Modelling spatial spread I - Exercises

Andrea Parisi

```
##
## Attaching package: 'deSolve'

## The following object is masked from 'package:pracma':
##
##     rk4

## Loading required package: viridisLite
```

Exercise 1

Increase the number of patches and observe how the infection curves will tend to overlap when such number becomes large. Can you explain why?

We start from 16 patches, and we increase the number to 50, 300, 1000.

```
patches <- 16
NN <- rep(10000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```
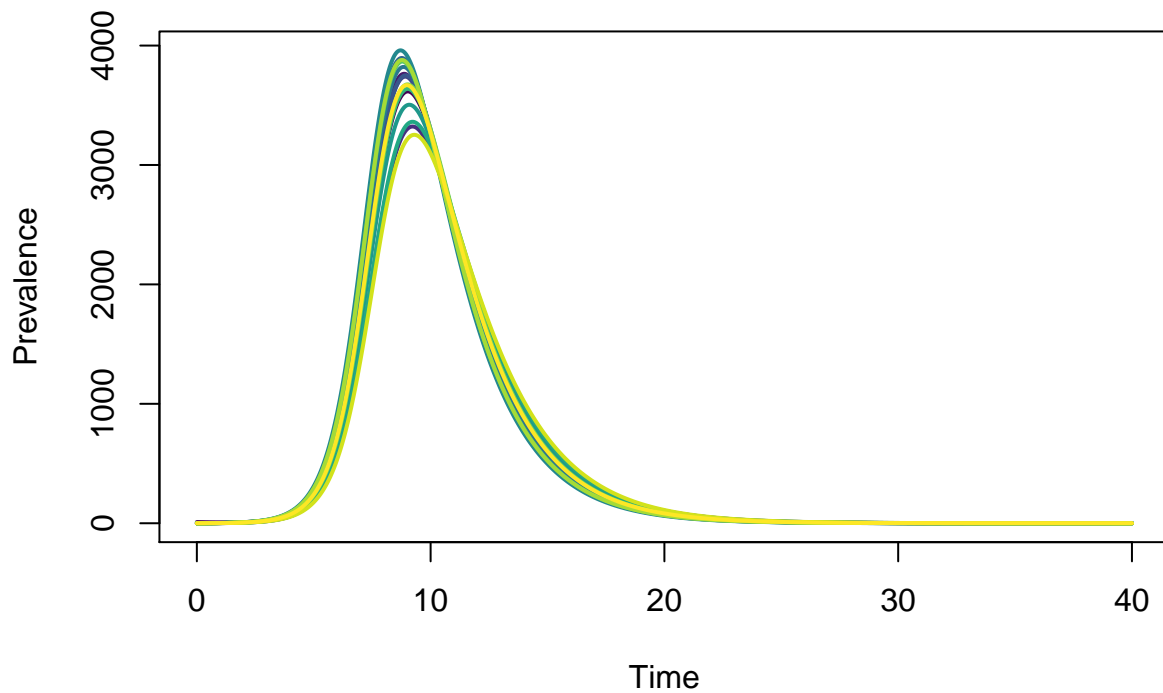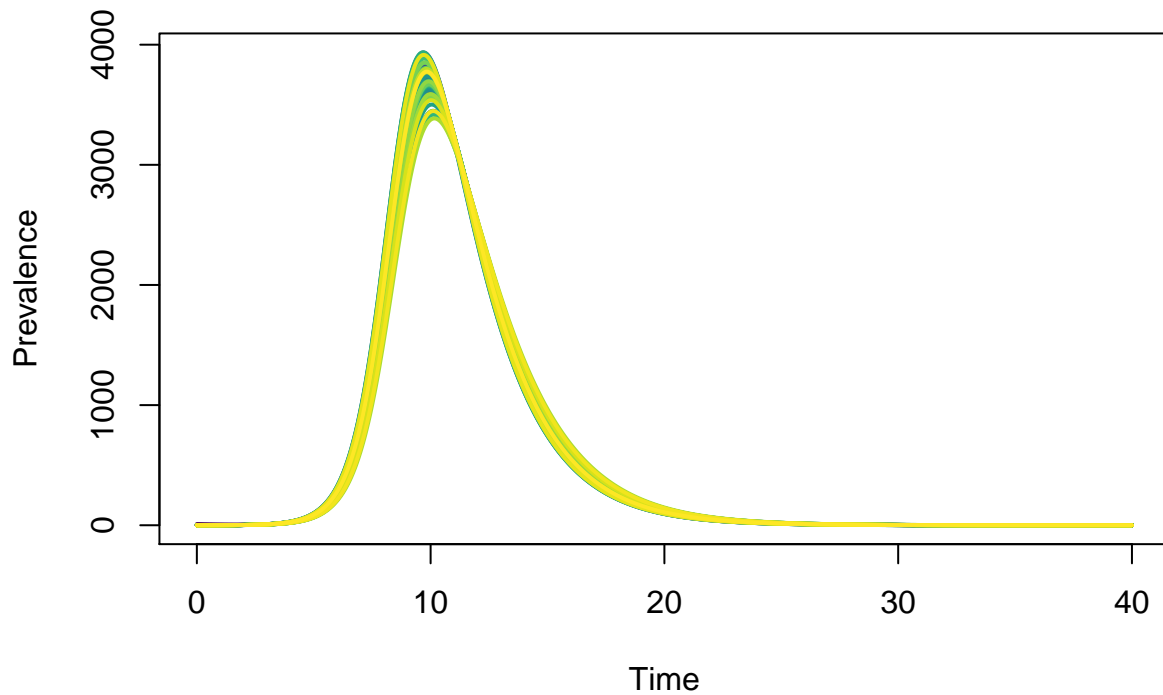
```
patches <- 50
NN <- rep(10000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```

```r
patches <- 300
NN <- rep(10000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```
