Structured models for host heterogeneities: Solutions

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Exercise 1. Modify the WAIFW matrix to reflect greater assortativity in mixing. What effect does this have on the epidemiological dynamics?

Greater assortativity means that potentiall infectious contacts occur at a relatively greater rate with individuals of the same age class than with individuals of other age classes. As in the handout, we set up an age-structured model with four classes.

```
> age.model<-function(t,x,parms){  #a function to return derivatives of age structured model
+  S<-x[1:4]      #S are the first four elements of x
+  E<-x[5:8]      #E are the next four elements of x
+  I<-x[9:12]     #I are the last four elements ofx
+  dx<-vector(length=12)   #a vector to store the derivatives
+   for(a in 1:4){   #loop over age classes
+     tmp <- (parms$beta[a,]%*%I)*S[a]    #temporary variable with infection rate
+     dx[a] <- parms$nu[a]*55/75 - tmp - parms$mu[a]*S[a]             #dS
+     dx[a+4] <- tmp - parms$sigma*E[a] - parms$mu[a]*E[a]            #dE
+     dx[a+8] <- parms$sigma*E[a] - parms$gamma*I[a] - parms$mu[a]*I[a]   #dI
+  }
+ return(list(dx))  #return the result
+ }
```

Solving this model will require the `deSolve` package.

```
> require(deSolve)
```

The state variables and initial conditions used previously are as follows.

```
> y0<-c(0.05, 0.01, 0.01, 0.008, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001, 0.0001)
> #initialize state variables
>
> #a list of model parameters
> parms<-list(beta=matrix(c(2.089, 2.089, 2.086, 2.037, 2.089, 9.336, 2.086, 2.037, 2.086, 2.086,
+             2.086, 2.037, 2.037, 2.037, 2.037,2.037),nrow=4,byrow=TRUE),
+             sigma=1/8, gamma=1/5, nu=c(1/(55*365),0,0,0),  mu=c(1/(55*365),0,0,0))
> parms

$beta
      [,1]  [,2]  [,3]  [,4]
[1,] 2.089 2.089 2.086 2.037
[2,] 2.089 9.336 2.086 2.037
[3,] 2.086 2.086 2.086 2.037
```

```
[4,] 2.037 2.037 2.037 2.037

$sigma
[1] 0.125

$gamma
[1] 0.2

$nu
[1] 4.98132e-05 0.00000e+00 0.00000e+00 0.00000e+00

$mu
[1] 4.98132e-05 0.00000e+00 0.00000e+00 0.00000e+00
```
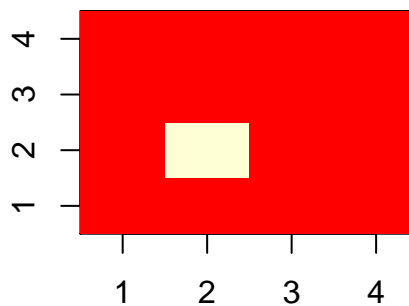
What is the average transmission rate (β)? We can compute this using `mean`.

```
> print(avg.beta <- mean(parms$beta))

[1] 2.51825
```

For a "fair" comparison, when we increase values of the transmission matrix correspoding to assortative mixing, we will want to decrease values elsewhere to achieve roughly the same average transmission rate. We can visualize the transmission matrix using the function `image`.

```
> image(x=seq(1,4), y=seq(1,4), parms$beta, xlab='', ylab='')
```


