Social Network Analysis Home Assignment 4

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Contents

Network Epidemics

Please send your reports to network.hse.2016@gmail.com with the subject of of the following structure: *[MAGOLEGO SNA 2016] {LastName} {First Name} HW{Number}*

Late submission policy: -1 point per day

Use this file as a template for your report.
Support your computations with figures and comments. Send ONLY .Rmd versions of your report.

```
##
## Attaching package: 'igraph'

## The following objects are masked from 'package:stats':
##
##     decompose, spectrum

## The following object is masked from 'package:base':
##
##     union
```

SIR Model

You need to perform epidemic SIR model on different types of networks: Try different parameters for network generation

```
gl <- list()
gl$ba <- barabasi.game(n = 6301,m = 4 , directed=FALSE)
gl$er <- erdos.renyi.game(n = 6301, p.or.m = 0.001, type=c("gnp"))
gl$ws <- watts.strogatz.game(dim = 1, size = 6301, nei = 3, p = 0.01)
data <- read.table("Net.txt")
data <- t(as.matrix(data))
data <- data+1
gl$net <- graph(data)
ev_er <- evcent(gl$er)$value
ev_ba <- evcent(gl$ba)$value
ev_ws <- evcent(gl$ws)$value
ev_net <- evcent(gl$net)$value
no.clusters(gl$er)
```

```
## [1] 19
```

```
no.clusters(gl$ba)
```

```
## [1] 1
```

```
no.clusters(gl$ws)
```

```
## [1] 1
```

```
no.clusters(gl$net)
```

```
## [1] 2
```

There are disconnected graphs! Moreover perform modeling on real peer-to-peer network here

Your goal is to perform a research on epidemics: Use different values of parameters listed below

```
beta <- 2
gamma <- 4
ntrials <- 100

# Running function sir for each element of list gl (list with graphs)
sim <- lapply(gl, sir, beta=beta, gamma=gamma, no.sim=ntrials)
```

```
## Warning in .Call("R_igraph_sir", graph, beta, gamma, no.sim, PACKAGE =
## "igraph"): At sir.c:126 :Edge directions are ignored in SIR model
```

at least 3 different versions, for example:

- betta (4 6 8)
- gamma (8 6 2)
- niter (100 500 1000)

For some reason **beta** *and* **gamma** *parameters should not be set below 0 and 1. Looks like they are somehow normilized during simulation.*

