Shiny map implementation for covid-19 positive cases in sri lanka

```r
  output$mymap<-renderLeaflet({


  iri<-read.csv(text =
getURL("https://raw.githubusercontent.com/ishancoderr/Covid_19_sri_lanka/main/Distribution_co
vid19.csv"))
  iri$Total_positive_cases=cut(iri$totalcase,
                  breaks = c(0,10,100,500,1000,2000,5000,10000),right = FALSE,
                  labels = c("1-10","10-100","100-500","500-1000","1000-2000","2000-
5000","5000-10000"))


  pal=colorFactor(palette = c("yellow","green","orange","red","brown","black","white"),domain =
iri$rangecase)


  leaflet(data = iri) %>%


  addTiles() %>%
  addProviderTiles(providers$Stamen.TonerLite, group = "Toner Lite") %>%
  addProviderTiles(providers$OpenStreetMap, group = "OSM") %>%
  addLayersControl(baseGroups = c( "Toner Lite","OSM")) %>%
  setView(lng=80.65167,lat =7.86,zoom = 7) %>%
  #addMarkers(lng= ~LON,lat = ~ LAT)
  addCircleMarkers(lng= ~LON,lat = ~ LAT,
            color =~pal(Total_positive_cases),
            radius = ~sqrt(totalcase)*1,
            label = paste("",iri$District,"POSITIVE:",iri$totalcase))%>%
  addLegend(position = "bottomright",pal = pal,values=~Total_positive_cases)
```
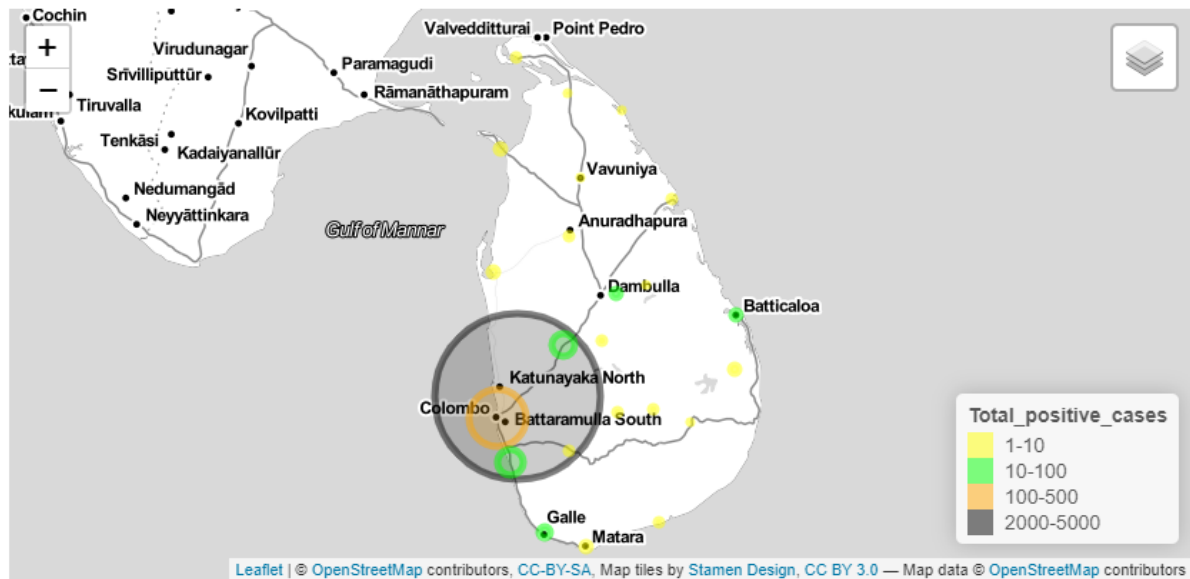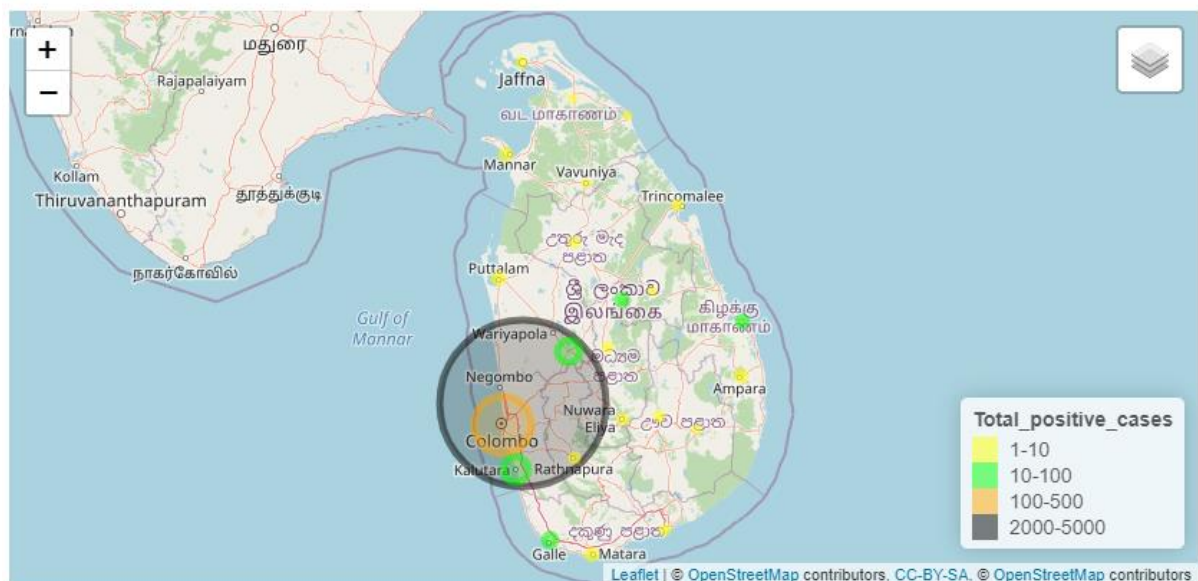
```
})
```

