly(x=~mpg, y=~disp, z=~wt, type="contour")

library(akima)
attach(mtcars)
s=interp(mpg,disp,wt, duplicate = "mean")
detach(mtcars)

plot_ly(x=~s$x, y=~s$y, z=~s$z, type="surface")

# symboldotMap ----------------------------------------------------------
library(plotly)
df <- read.csv('https://raw.githubusercontent.com/plotly/datasets/master/2011_february_us_airport_traff


g <- list(
  scope = 'usa'
)

p <- plot_geo(df, lat = ~lat, lon = ~long) %>%
  add_markers(
    text = ~paste(airport, city, state, paste("Arrivals:", cnt), sep = "<br />"),
    color = ~cnt, symbol = I("diamond"), hoverinfo = "text",
    colors=colorRamp(c("lightblue","darkblue"))
  )  %>%
  layout(geo = g)
p


#size adjustment

p <- plot_geo(df, lat = ~lat, lon = ~long) %>%
  add_markers(
    text = ~paste(airport, city, state, paste("Arrivals:", cnt), sep = "<br />"),
    size = ~cnt, symbol = I("diamond"), hoverinfo = "text",
    colors=colorRamp(c("lightblue","darkblue"))
  )  %>%
  layout(geo = g)
p

## Other countries than USA- ggplot2

##Example -UK

rds<-readRDS("gadm36_GBR_0_sf.rds")
df<-read.csv("GBcities.csv")
p<-ggplot()+geom_sf(data=rds)+
  geom_point(data=df, mapping = aes(longitude, latitude, color=Price))


p
##Use google chrome- does not work in explorer.

ggplotly(p)
```

```r
##Now with mapbox

p <- df %>%
  plot_mapbox(lat = ~latitude, lon = ~longitude,
              size = ~Price,
              mode = 'scattermapbox')
p
```

Topic 4

```r
# facettrellis ---------------------------------------------------------------
library(plotly)

df=lattice::barley

p<-ggplot(df, aes(y=variety, x=yield, color=year))+geom_point()+
  facet_grid(site~.)
p

ggplotly(p)

df1<-mpg

p1<-ggplot(df1, aes(cty, displ))+geom_point()+geom_smooth()+
  facet_wrap(~class, labeller = "label_both")


df3<-MASS::Aids2
Agerange<-lattice::equal.count(df3$age, number=6, overlap=0.03) #overlap is 3%

L<-matrix(unlist(levels(Agerange)), ncol=2, byrow = T)
L1<-data.frame(Lower=L[,1],Upper=L[,2], Interval=factor(1:nrow(L)))
ggplot(L1)+geom_linerange(aes(ymin = Lower, ymax = Upper, x=Interval))

index=c()
Class=c()
for(i in 1:nrow(L)){
  Cl=paste("[", L1$Lower[i], ",", L1$Upper[i], "]", sep="")
  ind=which(df3$age>=L1$Lower[i] &df3$age<=L1$Upper[i])
  index=c(index,ind)
  Class=c(Class, rep(Cl, length(ind)))
}

df4<-df3[index,]
df4$Class<-as.factor(Class)

ggplot(df4, aes(x=death-diag, fill="orange"))+ geom_histogram()+
  facet_wrap(~Class, labeller = "label_both")

# heatmap --------------------------------------------------------------------
```

```r
library(plotly)
mtscaled=scale(mtcars)

plot_ly(x=colnames(mtscaled), y=rownames(mtscaled),
        z=mtscaled, type="heatmap", colors =colorRamp(c("yellow", "red")))

# parallelcoord -------------------------------------------------------------
library(ggplot2)
library(plotly)


#Plotly - can not see observation ID
data=iris
p <- data %>%
  plot_ly(type = 'parcoords',
          #line = list(color = ~as.numeric(Species)),

          dimensions = list(
            list(label = 'Sepal Width', values = ~Sepal.Width),
            list(label = 'Sepal Length', values = ~Sepal.Length),
            list(label = 'Petal Length', values = ~Petal.Length)
          )
  )

p


## GGplot2 - can see observation ID, no interactivity
library(GGally)

obj<- ggparcoord(iris, columns=1:3)
ggplotly(obj)

#coloring lines
data=iris
data$Col=as.numeric(scale(data$Petal.Length)< -0.5)
obj<- ggparcoord(data, columns=1:3, scale="uniminmax", groupColumn = 6)

ggplotly(obj)

