

class_9_canvas

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#1. Loading and Installing EpiModel and NetDiffuseR

#loading the libraries I need

```
library(igraph)
library(ggraph)
library(EpiModel)
library(netdiffuseR)
library(gplots)
library(ggplot2)
library(ggpubr)
library(parallel)
library(dplyr)
library(tidyr)
```

#2. Loading in Data as iGraph

#loading in my nodes data

```
nodes <- read.csv('/Users/TomTheIntern/Desktop/Mendoza/Mod 4/Networks/Lab 2/nodelist.csv')
summary(nodes)
```

##	ID	Name	Age	Gender
##	Min. : 1.00	Length:12	Min. :21.00	Length:12
##	1st Qu.: 3.75	Class :character	1st Qu.:23.00	Class :character
##	Median : 6.50	Mode :character	Median :36.50	Mode :character
##	Mean : 6.50		Mean :38.00	
##	3rd Qu.: 9.25		3rd Qu.:45.75	
##	Max. :12.00		Max. :65.00	

#loading in my edges data

```
edges <- read.csv("/Users/TomTheIntern/Desktop/Mendoza/Mod 4/Networks/Lab 2/edgelist.csv")
summary(edges)
```

##	ego_num	alter_num	ego	alter
##	Min. : 1.000	Min. : 1.000	Length:40	Length:40
##	1st Qu.: 2.750	1st Qu.: 2.750	Class :character	Class :character
##	Median : 5.000	Median : 5.000	Mode :character	Mode :character
##	Mean : 5.575	Mean : 5.575		
##	3rd Qu.: 9.000	3rd Qu.: 9.000		
##	Max. :12.000	Max. :12.000		
##	type	strength		

```
## Length:40      Min.    :1.00
## Class :character 1st Qu.:2.00
## Mode  :character Median :4.00
##              Mean   :3.45
##              3rd Qu.:4.25
##              Max.    :5.00
```

```
#making it into an iGraph
```

```
net <-igraph::graph_from_data_frame(edges, directed = F, vertices = nodes)
net
```

```
## IGRAPH 387756f UN-- 12 40 --
## + attr: name (v/c), Name (v/c), Age (v/n), Gender (v/c), ego (e/c),
## | alter (e/c), type (e/c), strength (e/n)
## + edges from 387756f (vertex names):
## [1] 1 --2 1 --2 1 --5 1 --5 1 --3 1 --3 1 --4 1 --4 1 --6 1 --6
## [11] 1 --7 1 --7 1 --10 1 --10 2 --4 2 --4 2 --3 2 --3 3 --4 3 --4
## [21] 4 --6 4 --6 4 --5 4 --5 3 --5 3 --5 9 --10 9 --10 10--11 10--11
## [31] 10--12 10--12 9 --12 9 --12 11--12 11--12 6 --7 6 --7 7 --8 7 --8
```

#3. Running the Contagion Model

```
#base infection settings
```

```
param <- EpiModel::param.dcm(Inf.prob = 0.3, act.rate = 0.3)
```

```
# s.num = num initially susceptible, i.num = num initial infection
```

```
init <- EpiModel::init.dcm(s.num = 63, i.num = 1)
```

```
# type = contagion type to be modeled, nsteps = time steps to solve over
```

