

```
> restart;  
> xe1:=(mu-1)/(2*mu)+sqrt((mu+1)^2-4*mu/R0)/(2*mu);
```

$$xe1 := \frac{1}{2} \frac{\mu - 1}{\mu} + \frac{1}{2} \frac{\sqrt{(\mu + 1)^2 - \frac{4\mu}{R0}}}{\mu} \quad (1)$$

```
> xe2:=(mu-1)/(2*mu)-sqrt((mu+1)^2-4*mu/R0)/(2*mu);
```

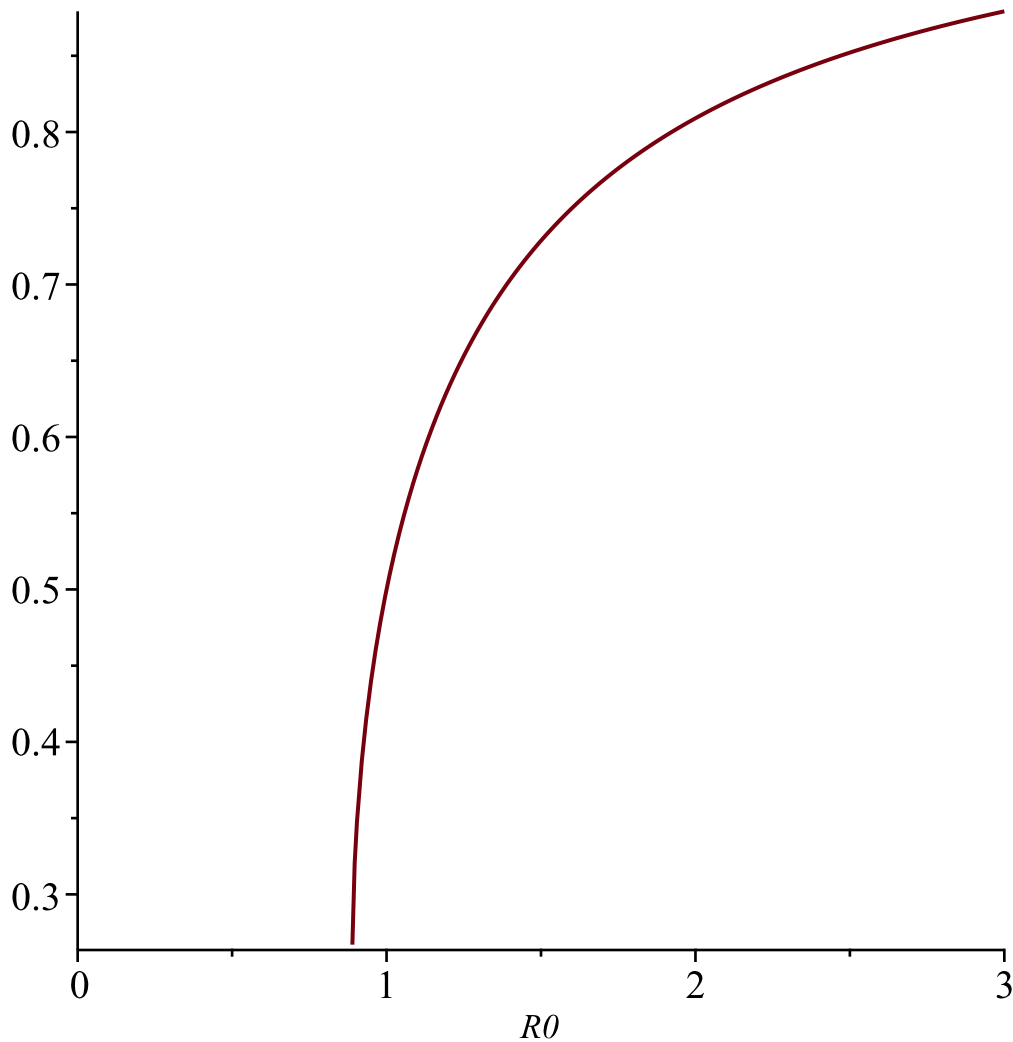
$$xe2 := \frac{1}{2} \frac{\mu - 1}{\mu} - \frac{1}{2} \frac{\sqrt{(\mu + 1)^2 - \frac{4\mu}{R0}}}{\mu} \quad (2)$$

```
> mu:=2;
```

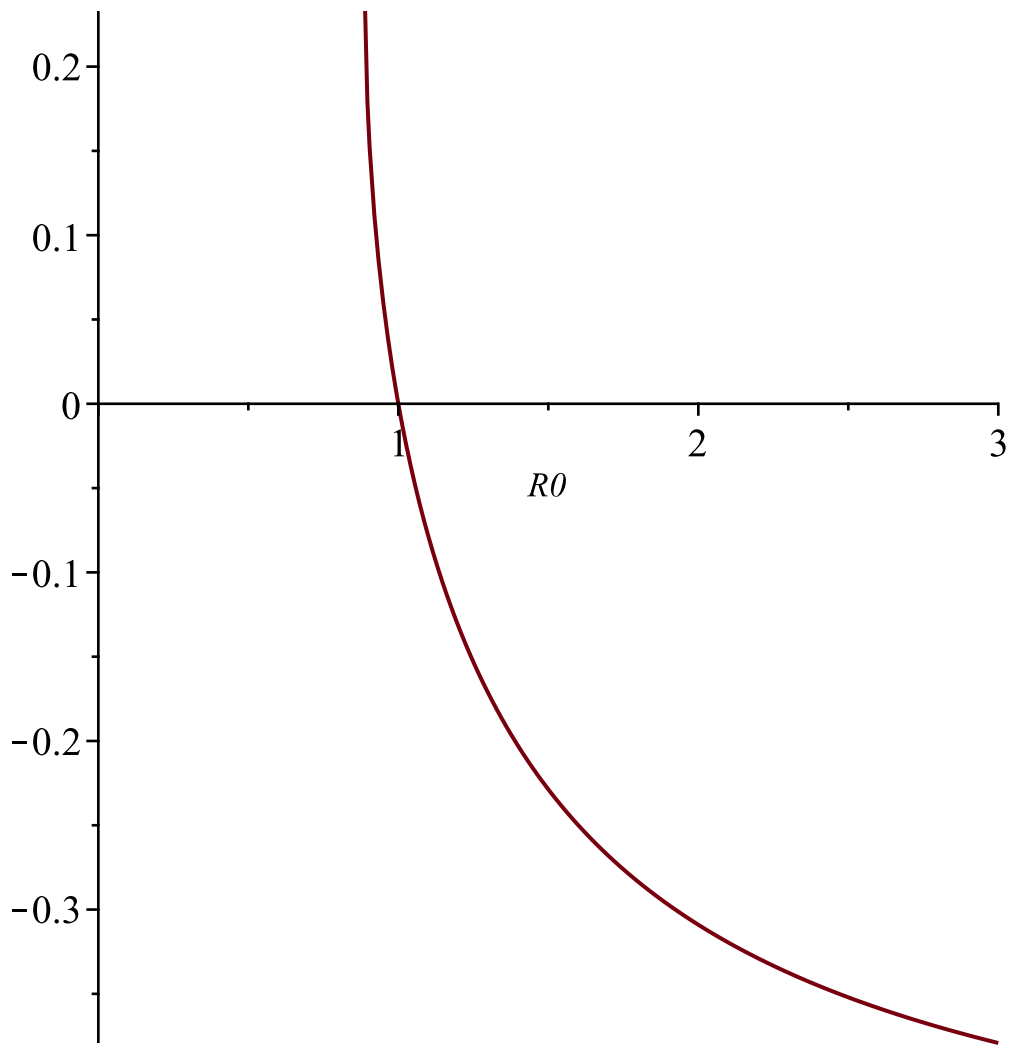
$$\mu := 2 \quad (3)$$

```
> with(plots):
```