#coloring by another variable
obj<- ggparcoord(data, columns=1:3, scale="uniminmax", groupColumn = 5)

ggplotly(obj)

# radarChart ----------------------------------------------------------------
library(plotly)

mtscaled=scale(mtcars)

#Superimposed
```

```r
p<- plot_ly(type='scatterpolar', fill = 'toself')

for (i in 1:3){
  p<-p%>% add_trace(r=c(mtscaled[i,], mtscaled[i,1]),
                    theta=c(colnames(mtscaled), colnames(mtscaled)[1]),
                    name=rownames(mtscaled)[i])
}

p <- p%>% layout(
  polar = list(
    radialaxis = list(
      visible = T
    )
  )
)

p

#Juxtaposed

#Ugly graphics
stars(mtcars,key.loc=c(15,2), draw.segments=F, col.stars =rep("Yellow", nrow(mtcars)))

##ggplot2
library(scales)
mtcars1<-mtcars%>% mutate_all(funs(rescale))
mtcars1$name=rownames(mtcars)
mtcars2 <- mtcars1%>%tidyr::gather(variable, value, -name, factor_key=T)%>%arrange(name)
p<-mtcars2 %>%
  ggplot(aes(x=variable, y=value, group=name)) +
  geom_polygon(fill="blue") +
  coord_polar() + theme_bw() + facet_wrap(~ name) +
  theme(axis.text.x = element_text(size = 5))
p

## Plotly

library(plotly)
library(dplyr)
library(scales)

Ps=list()
nPlot=10#nrow(mtcars)

mtcars %>%
  add_rownames( var = "group" ) %>%
  mutate_each(funs(rescale), -group) -> mtcars_radar

for (i in 1:nPlot){
  Ps[[i]] <- htmltools::tags$div(
    plot_ly(type = 'scatterpolar',
            r=as.numeric(mtcars_radar[i,-1]),
            theta= colnames(mtcars_radar)[-1],
```

```r
            fill="toself")%>%
      layout(title=mtcars_radar$group[i]), style="width: 25%;")
}

h <-htmltools::tags$div(style = "display: flex; flex-wrap: wrap", Ps)

htmltools::browsable(h)
# seriation ------------------------------------------------------------------
library(plotly)
library(seriation)

mtscaled=scale(mtcars[1:7])
rowdist<-dist(mtscaled)
coldist<-dist(t(mtscaled))

order1<-seriate(rowdist, "BBURCG")
order2<-seriate(coldist, "BBURCG")
ord1<-get_order(order1)
ord2<-get_order(order2)

reordmatr<-mtscaled[rev(ord1),ord2]

dims=list()
for( i in 1:ncol(reordmatr)){
  dims[[i]]=list( label=colnames(reordmatr)[i],
    values=as.formula(paste("~",colnames(reordmatr)[i])))
}

dims0=list()
for( i in 1:ncol(mtscaled)){
  dims0[[i]]=list( label=colnames(mtscaled)[i],
                  values=as.formula(paste("~",colnames(mtscaled)[i])))
}

p <- as.data.frame(mtscaled) %>%
  plot_ly(type = 'parcoords',
          #line = list(color = ~as.numeric(Species)),

          dimensions = dims0
  )

p

p1 <- as.data.frame(reordmatr) %>%
  plot_ly(type = 'parcoords',
          #line = list(color = ~as.numeric(Species)),

          dimensions = dims
  )

p1

plot_ly(x=colnames(reordmatr), y=rownames(reordmatr),
```

```
        z=reordmatr, type="heatmap", colors =colorRamp(c("yellow", "red")))
```

Topic 5

```
# interaction ------------------------------------------------------------
library(plotly)
library(crosstalk)
library(tidyr)

crabs<- read.csv("australian-crabs.csv")

d <- SharedData$new(crabs)

#LINKING EXAMPLES

#Bar-scatter
scatterCrab <- plot_ly(d, x = ~CL, y = ~RW) %>%
  add_markers(color = I("black"))


barCrab <-plot_ly(d, x=~sex)%>%add_histogram()%>%layout(barmode="overlay")

subplot(scatterCrab,barCrab)%>%
  highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%hide_legend()


