

# Modeling 4

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## 1 Logistic Population Model

A natural way to express population growth, especially for populations that have a negligibly small impact on their environment, is to say that the rate of increase is related to the number of individuals, namely:

$$\dot{P} \propto P \implies \dot{P} = kP \quad (1)$$

This can be easily integrated to give an exponential growth model:

$$P = P_0 e^{kt} \quad (2)$$

Where  $P_0$  is the initial population and  $t$  is time. However, no environment could support such a population indefinitely. Thus, it is necessary to introduce a growth-limiting factor which describes the carrying capacity of the environment. In this case, population growth is proportional to both the population and the square of the population.

$$\dot{P} \propto P, P^2 \implies \dot{P} = kP - \frac{P^2}{N} \quad (3)$$

Here,  $k$  is the population's growth factor, and  $N$  is the population's growth-limiting factor. Clearly, at larger populations the limiting term will approach the growth term, and the population change will approach 0, indicating the equilibrium population for the environment. This equation can be separated and integrated with the help of a variable substitution, yielding the final equation for the population as a function of time:

$$P = \frac{1}{\frac{1 - \frac{P_0}{N}}{1 - \frac{P_0}{N}} e^{-kt} - \frac{1}{N}} \quad (4)$$

This logistic growth equation is known as the Verhulst Model, after Belgian mathematician Pierre Verhulst. We'll use these models to investigate the population growth and carrying capacity of the United States, thanks to U.S. census data. Using the `scipy.optimize` package, the values for  $k$  and  $N$  of the Verhulst model were found to be:

k	0.020774672563165758
N	-494589190.54299223

This indicates that the U.S. has a carrying capacity of just under 5 billion. Plotting the Verhulst model also clearly indicates that the U.S. has not yet reached its carrying capacity. However, the effect of the limiting factor is clear when the Verhulst model is compared to the exponential model.

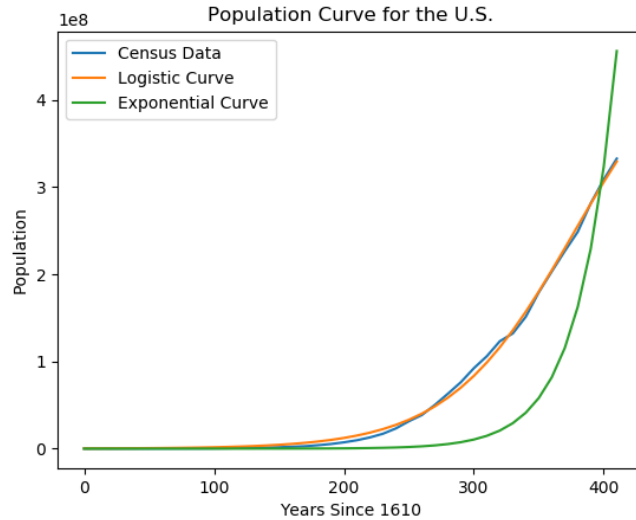


Figure 1: Population models for the U.S. Although the population is still in the growth phase, the limiting factor has caused significant deviation from the purely exponential model.

## 2 Predator-Prey Model

Another factor that can be incorporated into the population model of a certain species is the presence of a second, predatory species. We can create a highly simplified model using birth, death, and interaction rates. For this model, we'll consider a population of foxes and rabbits.

$$\begin{aligned}\dot{R} &= \alpha R - \beta RF = \alpha R \left(1 - \frac{\beta}{\alpha} F\right) \\ \dot{F} &= \gamma RF - \delta F = \delta F \left(\frac{\gamma}{\delta} R - 1\right)\end{aligned}$$

This model, known as the Lotka-Volterra model, makes some major assumptions namely that rabbits are only killed when they are eaten, every time a fox encounters a rabbit it eats it, and a population can recover from less than 1

individual. The coefficients in these can be reduced by reparameterizing  $R$  and  $F$  such that:

$$R' = \frac{\gamma}{\delta} R$$

$$F' = \frac{\beta}{\alpha} F$$

The differential equations reparameterized are then

$$\frac{1}{\alpha} \dot{R}' = R'(1 - F')$$

$$\frac{1}{\delta} \dot{F}' = F'(R' - 1)$$

Next, we can parameterize the time in our model

$$dt' = \alpha dt$$

which gives the equations

$$\frac{dR'}{dt'} = R'(1 - F')$$

$$\frac{1}{\delta\alpha} \frac{dF'}{dt'} = F'(R' - 1)$$

Finally, letting  $\eta = \frac{1}{\delta\alpha}$  we get our final equations characterized by a single parameter.

$$\frac{dR'}{dt'} = R'(1 - F') \tag{5}$$

$$\frac{dF'}{dt'} = \eta F'(R' - 1) \tag{6}$$

Letting  $\eta$  arbitrarily be  $\frac{3}{4}$  and the initial, reparameterized population be 10 rabbits and 1 fox, we can numerically solve for the rabbit and fox populations over time using the LSODA integrator.