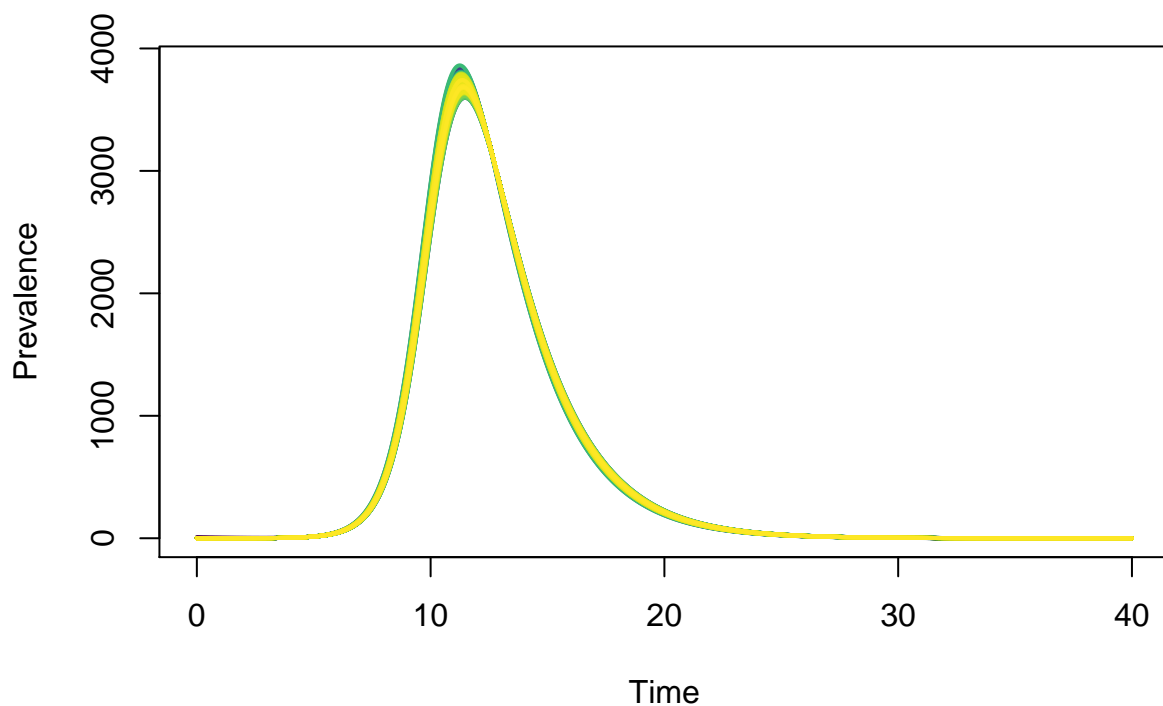
```r
patches <- 1000
NN <- rep(10000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```
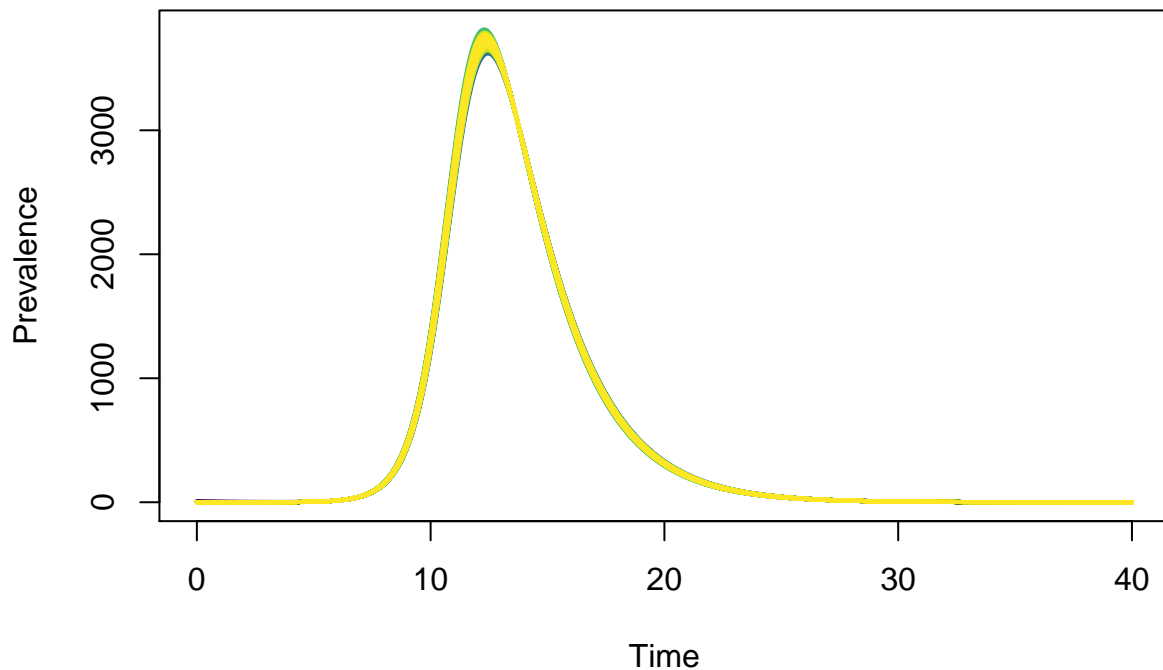
EACH patch will average out difference between influx from other patches: as the number of patches increases, all patches will see their influx converge towards a common average value.

