**CBS 810 Metapopulation models and other multiple-compartment models**

1. Learn to simulate simple metapopulation model
2. Compare the similarity and difference between multihost, vector-borne, and metapopulation models

**Recap – Comparison of three multi-compartment model transmission**

|  |  |  |
| --- | --- | --- |
| Type of Model | Within-group | Between-group |
| Multihost | sometimes | Y |
| Vector-borne | N | Y |
| Metapopulation | Y | Y |

**I2**

**S2**

**I1**

**S1**

***Metapopulation*** model: interacting ***subpopulations***

**I2**

**S2**

**I1**

**S1**

dS1/dt =

dI1/dt =

dS2/dt =

dI2/dt =

***Multihost*** model: (not necessarily) interacting ***populations***

**S1**

**I1**

**S2**

**I2**

dS1/dt =

dI1/dt =

dS2/dt =

dI2/dt =

***Vector-borne*** model: infection occurs between vector and host (**NOT** within them)

**S1**

**I1**

**S2**

**I2**

dS1/dt =

dI1/dt =

dS2/dt =

dI2/dt =

# Generic R code for simulation of multi-population model

library("deSolve")

parms <- c(beta1=1e-3, gamma=1e-1, beta2=1e-4, gamma2=1e-1)

inits <- c(S1=499,I1=1 ,S2=1990, I2=10) # H for host, V for vector

dt <- seq(0,100,0.1)

epi.sim <- function(t, x, parms){

with(as.list(c(parms,x)),{

dS1 <- -beta1\*S1\*I1

dI1 <- beta1\*S1\*I1 – gamma1\*I1

dS2 <- -beta2\*S2\*I2

dI2 <- beta2\*S2\*I2 – gamma2\*I2

der <- c(dS1, dI1, dS2, dI2)

list(der) # the output must be returned

}) # end of ’with’

} # end of function definition

sim.1 <- as.data.frame(lsoda(inits, dt, epi.sim, parms=parms))

plot.ts(sim.1$I1,lwd=2,ylim=c(0,1000))

lines(c(1:1001),sim.1$I2,col="blue",lty=2,lwd=2)

leg.txt<-c("Infected Group 1","Infected Group 2")

legend("topright",leg.txt,lty=c(1,2),col=c("black","blue"))