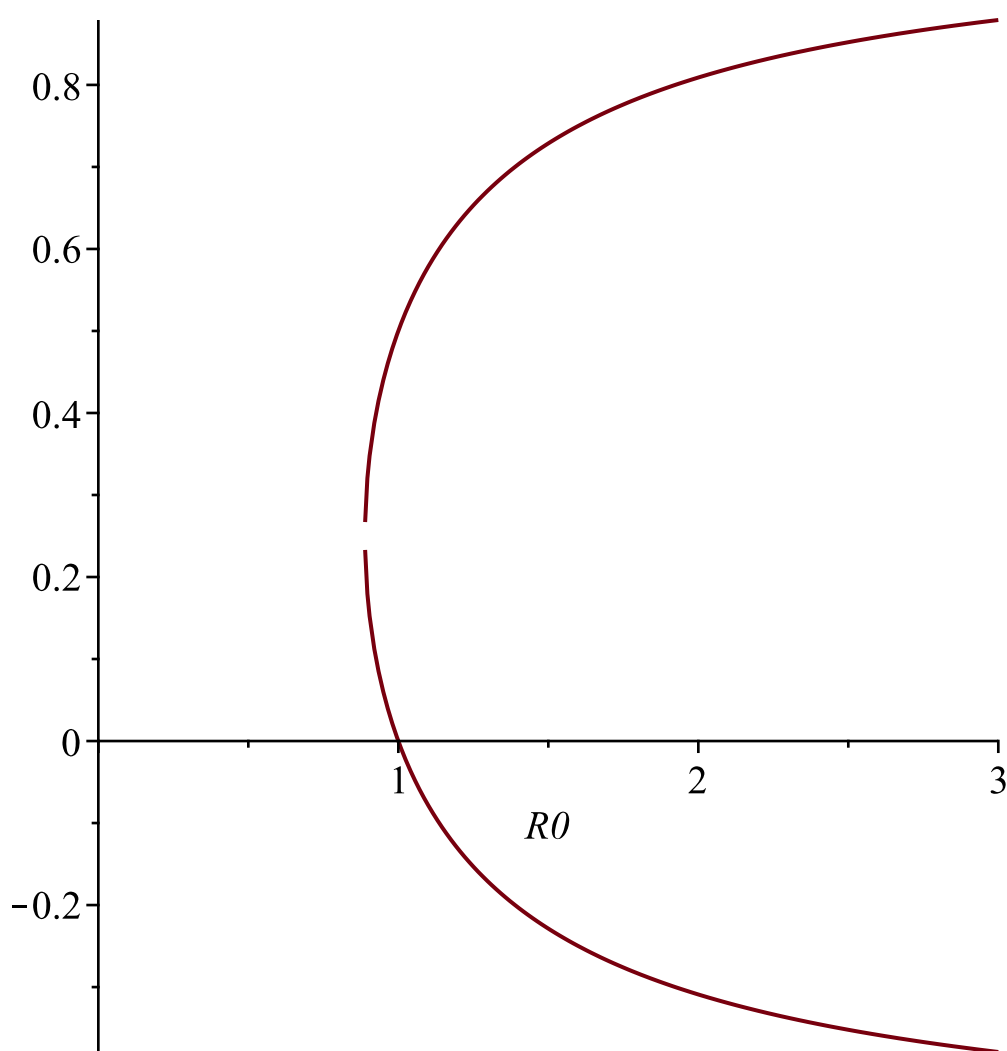
```
> p1:=plot(xe1,R0=0..3);
```



```
> p2:=plot(xe2,R0=0..3);
```



```
> display({p1,p2});
```



```
> restart;
```

```
> #Let's simulate the system with  $R_0 < 1$ , but larger than 8/9. In this range if the initial number of infected is large enough, we will have an endemic state.
```

```
> eq1:=diff(S(t),t)=b*N-lambda*(1+nu*I(t))/N*S(t)*I(t)+Gamma*R(t)-b*S(t);
```

$$eq1 := \frac{d}{dt} S(t) = bN - \frac{\lambda(1 + \nu I(t)) S(t) I(t)}{N} + \Gamma R(t) - b S(t) \quad (4)$$

```
> eq2:=diff(I(t),t)=lambda*(1+nu*I(t))*I(t)*S(t)/N-alpha*I(t)-b*I(t);
```

$$eq2 := \frac{d}{dt} I(t) = \frac{\lambda(1 + \nu I(t)) S(t) I(t)}{N} - \alpha I(t) - b I(t) \quad (5)$$

```
> eq3:=diff(R(t),t)=alpha*I(t)-Gamma*R(t)-b*R(t);
```

$$eq3 := \frac{d}{dt} R(t) = \alpha I(t) - \Gamma R(t) - b R(t) \quad (6)$$

```
> b:=0;
```