#Scatter-scatter

scatterCrab2 <- plot_ly(d, x = ~CL, y = ~BD) %>%
  add_markers(color = I("black"))
subplot(scatterCrab,scatterCrab2)%>%
  highlight(on="plotly_select", dynamic=T, persistent=T, opacityDim = I(1))%>%hide_legend()

#Parallel coords

library(GGally)
p<-ggparcoord(crabs, columns = c(4:6))

d<-plotly_data(ggplotly(p))%>%group_by(.ID)
d1<-SharedData$new(d, ~.ID, group="crab")
p1<-plot_ly(d1, x=~variable, y=~value)%>%
  add_lines(line=list(width=0.3))%>%
  add_markers(marker=list(size=0.3),
              text=~.ID, hoverinfo="text")


crabs2=crabs
crabs2$.ID=1:nrow(crabs)
d2<-SharedData$new(crabs2, ~.ID, group="crab")
p2<-plot_ly(d2, x=~factor(sex) )%>%add_histogram()%>%layout(barmode="stack")
```

```r
ps<-htmltools::tagList(p1%>%
  highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
  hide_legend(),
  p2%>%
    highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
    hide_legend()
  )
htmltools::browsable(ps)

#3D-plot and parcoord
df=read.csv("flea.csv")
d2<-SharedData$new(df)

p<-ggparcoord(flea, columns = c(6,7,2))

d<-plotly_data(ggplotly(p))%>%group_by(.ID)
d1<-SharedData$new(d, ~.ID, group="flea")
p1<-plot_ly(d1, x=~variable, y=~value)%>%
  add_lines(line=list(width=0.3))%>%
  add_markers(marker=list(size=0.3),
              text=~.ID, hoverinfo="text")
p1

flea2=flea[, c("tars1", "aede2", "aede3")]
flea2$.ID=1:nrow(flea)
d2<-SharedData$new(flea2, ~.ID, group="flea")

p3<-plot_ly(d2,x=~tars1,y=~aede2,z=~aede3)%>%add_markers()
bscols(p1%>%highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%
         hide_legend(),
       p3%>%highlight(on="plotly_click", dynamic=T, persistent = T)%>%hide_legend())

#Filter - check crosstalk package

d <- SharedData$new(crabs)
scatterCrab <- plot_ly(d, x = ~CL, y = ~RW) %>%
  add_markers(color = I("black"))


barCrab <-plot_ly(d, x=~sex)%>%add_histogram()%>%layout(barmode="overlay")

bscols(widths=c(2, NA),filter_slider("FL", "Frontal Lobe", d, ~FL)
        ,subplot(scatterCrab,barCrab)%>%
  highlight(on="plotly_select", dynamic=T, persistent = T, opacityDim = I(1))%>%hide_legend())


## Variable selection

ButtonsX=list()
for (i in 4:7){
  ButtonsX[[i-3]]= list(method = "restyle",
                        args = list( "x", list(crabs[[i]])),
                        label = colnames(crabs)[i])
```

```r
}

ButtonsY=list()
for (i in 4:7){
  ButtonsY[[i-3]]= list(method = "restyle",
                        args = list( "y", list(crabs[[i]])),
                        label = colnames(crabs)[i])
}

p <- plot_ly(d, x = ~CL, y = ~CW, alpha = 0.8) %>%
  add_markers() %>%
  layout(xaxis=list(title=""), yaxis=list(title=""),
    title = "Select variable:",
    updatemenus = list(
      list(y=0.9, buttons = ButtonsX),
      list(y=0.6, buttons = ButtonsY)
    )  )

p

# wordcloud ---------------------------------------------------------------

data<-read.table("romeo.txt",header=F, sep='\n') #Read file
library(tm)
library(wordcloud)
library(RColorBrewer)
data$doc_id=1:nrow(data)
colnames(data)[1]<-"text"

#Here we interpret each line in the document as separate document
mycorpus <- Corpus(DataframeSource(data)) #Creating corpus (collection of text data)
mycorpus <- tm_map(mycorpus, removePunctuation)
mycorpus <- tm_map(mycorpus, function(x) removeWords(x, stopwords("english")))
tdm <- TermDocumentMatrix(mycorpus) #Creating term-document matrix
m <- as.matrix(tdm)

