

SIR immunity shield

Code ▾

This R Markdown will recreate the SIR immunity shield model presented by Weitz et al., 2020. (You can access the article [here](https://www-nature-com/articles/s41591-020-0895-3/).)[\(https://www-nature-com/articles/s41591-020-0895-3/\)](https://www-nature-com/articles/s41591-020-0895-3/)

The original code was produced in MATLAB and can be viewed on the team's github. I recreated the model in R for an infectious disease midterm and am providing the code below!

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```
## create empty list for immune data to be pasted
total_s = as.list(c(1:30))
## base code is from lecture 1 scripts - sir_desolve.R - by Dr. Max Lau at Emory
require(deSolve)

## define the model ##
sir = function(t, y, parms) {
  # y is a list. each element is a vector storing values of a state variable over time
  S = y[1]
  I = y[2]
  R = y[3]
  # parms is a list storing parameter values
  beta = parms["beta"]
  gamma = parms["gamma"]
  N = parms["N"]
  alpha = parms["alpha"]
  # Define ode
  dS = -beta * S * I / (1 + alpha * R)
  dI = beta * S * I / (1 + alpha * R) - (gamma * I)
  dR = gamma * I
  res = c(dS, dI, dR)
  # Return list of the state variable values
  list(res)
}
```

The above is the model function. The standard SIR formulas have been adapted to reflect those in formula one of the journal article (i.e. replace N with $1 + \alpha R$ in the dS and dI equations).

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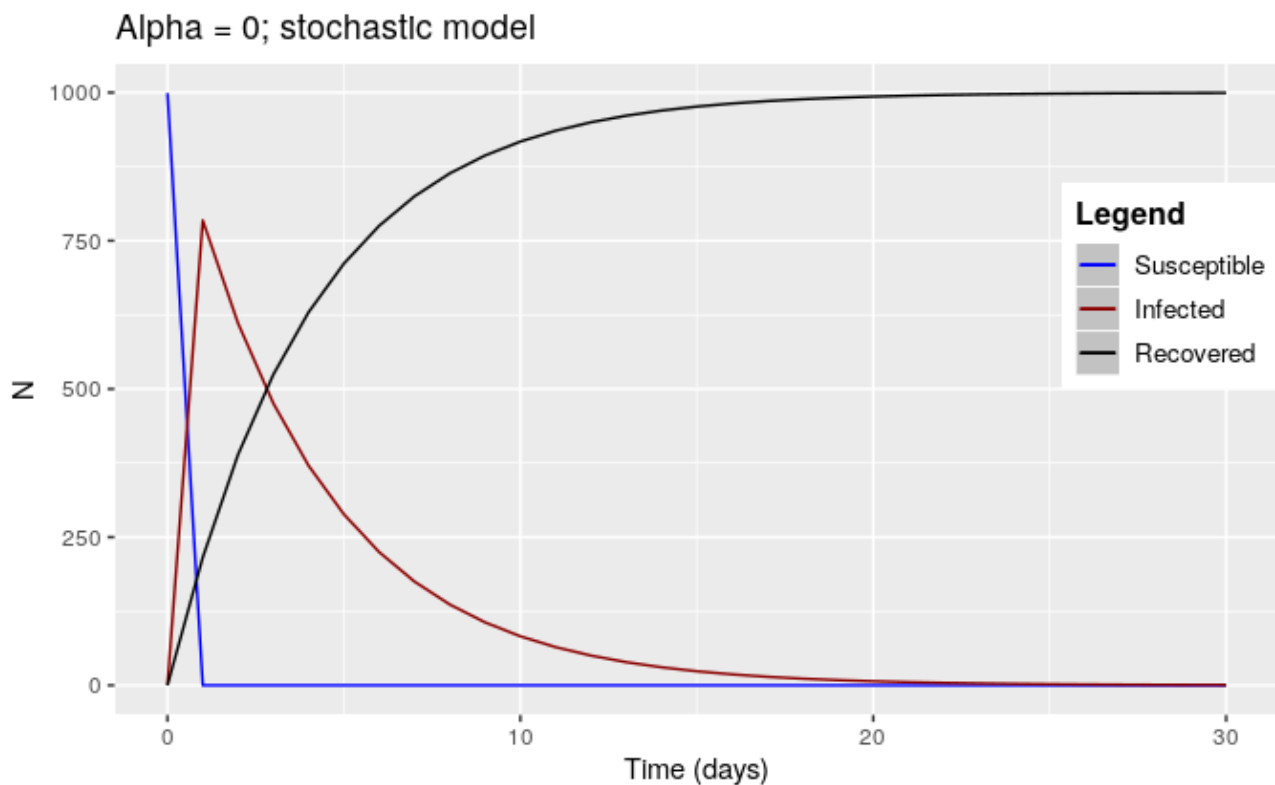
```
## set parameters and initial conditions ##
times = seq(0, 30, by = 1)
parms = c(N = 1000, beta = 0.25, gamma = 0.25, alpha=0)
start = c(S = 999, I = 1, R = 0) # note that S + I + R = N
```

This model is looking at change over 30 days. The transmission rate β is 0.25, and recovery rate γ is 0.25. In the initial model, alpha is zero. By doing this, we can compare the “normal” homogenous mixing SIR model to the SIR model with α built in. For each run, only the alpha value is being changed per run.

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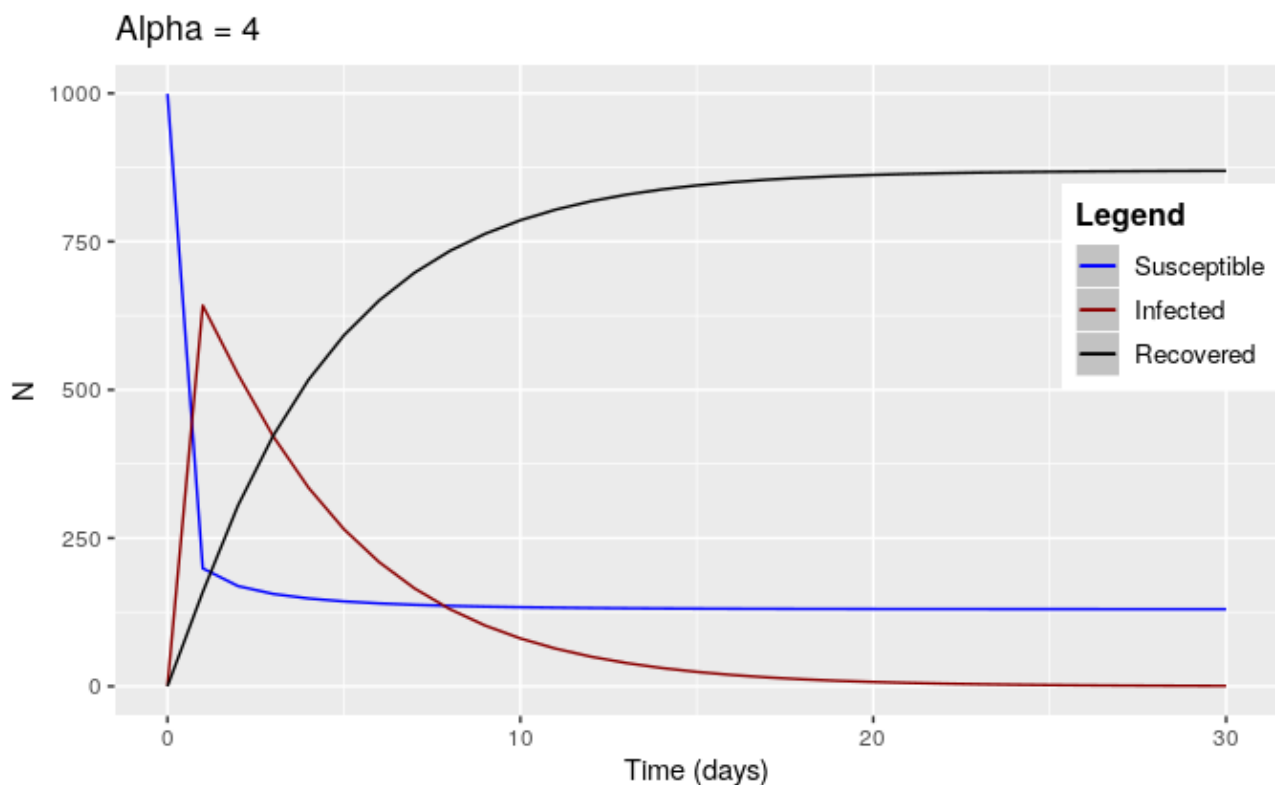
```
## perform numerical integration i.e. run the model ##
out=ode(y=start, times=times, func=sir, parms= parms)
## show and plot model outputs ##
out=as.data.frame(out)
total_s$alpha_0 = out$I