Alternatively, the population dynamics can be presented in the phase space of rabbit and fox populations. Emergent of iteration through initial population sizes and the initial ratio of rabbits to foxes is the existence of two fixed points and a set of stable points. The fixed point, in this parameterization, is occurs when the rabbit and fox populations are both 1. This point is a stable fixed point, a fact which becomes clear when consider small changes to the populations around (1,1). Equations 5 and 6 are 0 at this point due to their subtraction terms. If  $R'$  or  $F'$  is offset from 1 slightly, these terms will still be very close to 0, and thus the population will be attracted back toward that point. This attraction can be seen in the lack of other steady population states near (1,1) in phase space. Conversely, there is an unstable fixed point at (0,0). Perturbations at this point will result in rapid population growth. This too can be seen by the movement of population curve near (0,0) in phase space. Finally, there are

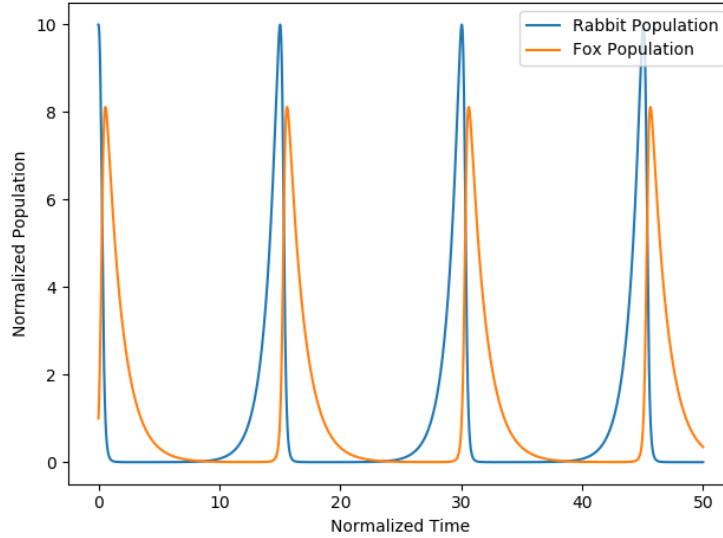


Figure 2: Rabbit and Fox population evolution as a function of time.

regions of stability along the curves seen in phase space. Each one represent the cyclic behavior of a given population based on its initial conditions, and in the absence of outside influences (which is the case by nature of the Lotka-Volterra model), the populations will not deviate from these curves.

It is possible to add a third population to the Lotka-Volterra model. In this example, we'll add dinosaurs. Dinosaurs eat both rabbits and foxes. The differential equations for this system are:

$$\begin{aligned}\dot{R} &= aR - bRF - cRD \\ \dot{F} &= dRF - eF - fFD \\ \dot{D} &= gDR + hDF - iD\end{aligned}$$

For the sake of my sanity and time, I did not attempt a reparameterization of these equations. Integrating these and plotting them yeild highly chaotic results. Small changes in the initial populations and coefficients can cause one predator to be completely out competed by other, the rabbits to grow uncontrollably because the dinosaurs eat too many foxes, etc. Plotting these in phase space would look akin to spaghetti. Instead, one of the best ways to represent three species (and in fact n species) is with the community matrix,  $\mathbf{J}$ . Consider the populations of rabbits, foxes, and dinosaurs to be a three vector in "animal space":

