

ME 406

S-I-R Model of Epidemics

Part 2

Vital Dynamics Included

`sysid`

Mathematica 4.1.5, DynPac 10.68, 4/29/2002

`intreset; plotreset;`

1. Introduction

■ Description of the Model

In this notebook, we include births and deaths in the standard S-I-R model for epidemics. The resulting model will allow us to look at events of longer duration. For the integration of the nonlinear differential equations, we use the package DynPac. Although some familiarity with DynPac is assumed, brief descriptions of some DynPac commands are given as they are used. The integrations in this notebook also can be done easily with the *Mathematica* function NDSolve.

The S-I-R model was introduced by W.O. Kermack and A.G. McKendrick ("A Contribution to the Mathematical Theory of Epidemics," Proc. Roy. Soc. London **A**, **115**, 700-721, 1927), and has played a major role in mathematical epidemiology. In later work, Kermack and McKendrick added the effects of vital dynamics (Proc. Roy. Soc. London **A**, **138** 55-83, 1932, and **141** 94-122, 1933). A summary of the model and its uses is given by Herbert W. Hethcote (*Applied Mathematical Ecology*, ed. S. A. Levin, T.G. Hallam, and L.J. Gross, Springer-Verlag, 1989, pp. 119-144). In the model, a population is divided into three groups: the susceptibles S , the infectives I , and the recovered R , with numbers s , i , and r respectively. The total population is

$$n = s + i + r . \tag{1}$$

The susceptibles are those who are not infected and not immune, the infectives are those who are infected and can transmit the disease, and the recovered are those who have been infected, have recovered and are permanently immune. We will include in the model the natural birth and death rates, although with simplifying assumptions. We assume that all births are into the susceptibles. We assume that the death rate is equal for members of all three classes, and we assume that the birth and death rates are equal so that the total population is stationary. Finally, we assume that this is a non-lethal disease so that the recovered are truly recovered and not dead.

■ Differential Equations and Parameters of the Model

The basic differential equations are as follows:

$$\frac{ds}{dt} = -\alpha si + \mu (s + i + r) - \mu s , \tag{2}$$

$$\frac{di}{dt} = \alpha si - \beta i - \mu i, \quad (3)$$

$$\frac{dr}{dt} = \beta i - \mu r. \quad (4)$$

These equations describe the transitions of individuals from S to I to R. The new parameter is the birth and death rate μ . By adding the three equations, we show easily that the total population n is constant. As before, the parameter α is the transmissivity and the parameter β the recovery rate. See Part 1 of this notebook and especially Part 2 of the SEIR notebook for a more detailed discussion of the transmissivity α .

In equation (2), we may replace the sum $s + i + r$ by the constant total population n . Then equations (2) and (3) constitute a set of two equations for s and i . After they are solved, we may calculate r from equation (1).

2. Defining the Equations for DynPac

In much of what follows, we will be integrating equations (2) and (3) numerically. In this section, we define the equations for DynPac. We start by resetting integration and plot options. de

```
intreset;
```

```
plotreset;
```

Now we tell DynPac that the state variables are i and s .

```
setstate[{s, i}];
```

We tell DynPac that the "official" system parameters are the transmissivity α , the recovery rate β , the birth and death rate μ , and the total population n .

```
setparm[{alpha, beta, mu, n}];
```

Finally, we define the slope vector of the equations for DynPac.

```
slopevec = {-alpha*s*i + mu*n - mu*s, alpha*s*i - (beta + mu)*i};
```

We will define integration parameters later. Our first step will be to look at the equilibrium states and their stability.

3. Equilibrium and Stability

We begin by looking for equilibrium states. The DynPac command `findpolyeq` finds equilibrium states for systems with polynomial slope vectors.

```
eq = findpolyeq
```

$$\left\{ \{n, 0\}, \left\{ \frac{\beta + \mu}{\alpha}, -\frac{\mu(-n\alpha + \beta + \mu)}{\alpha(\beta + \mu)} \right\} \right\}$$

The first state is one with no infectives, which we call eq1, and the second is an endemic state which we call eq2.

```
eq1 = eq[[1]]
```

```
{n, 0}
```

```
eq2 = eq[[2]]
```

$$\left\{ \frac{\beta + \mu}{\alpha}, -\frac{\mu(-n\alpha + \beta + \mu)}{\alpha(\beta + \mu)} \right\}$$

It is worth noting that although we can have a disease-free state with s and r both positive and i zero, it is not strictly speaking an equilibrium, because the recovered gradually die out and are not replaced. Only when all of the recovered are gone can the population distribution be stationary.