#here we merge all rows
v <- sort(rowSums(m),decreasing=TRUE) #Sum up the frequencies of each word
d <- data.frame(word = names(v),freq=v) #Create one column=names, second=frequences
pal <- brewer.pal(6,"Dark2")
pal <- pal[-(1:2)] #Create palette of colors
wordcloud(d$word,d$freq, scale=c(8,.3),min.freq=2,max.words=100, random.order=F, rot.per=.15, colors=pal
```

Topic 6

```r
# motion ------------------------------------------------------------------
library(plotly)

m=matrix(nrow=0,ncol=3)
for (a in seq(0,3,by=0.03)) {
  x<-seq(0,2,0.01)
```

```r
  y<-x^a
  m<-rbind(m,cbind(x,y,a))
}

df=as.data.frame(m)

plot_ly(df, x=~x, y=~y, frame =~a)%>%add_lines()%>%animation_opts(
  100, easing = "cubic", redraw = F
)
# network ----------------------------------------------------------------
library(ggraph)
library(igraph)
library(visNetwork)

nodes <- read.csv("Dataset1-Media-Example-NODES.csv", header=T, as.is=T)
links <- read.csv("Dataset1-Media-Example-EDGES.csv", header=T, as.is=T)

## Collapsing multiple links into one

links <- aggregate(links[,3], links[,-3], sum)
links <- links[order(links$from, links$to),]
colnames(links)[4] <- "weight"
rownames(links) <- NULL

nodes$label=nodes$media
#net <- graph_from_data_frame(d=links, vertices=nodes, directed=T)
#visIgraph(net)
visNetwork(nodes, links)

nodes$group=nodes$type.label
nodes$value=nodes$audience.size
links$width=links$weight
visNetwork(nodes, links)%>%visLegend()

visNetwork(nodes,links)%>%visIgraphLayout(layout="layout_in_circle")

# Community identification
nodes1<-nodes
net <- graph_from_data_frame(d=links, vertices=nodes, directed=F)
ceb <- cluster_edge_betweenness(net)
nodes1$group=ceb$membership
visNetwork(nodes1,links)%>%visIgraphLayout()


#adjacency representation

netm <- get.adjacency(net, attr="weight", sparse=F)
colnames(netm) <- V(net)$media
rownames(netm) <- V(net)$media

rowdist<-dist(netm)

library(seriation)
```

```r
order1<-seriate(rowdist, "HC")
ord1<-get_order(order1)

reordmatr<-netm[ord1,ord1]

library(plotly)

plot_ly(z=~reordmatr, x=~colnames(reordmatr),
        y=~rownames(reordmatr), type="heatmap")

# sunBurst ---------------------------------------------------------------
library(ggraph)
library(igraph)

graph <- graph_from_data_frame(flare$edges, vertices = flare$vertices)

ggraph(graph, 'partition', circular = TRUE) +
  geom_node_arc_bar(aes(fill = depth), size = 0.25)+
  geom_node_text(label=flare$vertices$shortName, size=3)

# treeMap ----------------------------------------------------------------
library(ggraph)
library(igraph)

flare1<-flare
flare1$vertices$mylabels=flare$vertices$shortName
graph <- graph_from_data_frame(flare1$edges, vertices = flare1$vertices)

ggraph(graph, 'treemap', weight = 'size') +
  geom_node_tile(aes(fill = depth), size = 0.25)+
  geom_node_text(aes(label=mylabels), size=3)

devtools::install_github("d3TreeR/d3TreeR")

library(treemap)
library(d3treeR)
data(GNI2014)
d3tree2(treemap(GNI2014,
        index=c("continent", "iso3"),
        vSize="population",
        vColor="GNI",
        type="value",
        format.legend = list(scientific = FALSE, big.mark = " ")),
rootname = "World")
# treeVis ----------------------------------------------------------------
library(ggraph)
library(igraph)
graph <- graph_from_data_frame(flare$edges, vertices = flare$vertices)

ggraph(graph, 'circlepack', weight = 'size') +
  geom_edge_link() +
  geom_node_point(aes(colour = depth)) +
  geom_node_text(label=flare$vertices$shortName, size=1)+
```

```r
  coord_fixed()

library(visNetwork)
library(rpart)

# Basic classification tree
crabs=read.csv("australian-crabs.csv")
res <- rpart(as.factor(sex)~., data=crabs)
visTree(res, main = "Iris classification Tree", width = "100%")
```