$$b := 0 \quad (7)$$

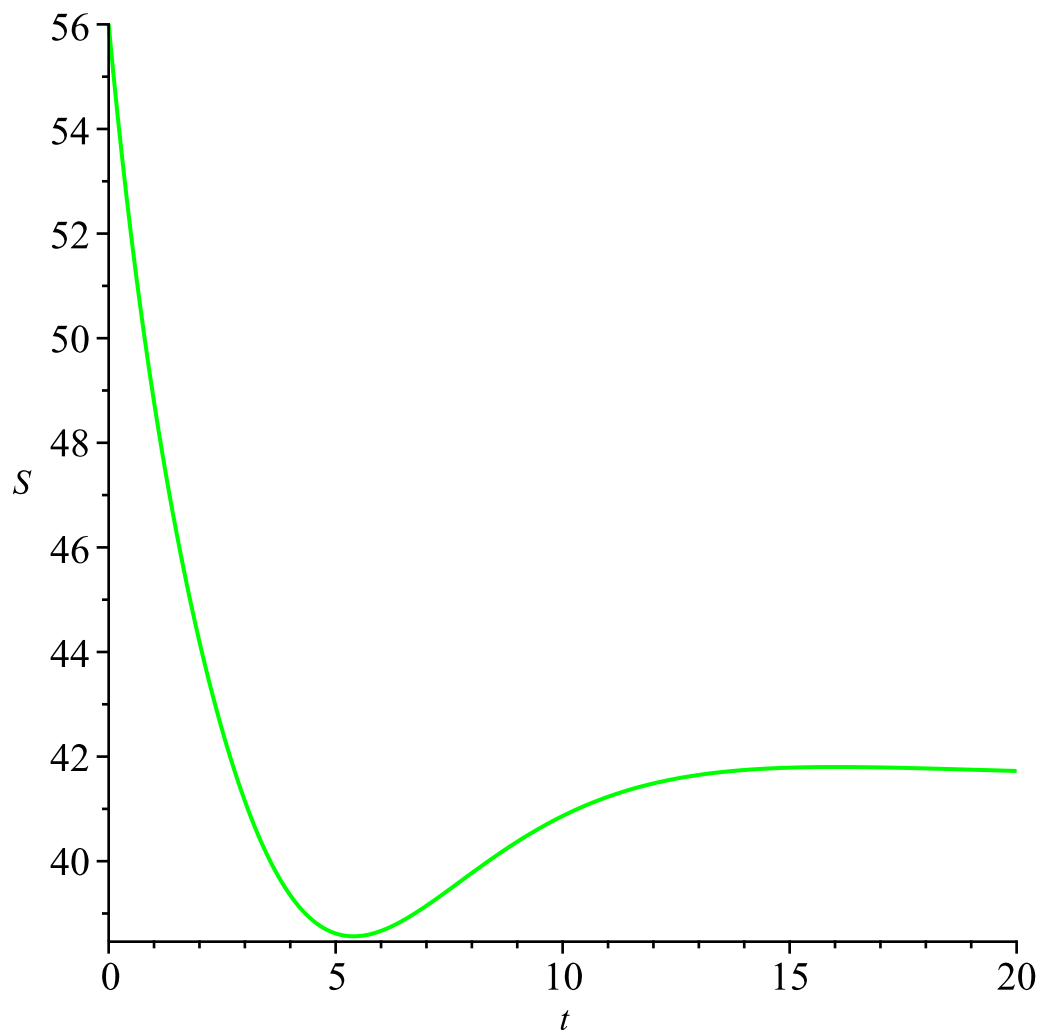
```
> alpha:=2;
```

$$\alpha := 2 \quad (8)$$

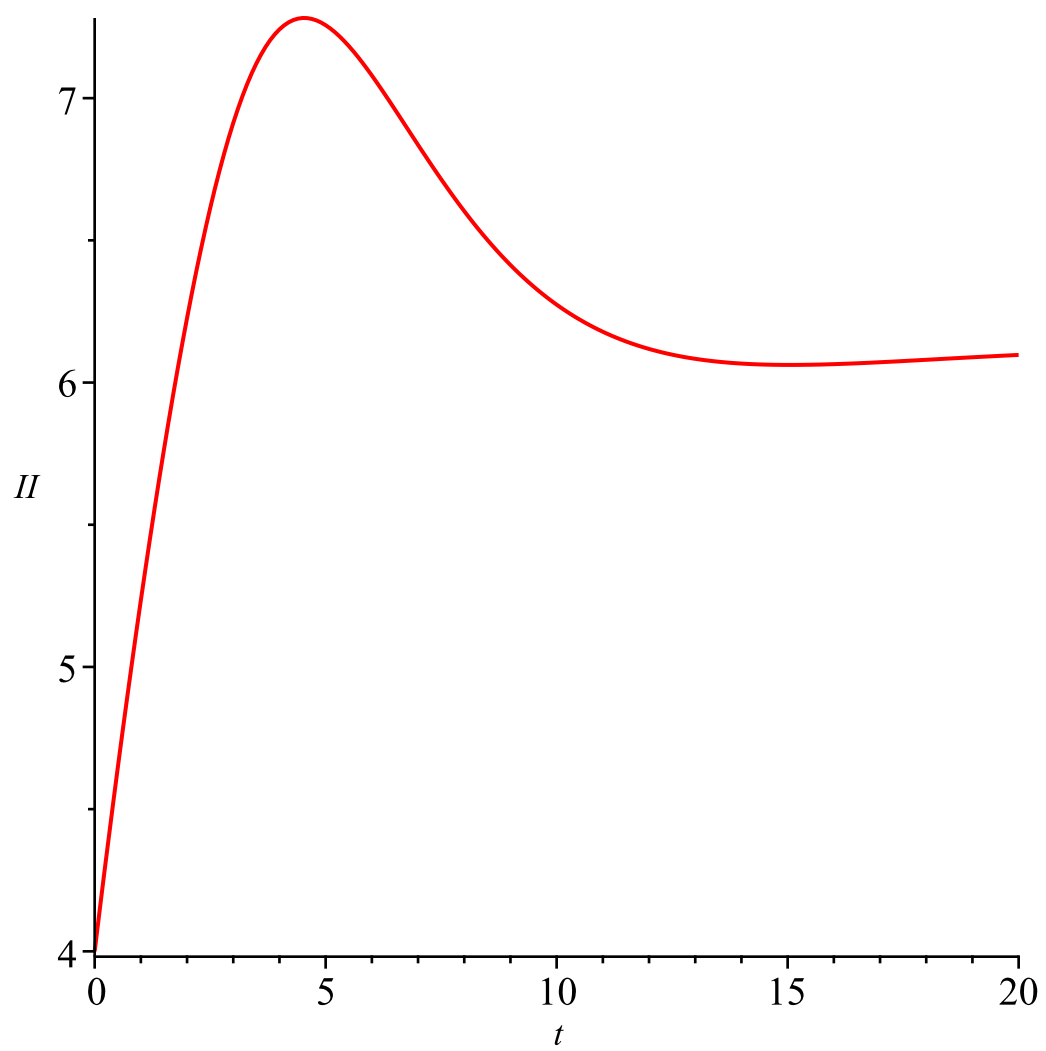
```

> Gamma:=1;
Γ := 1 (9)
> lambda:=16/9+.01;
λ := 1.787777778 (10)
> nu:=.1;
ν := 0.1 (11)
> N:=60;
N := 60 (12)
> R0:=lambda/(b+alpha);
R0 := 0.8938888890 (13)
> epsilon:=alpha/(b+Gamma);
ε := 2 (14)
> eta:=alpha/(b+alpha);
η := 1 (15)
> mu:=nu*N/(1+epsilon);
μ := 2.000000000 (16)
> # The critical value of x (it is the scaled number of infeted)
> xc:=(mu-1)/(2*mu)-1/(2*mu)*sqrt((mu+1)^2-4*mu/R0);
xc := 0.1939075384 (17)
> # The critical number of infrected (not scaled)
> Ic:=xc*N/(1+epsilon);
Ic := 3.878150767 (18)
> sol1:=dsolve({eq1,eq2,eq3,S(0)=56,I(0)=4,R(0)=0},{S(t),I(t),R
(t)},numeric);
sol1 := proc(x_rkf45) ... end proc (19)
> sol2:=dsolve({eq1,eq2,eq3,S(0)=58,I(0)=2,R(0)=0},{S(t),I(t),R
(t)},numeric);
sol2 := proc(x_rkf45) ... end proc (20)
> with(plots):
> p1:=odeplot(sol1,[t,S(t)],t=0..20,color='green');

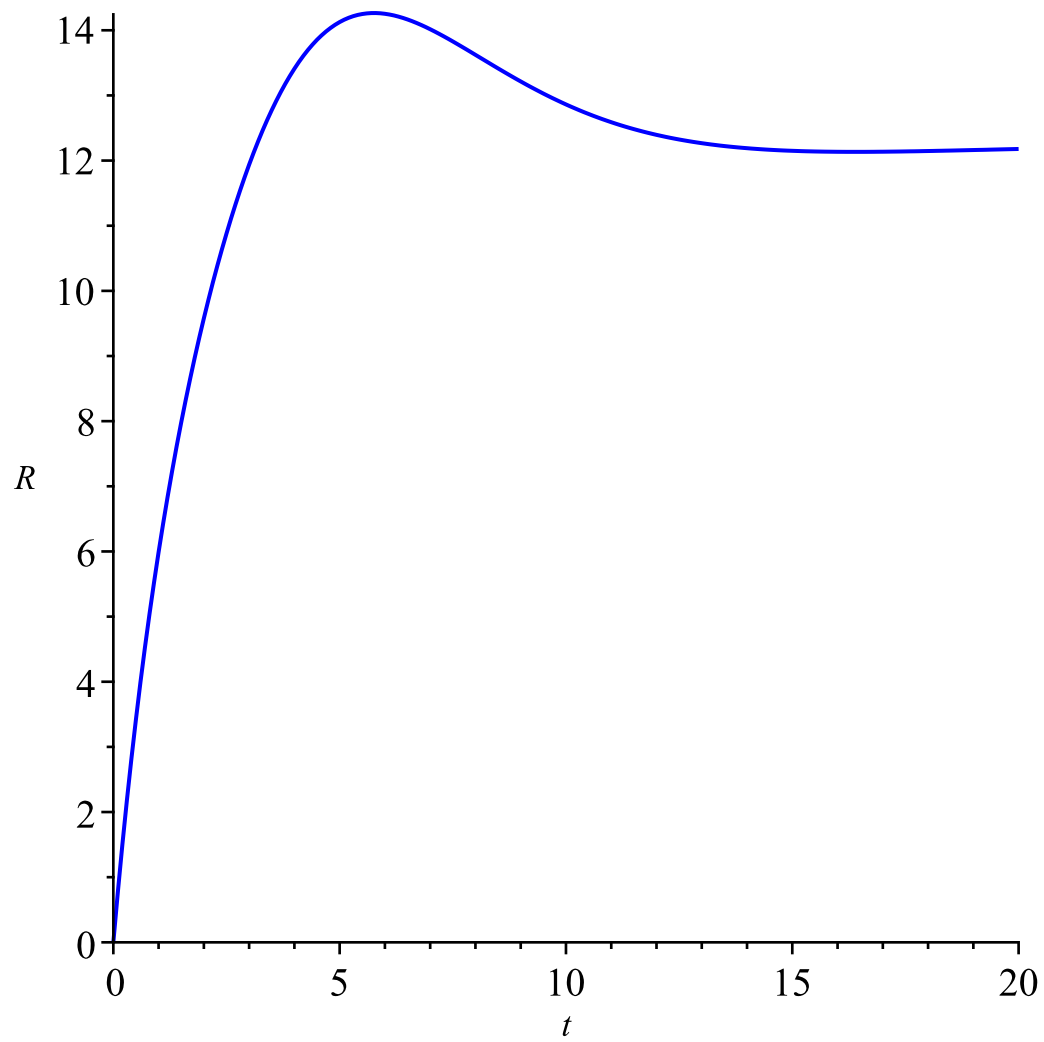
```



