

Social Networks Worksheet

Mathew Kiang

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Download the code*

<https://git.io/vy8vG>

Also download the data

<https://git.io/vy8v0>

**Question 1: Import a network, plot it, plot
the degree distribution**

Import a network

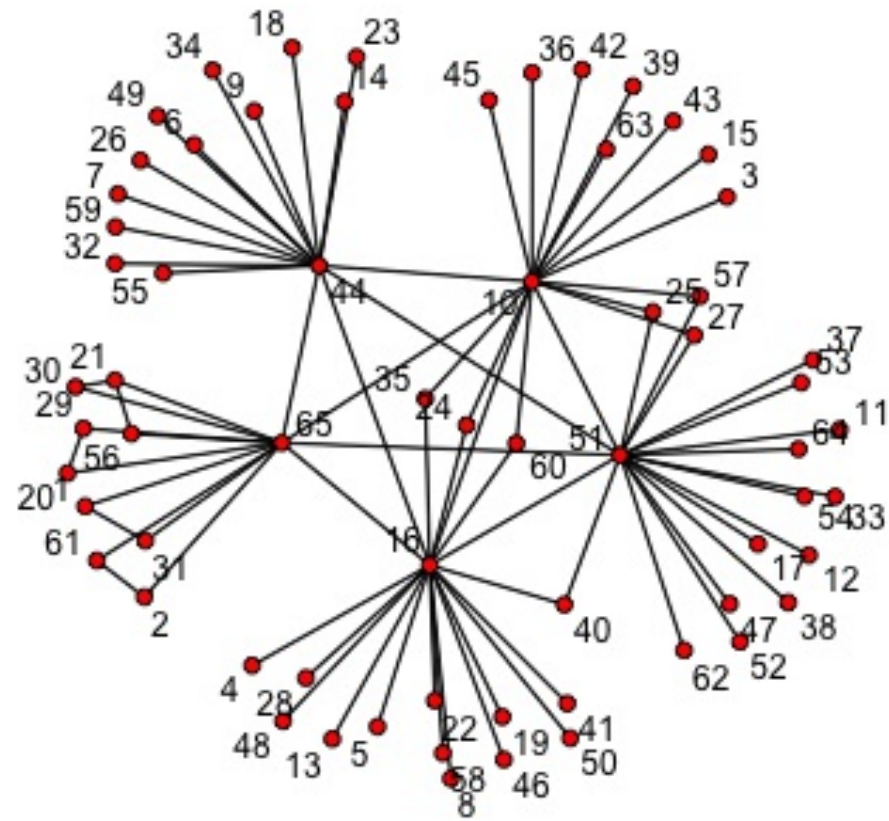
```
## Load the libraries (install if necessary)
library(network)
library(tidyverse)
source('./code/network_practical.R')

## Load up data (make sure you have the right file path)
mat1 <- read_csv('./data/unnamed_contact_network.csv', trim_ws = TRUE)

## Convert the matrix into a network
net1 <- as.network(mat1, directed = FALSE)
```