ggplot(out, aes(x = time)) +
  geom_line(aes(y=S,colour="Susceptible"))+
  geom_line(aes(y=I,colour="Infected"))+
  geom_line(aes(y=R,colour="Recovered"))+
  labs(x="Time (days)", y = "N", title= "Alpha = 0; stochastic model") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid"))+
  scale_colour_manual("Legend",
                      breaks=c("Susceptible","Infected","Recovered"),
                      values=c("blue","darkred","black"))
```


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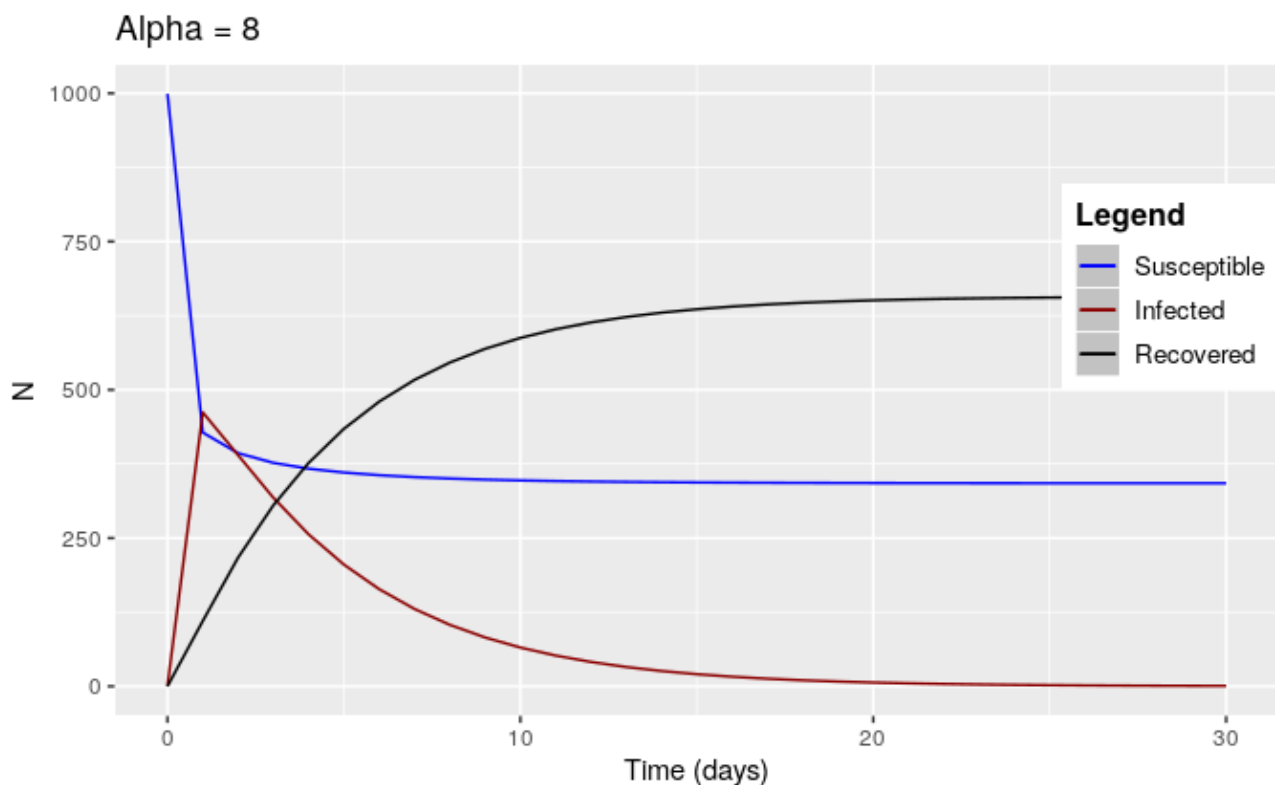
```
#####
parms = c(N = 1000, beta = 0.25, gamma = 0.25, alpha=4)
## perform numerical integration i.e. run the model ##
out=ode(y=start, times=times, func=sir, parms= parms)
## show and plot model outputs ##
out=as.data.frame(out)
total_s$alpha_4 = out$I

