

# Lotke-Volterra Equations: Population Models in Mathematica

Developed in the 1930s, the Lotke-Volterra Equations are a system of Ordinary Differential Equations (ODE) commonly used to model populations of species that are interacting with each other in a particular ecological environment. The most simple set of these are the Predator-Prey model, which is as follows:

$$\begin{aligned}x'(t) &= \alpha * x(t) - \beta * x(t) * y(t) \\ y'(t) &= -\gamma * y(t) + \delta * x(t) * y(t)\end{aligned}$$

where  $x(t)$  represents the prey population as a function of time, and  $y(t)$  performs a similar role for the predator.

$\alpha$  is the prey growth rate,  $\beta$  is the effect of predator presence on prey,  $\gamma$  is predator death rate and  $\delta$  is the effect of prey presence on predators.

In Mathematica these equations can be implemented as such:

```
In[ ]:= (*We implement the parameters shown above first*)
a = 0.5(*prey growth rate*);
b = 1(*predator effect on prey*);
c = 1(*predator death rate*);
d = 1(*prey effect on predator*);

preyInitialPopulation = 4;
predatorInitialPopulation = 2;



duration = 100;

In[ ]:= (*Then we can program the equations themselves*)
In[ ]:= predatorPreyEqns = {x'[t] == a * x[t] - b * x[t] * y[t], y'[t] == -c * y[t] + d * x[t] * y[t],
    x[0] == preyInitialPopulation, y[0] == predatorInitialPopulation}
Out[ ]:= {x'[t] == 0.5 x[t] - x[t] * y[t], y'[t] == -y[t] + x[t] * y[t], x[0] == 4, y[0] == 2}
```

Unfortunately the Lotke-Volterra Equations don't have algebraic solutions—the best we can do is numerical analysis using `NDSolve[]`.

```
In[ ]:= predatorPreySol = NDSolve[predatorPreyEqns, {x, y}, {t, 0, duration}]
```

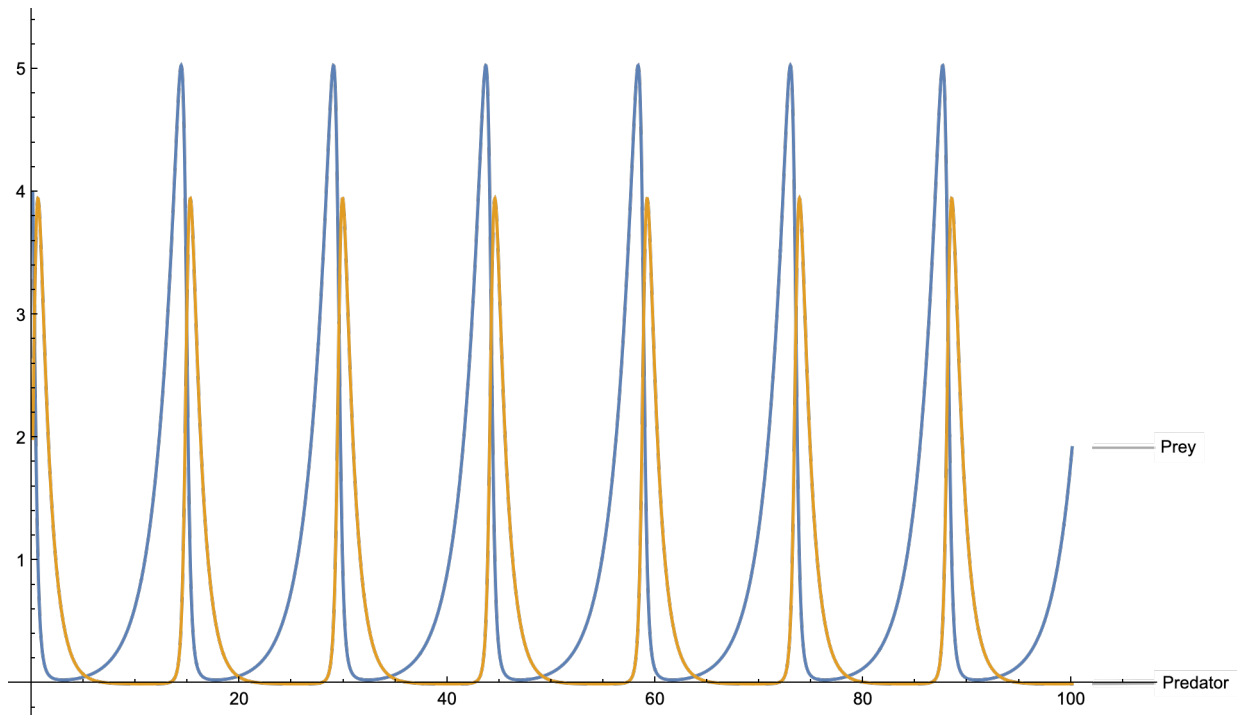
```
Out[ ]:=
```

```
{x -> InterpolatingFunction[ Domain: {{0., 100.}}  
Output: scalar],  
  
y -> InterpolatingFunction[ Domain: {{0., 100.}}  
Output: scalar]]}
```

And then we can plot the solution.

```
In[ ]:= Plot[Evaluate[{x[t], y[t]} /. predatorPreySol],  
             {t, 0, duration}, PlotRange -> All, PlotLabels -> {"Prey", "Predator"}]
```

```
Out[ ]:=
```



