

The Lotka-Volterra predator prey model.

Let $x(t)$ be the population of the prey at time t

Let $y(t)$ be the population of the predators at time t

> restart;

de1 := diff(x(t),t) = alpha1*x(t) - beta1*x(t)*y(t);

$$de1 := \frac{d}{dt} x(t) = \alpha_1 x(t) - \beta_1 x(t) y(t) \quad (1)$$

> de2 := diff(y(t),t) = beta2*x(t)*y(t) - alpha2*y(t);

$$de2 := \frac{d}{dt} y(t) = \beta_2 x(t) y(t) - \alpha_2 y(t) \quad (2)$$

> solve({rhs(de1)=0,rhs(de2)=0}, {x(t),y(t)});

$$\{x(t) = 0, y(t) = 0\}, \left\{ x(t) = \frac{\alpha_2}{\beta_2}, y(t) = \frac{\alpha_1}{\beta_1} \right\} \quad (3)$$

> alpha1 := 0.1;

beta1 := 0.1;

beta2 := 0.02;

alpha2 := 0.05;

$\alpha_1 := 0.1$

$\beta_1 := 0.1$

$\beta_2 := 0.02$

$\alpha_2 := 0.05$

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> F := dsolve({de1,de2,x(0)=1,y(0)=0.2}, numeric);

F:= proc(x_rkf45) ... end proc

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> F(0.0);

[t = 0., x(t) = 1., y(t) = 0.2000000000000000]

(6)

> F(0.1);

[t = 0.1, x(t) = 1.00803510126440, y(t) = 0.199402498979488]

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> F(2.0);

[t = 2.0, x(t) = 1.17484203973331, y(t) = 0.188993456628175]

(8)

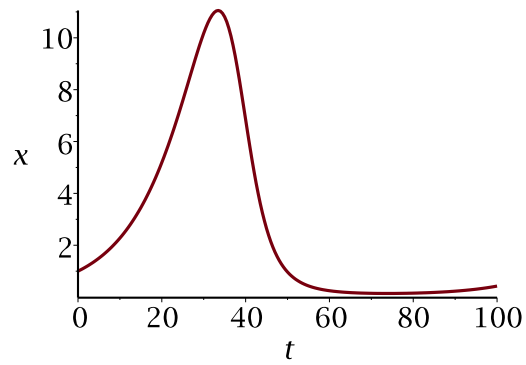
> F(-2.0);

[t = -2.0, x(t) = 0.853224170436178, y(t) = 0.213009874075132]

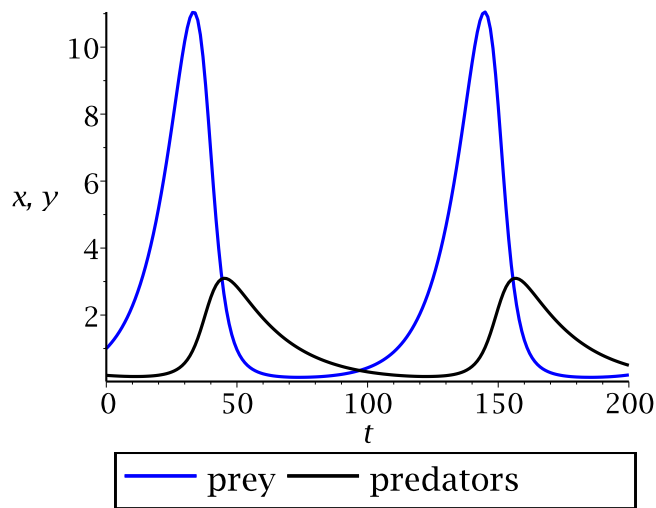
(9)

> with(plots):

> odeplot(F, [t,x(t)], t=0..100);



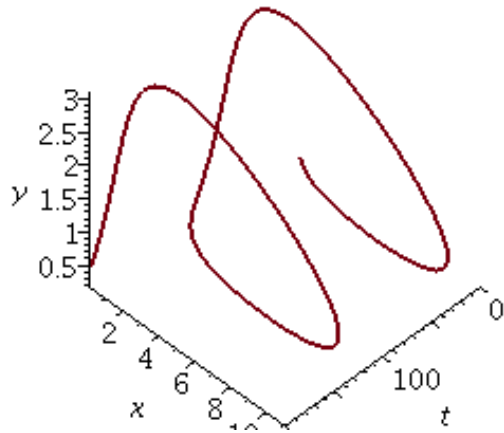
```
> odeplot( F, [[t,x(t)],[t,y(t)]], t=0..200, color=[blue,black], legend=
["prey","predators"] );
```