Let's look at the stability of the no-infectives state. We first evaluate the derivative matrix at that state.

```
dermat1 = dermat /. Thread[statevec -> eq1]
```

$$\{\{-\mu, -n\alpha\}, \{0, n\alpha - \beta - \mu\}\}$$

```
Eigensystem[dermat1]
```

$$\left\{ \{n\alpha - \beta - \mu, -\mu\}, \left\{ \left\{ -\frac{n\alpha}{n\alpha - \beta}, 1 \right\}, \{1, 0\} \right\} \right\}$$

The second eigenvalue $-\mu$ is always negative, hence the possibility of an epidemic hinges on the first eigenvalue. We see that the equilibrium is unstable and there will be an epidemic if

$$n\alpha - \beta - \mu > 0 \quad . \quad (5)$$

This is essentially our old condition that the initial reproductive ratio must exceed 1, only the recovery rate in the earlier formula is now replaced by the $\beta + \mu$, the sum of the recovery rate and the natural death rate. If (5) is satisfied and we introduce an infective, there will be an epidemic. In this case, the equilibrium is a saddle point, and the linear stable manifold, with eigenvalue μ , is the s axis -- that is, any perturbation in population with no infectives will go back to the equilibrium population with an e-folding time of $1/\mu$. The linear unstable manifold points in the direction of increasing i and decreasing s . (See the phase plane plot for an example in section 5 below.)

The endemic state is relevant only if the equilibrium values of i and s are positive. We see from the expression for eq2 above that this happens if and only if the condition (5) is satisfied. Therefore we get the endemic state only when the zero infective state is unstable. We would expect the endemic state to be stable in that case. Let's see if we can show that. We calculate the derivative matrix at eq2, and assign it to dermat2.

```
dermat2 = dermat /. Thread[statevec -> eq2]
```

$$\left\{ \left\{ -\mu + \frac{\mu(-n\alpha + \beta + \mu)}{\beta + \mu}, -\beta - \mu \right\}, \left\{ -\frac{\mu(-n\alpha + \beta + \mu)}{\beta + \mu}, 0 \right\} \right\}$$

Now we introduce some simplifying notation:

$$q = \beta + \mu, \quad p = (n\alpha - (\beta + \mu))/(\beta + \mu) \quad . \quad (6)$$

We use replacement rules to introduce these into dermat2:

```
dermat2 = Simplify[dermat2 /. \beta -> (q - \mu) /. n -> (q (p + 1)) / \alpha]
```

$$\{\{-(1+p)\mu, -q\}, \{p\mu, 0\}\}$$

Now we look at the characteristic polynomial:

```
Collect [CharacteristicPolynomial [dermat2, λ], λ]
```

$$\lambda^2 + p q \mu + \lambda (\mu + p \mu)$$

We see that for $p > 0$, the sum of the roots $-pq\mu$ is negative and the product of the roots $\mu + p\mu$ is positive, hence the equilibrium is strictly stable.

Summary of equilibrium and stability: (1) For $p < 0$, the only equilibrium is the state with all susceptibles and no infectives or recovered. This state is stable, and if infectives are introduced, the number of infectives will decrease with time -- that is, there will not be an epidemic. (2) For $p > 0$, the equilibrium with all susceptibles and no infectives or recovered still exists, but it is unstable. If any infectives are added, there is an epidemic and the number of infectives increases. The asymptotic state reached as $t \rightarrow \infty$ is the endemic state with coordinates given by eq2 above. This state is a stable equilibrium in which the disease persists with a constant number of susceptibles, infectives and recovered. For most diseases, the time required for an epidemic to peak is much less than the generational time represented by μ . Thus when we add infectives to a population in which $p > 0$, we expect to see a relatively rapid peak followed by a slow approach to the endemic state. We pursue these ideas next.