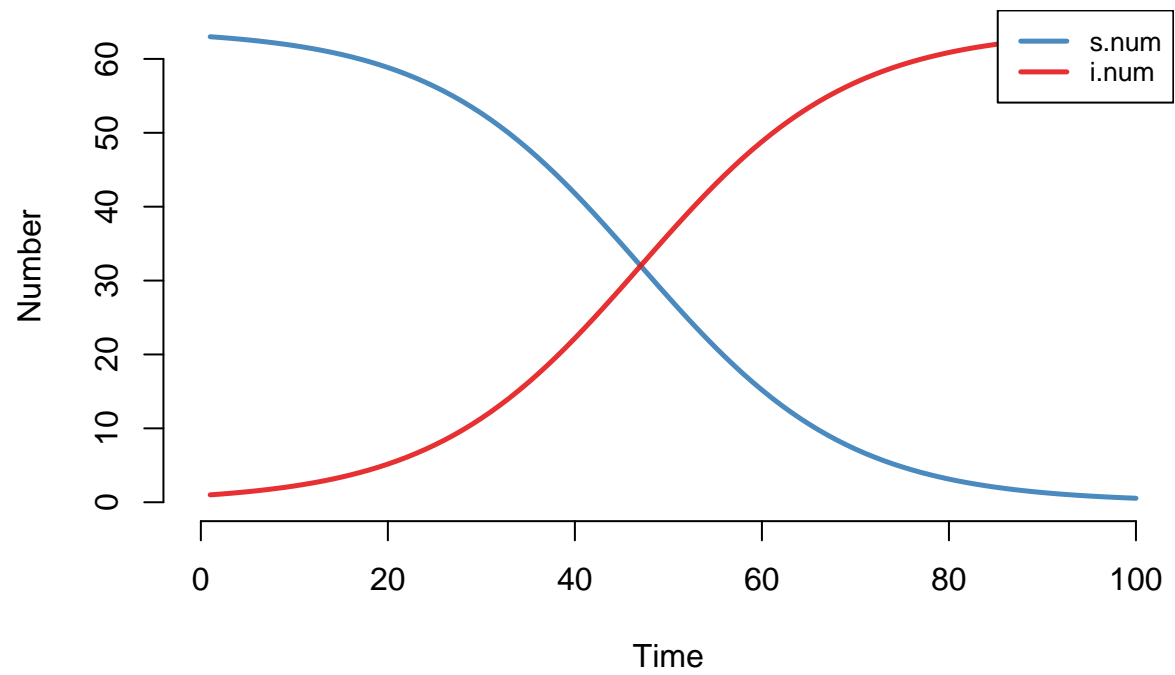
```
control <- EpiModel::control.dcm(type = "SI", nsteps = 100)
```

```
# We then combine those parameters in the dcm function.
```

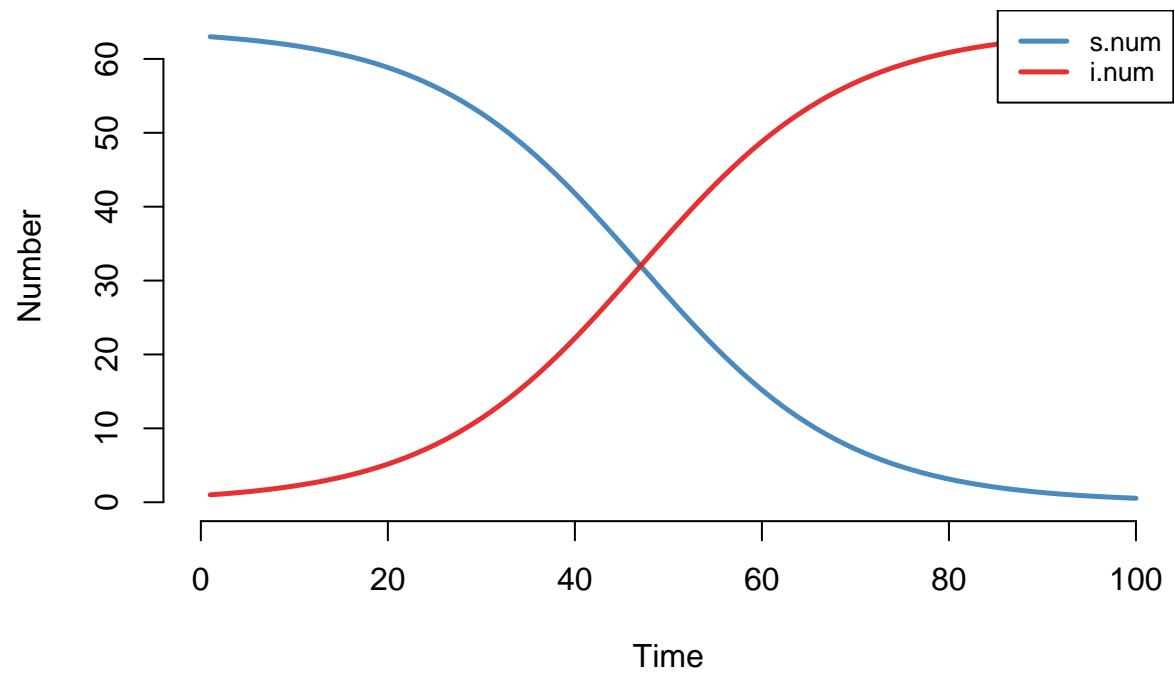
```
# We save that function as our model.
```

```
si_mod <- EpiModel::dcm(param, init, control)
```

