Zoonotic Spillover Problems 1.7

Amy Greer, Bonne Bay 2023

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PART ONE - Lets first go back the the simple SEIR model we set up last week in Problem set 1.1 (go back and find that code)

Let's assume that this model is for seasonal influenza in a human population (the parameter values are not in line with seasonal influenza but let's pretend for now).

```
require(deSolve)

 seirmod=function(t, y, parms){
   #Pull state variables from y vector
   S=y[1]
   E=y[2]
   I=y[3]
   R=y[4]
   #Pull the required parameter values from the parms vector
   beta=parms["beta"]
   kappa=parms["kappa"]
   alpha=parms["alpha"]
   N=parms["N"]
   #Define the equations (use what you wrote out in question 1) - 6 points
   dS = -(beta*S*I/N)
   dE = +(beta*S*I/N) - (kappa*E)
   dI = (kappa*E) - (alpha*I)
   dR = (alpha*I)
   res=c(dS, dE, dI, dR)
   #Return list of gradients
   list(res)
 }
```

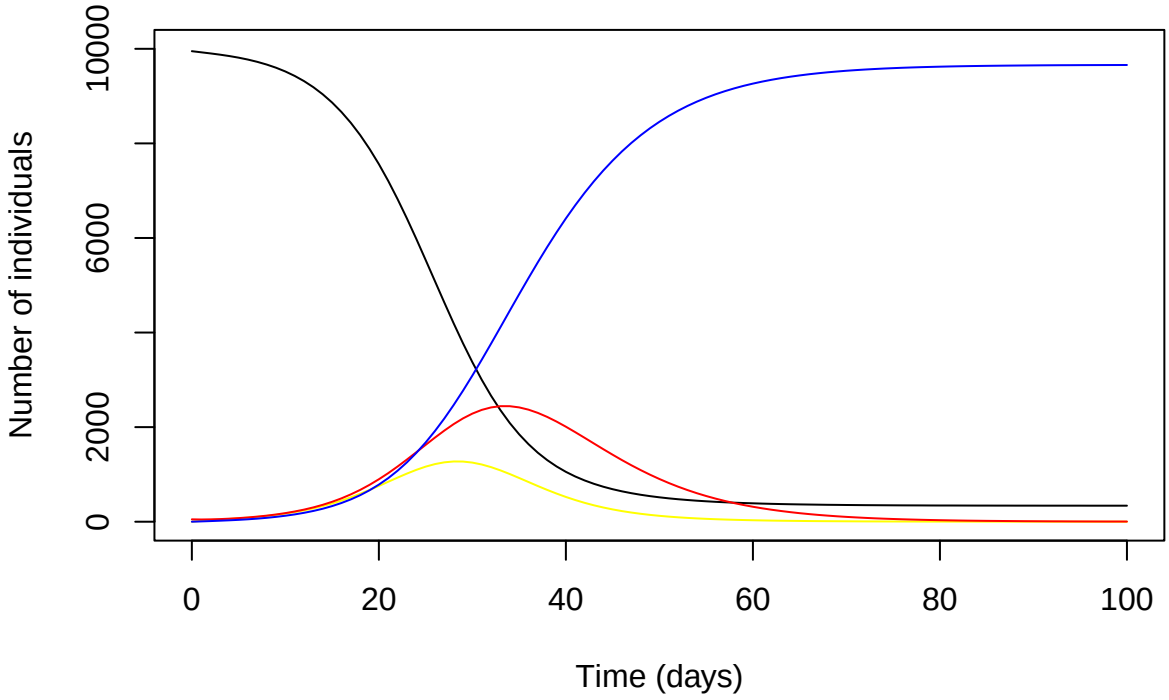
```
times  = seq(0, 100, by=1)
parms  = c(beta=0.5, kappa=1/3, alpha=1/7, N=10000)
start = c(S=9950, E=0, I=50, R = 0)
```

```
out = ode(y = start, times = times, func = seirmod,
     parms = parms)
out=as.data.frame(out)
head(round(out, 3))
```

```
##   time        S      E      I      R
## 1    0 9950.000  0.000 50.000  0.000
## 2    1 9926.254 20.155 46.764  6.827
## 3    2 9902.657 34.537 49.179 13.627
## 4    3 9876.950 46.678 55.318 21.054
```

```
## 5    4 9847.560 58.543 64.329 29.568
## 6    5 9813.193 71.306 75.945 39.557
```

```
plot(x = out$time, y = out$S, col = "black", ylab = "Number of individuals",
      xlab = "Time (days)", type = "l", xlim = c(0, 100), ylim = c(0,10000))
 lines(x = out$time, y = out$E, col = "yellow")
 lines(x = out$time, y = out$I, col = "red")
 lines(x = out$time, y = out$R, col = "blue")
```