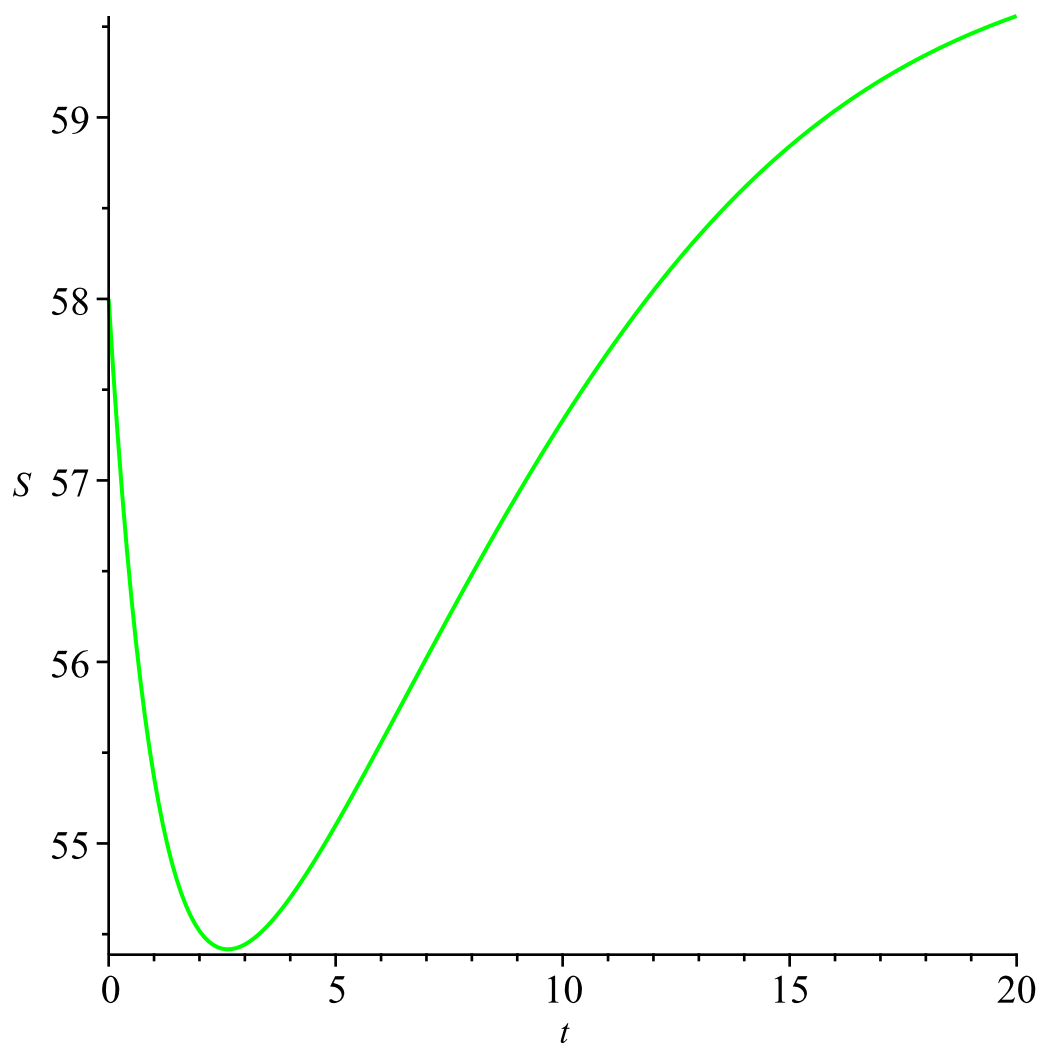
```
> p2:=odeplot(sol1,[t,I(t)],t=0..20,color='red');
```