ggplot(out, aes(x = time)) +
  geom_line(aes(y=S,colour="Susceptible"))+
  geom_line(aes(y=I,colour="Infected"))+
  geom_line(aes(y=R,colour="Recovered"))+
  labs(x="Time (days)", y = "N", title= "Alpha = 4") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid"))+
  scale_colour_manual("Legend",
                      breaks=c("Susceptible","Infected","Recovered"),
                      values=c("blue","darkred","black"))
```


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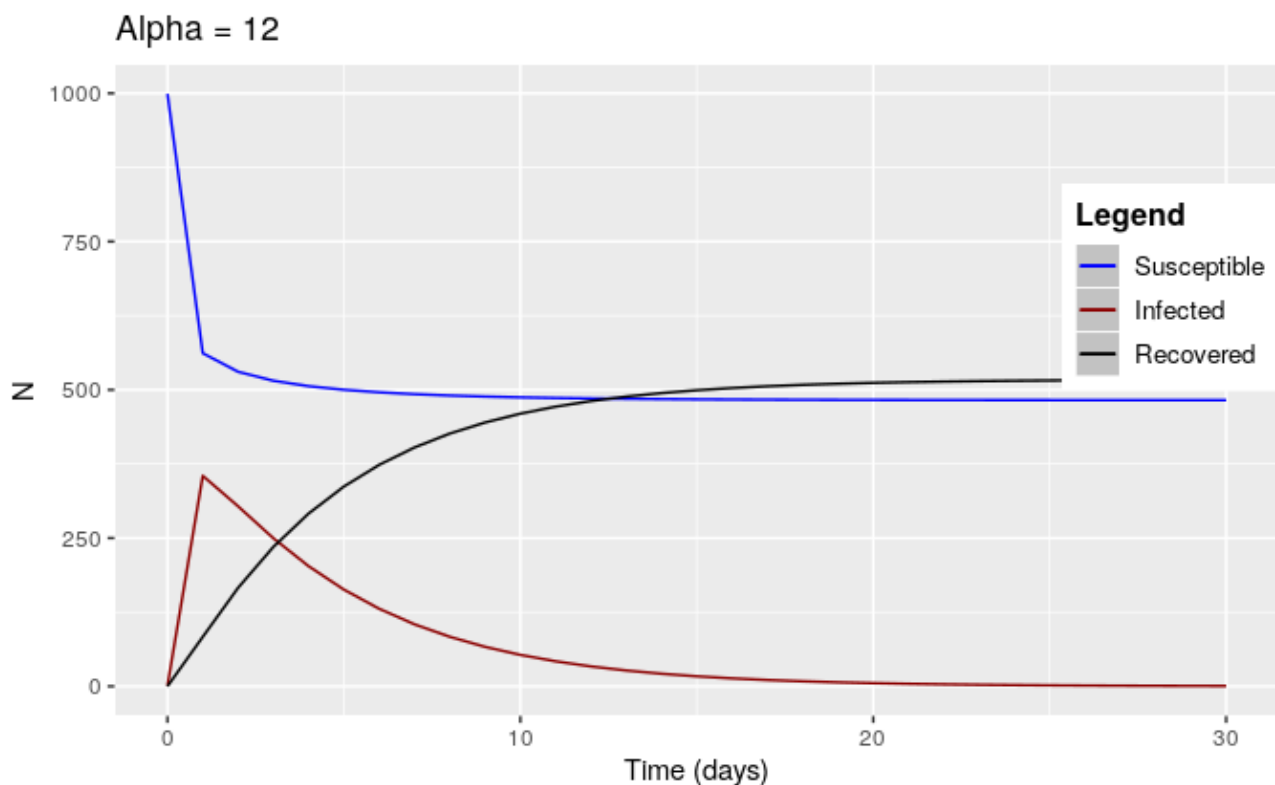
```
#####
parms = c(N = 1000, beta = 0.25, gamma = 0.25, alpha=8)
## perform numerical integration i.e. run the model ##
out=ode(y=start, times=times, func=sir, parms= parms)
## show and plot model outputs ##
out=as.data.frame(out)
total_s$alpha_8 = out$I

