**CBS810 Epidemiological models for disease control**

1. Review potential control methods for disease prevention
2. Learn to simulate simple control model

**Pathogen**

**Host**

**VECTOR**

**Environment**

**Table 1. Review of potential control methods**

|  |  |  |
| --- | --- | --- |
| **Factor 1** | **Factor 2** | **Potential Strategies** |
| **Pathogen** |  |  |
| **Host** |  |  |
| **Environment** |  |  |
| **Pathogen** | **Host** |  |
| **Pathogen** | **Environment** |  |
| **Host** | **Environment** |  |
| **Vector** |  |  |

# Generic R code for simulation of epidemiology model with control

library("deSolve")

parms <- c(beta=1e-3, gamma=1e-1)

inits <- c(S1=499,I1=1, R1=0)

dt <- seq(0,100,0.1)

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

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

dS <-

dI <-

dR <-

der <- c(dS, dI, dR)

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$I,lwd=2,ylim=c(0,1000))