The code below can help you with plotting

```
x.max <- max(sapply(sapply(sim, time_bins), max))
y.max <- 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NI"]]), max, na.rm=TRUE))

plot(time_bins(sim$er),  median(sim$er)[["NI"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NI"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NI"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NI"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)
```
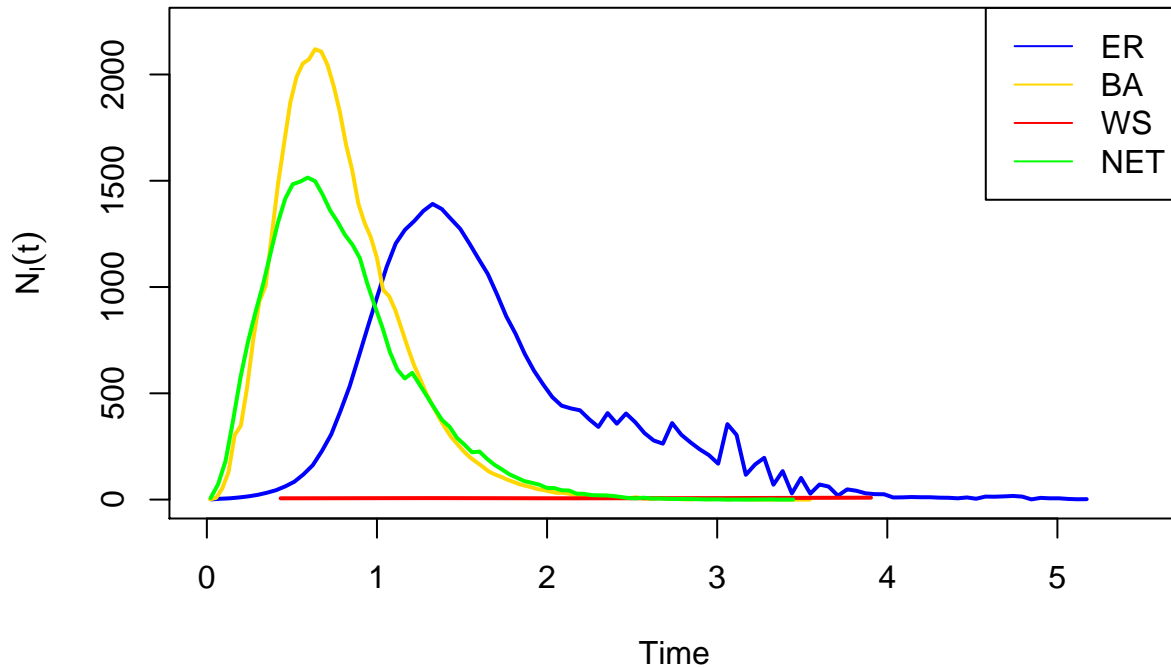
You need to plot three values on the graphics: Number of infected, number of suseprible, number of recovered - all depends on time. As a result of this task, you need to provide 12 plots (one for each network with 3 diferent parameters) with explanation.

```r
par(mfrow=c(3,1))
beta <- 2
gamma <- 4
ntrials <- 100

sim <- lapply(gl, sir, beta=beta, gamma=gamma, no.sim=ntrials)
x.max <- max(sapply(sapply(sim, time_bins), max))
y.max <- 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NI"]]), max, na.rm=TRUE))