4. Small μ Approximations

We derive here some simple approximations for μ small. We assume throughout this section that $p > 1$, so that there is an epidemic. The positive eigenvalue calculated above for the initial equilibrium of no infectives is $n\alpha - \beta - \mu$, which is approximately $n\alpha - \beta$, exactly what it is in the S-I-R model without vital dynamics. For the final approach to the endemic state, the time scales are determined by the eigenvalues in the endemic state. It is easy to show from the characteristic equation that, correct to first order in μ , we get eigenvalues

$$-\frac{\mu\alpha n}{2\beta} \pm \sqrt{\frac{\mu}{\beta}(n\alpha - \beta)} \quad . \quad (7)$$

From the fact that μ is small, we see that both the oscillation and decay time scales are long, but that the decay scale is the longer of the two. Now we look at a numerical example of this.

5. Examples

This example is strictly fictional, but the scales are chosen to illustrate the basic points. We suppose that the recovery period for the disease is one week, that the population is 1000, that the birth/death rate μ is 5×10^{-2} (inverse weeks), and that α is 3×10^{-3} (inverse weeks). We set these parameter values for DynPac:

```
parmval = {3. * 10-3, 1.0, 5. * 10-2, 1000};
```

Now we set the integration parameters -- the initial time t_0 , the time step h , the initial vector $initvec$, and the number of time steps $nsteps$. For the initial vector, we assume that 10 of the 1000 are infected initially.

```
t0 = 0.0; h = 0.1; initvec = {990, 10}; nsteps = 800;
```

Thus our time step is 0.1 weeks, and we are integrating out to 80 weeks.

```
soll = integrate[initvec, t0, h, nsteps];
```

We set the aspect ratio to 1.

```
asprat = 1;
```

We set the plot range to $\{0,1000\}$ in both s and i .

```
plrange = {{0, 1000}, {0, 1000}};
```

We set the system name to SIR, and we ask for arrows on the phase diagram -- specifically one arrow at the midpoint of the integral curve.

```
sysname = "SIR";
```

```
arrowflag = True;
```