Exercise 2

Increase or decrease the population size and the initial number of infectives of each patch by the same amount. What happens to the infection curves? Why?
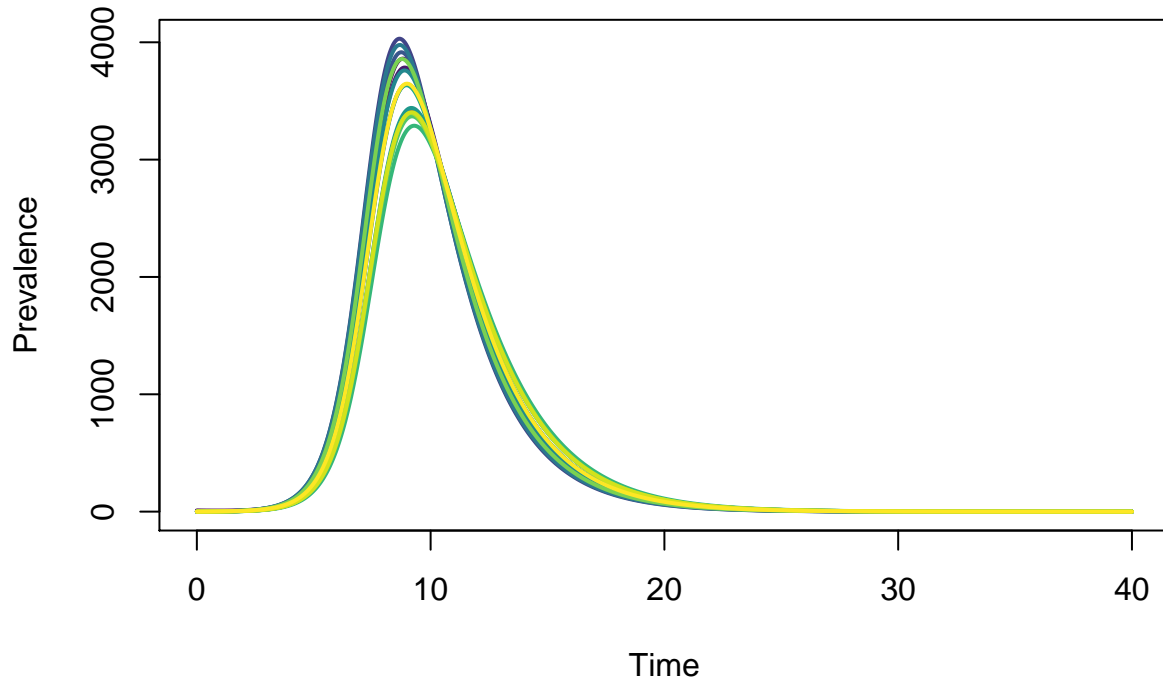
```
side <- 4
patches <- 16
NN <- rep(10000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)
```

```
res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```
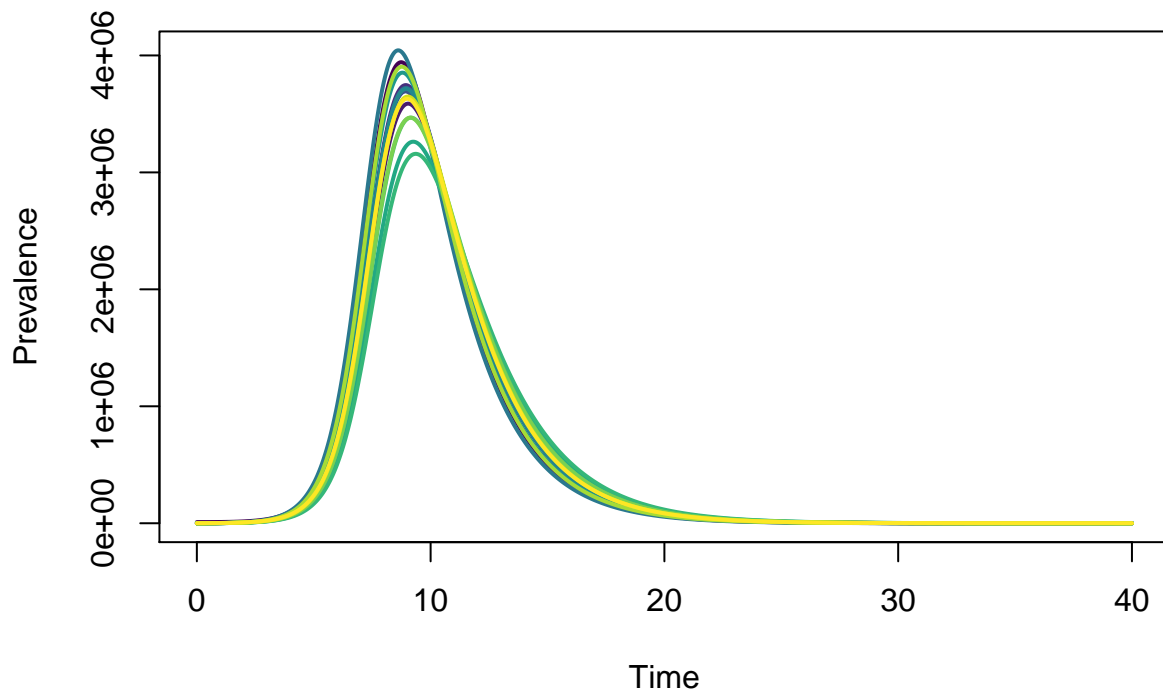


```
patches <- 16
NN <- rep(10000000, patches)

rho <- randomContactMatrix(patches)

start.I0 <- rep(0, patches)
start.I0[1] <- 10000
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```