Island wide confirmed cases

Island wide confirmed cases

Full Shiny app

Link→ https://ishanweerakoon11.shinyapps.io/covid_sri_lanka/

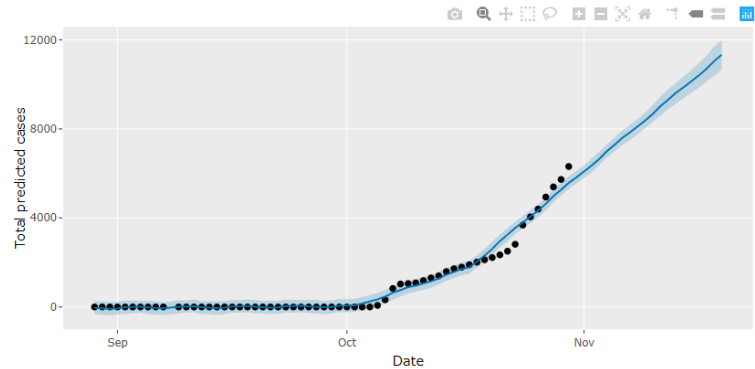Analytics details→ model_report-1.html

                    Data_analysis.html
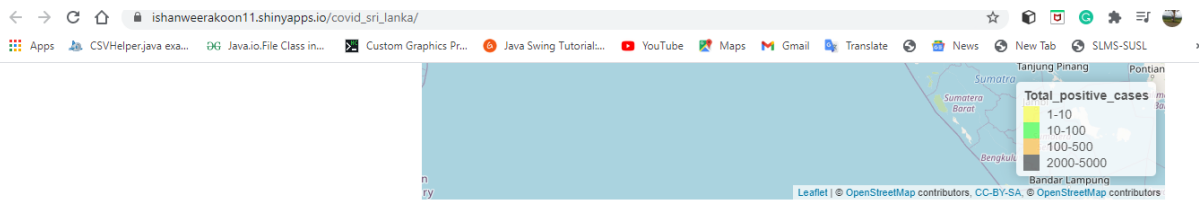
Source code→covid_web_app.r