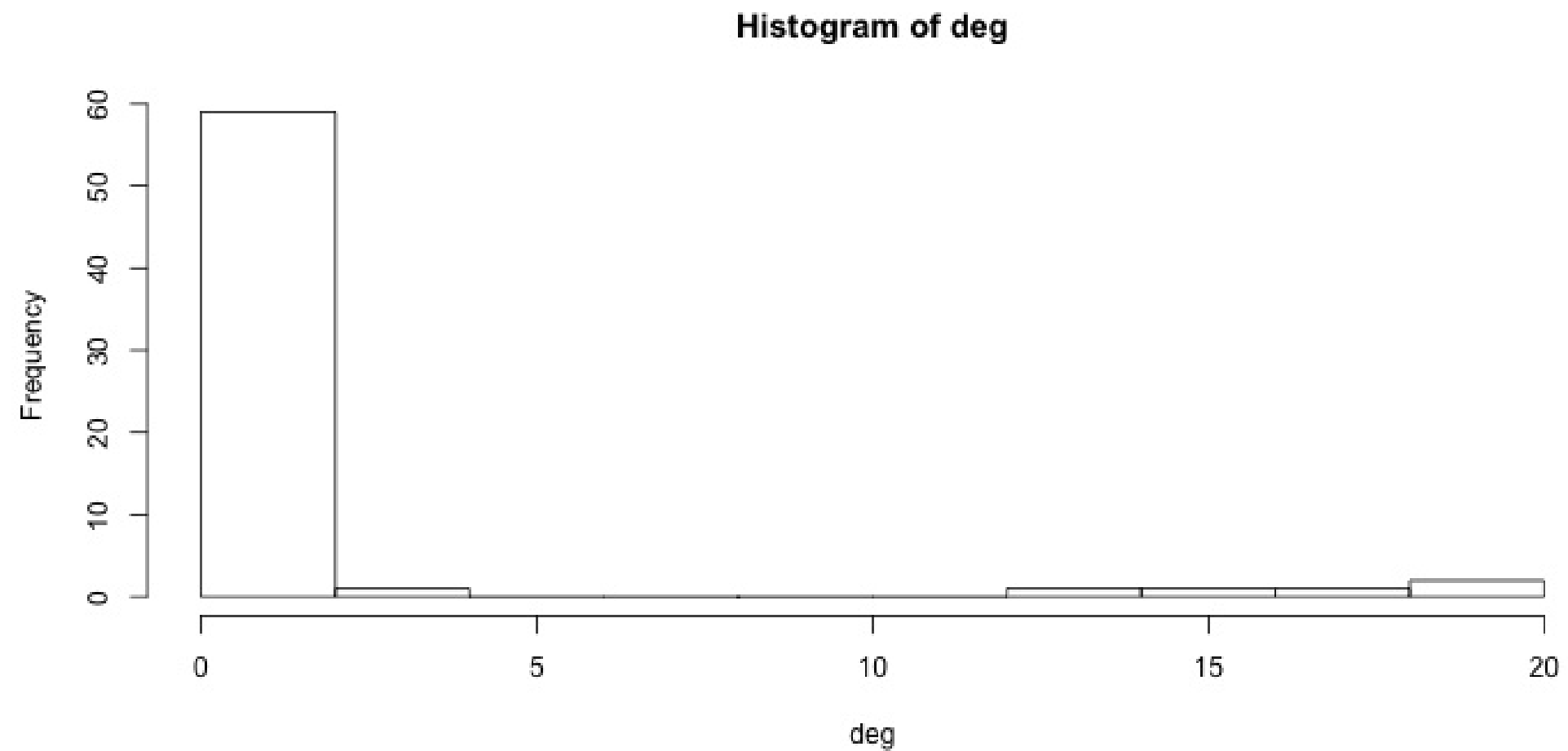
Plot the network

```
## Take a look at the network  
plot(net1, label = network.vertex.names(net1))
```



Plot the degree distribution

```
deg <- NULL
for(i in 1:network.size(net1)) {
  deg <- rbind(deg, length(get.neighborhood(net1, i)))
}
hist(deg)
```