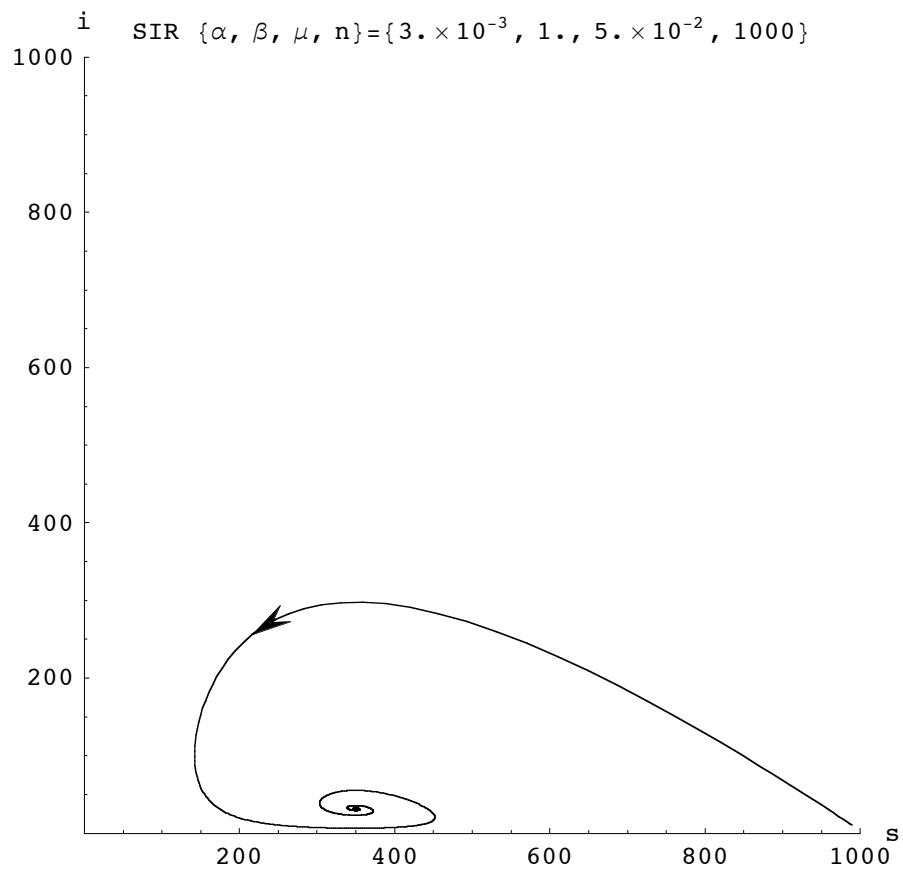
```
arrowvec = {1 / 2};
```

Finally, we ask for scientific notation to be used for the parameter values printed in the graph label.

```
decdig = 3;
```

```
sciflag = True;
```

```
phaser[sol1];
```



We see the rapid development of the epidemic and the slow spiral into the endemic state. That state is

```
eqstateval[eq2]
```

```
{350., 30.9524}
```

The number of recovered is

```
1000 - 350 - 31
```

```
619
```

We look at our last integration point to see that we have actually arrived at the endemic state:

```
lasttx
```

```
{80., 351.14, 30.717}
```

We are almost at the final endemic state -- close enough for now.

Now let's look at a time plot of the number of infectives. We first check the range in the solution.

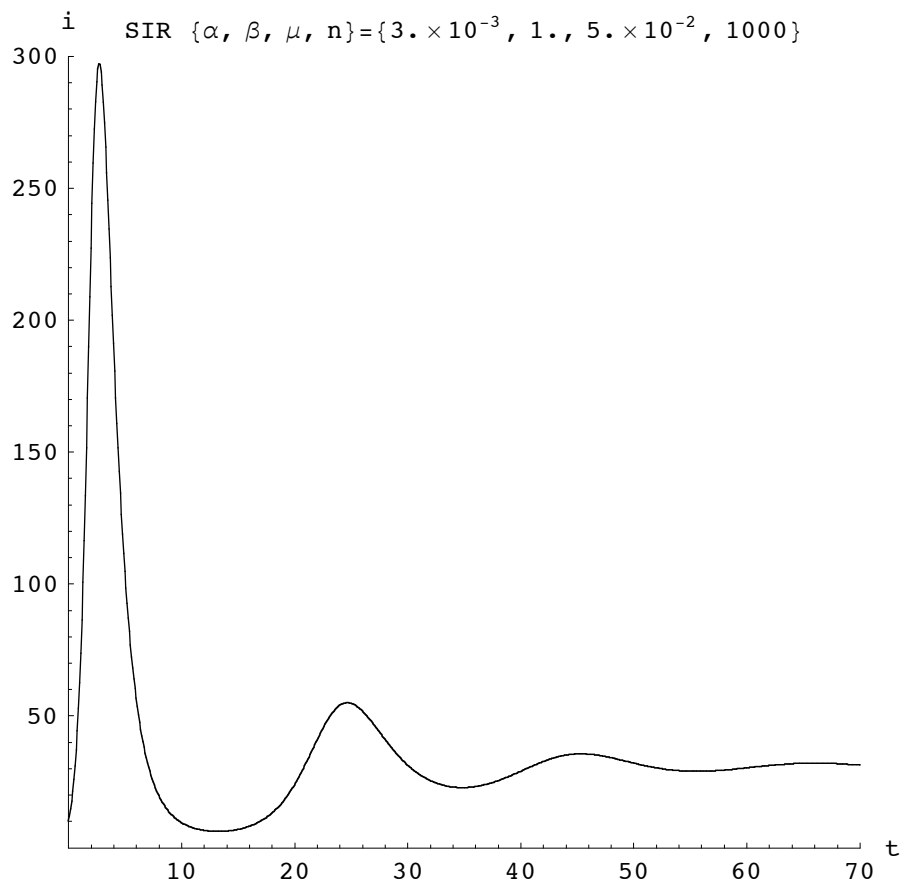
```
staterange[sol1]
```

```
{{s, {142.592, 5.1}, {990, 0.}}, {i, {6.12809, 13.2}, {297.239, 2.7}}}
```