plot(time_bins(sim$er), median(sim$er)[["NI"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NI"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NI"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NI"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NS"]]), max, na.rm=TRUE))
plot(time_bins(sim$er), median(sim$er)[["NS"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NS"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NS"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NS"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
```
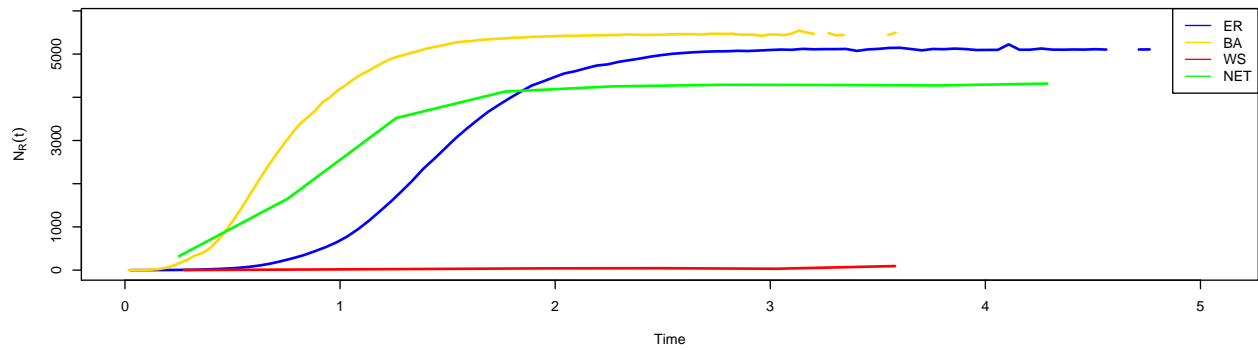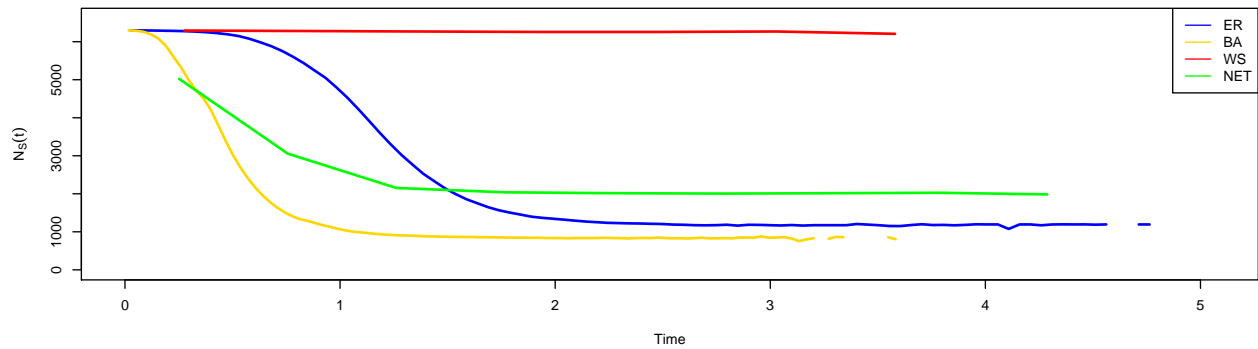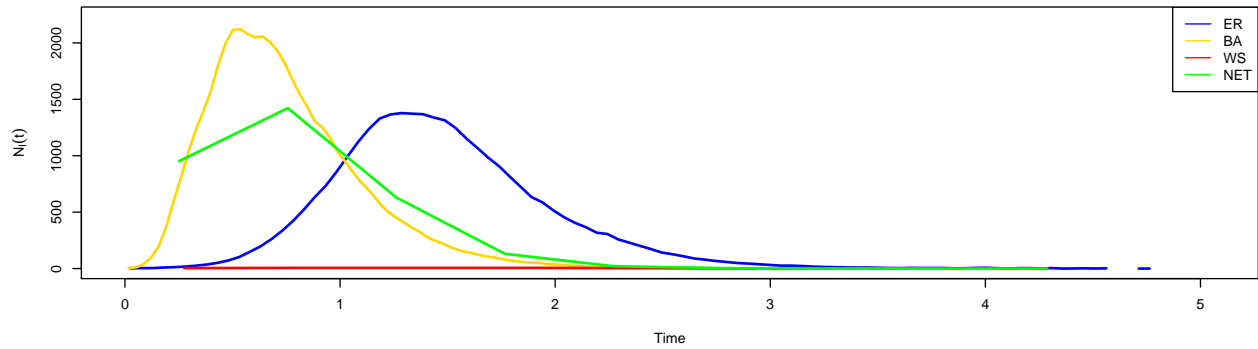
```
## [1] 5544
```

```
plot(time_bins(sim$er), median(sim$er)[["NR"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NR"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NR"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NR"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)
```


