Numerical solution of deterministic epidemiological models^{*}

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1 Introduction

Many of the core theories of epidemic propagation are expressed is a system of *ordinary differential equations* known as a *compartmental model*. This session introduces techniques for numerically solve systems of nonlinear differential equations with an adaptive step size solver.

2 The SIR model

As we introduced in the lecture, the classical *SIR* compartmental model tracks the fraction of the population in each of three classes (susceptible, infected, recovered). In a *demographically closed* system, flow out of one class must enter another class, giving rise to a *conservation property*. The state variables change according to the following system of differential equations:

$$\begin{split} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma \, I \\ \frac{dR}{dt} &= \gamma \, I \end{split}$$

where S, I, and R are the proportion of susceptible, infected, and recovered individuals and γ is the recovery rate.

In a *demographically open* system, the number of individuals in the population may change due to births and deaths that happen at *per capita* rates α and μ . The we have

$$\frac{dS}{dt} = \alpha - \beta SI - \mu S$$
$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

If we set $\alpha = \mu$ then births exactly balance deaths and the population remains at a constant size, yielding

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$$\frac{dS}{dt} = \mu - \beta SI - \mu S$$
$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

Like many epidemiological models, one can't solve the *SIR* equations analytically. Rather, to find the *trajectory* of a continuous-time model such as the *SIR*, we integrate these equations numerically. What we mean by this is that we use a computer algorithm to approximate the solution. In general, this can be a tricky business. Fortunately, this is a well studied problem in numerical analysis and (when the equations are smooth, well-behaved functions of a relatively small number of variables) standard numerical integration schemes are available to approximate the integral with arbitrary precision. Particularly, R has a very sophisticated ODE solver, which (for many problems) will give highly accurate solutions. To use the numerical integration package, we must load the package

```
> require(deSolve)
```

#deSolve library needed for this computing session

The ODE solver needs to know the right-hand sides of the ODE. We give it this information as a function (sub-routine). Note that the form of the arguments and output of this function must exactly match what is expected by the ode routine. Thus, for instance, the time variable t must be the first argument even if the function is *autonomous* or *time-invariant* so that t is neglected in the calculation. Here we right a function to return the derivatives of the closed SIR model.

```
> sir.model.closed <- function (t, x, params) {</pre>
                                                      #here we begin a function with three arguments
    S < -x[1]
                                              #create local variable S, the first element of x
+
    I <- x[2]
+
                                              #create local variable I
+
    R < -x[3]
                                              #create local variable R
+
    with(
                                              #we can simplify code using "with"
                                              #this argument to "with" lets us use the variable names
+
         as.list(params),
         {
+
                                              #the system of rate equations
           dS <- -beta*S*I
+
+
           dI <- beta*S*I-gamma*I
+
           dR <- gamma*I
           dx < - c(dS, dI, dR)
+
                                              #combine results into a single vector dx
           list(dx)
                                              #return result as a list
+
         }
+
         )
+
+ }
```

Notice that here, we've assumed β is constant.

[Note: In case the with function is unfamiliar, it serves here to make the parameters params available to the expressions in the brackets, as if they were variables. One could achieve the same effect by, for example, dS <- params["mu"]*(1-S)-params["beta"]*S*I and so on.]

We now state the times at which we want solutions, assign some values to the parameters, and specify the *initial conditions*, *i.e.*, the values of the state variables S, I, and R at the beginning of the simulation:

| > times <- seq(0,120,by=5) | #function seq returns a sequence |
|---|---|
| > params <- c(beta=0.3,gamma=1/7) | #function c "c"ombines values into a vector |
| > xstart <- c(S=9999/10000,I=1/10000,R=0) | #initial conditions |

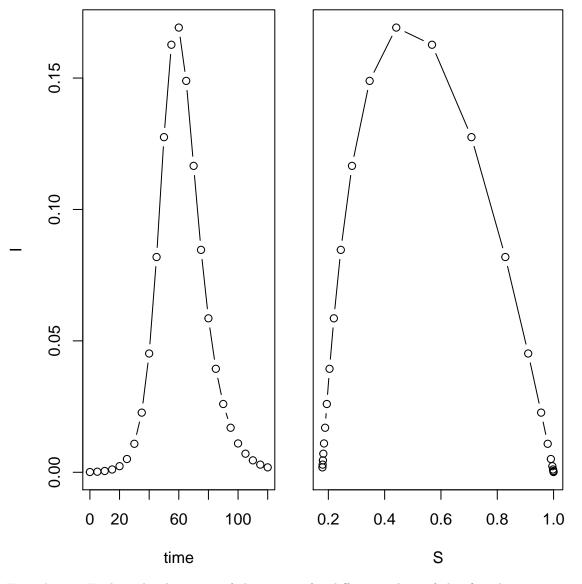
Next, we simulate a model trajectory with the ode command:

> out <- as.data.frame(ode(xstart,times,sir.model.closed,params)) #result stored in dataframe

and plot the results

```
> op <- par(fig=c(0,0.5,0,1),mar=c(4,4,1,1))
> plot(I~time,data=out,type='b')
> par(fig=c(0.5,1,0,1),mar=c(4,1,1,1),new=T)
> plot(I~S,data=out,type='b',yaxt='n',xlab='S')
> par(op)
```

#set graphical parameters
#plot the I variable against time
#re-set graphical parameters
#plot phase portrait
#re-set graphical parameters



Exercise 1. Explore the dynamics of the system for different values of the β and γ parameters by simulating and plotting trajectories as time series and in phase space (e.g., I vs. S).

Exercise 2. Explore the dynamics of the system for one set of β and γ at different initial conditions. What happens if there is pre-existing immunity in the population?

Exercise 3. Modify the codes given to study the dynamics of a demographically open SIR model.

*Exercise 4. Modify the codes given to study the dynamics of an SEIR model.