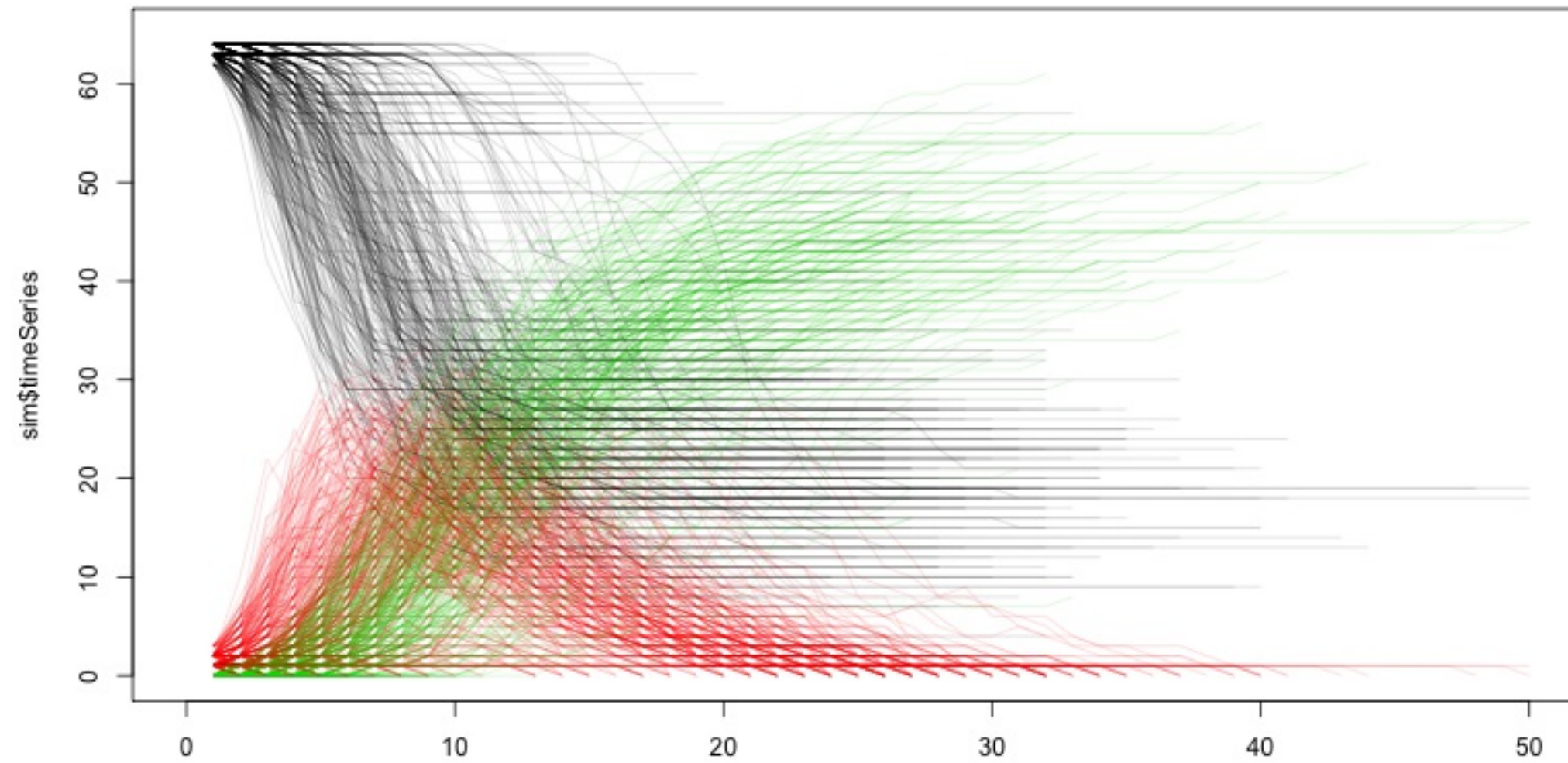
Visualizing randomness

500 simulations plotted

```
## This just loops through n_sims times and makes that many lines/simulations
## NOTE: There's a difference between matplot and matlines
n_sims <- 500
for (i in 1:n_sims) {
  sim <- networkPractical(net1, .2, .2, runTime = 50)
  ## If it is the first simulation, we need to create the plot canvas
  if (i == 1) {
    matplot(sim$timeSeries, lty = 1, type = "l", xlim = c(0, 50),
            ylim = c(0, network.size(net1)), col = alpha(1:3, .15))
    ## If it is not the first one, we just draw on top of the existing canvas
  } else {
    matlines(sim$timeSeries, lty = 1, type = "l", col = alpha(1:3, .15))
  }
}
```

Play with the parameters and see how this affects the plots.