beta/gamma

```
## [1] 0.5
```

1/ev_er

```
## [1] 0.1337772
```

4

```
1/ev_ba
```

```
## [1] 0.04661436
```

```
1/ev_ws
```

```
## [1] 0.1653076
```

```
1/ev_net
```

```
## [1] 0.03524172
```

There is not epidemic spread. Because of the high rate of regeneration. WS is not affected at all. NET and BA has similar EV and has similar form.

```
par(mfrow=c(3,1))
beta <- 6
gamma <- 6
ntrials <- 500

sim <- lapply(gl, sir, beta=beta, gamma=gamma, no.sim=ntrials)
x.max <- max(sapply(sapply(sim, time_bins), max))
y.max <- 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NI"]]), max, na.rm=TRUE))

plot(time_bins(sim$er), median(sim$er)[["NI"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NI"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NI"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NI"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NS"]]), max, na.rm=TRUE))
plot(time_bins(sim$er), median(sim$er)[["NS"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NS"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NS"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NS"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
```
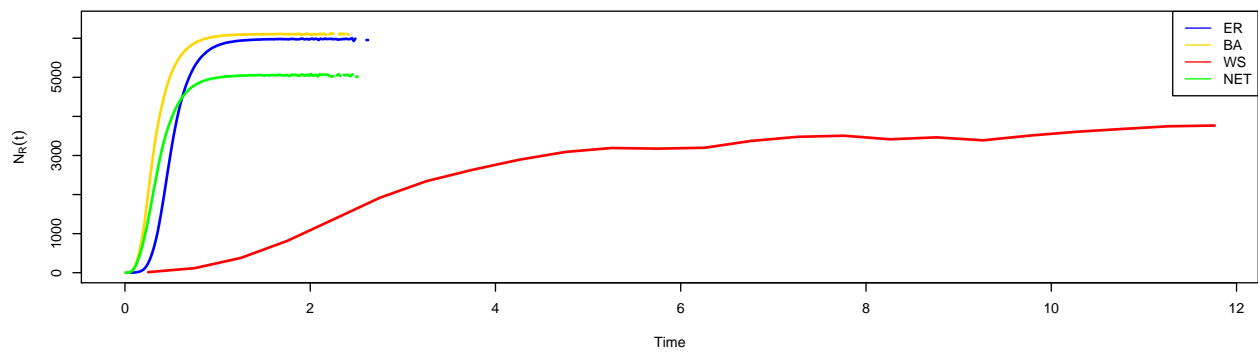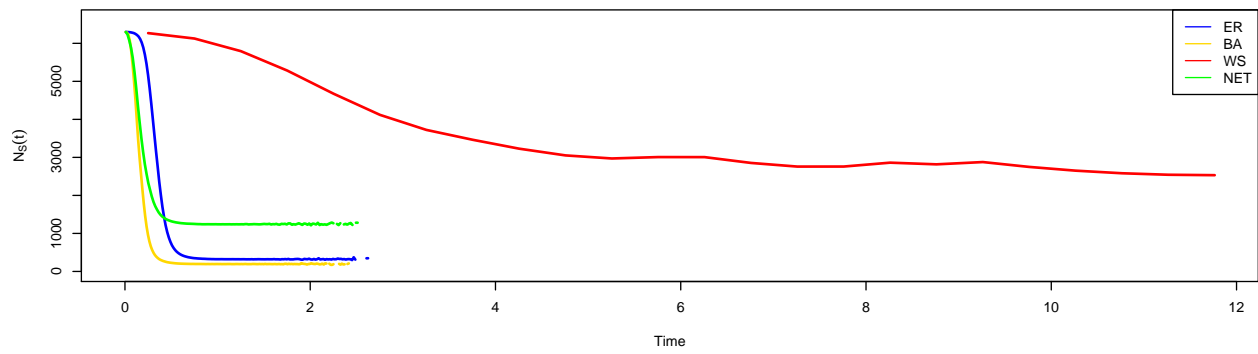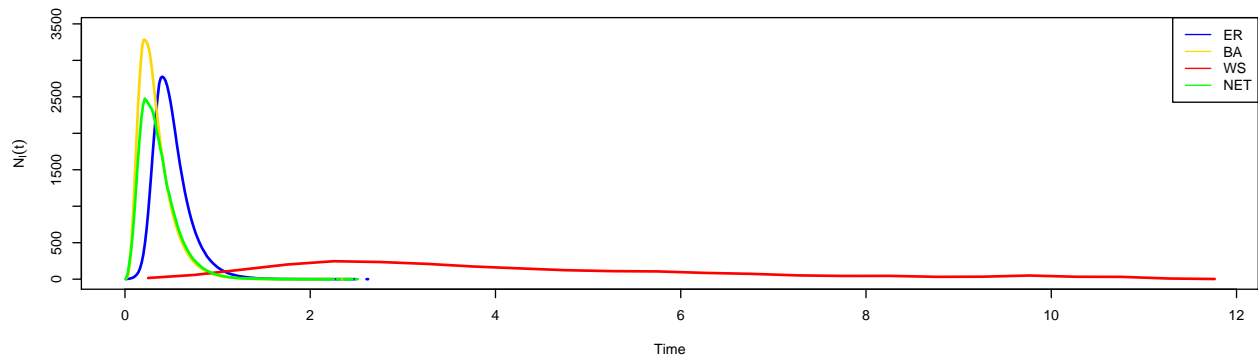
```
## [1] 6129
```

```
plot(time_bins(sim$er), median(sim$er)[["NR"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NR"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NR"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NR"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)
```

```
beta/gamma
```

```
## [1] 1
```

```
1/ev_er
```

```
## [1] 0.1337772
```

```
1/ev_ba
```

```
## [1] 0.04661436
```

```
1/ev_ws
```

```
## [1] 0.1653076
```

```
1/ev_net
```

```
## [1] 0.03524172
```