$$\begin{bmatrix} R \\ F \\ D \end{bmatrix}$$

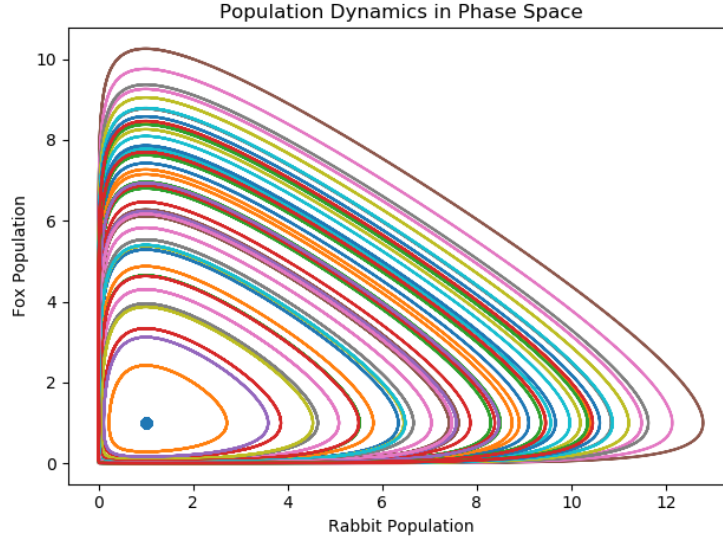


Figure 3: Rabbit and Fox population dynamics in phase space.

Then, we can write our differential equations in matrix form:

$$\begin{bmatrix} \dot{R} \\ \dot{F} \\ \dot{D} \end{bmatrix} = \begin{bmatrix} aR - bRF - cRD \\ dRF - eF - fFD \\ gDR + hDF - iD \end{bmatrix} \quad (7)$$

This can be written as a vector transformation utilizing the community matrix  $\mathbf{J}$ , the Jacobian of the differential equation matrix evaluated at the equilibrium population. This yields the final result:

$$\begin{bmatrix} \dot{R} \\ \dot{F} \\ \dot{D} \end{bmatrix} = \begin{bmatrix} a & -bR_e & -cR_e \\ dF_e & -e & -fF_e \\ gD_e & hD_e & -i \end{bmatrix} \begin{bmatrix} R \\ F \\ D \end{bmatrix} \quad (8)$$

An interesting property that is immediately clear is that the trace of  $\mathbf{J}$  is the total natural birth and death rate of all animals in the system. Additionally, by the stable manifold theorem, if one or more of the eigenvalues of  $\mathbf{J}$  have positive real components the equilibrium is unstable, but if both have negative real parts it is stable.<sup>1</sup> Evaluating the community matrix of the reparameterized two species model at its two equilibrium points, we find it to be:

$$\begin{bmatrix} 1 - F'_e & -R'_e \\ \eta F'_e & \eta R'_e - 1 \end{bmatrix}$$

<sup>1</sup>Community matrix and stable manifold theorem from: [https://en.wikipedia.org/wiki/Community\\_matrix](https://en.wikipedia.org/wiki/Community_matrix)

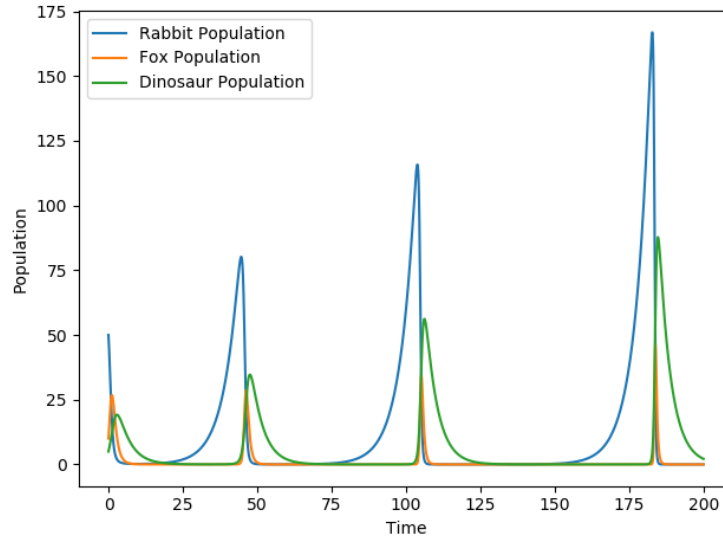


Figure 4: Chaotic and runaway population dynamics with the introduction of the third species, dinosaurs.

At  $(0,0)$  and  $\eta = \frac{3}{4}$  it evaluates to:

$$\begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix}$$

And at  $(1,1)$  this evaluates to:

$$\begin{bmatrix} 0 & -1 \\ \frac{3}{4} & -\frac{1}{4} \end{bmatrix}$$

Indeed, the eigenvalues for the  $(0,0)$  matrix are 1 and -1, indicating an unstable equilibrium, while the eigenvalues for the the  $(1,1)$  equilibrium point are  $(-\frac{1}{8} + i\frac{\sqrt{47}}{8}, -\frac{1}{8} - i\frac{\sqrt{47}}{8})$ , indicating a stable equilibrium point!