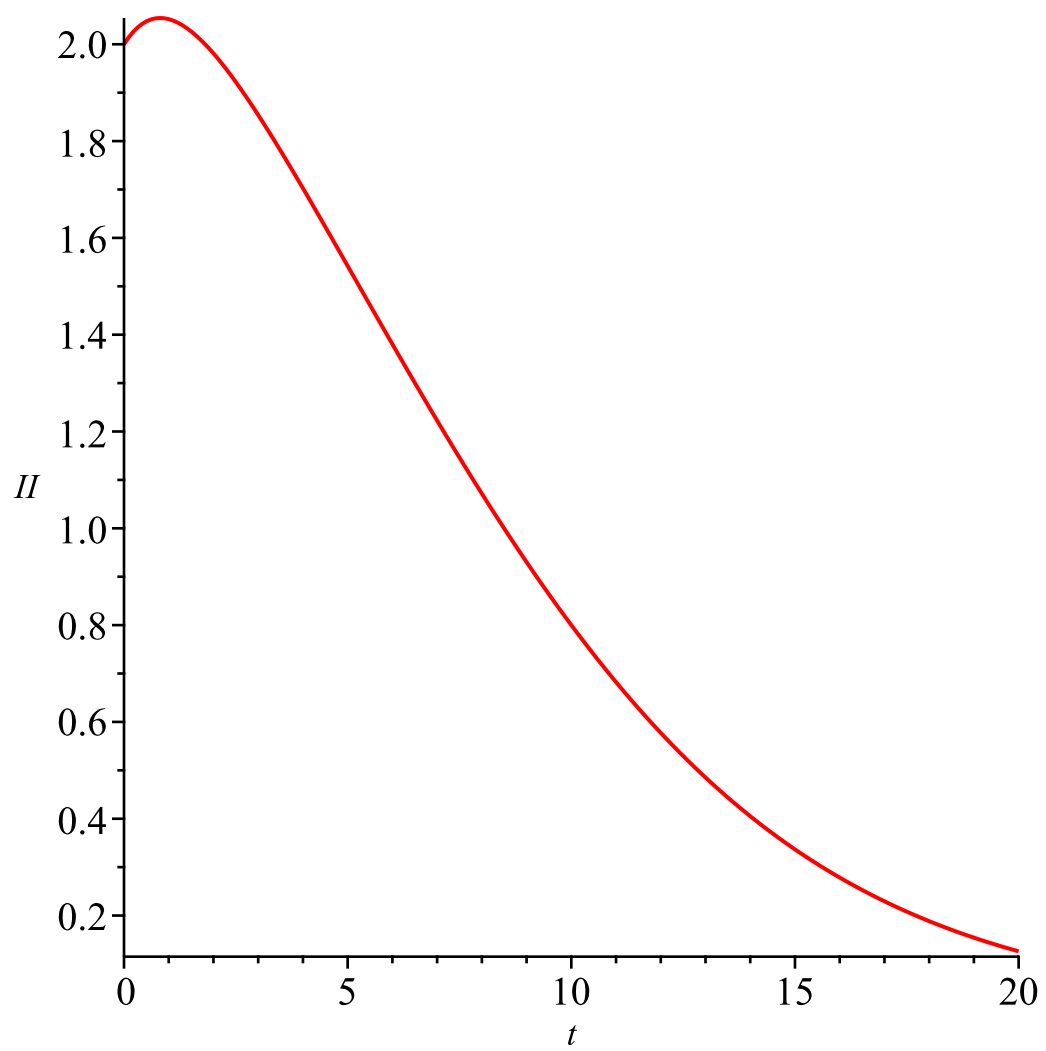
```
> p3:=odeplot(sol1,[t,R(t)],t=0..20,color='blue');
```



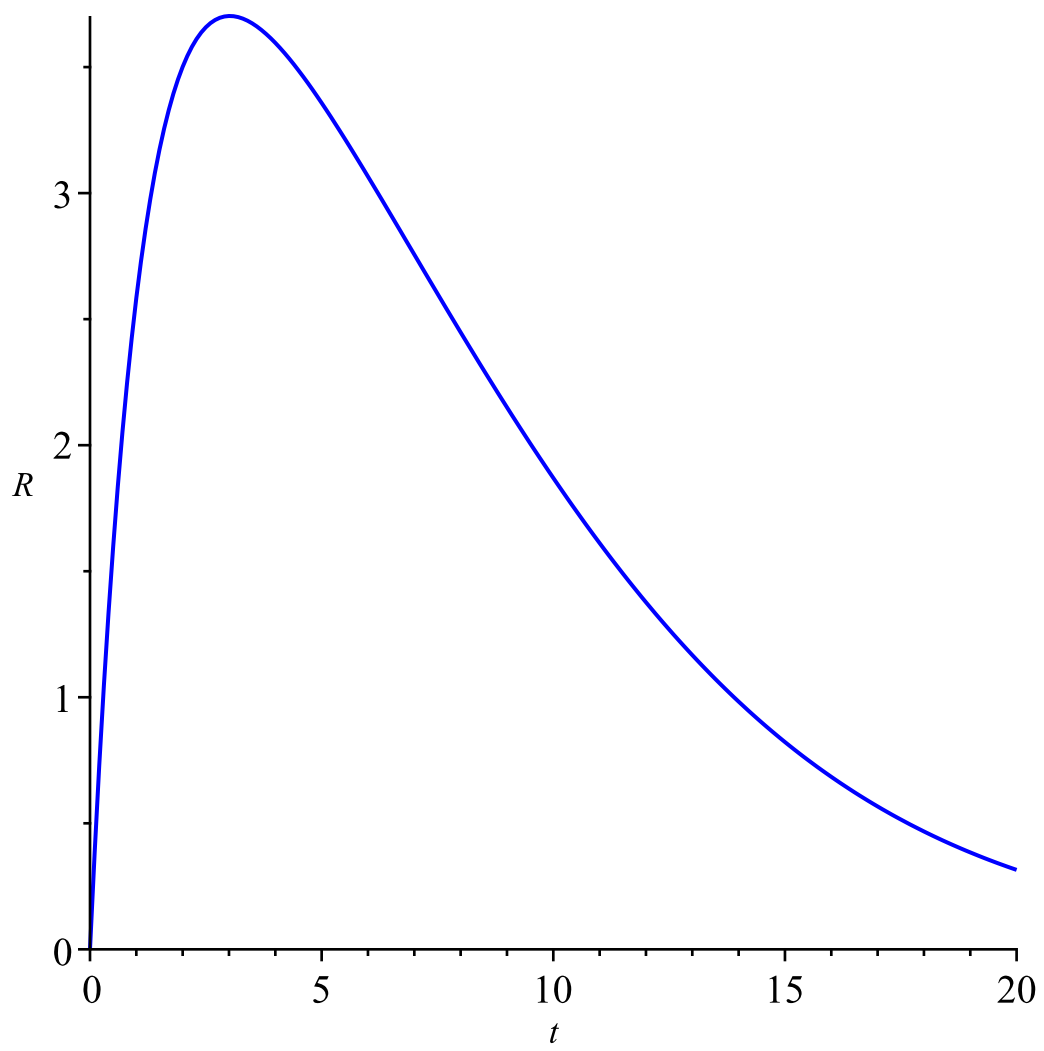
```
> p4:=odeplot(sol2,[t,S(t)],t=0..20,color='green');
```