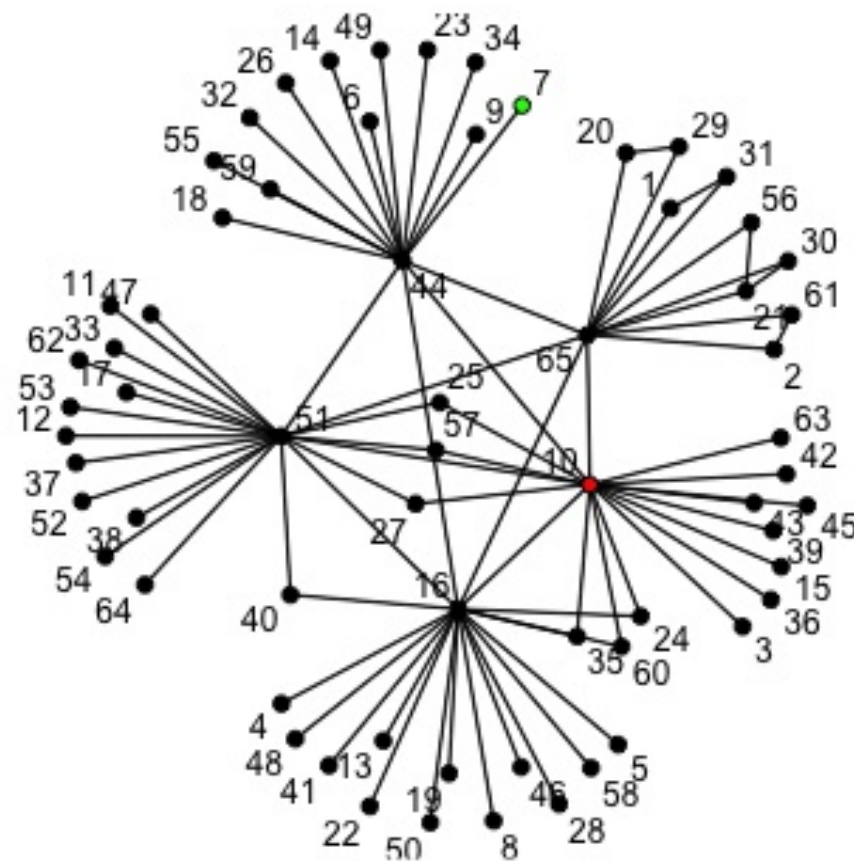
500 simulations plotted



**How does the starting infectious person
change our model?**

Plot the network

```
vert_cols <- rep("black", network.size(net1))  
vert_cols[c(7, 10)] <- c("green", "red")  
plot(net1, label = network.vertex.names(net1), vertex.col = vert_cols)
```