We replicate the analysis from the handout and plot.
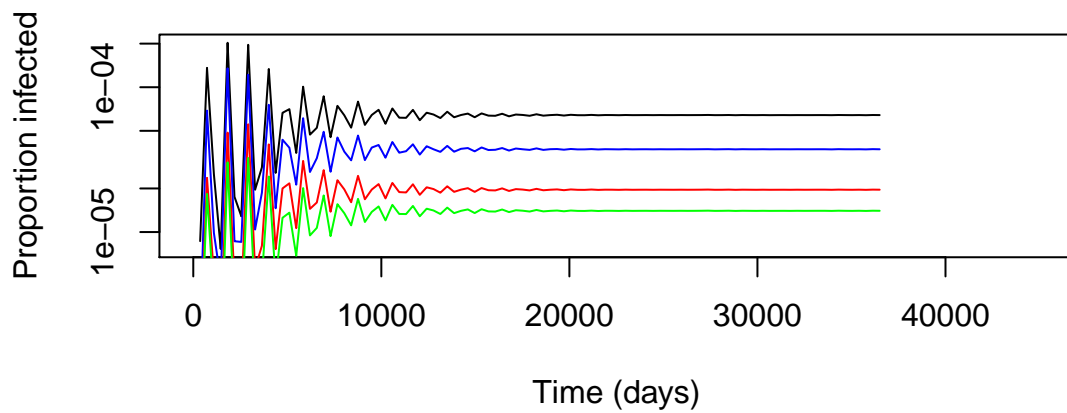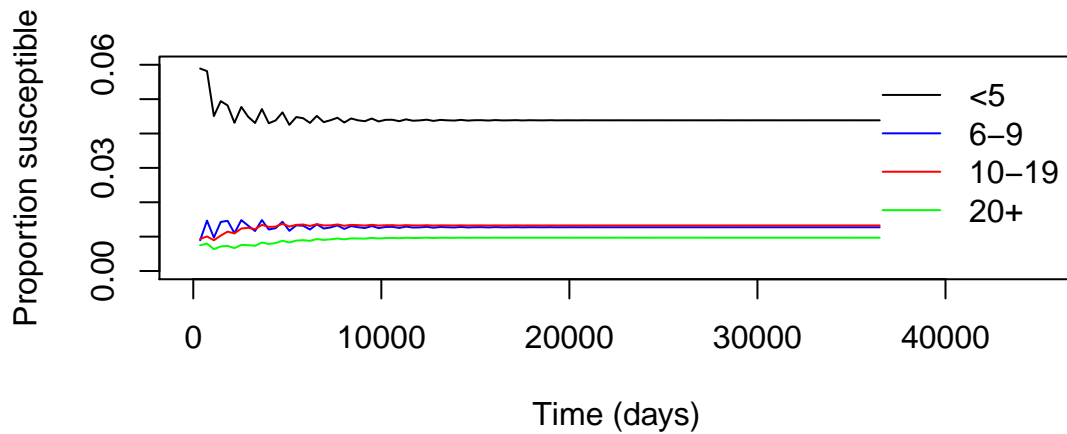
```
> n=c(6,4,10,55)/75   #number of years in each age class
> maxTime <- 100*365  #number of days in 100 years
```

```
> T0 <- 0                    #initial time
> S <- c()                   #initialize S
> E <- c()                   #initialize E
> I <- c()                   #initialize I
> T <- c()                   #initialize T, a vector to hold times
> while(T0<maxTime){  #loop over times
+   y <- lsoda(y0,c(T0, T0+365),age.model,parms) #solve diff'l equation for each time
+   T <- rbind(T, y[2,1])        #store results
+   S <- rbind(S, y[2,2:5])
+   E <- rbind(E, y[2,6:9])
+   I <- rbind(I, y[2,10:13])
+   #Now do the yearly movements
+   #Note use of "tail" to pull off the last value in a vector
+   y0[1] <- tail(y,1)[2]-tail(y,1)[2]/6
+   y0[2] <- tail(y,1)[3]+tail(y,1)[2]/6 - tail(y,1)[3]/4
+   y0[3] <- tail(y,1)[4]+tail(y,1)[3]/4 - tail(y,1)[4]/10
+   y0[4] <- tail(y,1)[5]+tail(y,1)[4]/10
+   y0[5] <- tail(y,1)[6]-tail(y,1)[6]/6
+   y0[6] <- tail(y,1)[7]+tail(y,1)[6]/6 - tail(y,1)[7]/4
+   y0[7] <- tail(y,1)[8]+tail(y,1)[7]/4 - tail(y,1)[8]/10
+   y0[8] <- tail(y,1)[9]+tail(y,1)[8]/10
+   y0[9] <- tail(y,1)[10]-tail(y,1)[10]/6
+   y0[10] <- tail(y,1)[11]+tail(y,1)[10]/6 - tail(y,1)[11]/4
+   y0[11] <- tail(y,1)[12]+tail(y,1)[11]/4 - tail(y,1)[12]/10
+   y0[12] <- tail(y,1)[13]+tail(y,1)[12]/10
+   T0 <- tail(T,1)
+ }


> #plot
> par(mfrow=c(2,1))     #set up plotting region
> plot(T,S[,1],type='l',xlim=c(0,45000),ylim=c(0,0.06),xlab='Time (days)',
+     ylab='Proportion susceptible') #plot susceptibles in youngest age class
> lines(T,S[,2],col='blue')           #susceptibles in second age class
> lines(T,S[,3],col='red')            #susceptibles in third age class
> lines(T,S[,4],col='green')          #susceptibles in oldest age class
> legend(x='topright',legend=c('<5','6-9','10-19','20+'),  #add legent
+     col=c('black','blue','red','green'),lty=1,bty='n')
> plot(T,I[,1],type='l',log='y',xlim=c(0,45000),xlab='Time (days)', #plot infected
+     ylab='Proportion infected')
> lines(T,I[,2],col='blue')
> lines(T,I[,3],col='red')
> lines(T,I[,4],col='green')
```