#

Adding in Spillover

In this example, we are going to assume that humans in the model can become infected with seasonal influenza (the model above) but that people in this population also visit live bird markets (LBM) with some frequency. These LBM visits represent contact between poultry in the market with humans visiting the market. Additionally, organizations like FAO conduct sink surveillance which is a way to estimate prevalence of a pathogen like highly pathogenic avaian influenza (HPAI) within a market setting without having to test individual poultry and in a way that is easy, low cost, and non-invasive (https://www.fao.org/3/i2252e/i2252e.pdf). We are going to use an approach described by Iacono et al. (2016) to model spillover of HPAI from poultry into people who have exposure to the pathogen as a result of visiting LBM.

Our new model structure will include individuals infected with seasonal influenza, or HPAI (spillover from poultry). The compartment diagram looks like this (you can see I have used subscripts to differentiate between human and poultry viruses).

Since the spillover component of the model is going to need to be stochastic, we first need to provide some code to to set up the stochasticity where we will draw a parameter value from a distribution for the spillover equation.

```
set.seed(142)
nsamp <-1000 # run 1000 iterations of the model
sampseed<-sample(1:10e5, nsamp, replace=F)
sampseed<-as.data.frame(sampseed)
```

We also need to provide someplace for the data from each iteration to be stored.

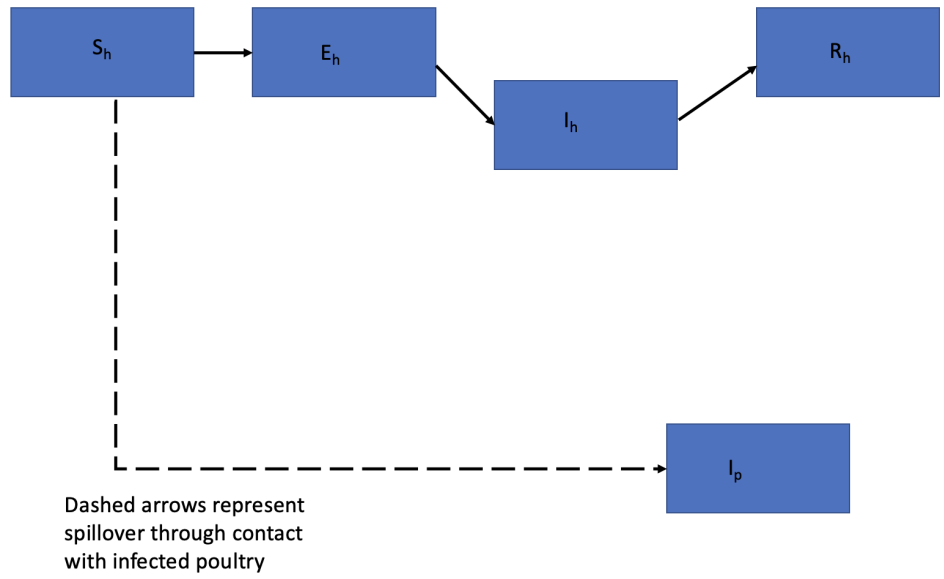


Figure 1: Updated SEIR Spillover Compartment model

Spillover rate (Iacono 2016)

- Probability that K spillover events occur during time τ is described by a stochastic Poisson process
  - $P(k) = \frac{exp^{-\lambda\tau}(\lambda\tau)^k}{k!}$,
  - Where λ is the expected number of zoonotic spillovers per unit time, which is specified as
    - $\lambda = N_h(t) Pr_R(N_R)\, \chi_R \eta_R(N_R)$
      - $N_h(t)$= *Number of susceptible humans at time t, initial population size*
      - $Pr_R(N_R)$ = *Prevalence of infected poultry , calibrated using average prevalence of AIV in poultry from Sink Surveillance data in DCC = 52% in 2018*
      - χ_R = *infection response efficiency , estimated as 0.0001 (high uncertainty)*
      - $\eta_R(N_R)$ =
        Average human exposure to poultry in LBM, calibrated using DCC mobile phone survey =30.2/365= 0.082

