Module 3

Application of SOMs in Real Life: Modelling the COVID-19 Pandemic in India

The COVID-19 pandemic has had a devastating impact across the world in the years 2020 and 2021. In an attempt to study the dynamics of the pandemic we need to analyze the number of rising cases and deaths and find patterns in the trends of the pandemic impact. But the sheer amount of data available on the pandemic makes this task difficult, as the voluminous numbers need to be reduced to concise insights for usage in real life. Out of the many approaches to dimensionality reduction, we show an implementation of self organizing maps on the COVID-19 data for India. We also present the patterns visually in the form of dynamic Self Organizing Map charts and their spatial representation using the India map. The data used in this implementation ranges from 1st March 2021 to 1st June 2021 and contains data on all the states in India as of 2021. The data has been sourced from (“COVID Data Source,” n.d.),(“COVID Data Original Source,” n.d.),(“COVID Data Official Government Website,” n.d.).

Part 1: Loading and installing necessary libraries.

```r
 # install.packages("readr")
 # install.packages("dplyr")
 # install.packages("rgdal")
 # install.packages("sf")
 # install.packages("ggplot2")
 # install.packages("magick")

#--Libraries required--#

suppressWarnings(library(readr))
suppressWarnings(library(dplyr))
suppressWarnings(library(rgdal))
suppressWarnings(library(sf))
suppressWarnings(library(ggplot2))
suppressWarnings(library(magick))
```