Now, we change the values of β along the diagonal, say $\beta_{1,1} = 4$, $\beta_{3,3} = 3.2$, and $\beta_{4,4} = 3.1$.

```
> parms$beta <- matrix(c(6.4, 2.089, 2.086, 2.037, 2.089, 9.336, 2.086, 2.037, 2.086, 2.086,
+              6.4, 2.037, 2.037, 2.037, 2.037, 5.8), nrow=4,byrow=TRUE)
```
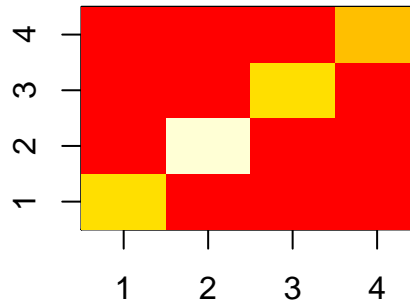
We check what the average is.

```
> print(avg.beta.try <- mean(parms$beta))
```

```
[1] 3.2925
```

to achieve the same average as in the example we multiply this matrix by a factor `average.beta/avg.beta.try`.

```
> parms$beta <- parms$beta*(avg.beta/avg.beta.try)
```

```
> image(x=seq(1,4), y=seq(1,4), parms$beta, xlab='', ylab='')
```