Figure 2: Spillover process

```
#save results dataframe
res_S <- matrix(0,366,nsamp) #matrix for the samples
res_E <- matrix(0,366,nsamp) #matrix for the samples
res_I <- matrix(0,366,nsamp) #matrix for the samples
res_R <- matrix(0,366,nsamp) #matrix for the samples
res_P <- matrix(0,366,nsamp) #matrix for the samples
res_xr <-matrix(0,1,nsamp)  #matrix for the samples

for (i in 1:nsamp)
  {set.seed(sampseed[i,])}
```

Now we will set up the compartment model structure.

```
 seirmod=function(t, y, parms){
   #Create state variables from y vector
   S=y[1]
   E=y[2]
   I=y[3]
   R=y[4]
   P=y[5]

    with (
      as.list (parms), {
        L1 = rpois(1,lambda=(S*pr*xr*nr*intervention)) # this is the distribution we will draw from for
        dS = -(beta*S*I/N)- L1
        dE = +(beta*S*I/N) - (kappa*E)
        dI = (kappa*E) - (alpha*I)
        dR = (alpha*I)
        dP = L1


        # combine results
        res = c (dS, dE, dI, dR, dP)
        list (res)
      })
  }

 ### Defining Parameters
beta=0.5
kappa=1/3
alpha=1/7
N=100000
intervention=1 # this indicates no intervention on the spillover side to reduce risk
pr=0.52 #prevalence of HPAI in infected poultry at the LBM
nr=30.2/365 #(average number of exposures to poultry in LBM in 1 year)
xr= rgamma(1, shape=0.005, scale=1) #infection response efficiency. low efficiency (for high efficiency

#save the xr values for each run -- so we can see what proportion were above threshold
  res_xr[,i]<-xr

#when xr is too big it won't run, so we have set it to shape
  #if(xr > 0.01){
   # xr<-0.005
  #}
```

```
### fill named vectors with our parameter values and initial conditions
parms = c(beta=beta, kappa=kappa, alpha=alpha, N=N, intervention=intervention, pr=pr, nr=nr, xr=xr)
inits = c(S=999500,E=0,I=50,R=0, P=0)
times  = seq(0, 365, by=1)

solved_model = as.data.frame(ode(inits, times, seirmod, parms, method="rk4", hini=0.01))
  res_S[,i]<- solved_model$S
  res_E[,i]<- solved_model$E
  res_I[,i]<- solved_model$I
  res_R[,i]<-solved_model$R
  res_P[,i]<- solved_model$P


# Tell about progress
  cat('Completed', i, 'of', nsamp,'\n')
```

```
## Completed 1000 of 1000
```

```
#beep when finished running
beep(3)
```

```
#Write outcomes
write.csv(res_S, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Aca
write.csv(res_E, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Aca
write.csv(res_I, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Aca
write.csv(res_R, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Aca
write.csv(res_P, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Aca
write.csv(res_xr, "/Users/amygreer/Library/CloudStorage/OneDrive-UniversityofGuelph/Guelph/2022-2023 Ac
```

Questions for your consideration (20 points)

1) Compare your results with a classmate. Do you get the same results? Why or why not? (4 points)
2) In your model iterations did you see any spillover events happen? If so, in how many simulation runs did you observe one of more spillover events happening and how many events did you observe? (2 points)
3) Describe some of the reasons why spillover might *not* happen have been observed in your model. Can any of these factors be adjusted to increase your chance of observing spillover events in this model? If so, what could you try? (6 points)
4) Choose at least one of the factors you described above and try modifying your model code and rerunning the simulations to increase the chance that you observe a spillover event (which are rare). Why do you think these modifications will increase the occurrence of spillover events? Describe what you changed, why you hypothesize that the change will increase spillover risk, and then describe your updated model results. If the change you implement does not increase the spillover risk what is your possible explanation for that and how would you revise your hypothesis as a result? (8 points)