ggplot(out, aes(x = time)) +
  geom_line(aes(y=S,colour="Susceptible"))+
  geom_line(aes(y=I,colour="Infected"))+
  geom_line(aes(y=R,colour="Recovered"))+
  labs(x="Time (days)", y = "N", title= "Alpha = 8") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid"))+
  scale_colour_manual("Legend",
                      breaks=c("Susceptible","Infected","Recovered"),
                      values=c("blue","darkred","black"))
```


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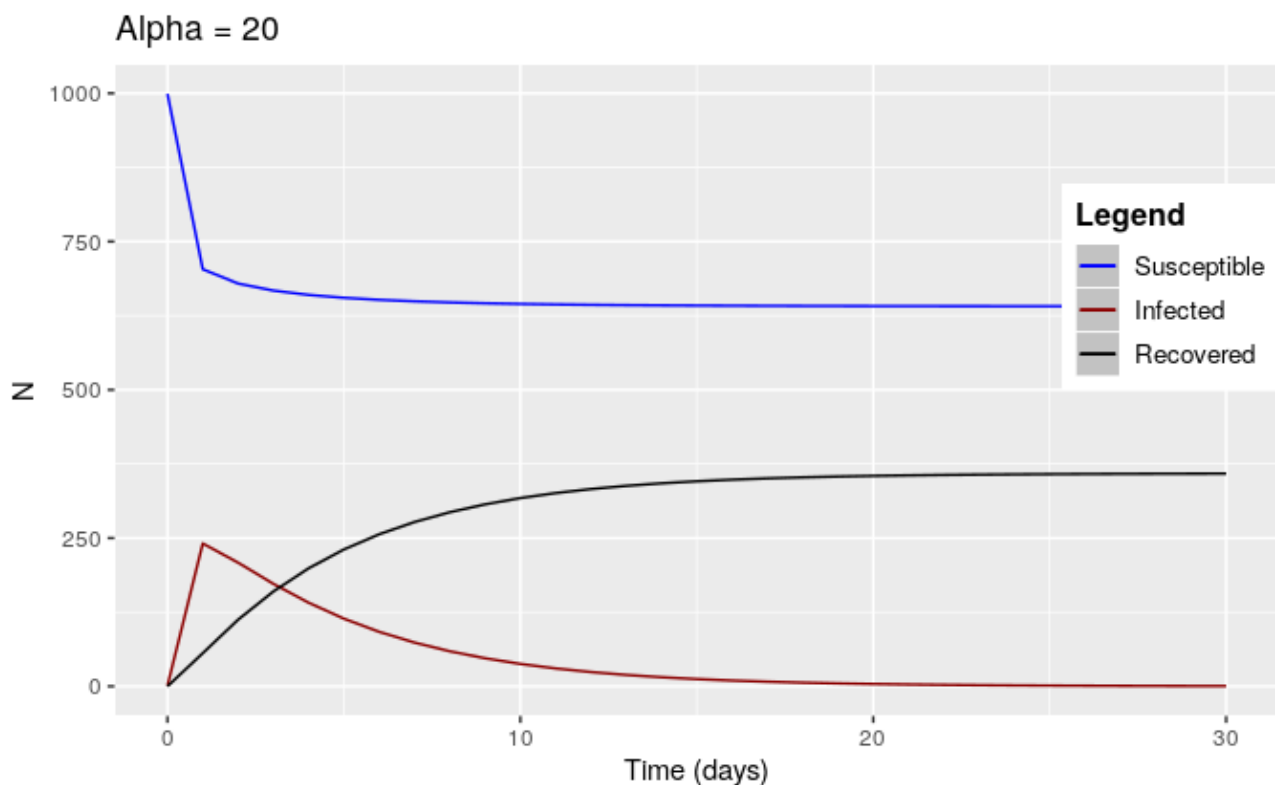
```
#####
parms = c(N = 1000, beta = 0.25, gamma = 0.25, alpha=12)
## perform numerical integration i.e. run the model ##
out=ode(y=start, times=times, func=sir, parms= parms)
## show and plot model outputs ##
out=as.data.frame(out)
total_s$alpha_12 = out$I