Modifying the population size does not have any effect since these are continuous model and the contact matrix represents population fractions.
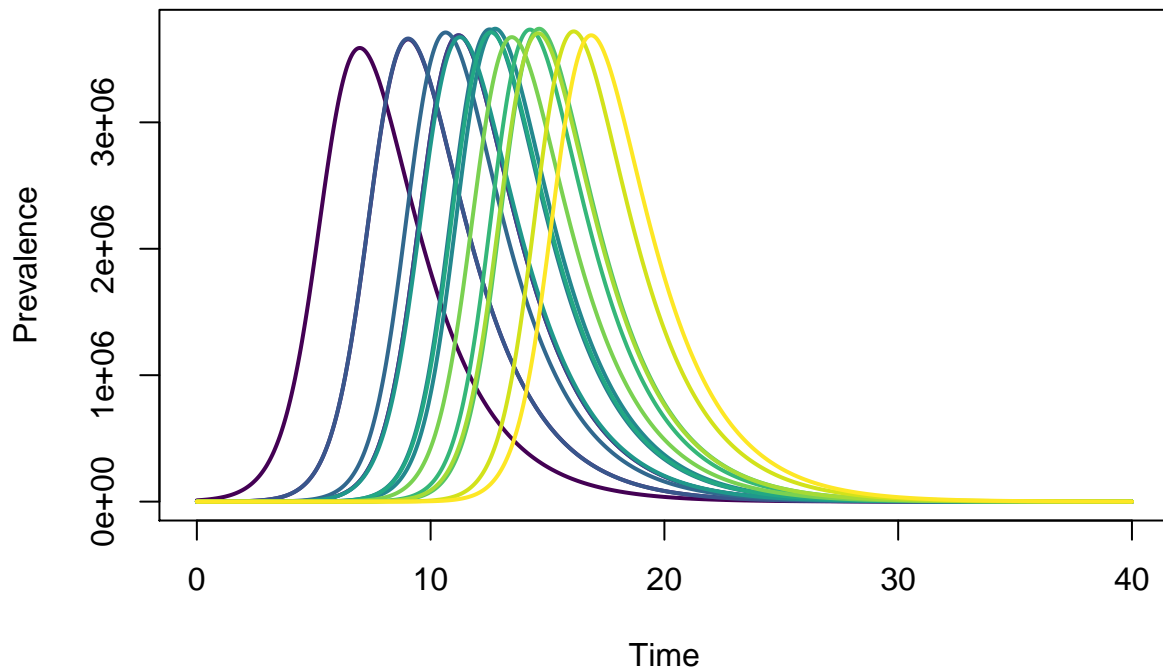
Exercise 3

This is the original nearest-neighbours matrix

```
entry <- 1
rho <- zeros(patches) # Generates a matrix of zeros
for (dst in 1:patches)  {
    for (src in 1:patches)  {
        if (dst == src)  {
            rho[dst,src] <- 0.96 # 1 - 4*0.01 - 4*0.05
        } else if (dst == src+side || dst == src-side ||
                    dst == src+1 || dst == src-1)  {
            rho[dst,src] <- 0.01
        }
    }
}
params <- list(patches, mu, gamma, beta, rho, NN)
```

```
res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```


This is a contact matrix with additional tranmission to second nearest neighbours