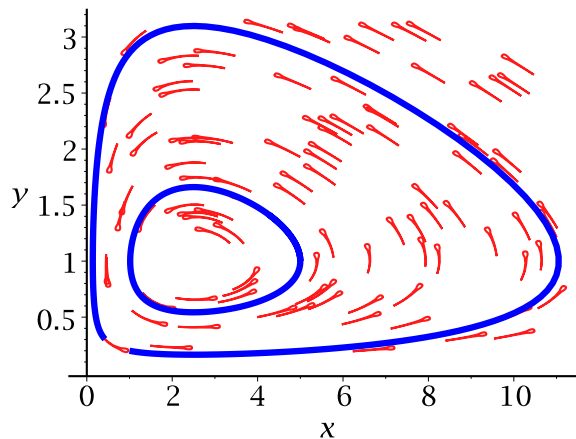
```
> ?odeplot
```

Animation, in 3D, etc.

```
> odeplot( F, [t,x(t),y(t)], t=0..200, thickness=2, axes=frame);
```



```
> with(DEtools):
> DEplot( {de1,de2}, [x(t),y(t)], t=0..100, [[x(0)=1,y(0)=0.2],[x(0)=5,y(0)=1]],
linecolor=blue, numpoints=200, dirfield=100, arrows=comet );
```



What happens if we modify the differential equation for the predator to be

```
> de2 := diff(y(t),t) = -beta2*x(t)-alpha2*y(t);
```

$$de2 := \frac{d}{dt} y(t) = -0.02 x(t) - 0.05 y(t) \tag{10}$$

Go back and experiment with that

```
> restart;
interface(imaginaryunit=_i);
```

$$I \tag{11}$$

```
> I^2;
```

$$I^2 \tag{12}$$

The SIR (Kermack McKendrick) virus spread model

S(t) is the number of susceptibles, I(t) is the number of infecteds, R(t) is the number of

recovereds

```
> deS := diff(S(t),t) = -beta*S(t)*I(t);  
del := diff(I(t),t) = beta*S(t)*I(t)-alpha*I(t);  
deR := diff(R(t),t) = alpha*I(t);
```

$$deS := \frac{d}{dt} S(t) = -\beta S(t) I(t)$$

$$deI := \frac{d}{dt} I(t) = \beta S(t) I(t) - \alpha I(t)$$

$$deR := \frac{d}{dt} R(t) = \alpha I(t) \quad (13)$$

```
> beta := 0.3;
```

$$\beta := 0.3 \quad (14)$$

```
> alpha := 0.1;
```

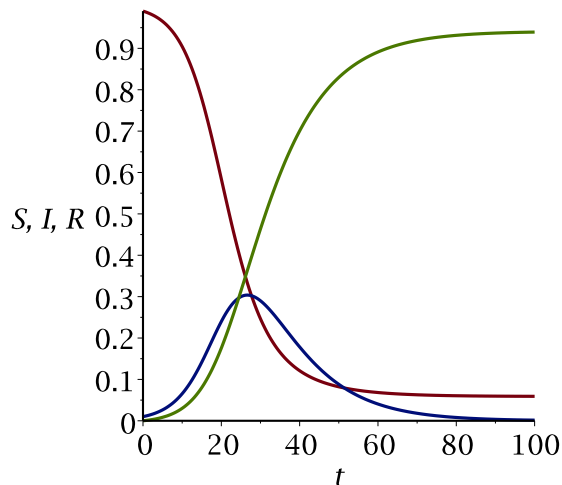
$$\alpha := 0.1 \quad (15)$$

The initial values $S(0)=0.99$, $I(0)=0.01$, $R(0)=0$ mean 1% are infected, 99% are susceptible, and none have recovered at time 0.

```
> F := dsolve( {deS, del, deR, S(0)=0.99, I(0)=0.01, R(0)=0}, {S(t), I(t), R(t)}, numeric );  
F := proc(x_rkf45) ... end proc \quad (16)
```

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

```
> odeplot( F, [[t,S(t)],[t,I(t)],[t,R(t)]], t=0..100, numpoints=200 );
```



The plot shows that the virus is epidemic, that is, growing since $I(t)$ (in blue) is increasing at time $t=0$.

We can't take the $\lim_{t \rightarrow \infty} S(t)$ to determine what happens to the survivors but the following shows that at $t=300$ the number of infecteds is nearly 0 and hence the virus has died out and the number of survivors is 5.88%.

```
> F(300);
```

```
[t = 300., I(t) = 2.35201393323179 10-9, R(t) = 0.941202616250399, S(t) \quad (17)
```

```
= 0.0587973813975870]
```

```
Reexecute the above using
```

```
> beta := 0.1;  
alpha := 0.3;
```

```
beta := 0.1
```

```
alpha := 0.3
```

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```
> F := dsolve( {deS, deI, deR, S(0)=0.99, I(0)=0.01, R(0)=0}, {S(t), I(t),  
R(t)}, numeric );
```

```
F:=proc(x_rkf45) ... end proc
```

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```
> odeplot( F, [[t,S(t)],[t,I(t)],[t,R(t)]], t=0..200, view=[0..200,0.  
.05], numpoints=200 );
```