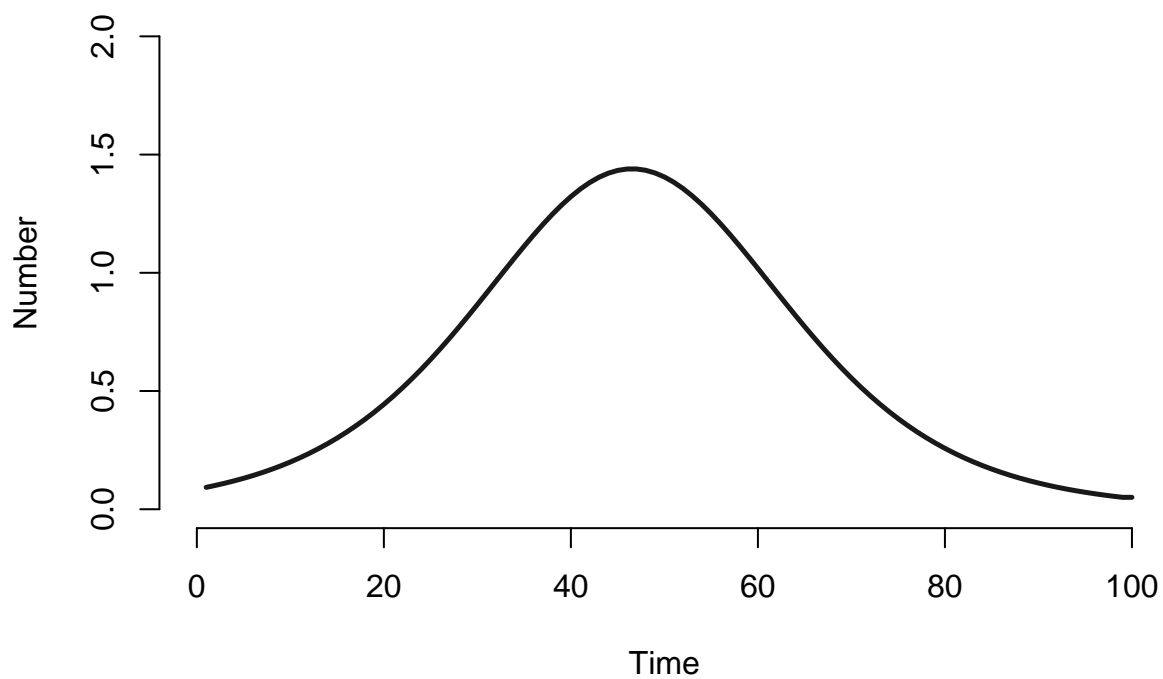
```
plot(si_mod)
```



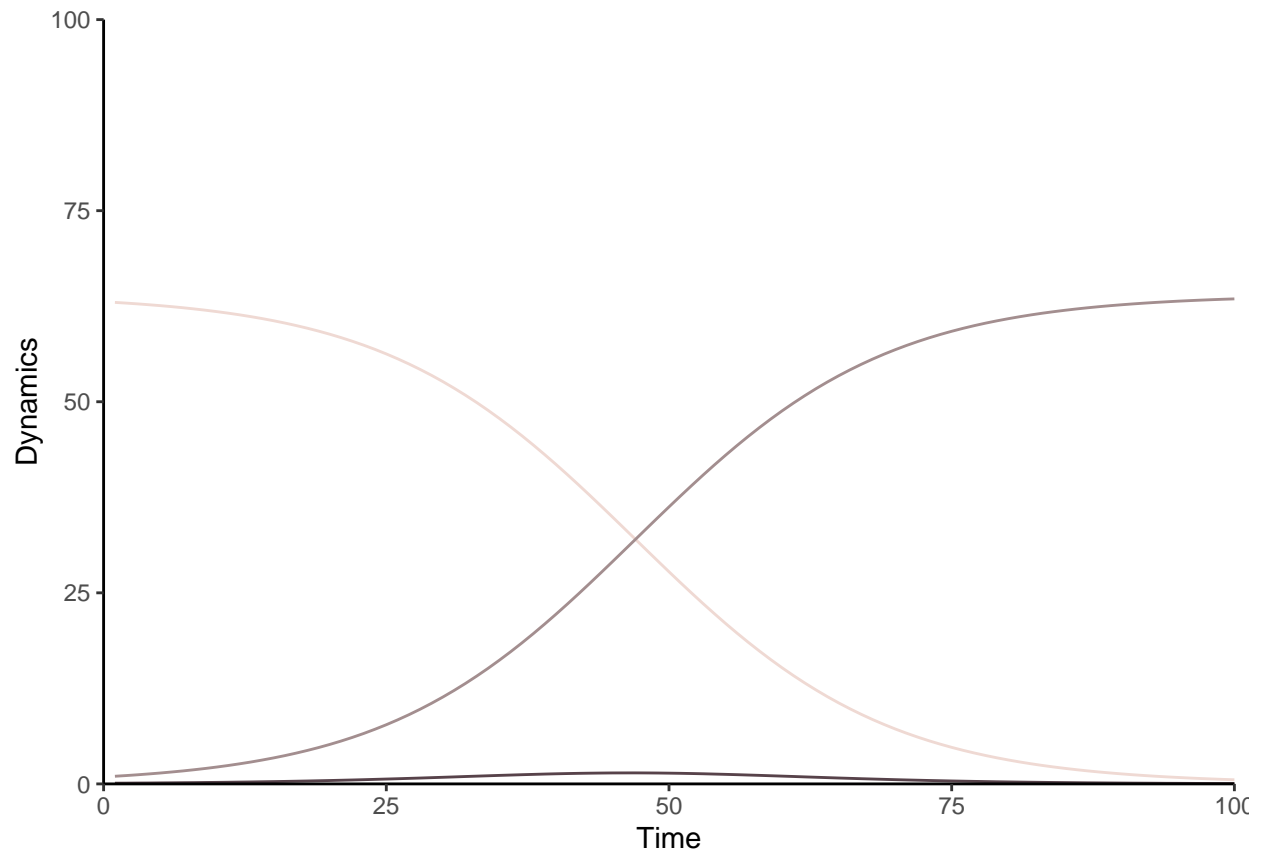
```
#Making it into a dataframe  
si_mod_df <- as.data.frame(si_mod)  
  
plot(si_mod)
```



```
plot(si_mod, y = "si.flow")
```



```
#Using the df to make a plot
ggplot2::ggplot(si_mod_df) +
  geom_line(aes(x = time, y = s.num), colour="#EFD9D3") +
  geom_line(aes(x = time, y = i.num), colour="#A38E8F") +
  geom_line(aes(x = time, y = si.flow), colour="#57424A") +
  scale_x_continuous(limits = c(0,100), expand = c(0, 0)) +
  scale_y_continuous(limits = c(0,100), expand = c(0, 0)) +
  xlab("Time") + ylab("Dynamics") +
  theme_classic()
```



#4. Analysis

Assuming that time is in days, it looks like susceptibility and infected intersect around day 47, with a peak infection flow to match. In general, because I lowered the infection rate to .30, it took the infection much longer to spread through the network.