## Week 1 - Solving DEs - Self

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# defining model parameters

```
# initialized params and state variables here ... these are fixed nnonetheless
alpha.0 = 1/3; beta.0 = 0.5; N.0=7900000; prop.val <- FALSE; delta <- 1
times \leftarrow seq(0, 150, by = delta)
S.0 = 7900000; I.0 = 10; R.0 = 0
# alpha: recovery rate, beta: contacts per given time sufficient for spread
params <- c(alpha = alpha.0, beta = beta.0, N=N.0)
# state variables
if(prop.val){
  state <-c(S = S.0/N.0, I=I.0/N.0, R = R.0/N.0)
  state <- c(S = S.0, I=I.0, R = R.0)
# self implementation
RateOfChange.Self <- function(times, state, params)</pre>
 df <- data.frame(time = times)</pre>
 S.list <- c(NULL); I.list <- c(NULL); R.list <- c(NULL)
  # convert the rates into named list
  with(as.list(c(state, params)), {
    for (time in times){
      # this is to ensure that the first values are the initials
      # update the variables 1
      S.list \leftarrow c(S.list, S); I.list \leftarrow c(I.list, I); R.list \leftarrow c(R.list, R);
      # rate of change of subsceptible population
      S.change <- S*(1 - delta*beta*(I/N))
      \#dS \leftarrow (S.change - S)/delta
      # rate of change of the recovered population
      #dR <- alpha*I
      R.change <- R + delta*alpha*I
      # rate of change of the infectious population
      I.change <- N - S.change - R.change
```

```
#dI <- beta*(S/N)*I - alpha*I

# update the variables 2
S <- S.change; I <- I.change; R <- R.change
}

df$S <- S.list; df$I <- I.list; df$R <- R.list
    return(df)
})</pre>
```

```
data <- RateOfChange.Self(times, state, params)
head(data)</pre>
```

```
## time S I R
## 1 0 790000 10.00000 0.00000
## 2 1 7899995 1.666667 3.333333
## 3 2 7899994 1.944444 3.888889
## 4 3 7899993 2.268517 4.537037
## 5 4 7899992 2.646602 5.293209
## 6 5 7899991 3.087701 6.175410
```

```
# make a combine plot
ggplot(data = data, aes(time)) + geom_line(aes(y = S, colour = "blue")) +
geom_line(aes(y = I, colour = "red")) +
geom_line(aes(y = R, colour = "green"))
```