We now set the plot range for i .

```
plrange = {{0, 70}, {0, 300}};
```

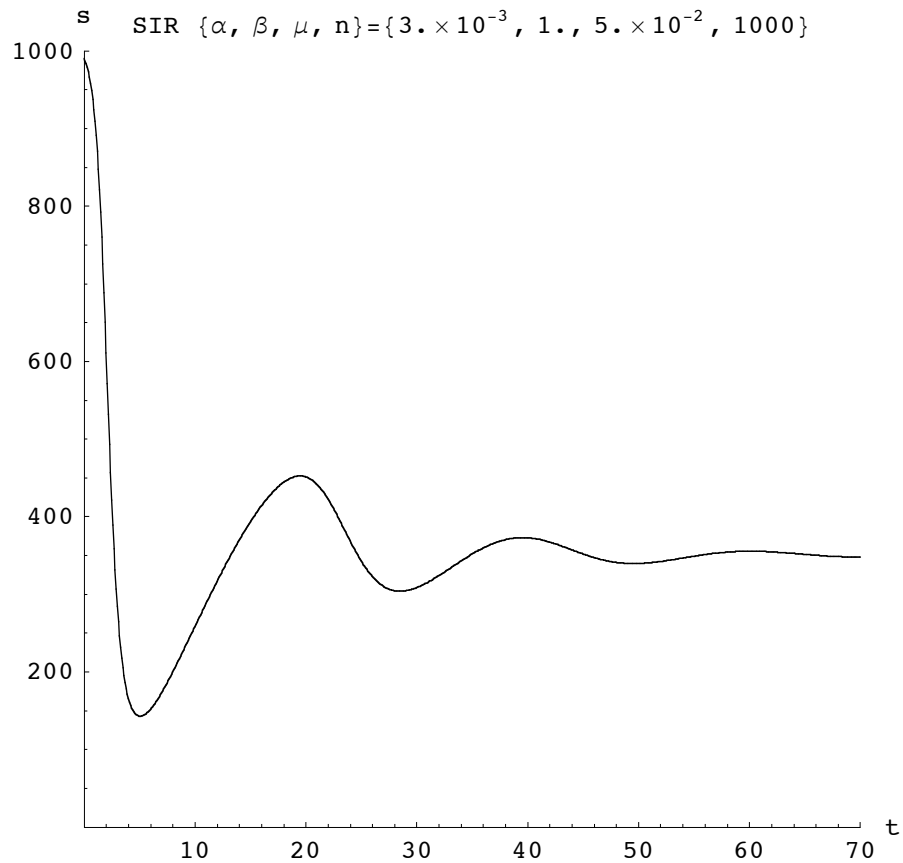
```
timeplot[sol1, 2];
```



We see the strong rapid peak in the epidemic, followed by decaying oscillations to the final endemic state. Let's do the time plot for the number of susceptibles.

```
plrange = {{0, 70}, {0, 1000}};
```

```
timeplot[sol1, 1];
```



Once again the strong epidemic peak followed by an oscillatory approach to the endemic state.

Once the endemic state is established, any small perturbations which occur will be damped oscillations, with frequency and damping rate determined by the eigenvalues of that state. These eigenvalues are

```
Eigenvalues[dermatval[eq2]]
```

```
{-0.0714286 + 0.30397 i, -0.0714286 - 0.30397 i}
```

We see that the imaginary part is larger than the real part, as we would expect from equation (7). The e-folding decay scale is

```
1 / 0.0714286
```

```
14.
```

hence 14 weeks, and the oscillation period is

```
2 * Pi / (0.30397)
```

```
20.6704
```

a little under 20 weeks.