```
entry <- 1
rho <- zeros(patches) # Generates a patches x patches matrix of zeros
for (dst in 1:patches) {
    for (src in 1:patches) {
        if (dst == src) {
            rho[dst,src] <- 0.94 # 1 - 4*0.01 - 4*0.05
        } else if (dst == src+side || dst == src-side ||
                    dst == src+1 || dst == src-1) {
            rho[dst,src] <- 0.01
        } else if (dst == src+side-1 || dst == src-side-1 ||
                    dst == src+side+1 || dst == src-side+1) {
            rho[dst,src] <- 0.005
        }
    }
}
```
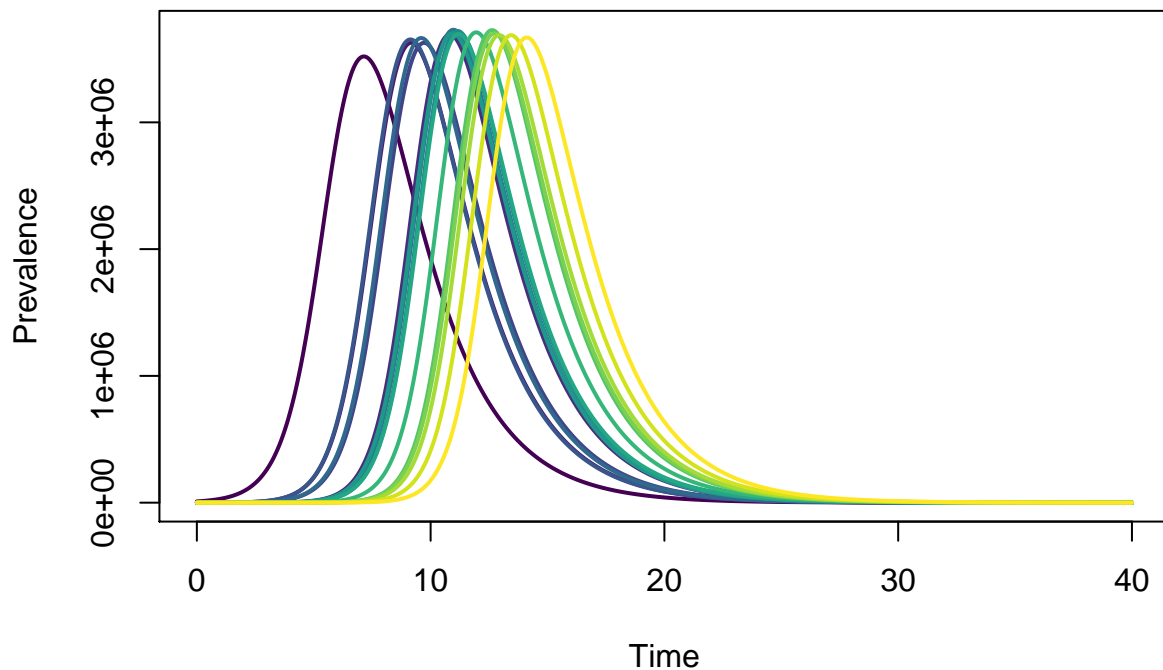
```
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```


Increasing the coupling between counties makes outbreaks in far countries occur earlier.

