SICR model with a carrier class

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## It is the SICR which includes a carrier class.

## Parameters:
# miu: Per captia death rate, and the population level birth rate;
# beta: Product of contact rates and transmission probability;
# gamma: Recovery Rate;
# epsilon: Proportion reduction in transmission from carriers compared to stan
dard infectious individuals;
# q: Proportion of infected individuals that become carriers rather than fully
recover;
# Gamma: Recovery rate associated with carriers;
# S: Proportion of the population that are susceptible;
# I: Proportion of the population that are infectious;
# C: Proportion of the population that are carriers;
# R: Proportion of the population that are recovered.

library(deSolve)SICR = function(time, state, pars) {
  with(as.list(c(state,pars)), {
    dS = miu - (beta * I0 + epsilon * beta * C0) * S0 - miu * S0
    dI = (beta * I0 + epsilon * beta * C0) * S0 - (miu + gamma) * I0
    dC = gamma * q * I0 - Gamma * C0 - miu * C0
    dR = gamma * (1 - q) * I0 + Gamma * C0 - miu * R0
    return(list(c(dS,dI,dC,dR)))
  })
}
yini = c(S0 = 0.2,I0 = 1e-4,C0 = 1e-3, R0 = 1-0.2-1e-4-1e-3)
pars = c(miu = 1/(50*365), beta = 0.2,gamma = 0.01, epsilon = 0.1, q = 0.4, Ga
mma = 0.001)
times = seq(0,700,by = 1)


out = ode(func = SICR, y = yini, parms = pars, times = times)
out = as.data.frame(out)
out$time = NULL

matplot(times,out,type = "l", xlab = "Time(days)", ylab = "Susceptibles and Re
covereds", main = "SEIR Model",
        lwd = 2, lty = 1, col = 2:5)
legend(60,0.5,c("Susceptibles","Infecteds","Carriers","Recovereds"),pch = 1, c
ol = 2:5, bty = "n")
```

SEIR Model