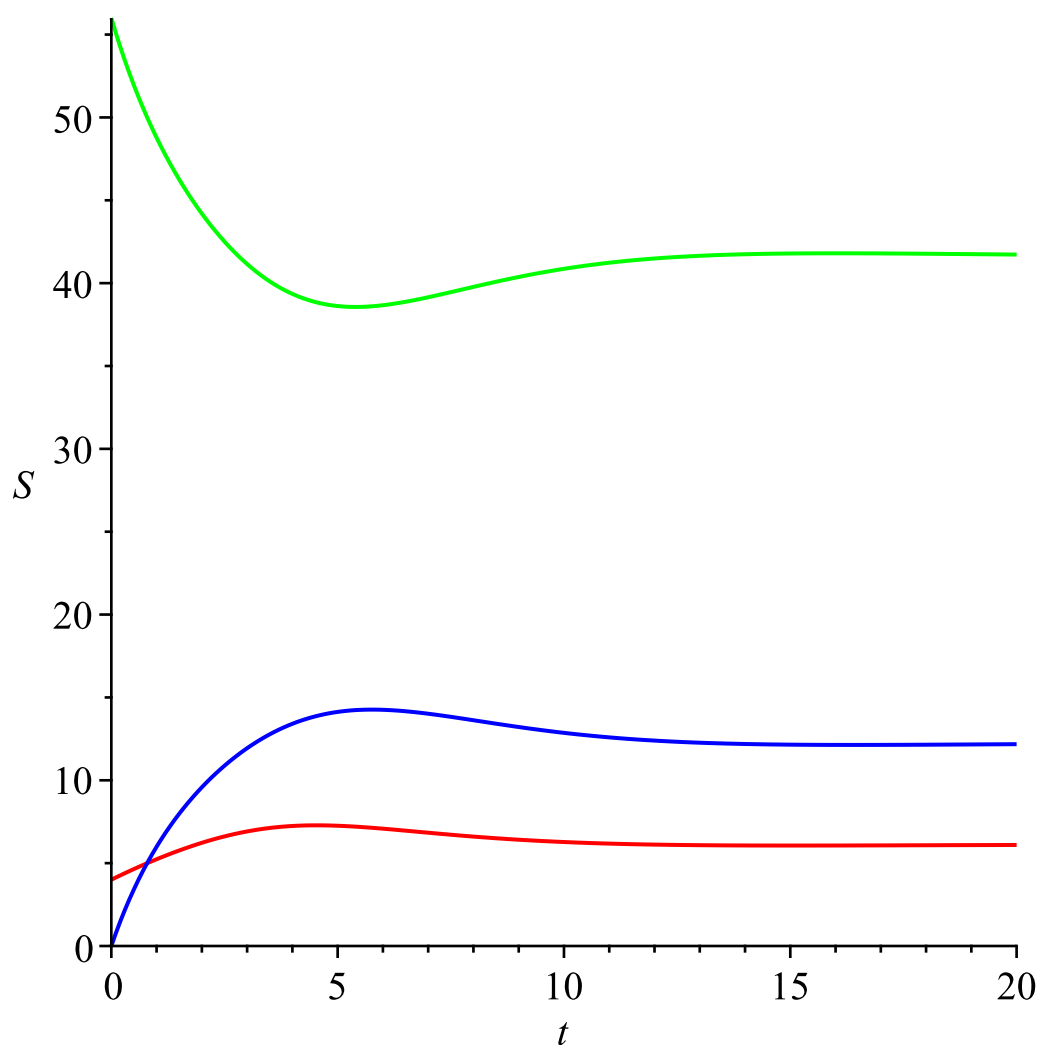
```
> p5:=odeplot(sol2,[t,II(t)],t=0..20,color='red');
```

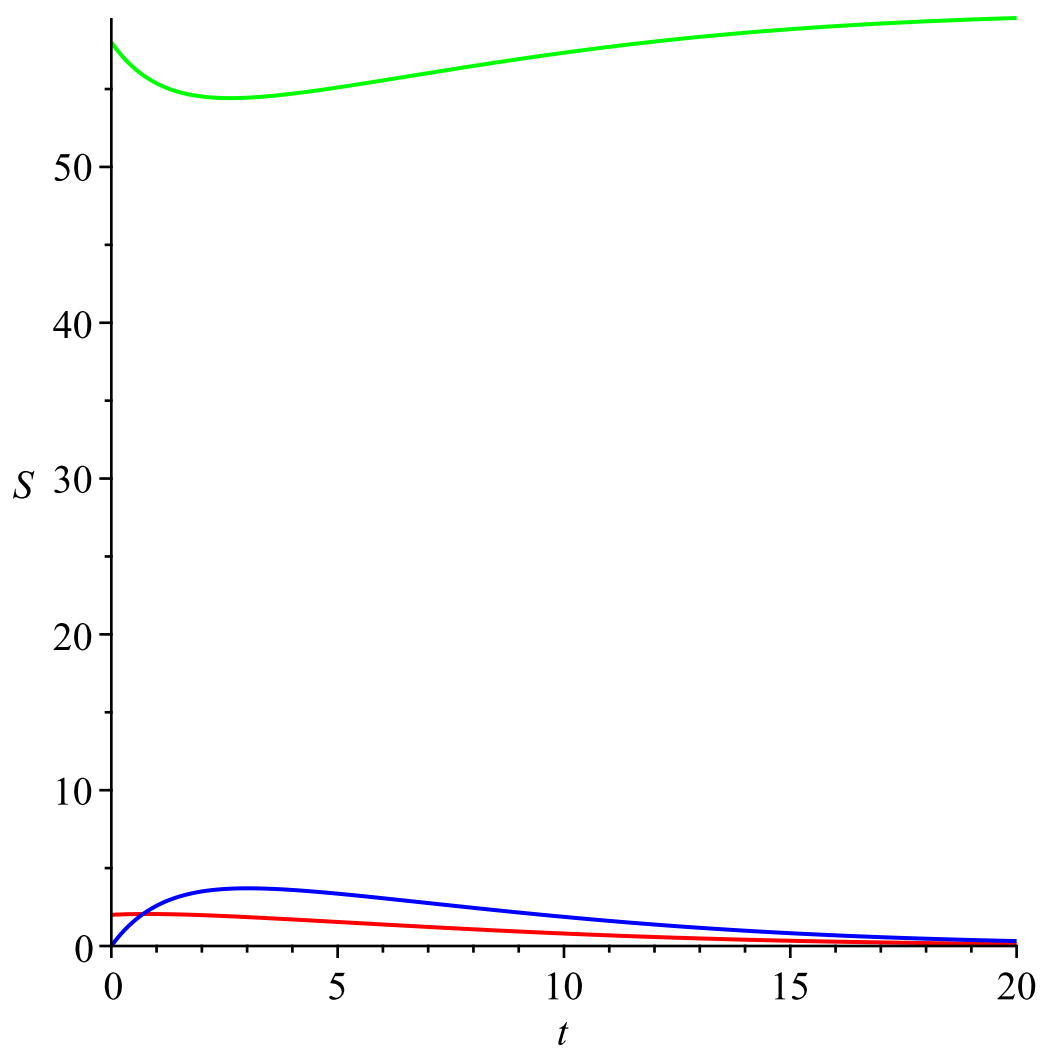
```
> p6:=odeplot(sol2,[t,R(t)],t=0..20,color='blue');
```