ggplot(out, aes(x = time)) +
  geom_line(aes(y=S,colour="Susceptible"))+
  geom_line(aes(y=I,colour="Infected"))+
  geom_line(aes(y=R,colour="Recovered"))+
  labs(x="Time (days)", y = "N", title= "Alpha = 12") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid"))+
  scale_colour_manual("Legend",
                      breaks=c("Susceptible","Infected","Recovered"),
                      values=c("blue","darkred","black"))
```


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```
#####
parms = c(N = 1000, beta = 0.25, gamma = 0.25, alpha=20)
## perform numerical integration i.e. run the model ##
out=ode(y=start, times=times, func=sir, parms= parms)
## show and plot model outputs ##
out=as.data.frame(out)
total_s$alpha_20 = out$I

ggplot(out, aes(x = time)) +
  geom_line(aes(y=S,colour="Susceptible"))+
  geom_line(aes(y=I,colour="Infected"))+
  geom_line(aes(y=R,colour="Recovered"))+
  labs(x="Time (days)", y = "N", title= "Alpha = 20") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid"))+
  scale_colour_manual("Legend",
                      breaks=c("Susceptible","Infected","Recovered"),
                      values=c("blue","darkred","black"))
```


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```
#####

ts <- as.data.frame(total_s)
ts <- ts %>% dplyr::select(alpha_0:alpha_20)
ts$time <- out$time
ggplot(ts, aes(x = time)) +
  geom_line(aes(y=alpha_0, colour="Alpha 0"))+
  geom_line(aes(y=alpha_4, colour="Alpha 4"))+
  geom_line(aes(y=alpha_8, colour="Alpha 8"))+
  geom_line(aes(y=alpha_12, colour="Alpha 12"))+
  geom_line(aes(y=alpha_20, colour="Alpha 20"))+
  labs(x="Time (days)", y = "N", title= "Proportion Infected curve for different alpha va
lues, like Figure 2A") +
  theme(legend.justification=c(1,0), legend.position=c(1,0.5))+
  theme(legend.title=element_text(size=12,face="bold"),
        legend.background = element_rect(fill='#FFFFFF',
        size=0.5,linetype="solid"),
        legend.text=element_text(size=10),
        legend.key=element_rect(colour="#FFFFFF",
        fill='#C2C2C2',
        size=0.25,
        linetype="solid")) +
  scale_colour_manual("Legend",
                      breaks=c("Alpha 0", "Alpha 4", "Alpha 8", "Alpha 12", "Alpha 2
0"),
                      values=c("steelblue","darkblue","blue", "lightskyblue", "lightsky
blue1"))
```