The next level of complexity arises when we introduce the concept of carrying capacity—which refers to the maximum population a species can take on in the environment before overpopulation begins to decrease the number of individuals. The system (known as the Lotke-Volterra Competitive Equations) becomes this:

$$\begin{aligned} x'(t) &= r_1 * x(t) * \left(1 - \frac{x(t) + \alpha_{12} y(t)}{k_1}\right) \\ y'(t) &= r_2 * y(t) * \left(1 - \frac{y(t) + \alpha_{21} x(t)}{k_2}\right) \end{aligned}$$

where  $r_i$  and  $k_i$  refer to growth and carrying capacity respectively, and  $\alpha_{i,j}$  is now redefined as the effect species  $j$  has on species  $i$  (in this case,  $x$  is 1 and  $y$  is 2).

```
In[ ]:= (*Parameter implementation*)
```

```
r1 = 0.2;
k1 = 100;
r2 = 0.5;
k2 = 100;
α12 = 0.1;
α21 = 0.1;
xInit = 4;
yInit = 2;
```



```
In[ ]:= compEqns = {x'[t] == r1 * x[t] * (1 - (x[t] + α12 * y[t]) / k1),
                    y'[t] == r2 * y[t] * (1 - (y[t] + α21 * x[t]) / k2), x[0] == xInit, y[0] == yInit}
```

```
Out[ ]:=
```

```
{x'[t] == 0.2 * x[t] * (1 + (1/100) * (-x[t] - 0.1 * y[t])),
 y'[t] == 0.5 * (1 + (1/100) * (-0.1 * x[t] - y[t])) * y[t], x[0] == 4, y[0] == 2}
```

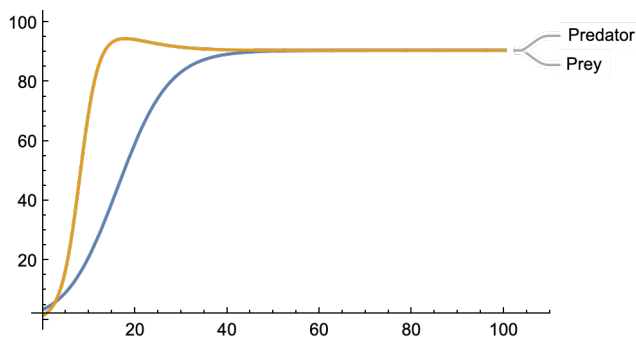
```
In[ ]:= compSol = NDSolve[compEqns, {x, y}, {t, 0, duration}]
```

```
Out[ ]:=
```

```
{ {x -> InterpolatingFunction[ Domain: {{0., 100.}} Output: scalar],
  y -> InterpolatingFunction[ Domain: {{0., 100.}} Output: scalar]}]}
```

```
In[ ]:= Plot[Evaluate[{x[t], y[t]} /. compSol], {t, 0, duration},
             PlotRange -> All, PlotLabels -> {"Prey", "Predator"}]
```

```
Out[ ]:=
```



The ultimate system utilised are the Generalised Lotke-Volterra Equations, which can model n number of species. This is done using the generalised formula:

$$x_i'(t) = (r_i + A) x$$

here A represents a matrix of interactions between various species. Each row of the matrix has 3 inputs,

{effect of species a on species b, effect of species b on species a, and effect of species a on itself}. An example with three species is implemented below.

```
identities = {x, y, z};
growthRates = {3, 4, 7.2};
initials = {0.1, 0.8, 0.3};
interactionMatrix = {{-0.5, -1, 0}, {0, -1, -2}, {-2.6, -1.6, -3}};
(*Creating the interaction matrix*)
Grid[interactionMatrix] (*Visualisation*)
```

Out[ ]=

```
-0.5  -1   0
  0   -1  -2
-2.6 -1.6 -3
```

```
n = 3;
system = Table[Flatten[{identities[[i]]'[t] == (growthRates[[i]] +
    Total[Table[interactionMatrix[[i]][[j]] * identities[[j]][t], {j, n}]]] *
    identities[[i]][t], identities[[i]]'[0] == initials[[i]]}], {i, n}];
(*Generating a system of equations from the parameters*)
Column[system]
```

Out[ ]=

```
{x'[t] == x[t] (3 - 0.5 x[t] - y[t]), x'[0] == 0.1}
{y'[t] == y[t] (4 - y[t] - 2 z[t]), y'[0] == 0.8}
{z'[t] == (7.2 - 2.6 x[t] - 1.6 y[t] - 3 z[t]) z[t], z'[0] == 0.3}
```

In[ ]:= genEq = Flatten[system]

Out[ ]=

```
{x'[t] == x[t] (3 - 0.5 x[t] - y[t]), x'[0] == 0.1, y'[t] == y[t] (4 - y[t] - 2 z[t]),
 y'[0] == 0.8, z'[t] == (7.2 - 2.6 x[t] - 1.6 y[t] - 3 z[t]) z[t], z'[0] == 0.3}
```

In[ ]:= genSol = NDSolve[genEq, identities, {t, 0, duration}]

Out[ ]=

```
{ {x → InterpolatingFunction[ Domain: {{0., 100.}} Output: scalar] },
  y → InterpolatingFunction[ Domain: {{0., 100.}} Output: scalar] },
  z → InterpolatingFunction[ Domain: {{0., 100.}} Output: scalar] ] }
```

```
In[ ]:= Plot[Evaluate[{x[t], y[t], z[t]} /. genSol],  
             {t, 0, duration}, PlotLabels -> {"x", "y", "z"}]
```