We initialize new state variables, evaluate the model again, and plot.

```
> T0 <- 0                   #initial time
> S2 <- c()                 #initialize S
> E2 <- c()                 #initialize E
> I2 <- c()                 #initialize E
> T2 <- c()                 #initialize T, a vector to hold times
> while(T0<maxTime){  #loop over times
+   y <- lsoda(y0,c(T0, T0+365),age.model,parms) #solve diff'l equation for each time
+   T2 <- rbind(T2, y[2,1])      #store results
+   S2 <- rbind(S2, y[2,2:5])
+   E2 <- rbind(E2, y[2,6:9])
+   I2 <- rbind(I2, y[2,10:13])
+   #Now do the yearly movements
+   #Note use of "tail" to pull off the last value in a vector
+   y0[1] <- tail(y,1)[2]-tail(y,1)[2]/6
+   y0[2] <- tail(y,1)[3]+tail(y,1)[2]/6 - tail(y,1)[3]/4
+   y0[3] <- tail(y,1)[4]+tail(y,1)[3]/4 - tail(y,1)[4]/10
+   y0[4] <- tail(y,1)[5]+tail(y,1)[4]/10
+   y0[5] <- tail(y,1)[6]-tail(y,1)[6]/6
+   y0[6] <- tail(y,1)[7]+tail(y,1)[6]/6 - tail(y,1)[7]/4
+   y0[7] <- tail(y,1)[8]+tail(y,1)[7]/4 - tail(y,1)[8]/10
+   y0[8] <- tail(y,1)[9]+tail(y,1)[8]/10
+   y0[9] <- tail(y,1)[10]-tail(y,1)[10]/6
+   y0[10] <- tail(y,1)[11]+tail(y,1)[10]/6 - tail(y,1)[11]/4
+   y0[11] <- tail(y,1)[12]+tail(y,1)[11]/4 - tail(y,1)[12]/10
+   y0[12] <- tail(y,1)[13]+tail(y,1)[12]/10
+   T0 <- tail(T2,1)
+ }
```
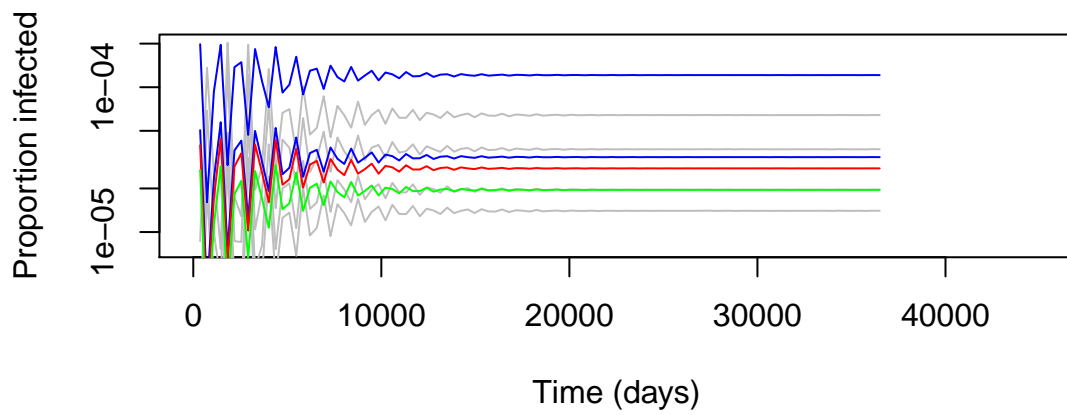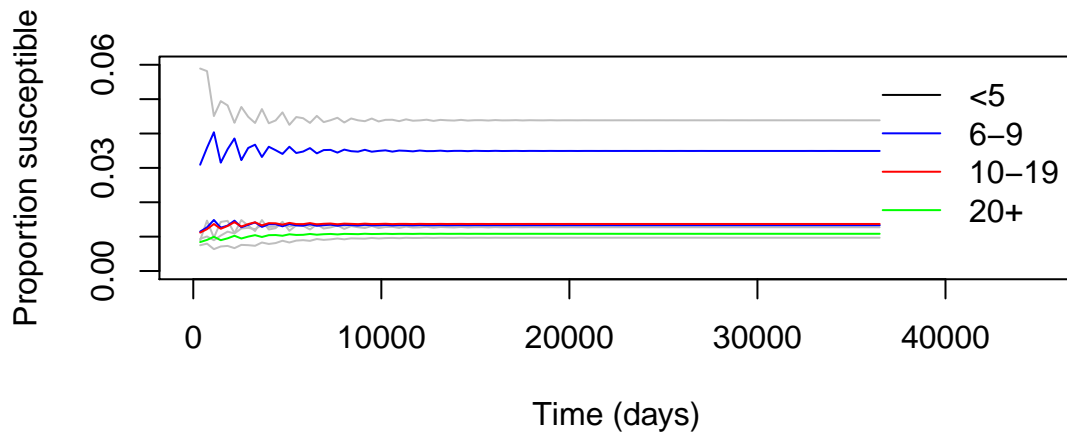
For comparison, we plot the earlier reuslts in gray, overplotting our new results in color

```
> #plot
> par(mfrow=c(2,1))     #set up plotting region
> plot(T,S[,1],type='l',xlim=c(0,45000),ylim=c(0,0.06),xlab='Time (days)', col='grey',
+      ylab='Proportion susceptible') #plot susceptibles in youngest age class
> lines(T,S[,2],col='grey')            #susceptibles in second age class
> lines(T,S[,3],col='grey')            #susceptibles in third age class
> lines(T,S[,4],col='grey')            #susceptibles in oldest age class
> lines(T,S2[,1],col='blue')            #susceptibles in second age class
> lines(T,S2[,2],col='blue')            #susceptibles in second age class
> lines(T,S2[,3],col='red')             #susceptibles in third age class
> lines(T,S2[,4],col='green')           #susceptibles in oldest age class
> legend(x='topright',legend=c('<5','6-9','10-19','20+'),  #add legend
+      col=c('black','blue','red','green'),lty=1,bty='n')
> plot(T,I[,1],type='l',log='y',xlim=c(0,45000),xlab='Time (days)', #plot infected
+      ylab='Proportion infected', col='grey')
> lines(T,I[,2],col='grey')
> lines(T,I[,3],col='grey')
> lines(T,I[,4],col='grey')
> lines(T,I2[,1],col='blue')            #susceptibles in second age class
> lines(T,I2[,2],col='blue')            #susceptibles in second age class
> lines(T,I2[,3],col='red')             #susceptibles in third age class
> lines(T,I2[,4],col='green')           #susceptibles in oldest age class
```

Evidently, increasing assortativity increases the number of individuals in all age classes, while simultaneously shifting the age-distribution of infections toward younder age classes.