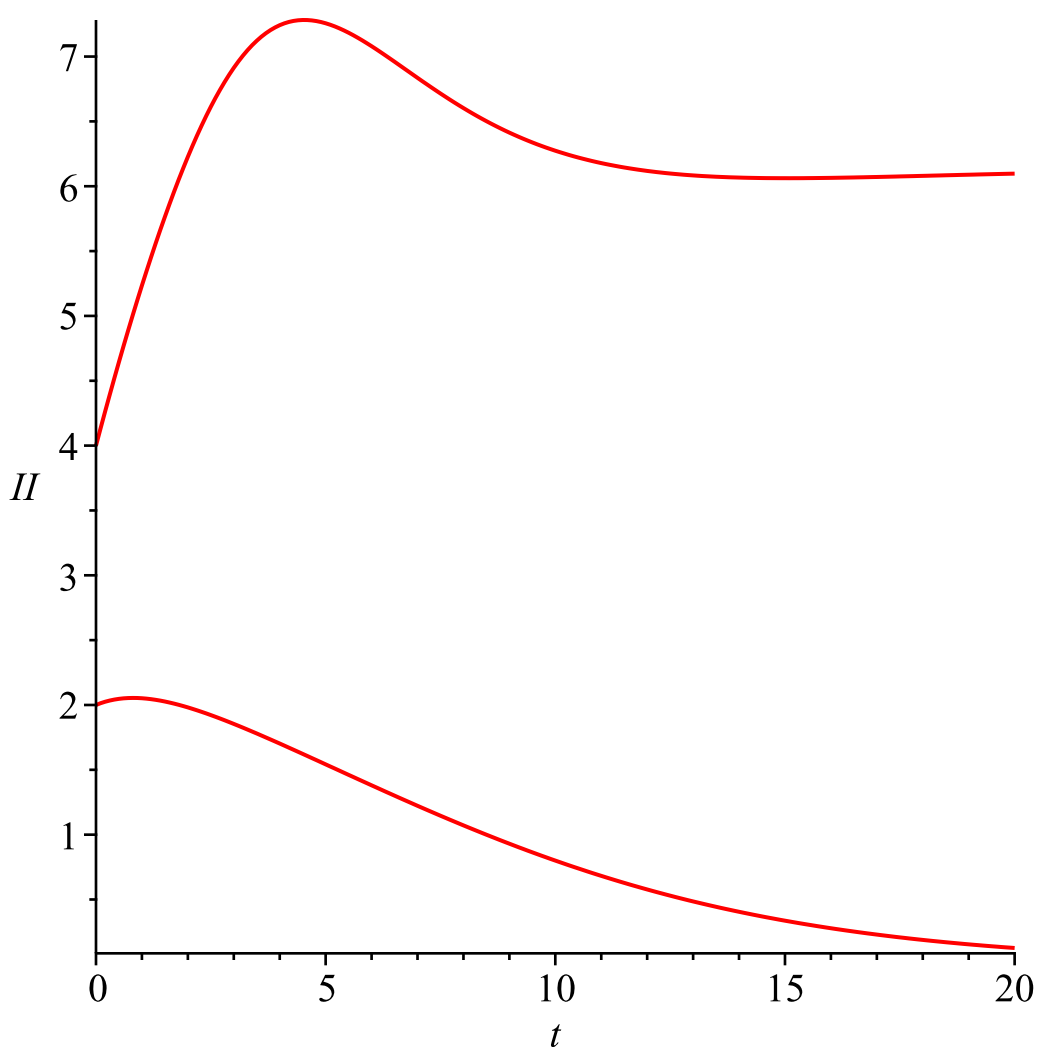
```
> display({p1,p2,p3});
```



```
> display({p4,p5,p6});
```



```
> display({p2,p5});
```



> # Here I will show how a small change in R0 can have a big change in the magnitude of the solution

> #

> restart;

> # I will use the scaled system as it is easier to see what is happening if R0 is a parameter

> eq1:=diff(x(t),t)=R0*(1+chi*x(t))*(1-(x(t)+y(t))/(1+epsilon))*x(t)-x(t);

$$eq1 := \frac{d}{dt} x(t) = R0 (1 + \chi x(t)) \left(1 - \frac{x(t) + y(t)}{1 + \epsilon} \right) x(t) - x(t) \quad (21)$$

> eq2:=diff(y(t),t)=eta*(x(t)-y(t)/epsilon);

$$eq2 := \frac{d}{dt} y(t) = \eta \left(x(t) - \frac{y(t)}{\epsilon} \right) \quad (22)$$

> chi:=2:epsilon:=1:eta:=1:

> # First I pick R0 very close to 1 but under 1.

> R0:=.99;

$$R0 := 0.99 \quad (23)$$

> # This is the critical value of infected. We must start with an initial value below this.