COVID-PREDICTOR
SRI LANKA
#Team cifra
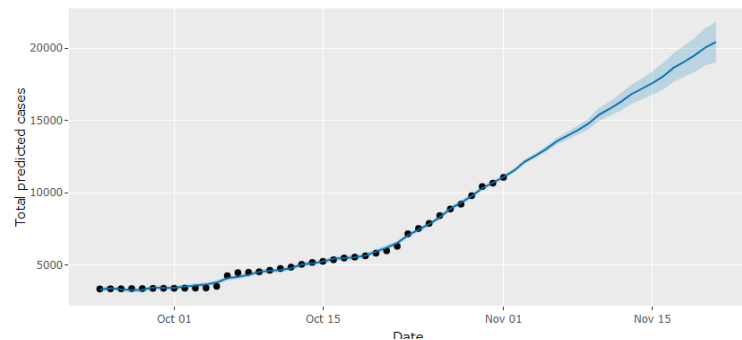
brandex cluster cases for next 20 days

overseas cluster cases for next 20days

Island wide predicted cases for next 20 days

Susceptible, Exposed, Infected, Recovered model for COVID-19 Sri Lanka

S = Susceptible

I = Infective

R = Removed

Assumptions

1. Population remains constants
2. Rate of infective & contacts
3. Infective recover and die in constant rate

r = rate of contact

$$\frac{dS}{dt} = -rIS$$

$$\frac{dI}{dt} = rIS - aI$$

$$\frac{dR}{dt} = aI$$

Implementing these models, we can get these formulas

Here we wish to understand the dynamics of these categories through time t.

- Let Susceptible be denoted as $S(t)$
- Exposed be denoted as $E(t)$
- Infected be denoted as $l(t)$
- Recovered be denoted as $R(t)$
- Morality be denoted as $D(t)$

These are functions through time, hence the (t) notation.

Basically, these are "counts" of the number of people in each category.

For these simple models with two compartments S and I we can write the model as a system of two ordinary differential equation.

$$\frac{\partial S(t)}{\partial t} = -\partial S(t)t(t)$$

$$\frac{\partial l(t)}{\partial t} = -\partial S(t)l(t)$$

Let's do some math to make this simple!

$$\partial S(t) = \partial t\big(-\propto S(t)l(t)\big)$$

$$\partial l(t) = \partial t(\propto S(t)l(t))$$

Put in the fact that the ∂ means difference.

$$S(t) - S(t - \partial t) = \partial t(-\propto S(t)l(t))$$

$$l(t) - l(t - \partial t) = \partial t(\propto S(t)l(t))$$

Some more simplification:

$$S(t) - S(t - \partial t) = \partial t(-\propto S(t)l(t))$$

$$l(t) - l(t - \partial t) = \partial t(\propto S(t)l(t))$$

We for our application we know the difference in time ∂t is 1 day.

$$S(t) - S(t \ \sigma \ 1) = (-\propto S(t-1)l(t-1))$$

$$l(t) - l(t - 1) = (\propto S(t-1)l(t-1))$$

Isolate $S(t)$ and $l(t)$

$$S(t) = S(t-1) -\propto S(t-1)l(t-1)$$

$$l(t) = l(t-1) +\propto S(t-1)l(t-1)$$

A little more complicated model is to add a recovered category.

$$\frac{\partial S(t)}{\partial t} = -\propto S(t)E(t)$$

$$\frac{\partial E(t)}{\partial t} = \propto S(t)E(t) - \beta E(t)$$

$$\frac{\partial I(\delta)}{\partial t} = \beta E(t) - \gamma R(t)$$

$$\frac{\partial R(t)}{\partial t} = \gamma I(t)$$

Which we will do the same process and turn it into:

$$S(t) = S(t-1) -\propto S(t-1)I(t-1)$$

$$E(t) = E(t-1) +\propto S(t-1)E(t-1) - \beta E(t)$$

$$I(t) = I(t-1) - \beta E(t) - \gamma I(t-1)$$

$$R(t) = R(t-1) - \gamma I(t-1)$$

According to these formulas we can implement model.