We now look at a second example, given by R.M Anderson and R.M May in **Infectious Diseases of Humans**, Oxford University Press, 1991, p. 123-124. The model is the same as that discussed here. The parameter values are (the time unit is years; our numbers differ somewhat from May's)

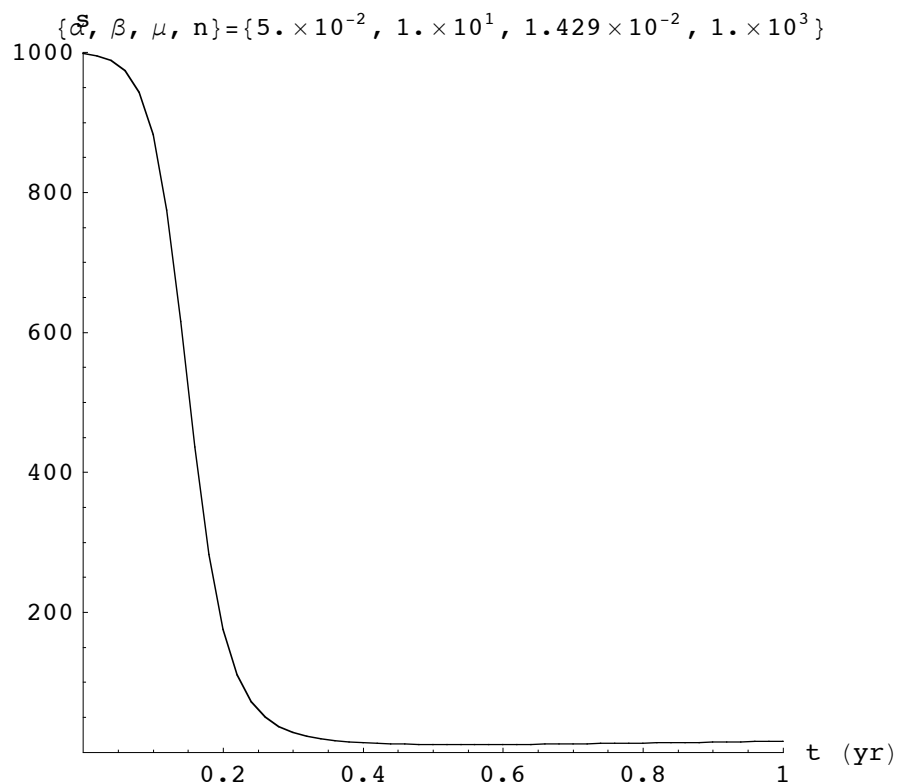
```
parmval = {0.05, 10.0, 1.0 / 70.0, 1000.0};
```

We start with two infectives in a population of 1000, and we integrate for 100 years.

```
maysol = integrate[{998, 2}, 0.0, 0.02, 5000];
```

We first look at the solution over a short time scale.

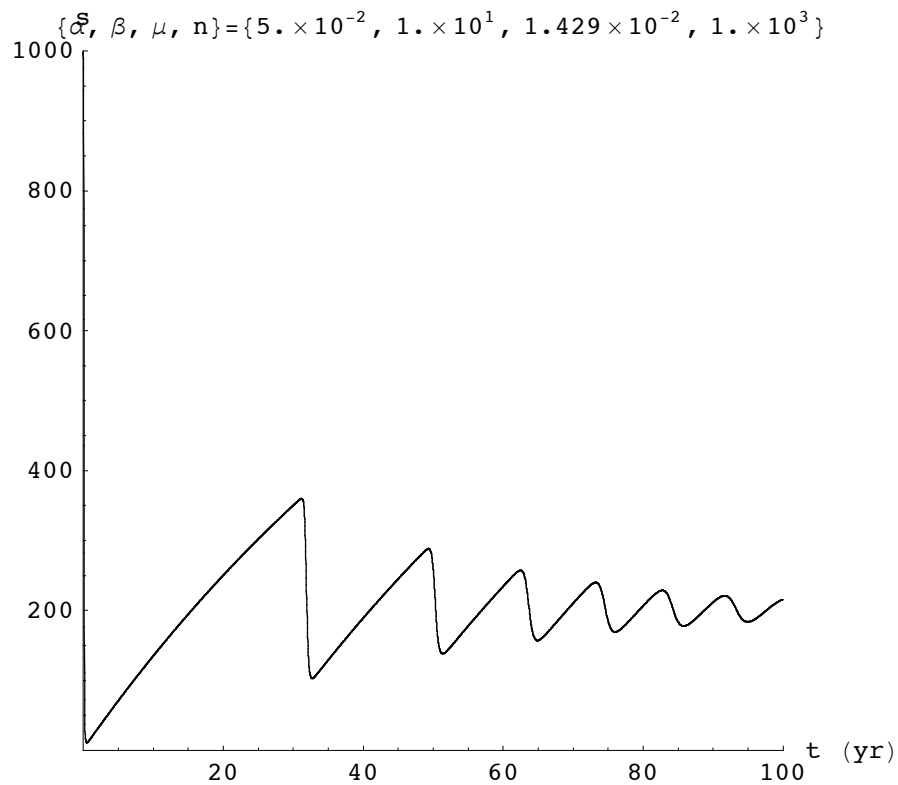
```
sysname = "";
plrange = {{0, 1}, {0, 1000}};
timeunit = "yr";
timeplot[maysol, 1];
```