Part 2: Creating the functions necessary for working of SOMs. Refer to Module 1 for learning about the same.

```r
# 1) A function to return the sum of squared distance between x and y.

euclidean_distance <- function(x, y) {
  ret <- sqrt(sum((x - y)^2))
  return(ret)
```

```r
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------


# 2) Function to create a SOM grid.
# n is the number of neurons.
# p is the number of columns in the original dataframe.
# data table is used for faster computation.

create_grid <- function(x,y,p) {
  ret <- matrix(data = rnorm(x * y * p), nrow = x * y, ncol = p)
  return(ret)
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------


# 3) Function to decay the radius exponentially over time.
# rds is the initial radius that is passed.
# cur_iter represents the current iteration.
# time_constant is the time constant that is calculated before the

decay_radius_function <- function(radius, current_iteration, time_constant) {
  ret <- radius * exp(-current_iteration / time_constant)
  return(ret)
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------


# 4) Function to decay the learning rate.
# learning_rate is the current learning rate.
# current_iteration is the current iteration
# n_iteration is the number of iterations.

decay_learning_rate <- function(learning_rate, current_iteration,
n_iteration) {
  ret <- learning_rate * exp(-current_iteration / n_iteration)
  return(ret)
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------


# 5) A function to calculate influence over neighboring neurons
#distance is the lateral distance.
#rds is the current neighbourhood radius.
```

```
influence_calculation <- function(distance, radius) {
  ret <- exp(-(distance^2) / (2 * (radius^2)))
  return(ret)
}


#-----------------------------------------------------------------------------
--------------------------------------------------------------------

# 6) A functionto find the winning neuron / Best Matching unit of a SOM grid

# Simple BMU Implementation - Function to return the winning neuron.
# x is a single row of data and input_grid is the grid

BMU <- function(x, input_grid) {
  distance <- 0
  min_distance <- 10000000 # Setting high min dist value
  min_ind <- -1 # Setting random min_ind value
  for (e in 1:nrow(input_grid)) # Iterating through grid
  {
    distance <- euclidean_distance(x, input_grid[e, ]) # euclidean_distance
distance
    if (distance < min_distance) {
      min_distance <- distance # Updating min distance for winning unit
      min_ind <- e # Updating winning neuron
    }
  }
  return(min_ind-1) #returns index of BMU
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------

#7) Fastest BMU Implementation using vectorisation. You can opt in for this
function over the regular BMU function for faster execution.
#x is a single row of data and input_grid is the grid

BMU_Vectorised <- function(x, input_grid) {
  dist_mtrx=rowSums(sweep(input_grid,2,x)^2) #Calculating the distance of
this row from all the neurons using matrix operations.
  min_ind=which.min(dist_mtrx) #Finding the location of the neuron with the
minimum distance.
  return (min_ind-1) #Returning the zero-indexed value of the winning neuron.
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------

#8) A function to encapulate the entire creation, working and updating of SOM
```

```
over the training period.
#x is the input and input_grid is the SOM grid that will be updated
iteratively.

SOM <- function(x, input_grid) {
  breaker <- 0
  n_iteration <- nrow(x) # Defining number of iterations
  initial_learning_rate <- 0.5 # Defining initial learning rate
  initial_radius <- 15 # Defining initial radius
  time_constant <- n_iteration / log(initial_radius) # Initializing time
constant

lateral_distance_points=expand.grid(1:sqrt(nrow(input_grid)),1:sqrt(nrow(inpu
t_grid)))#Initialising physical locations of neurons to figure out lateral
distance.
  rows=sqrt(nrow(input_grid)) #The square grid is used here - so taking the
number of rows as square root of number of entries in the grid.
  n_epochs=40 #Defining the number of epochs.
  new_radius <- initial_radius
  l <- c()
  for(ne in 1:n_epochs)
  {
    extra <- ((ne-1)*400)
    for (i in 1:n_iteration) # Looping through for training
    {
      old_grid=input_grid
      curr_i <- extra + i
      sample_input_row <- as.vector(unlist(x[sample(1:nrow(x), size = 1,
replace = F), ])) # Selecting random input row from given data set
      new_radius <- decay_radius_function(initial_radius, curr_i,
time_constant) # Decaying radius
      new_learning_rate <- decay_learning_rate(initial_learning_rate,curr_i,
n_iteration) # Decaying learning rate
      index_temp <- BMU_Vectorised(sample_input_row, input_grid) # Finding
best matching unit for given input row
      index_new=c((as.integer(index_temp/rows)+1),(index_temp%%rows)+1)
#Converting a 1D co-ordinate to a 2D co-ordinate for finding lateral distance
on the map.

lateral_distance=sqrt(abs(rowSums(sweep(lateral_distance_points,2,index_new)^
2))) #Finding Euclidean distance between the given best matching units and
all units on the map.
      rn=which(lateral_distance<=new_radius) #Finding neurons that are within
the radius of the winning unit.
      inf=influence_calculation(lateral_distance[rn],new_radius)#Calculating
the influence of the winning neuron on neighbours.
      if(length(rn)!=1) #Updating multiple rows if neighbourhood is large
      {
        #Calculating the influence of the winning neuron on neighbours.
        diff_grid=(sweep(input_grid[rn,],2,sample_input_row))*-1 #A temporary
matrix that stores the difference between the data point and the weights of
the winning neuron & neighbours.
        updated_weights=new_learning_rate*inf*diff_grid #The updating
operation on the winning and neighbouring neurons.
        input_grid[rn,]=input_grid[rn,]+updated_weights #Now updating those
grid entries that are either the winning neuron or its neighbours.
      }
      else #Updating only winning neuron.
      {
        diff_row=(input_grid[rn,]-sample_input_row)*-1 #A temporary matrix
that stores the difference between the data point and the weights of the
winning neuron & neighbours.
        updated_weights=new_learning_rate*inf*diff_row #The updating
operation on the winning and neighbouring neurons.
        input_grid[rn,]=input_grid[rn,]+updated_weights #Now updating those
grid entries that are either the winning neuron or its neighbours.
      }
      l <- c(l,euclidean_distance(old_grid,input_grid))
      if(isTRUE(all.equal(old_grid,input_grid)))
      {
        breaker <- 1
        break
      }
    }
    if(breaker ==1)
    {
      break
    }
  }
  return(list(input_grid,l)) #Returning the updated SOM weights.
}

#-----------------------------------------------------------------------------
--------------------------------------------------------------------
# 9) A function to visualize the weights of SOM in a graphical format.

drawGrid<- function(weight,dimension,showPlot=TRUE){

  # Converting to a matrix
  weight<-as.matrix(weight, ncol = ncol(weight))

  norm.matrix<-NULL

  # Calculation of the norm
  for(i in 1:length(weight[,1])){
    a<-norm(weight[i,], type = "2")
    norm.matrix<-rbind(norm.matrix,a)
  }
  ## Mapping to range 5 to 20
  input_start<-min(norm.matrix)
  input_end<-max(norm.matrix)
  output_start<-5
  output_end<-20


  ## Calculating wavelength based on norm
  color<-NULL
  for(i in 1:length(norm.matrix)){
    input = norm.matrix[i]
    output = output_start + ((output_end - output_start) / (input_end -
input_start)) * (input - input_start)
    color<-rbind(color,output)
  }

  # Getting the colors (hex values) from the wavelength
  #color.rgb<-w_length2rgb(color)
  color.rgb<-rainbow(20, rev = T)[color]

  # Plotting the grid
  if(showPlot){
    dim<-max(dimension)+1
    plot(1:dim, type = "n")

    for (i in 1:dimension[1]) {
      for(j in 1:dimension[2]){
        #draw.circle(i*2,j*6, radius =.5, col = color.rgb[i*dimension[1]+j -
dimension[1]])
        rect(i,j,i+1,j+1, col = color.rgb[i*dimension[1]+j - dimension[1]])
      }
    }
  }

  return(color.rgb)
}
```