> xc:=(chi-1)/(2*chi)-sqrt((chi+1)^2-4*chi/R0)/(2*chi);

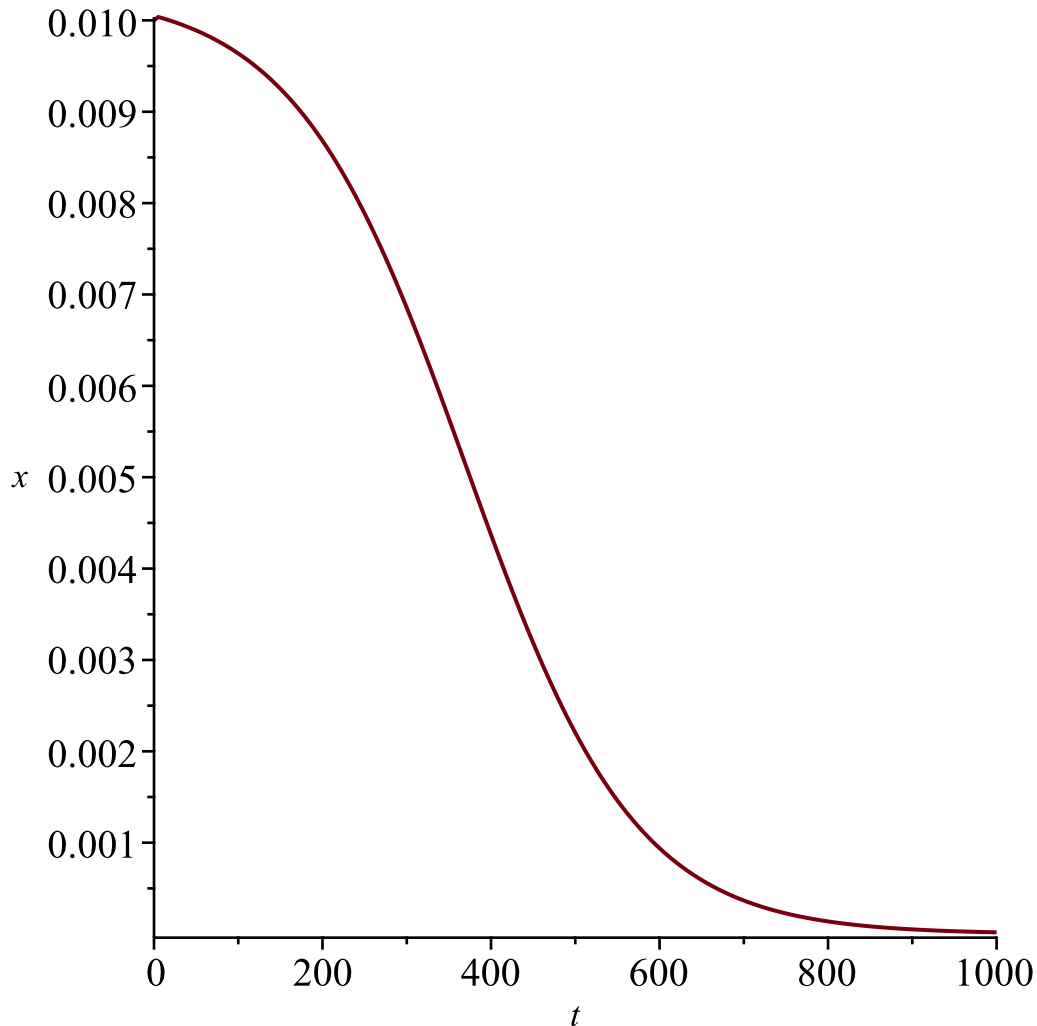
`xc := 0.0103137572`

(24)

```
> sol:=dsolve({eq1,eq2,x(0)=0.01,y(0)=0},{x(t),y(t)},numeric);  
sol := proc(x_rkf45) ... end proc
```

(25)

```
> with(plots):  
> odeplot(sol,t=0..1000);
```



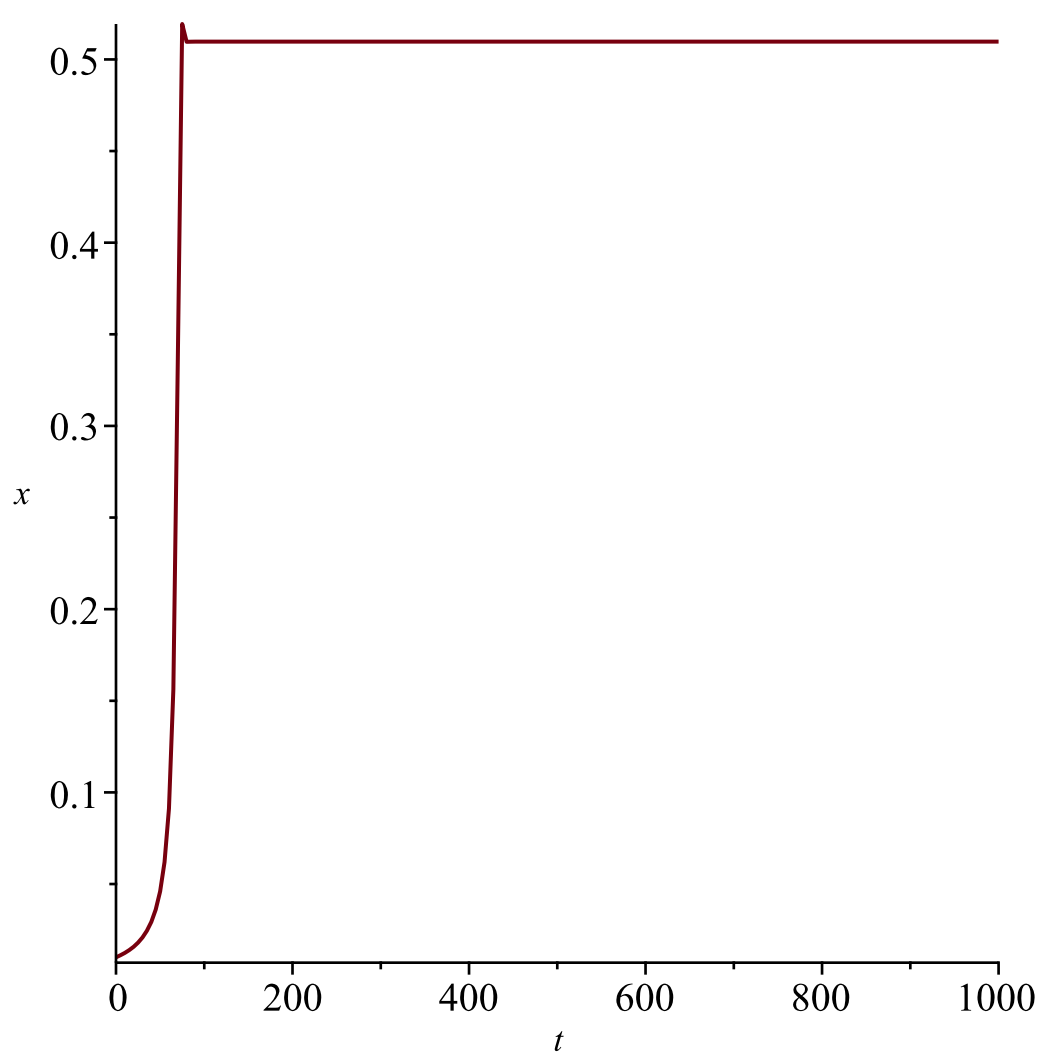
```
> # Now I make a very small change to R0 and leave the rest of the  
system the same  
> R0:=1.01;
```

`R0 := 1.01`

(26)

```
> sol1:=dsolve({eq1,eq2,x(0)=0.01,y(0)=0},{x(t),y(t)},numeric);  
sol1 := proc(x_rkf45) ... end proc  
> odeplot(sol1,t=0..1000);
```

(27)



- > # Remember that x is the scaled number of infected individuals. With this very small change in parameters, we jump from 0
- > # to a relatively large number of infected.