The epidemic is essentially over in four or five months. Now we look at the solution over much longer times:

```
plrange = {{0, 100}, {0, 1000}};
```

```
timeplot[maysol, 1];
```

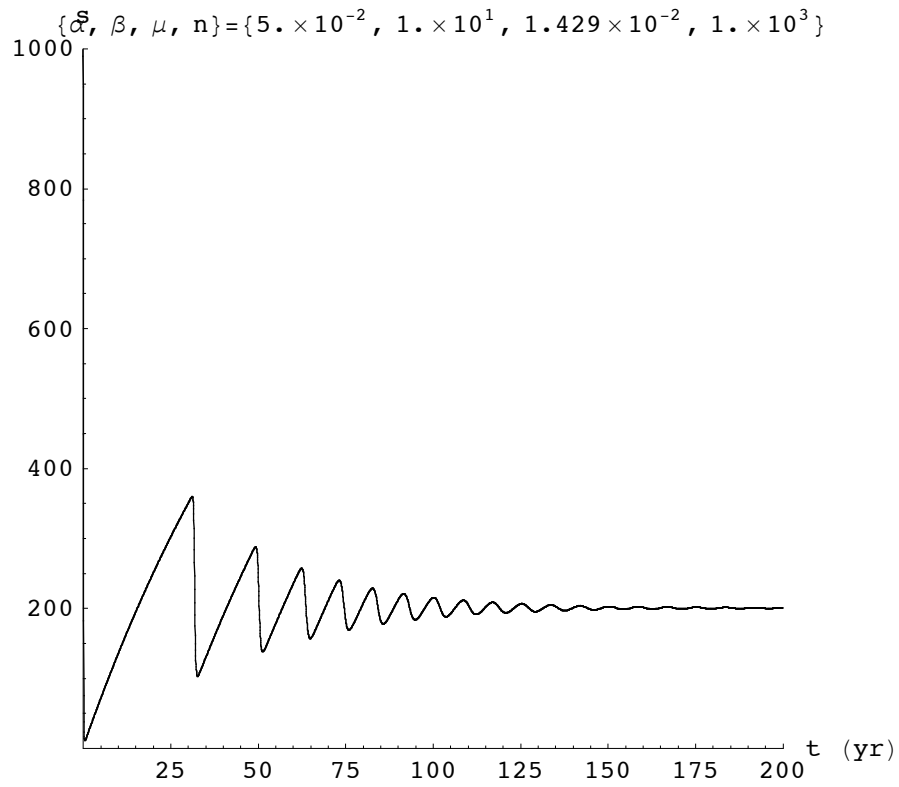


This rather striking curve can be described as a succession of epidemics, of ever-diminishing amplitude. Eventually, these oscillations disappear and the system settles in to the stable endemic equilibrium. Let's track it a little further in time to see this. We use a coarser time step and go twice as far.

```
maysol2 = integrate[{998, 2}, 0.0, 0.04, 5000];
```

```
plrange = {{0, 200}, {0, 1000}};
```

```
timeplot[maysol2, 1];
```



The system requires 200 years to settle into the endemic state!

The most characteristic feature of this system is the existence of two very different time scales -- the short time scale of a single epidemic, and the long generational time scale on which susceptibles are replenished.