Part 3: Loading the data and necessary files for implementation.

```
#-- Output directory for storing SOMs--#
dir.create("SOM_Maps")
dir_out <-  paste0(getwd(),"/SOM_Maps/")

#--Mapping files--#
isro<-st_read("cauvery-INDIA_STATE_250K.kml")

## Reading layer `cauvery:INDIA_STATE_250K' from data source
##   `C:\Users\Aboli\Desktop\FOSSEE\Final_Documentation\cauvery-
```

```
INDIA_STATE_250K.kml'
##   using driver `KML'
## Simple feature collection with 36 features and 2 fields
## Geometry type: GEOMETRYCOLLECTION
## Dimension:     XY
## Bounding box:  xmin: 68.10606 ymin: 6.679998 xmax: 97.41535 ymax: 37.07833
## Geodetic CRS:  WGS 84

isro<-isro[-1,] # ambiguous


#--New COVID Data--#
covid<-read.csv("covid_19_india.csv")
head(covid)

##   ï..Sno       Date    Time State.UnionTerritory ConfirmedIndianNational
## 1      1 2020-01-30 6:00 PM               Kerala                       1
## 2      2 2020-01-31 6:00 PM               Kerala                       1
## 3      3 2020-02-01 6:00 PM               Kerala                       2
## 4      4 2020-02-02 6:00 PM               Kerala                       3
## 5      5 2020-02-03 6:00 PM               Kerala                       3
## 6      6 2020-02-04 6:00 PM               Kerala                       3
##   ConfirmedForeignNational Cured Deaths Confirmed
## 1                        0     0      0         1
## 2                        0     0      0         1
## 3                        0     0      0         2
## 4                        0     0      0         3
## 5                        0     0      0         3
## 6                        0     0      0         3

# Taking deaths [8] and conformed cases [9]
data<-covid[,c(2,4,8,9)]


#Note: rows corresponding to dates
#   1) 12207 for march 1
#   2) 14655 for may 8

data<-data[12207:length(data[,1]),] %>% arrange(Date,State.UnionTerritory)
average.length<-7
iteration<-0
date.range<-seq(from = as.Date("2021/3/1"), to = as.Date("2021/6/1"),by =
"day")

head(data)

##         Date        State.UnionTerritory Deaths Confirmed
## 1 2021-03-01 Andaman and Nicobar Islands     62      5020
## 2 2021-03-01              Andhra Pradesh   7169    889916
## 3 2021-03-01           Arunachal Pradesh     56     16836
## 4 2021-03-01                       Assam   1092    216445
## 5 2021-03-01                       Bihar   1541    262534
## 6 2021-03-01                  Chandigarh    352     21770
```