CODE$\rightarrow$

```
#########################################
#Suspectable, Infected and recovered Model
```

```r
##sri lanka covid 19

#########################################

S0<- 21803000 #sri lanka population

I0<- 1      #Initial infected

R0<- 0     #intial recovers

E0<- 10 #they have virus but they don't know about that

#parameters

alpha1<-1/100000000

alpha2<-1/100000000

beta1<-1/14

gamma1<-1/7

gamma2<-1/21

out1<-matrix(0,ncol = 4,nrow = 1000)

for(i in 1:1000){

  E0n<-E0

  S0n<- S0

  I0n<- I0

  R0n<- R0

  S0<-max(0,S0n-alpha1*E0n*S0n-alpha2*S0n*I0n)

  E0<-max(0,E0n+alpha1*E0n*S0n+alpha2*S0n*I0n-gamma1*E0n-gamma2*E0n)

  I0<-max(0,I0n+gamma1*E0n-beta1*I0n)

  R0<-max(0,R0n+beta1*I0n+gamma2*E0n)

  out1[i,1] <- S0

  out1[i,2] <- E0

  out1[i,3] <- I0

  out1[i,4] <- R0


}

plot(1:1000,out1[,1],type="l",ylim=c(0,21803000))

lines(1:1000,out1[,2],col="orange")

lines(1:1000,out1[,3],col="red")
```
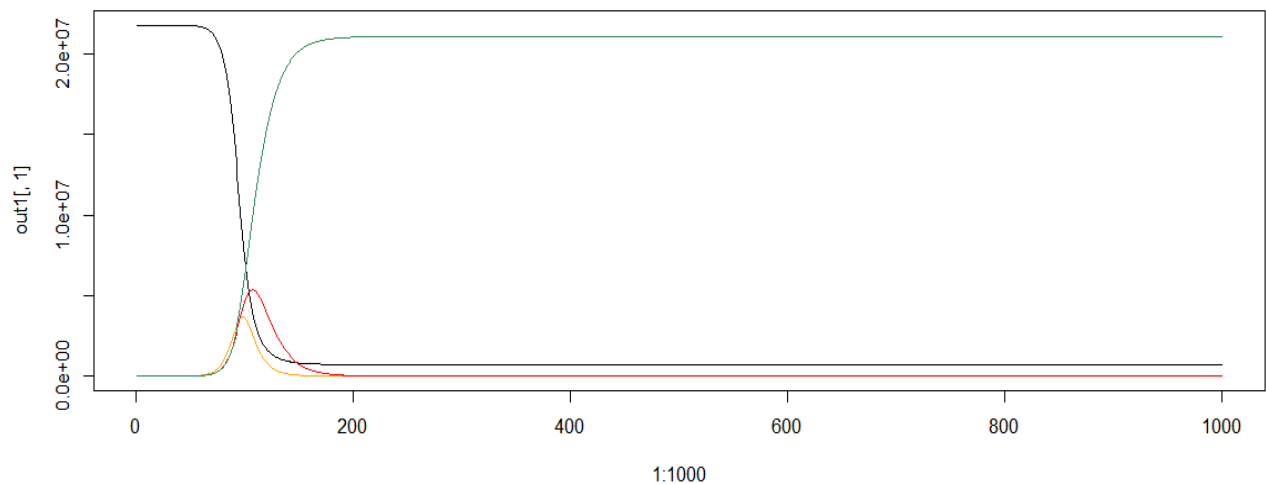
lines(1:1000,out1[,4],col="seagreen")

Output→

Black line-many people are susceptible, and few people are infected, after 100 days it becomes large susceptive people come to low and infected people come to high.

In this programme beta1 variable represent how many people recover from the virus I am getting it as 1/14 every day

Green line-represent who are recovered people

Red line-who are the infected people

In this programme gamma1 variable number of people who are exposed to transition actually been sick

Orange line- exposed to virus and no go to sick they are recovered

In this programme gamma2 variable the come to recover group skipping infection group, they were no infection.

In this programme alpha2 variable some sick people actually interact with healthy people. quarantine valuable in this case. Add this variable we can the considerable difference in chart

Code file→SIR.r