Betta and alpha are equal. Total time depends on the graph structure. ER, BA and NET have leap but WS is sloping. Threshold for SIR is not 1/ev!! There was not epidemic but it was really close. We can see how graphs with similar EV differ because of the structure.

```r
par(mfrow=c(3,1))
beta <- 8
gamma <- 2
ntrials <- 1000

sim <- lapply(gl, sir, beta=beta, gamma=gamma, no.sim=ntrials)
x.max <- max(sapply(sapply(sim, time_bins), max))
y.max <- 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NI"]]), max, na.rm=TRUE))

plot(time_bins(sim$er), median(sim$er)[["NI"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NI"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NI"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NI"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NS"]]), max, na.rm=TRUE))
plot(time_bins(sim$er), median(sim$er)[["NS"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NS"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NS"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NS"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)

y.max = 1.05 * max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
max(sapply(sapply(sim, function(x) median(x)[["NR"]]), max, na.rm=TRUE))
```
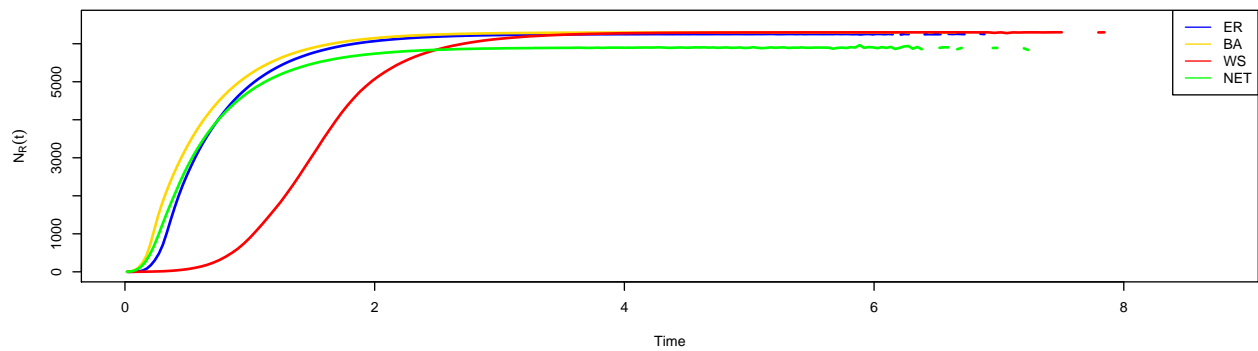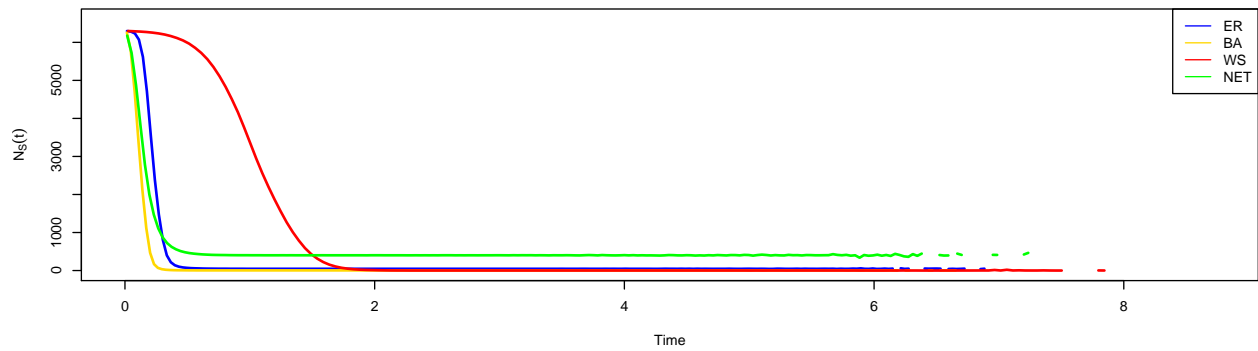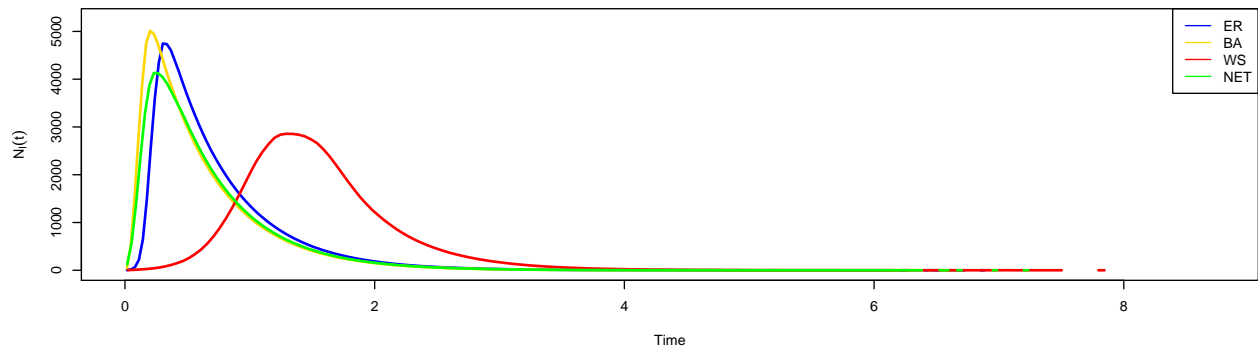
```
## [1] 6301
```

```r
plot(time_bins(sim$er), median(sim$er)[["NR"]], type="l", lwd=2, col="blue", xlim=c(0, x.max), ylim=c(0
lines(time_bins(sim$ba), median(sim$ba)[["NR"]], lwd=2, col="gold")
lines(time_bins(sim$ws), median(sim$ws)[["NR"]],lwd=2, col="red")
lines(time_bins(sim$net), median(sim$net)[["NR"]],lwd=2, col="green")
legend("topright", c("ER", "BA", "WS", "NET"),col=c("blue", "gold", "red", "green"), lty=1)
```

```
beta/gamma
```

```
## [1] 4
```

```
1/ev_er
```

```
## [1] 0.1337772
```

```
1/ev_ba
```

```
## [1] 0.04661436
```

```
1/ev_ws
```

```
## [1] 0.1653076
```

```
1/ev_net
```

```
## [1] 0.03524172
```

There was not an epidemic for NET even with such high value of betta. I think the cause may be disconnected or "bridge" graph structure.