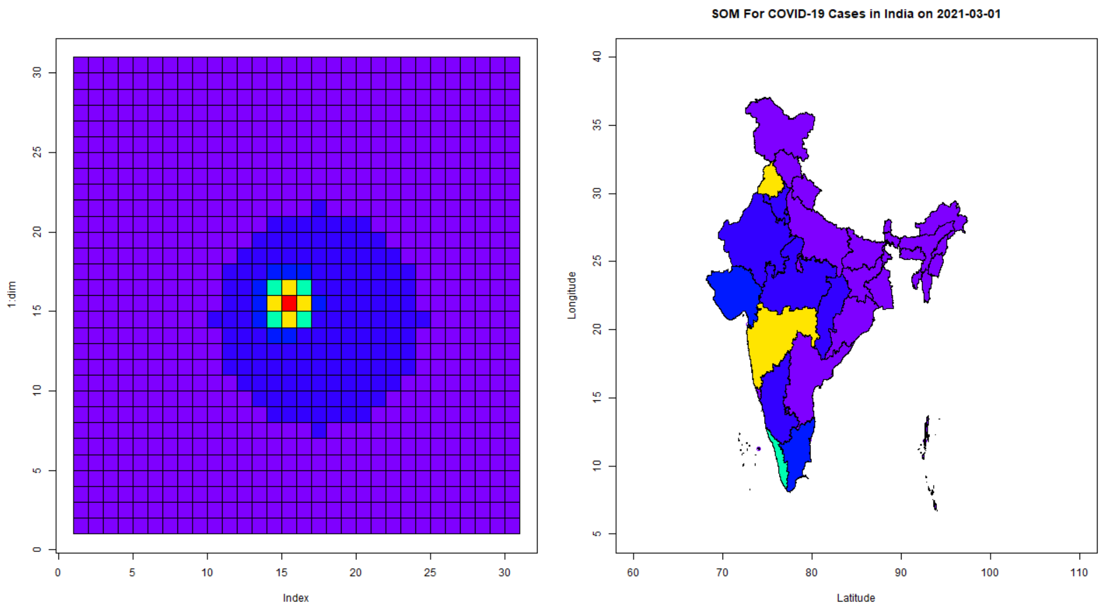
Part 4: Generating the Self Organizing Maps for each date and saving the plots.

```
# Iterating over all the dates present in dataset
for(iteration in 0:(length(date.range)-1)){

    start<-36*iteration+1
    end<-start+36*average.length

    previous.range<-seq(start,start+35)
    later.range<-seq(end,end+35)

    week<-cbind.data.frame(Name = data[1:36,2],
                           Deaths = (data[later.range,3] -
data[previous.range,3])/average.length,
                           Conformed = (data[later.range,4] -
data[previous.range,4])/average.length
    )


    #Note : change below mentioned line to
    #       data.set<-week_1[,-1] if running for individual weeks

    data.set<-week[,-1]  # removing the names


    #--Creating the Grid--#

    #Creating a 4*4 grid using the function defined above.
    set.seed(222)
    grid <- create_grid(30,30,2)

    #--Training the model--#
    y <- SOM(data.set,grid)

    # These are the returned weights for 900 neurons i.e. 30X30 grid
    gridSOM <- y[1]



    # For saving the plot
    path1 <- paste0(dir_out,"Week ")
    img.name<-paste0(path1,iteration+1," ",date.range[iteration+1],".png",sep
= "")
    png(img.name, width = 1280, height = 720)
    par(mfrow =c(1,2))

      #--Retrieving the weights and plotting the map--#

    gridSOM<-matrix(unlist(gridSOM),ncol=2)
    color.rgb<-drawGrid(gridSOM,c(30,30),TRUE)

      #--Indexing showing which state corresponds to which neuron--#

    index<-NULL


    for(i in 1:nrow(data.set)){
        k<-as.matrix(data.set[i,],ncol = 2)
        index<-rbind(index,c(week[i,1],BMU_Vectorised(k,gridSOM)))
      }

      # removing states which are not present in the map
    index<-rbind(index[1:8,],index[8,],index[9:36,])
    index<-index[-c(19,33),]


    index.numbers<-as.numeric(index[,2])
    color.index<-color.rgb[index.numbers]

      # Plotting the grid
    title_string <- paste0("SOM For COVID-19 Cases in India on
",date.range[iteration+1])
    plot(1:100, type ="n", xlim=c(60,110), ylim=c(5,40), xlab="Latitude",
ylab="Longitude", main=title_string)
    for(i in 1:36){
        plot(st_geometry(isro[i,]),col =color.index[i], add =TRUE)
      }

    dev.off()
}
```

Part 5: Generating an animated gif to combine all the plots sequentially.

```
# Obtaining all the maps in one list
imgs <- list.files(dir_out, full.names = TRUE)
img_list <- lapply(imgs, image_read)
# join the images together
img_joined <- image_join(img_list)
# animate at 2 frames per second
img_animated <- image_animate(img_joined, fps = 4)
```

```
# view animated image
img_animated
```



```
# save to disk
image_write(image = img_animated,path = "som_map_animation.gif")
```

Thus we have successfully implemented Self Organizing Maps in R for dimensionality reduction for the COVID-19 cases in India in 2021 and have observed the patterns in the number of cases and deaths over time as the pandemic crossed the country.

Part 6: References

"COVID Data Official Government Website." n.d. https://www.mohfw.gov.in/.

"COVID Data Original Source." n.d. https://www.covid19india.org/.

"COVID Data Source." n.d. https://www.kaggle.com/sudalairajkumar/covid19-in-india.