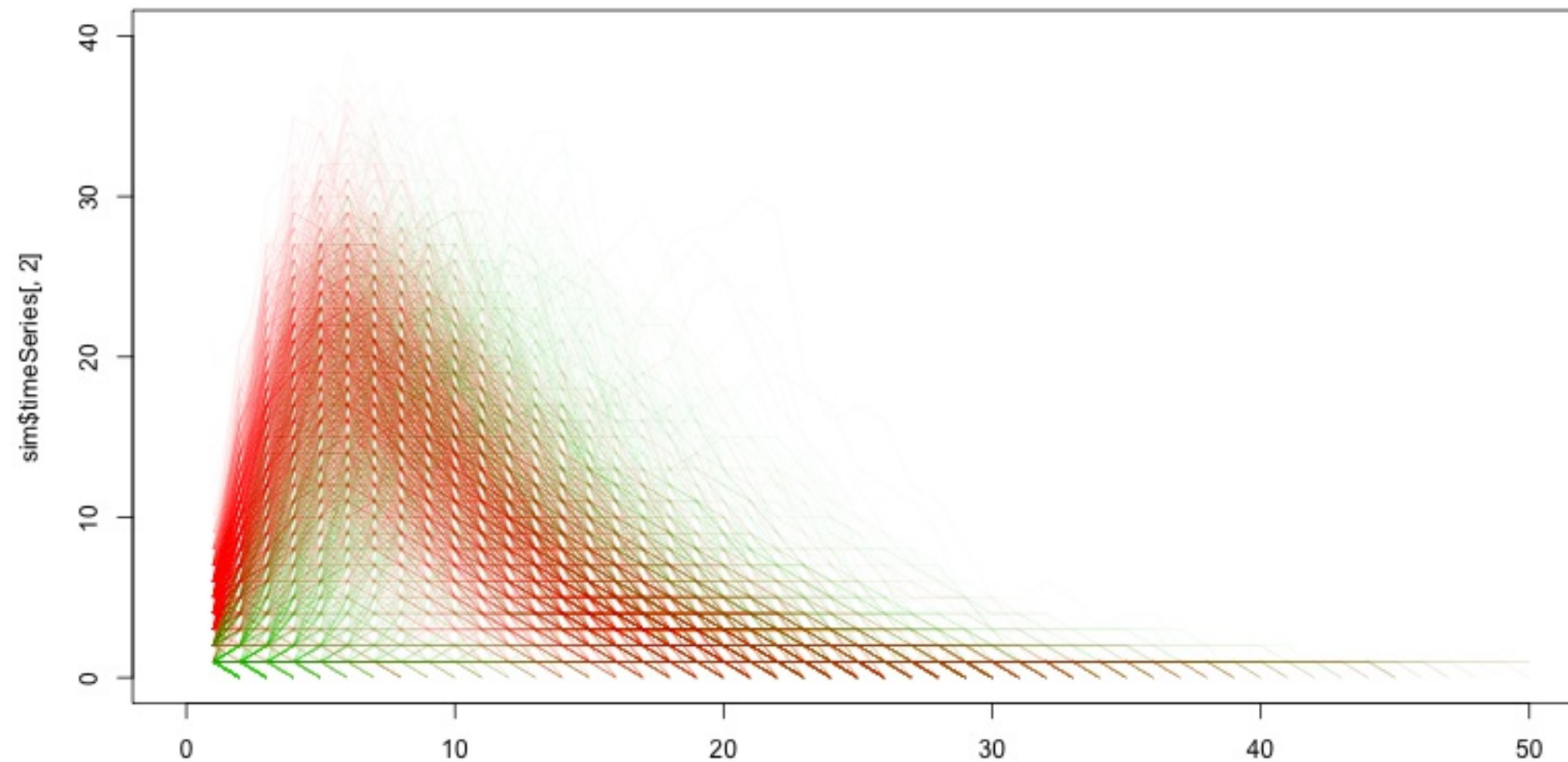


Node 7 (green) vs Node 10 (red)

```
n_sims <- 2000
for (i in 1:n_sims) {
  sim <- networkPractical(net1, .2, .2, runTime = 50, start_infected = 7)
  sim2 <- networkPractical(net1, .2, .2, runTime = 50, start_infected = 10)
  ## If it is the first simulation, we need to create the plot canvas
  if (i == 1) {
    matplot(sim$timeSeries[, 2], lty = 1, type = "l", xlim = c(0, 50),
            ylim = c(0, 40), col = alpha(3, .03))
    matlines(sim2$timeSeries[, 2], lty = 1, type = "l",
             col = alpha(2, .03))
    ## If it is not the first one, we just draw on top of the existing canvas
  } else {
    matlines(sim$timeSeries[, 2], lty = 1, type = "l", col = alpha(3, .03)
    matlines(sim2$timeSeries[, 2], lty = 1, type = "l",
             col = alpha(2, .03))
  }
}
```

Modified the loop from before so that now we run two simulations -- one starting on Node 7 (green lines) and one starting on Node 10 (red lines). We plot only the infectious curve.

Node 7 (green) vs Node 10 (red)



What does the variation between the two colors tell you? What does this imply for network structure and infectious diseases?

That's it.

Thanks