Exercise 4

```
## Linking to GEOS 3.6.2, GDAL 2.2.3, PROJ 4.9.3
NN <- counties.wsg84$pop
beta <- 1.66
times <- seq( from = 0, to = 40, by = 0.05)

rho <- build.contact.matrix( counties.wsg84, comm, "Total" )
patches <- nrow(rho)

# Find counties 'Modoc' and 'Los Angeles'
```
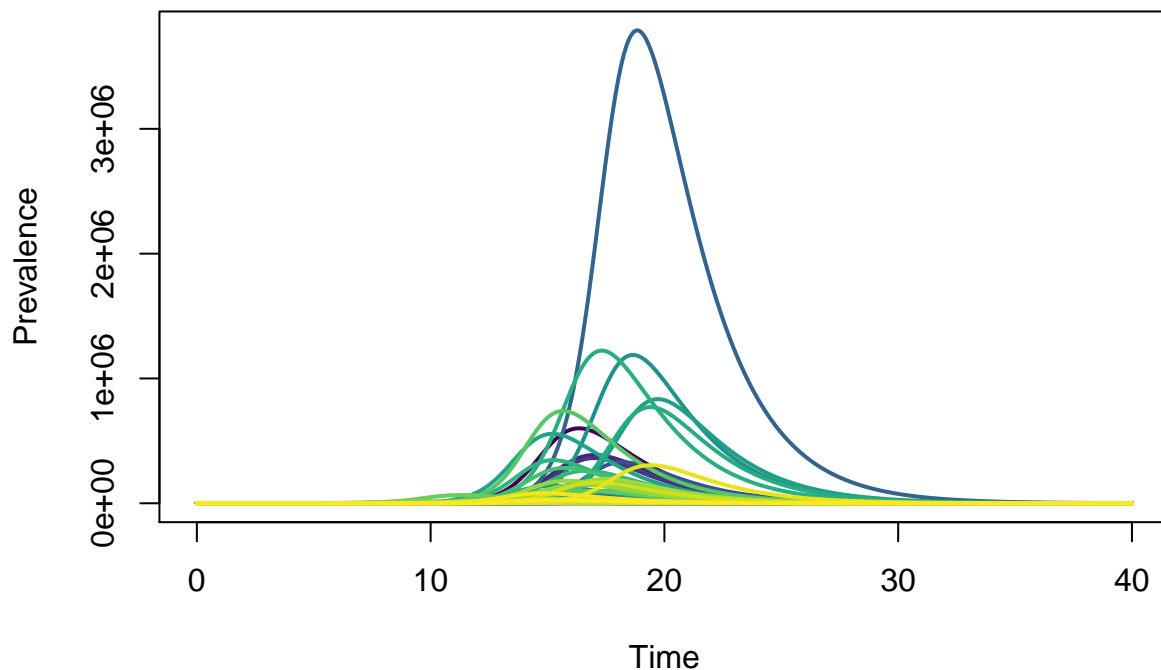
```
modoc <- which(counties.wsg84$NAME == "Modoc")
start.I0 <- rep(0, patches)
start.I0[modoc] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )

output <- data.frame( res )
showOutput(output, patches, NN)
```
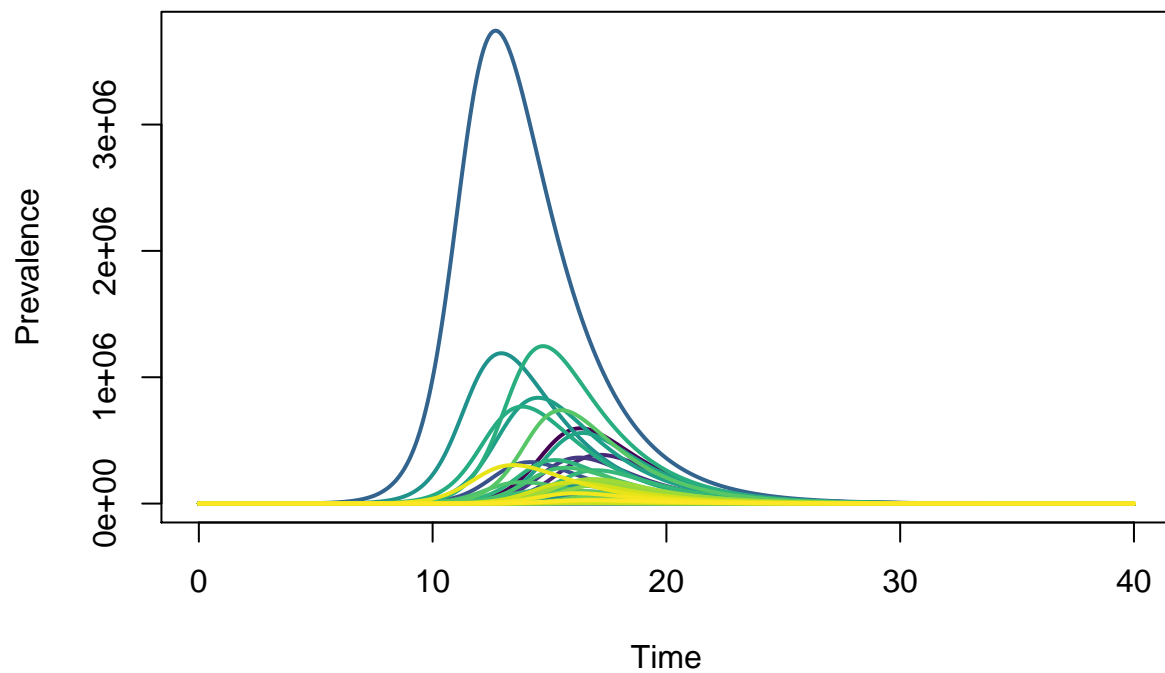


```
losangeles <- which(counties.wsg84$NAME == "Los Angeles")
start.I0 <- rep(0, patches)
start.I0[losangeles] <- 10
start.S0 <- NN-start.I0
xstart <- c( start.S0, start.I0 )
params <- list(patches, mu, gamma, beta, rho, NN)

res <- deSolve::ode( xstart, times, sir.model, params, method=deSolve::rk4 )
```

```
output <- data.frame( res )
showOutput(output, patches, NN)
```


Los Angeles has higher connections than the Modoc county, thus an initial infective in Los Angeles would cause a faster epidemic throughout California.