### 3 Epidemic Model

A population of  $N$  individuals (people) in the midst of an epidemic can be partitioned into three groups: Healthy, Sick, and Immune (it should be noted that dead people are immune to all diseases). Thus,

$$N = H + S + I$$

We can describe the spread of the disease in a closed population with the following equations:

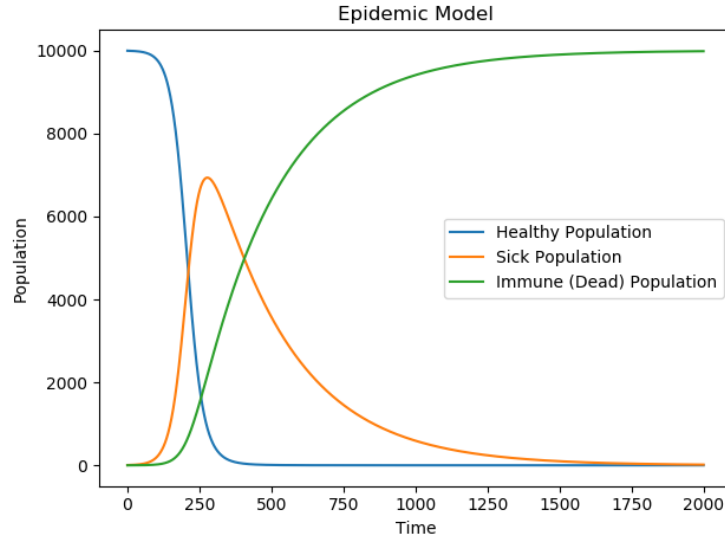


Figure 5: Disease spread through a population with no immunization or treatment.

$$\begin{aligned}\dot{H} &= -\alpha HS \\ \dot{S} &= \alpha HS - \beta S \\ \dot{I} &= \beta S\end{aligned}$$

Where  $\alpha$  describes the transmission between sick and healthy individuals and  $\beta$  describes the recover (death) rate of sick individuals. The coefficients were chosen as such to maintain a steady population, satisfying:

$$\dot{H} + \dot{S} + \dot{I} = 0$$

Letting  $\alpha = .000004$  and  $\beta = .0036$  we find the relatively realistic scenario in which a serious epidemic infects a population of 10,000 people over the course of about 2.5 years with no effort to control or prevent the disease.

We can model the epidemic again, but this time include efforts to decrease the transmission rate by reducing  $\alpha$  by a factor of 4. The disease takes much longer to take hold of the population and infects about one third less people.

Similarly, we can immunize a share of the population. Using the original value of  $\alpha$ , we see that the population infects less people and takes longer to spread.

Unsurprisingly, immunization can increase or decrease the transmission rate to the point where the sick population is reduced to patient zero, or a minute number of individuals, while the rest of the population remains unaffected. However, this simple model does not account for numerous factors, including

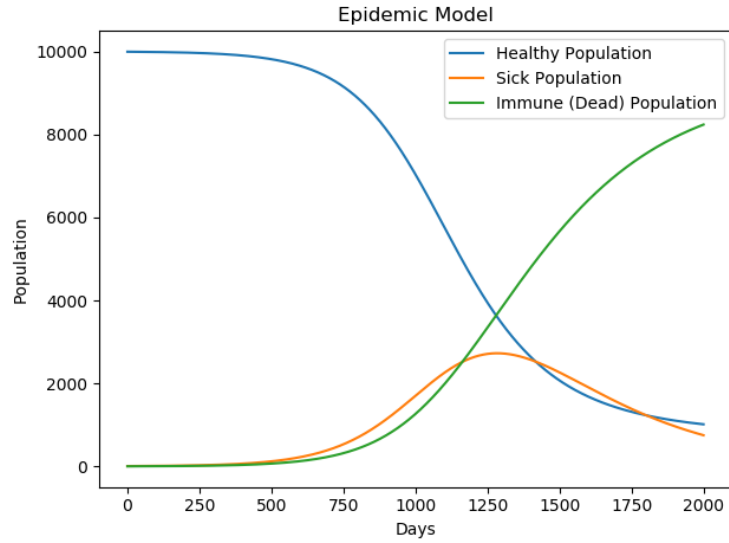


Figure 6: Disease spread through a population with efforts to reduce transmission.

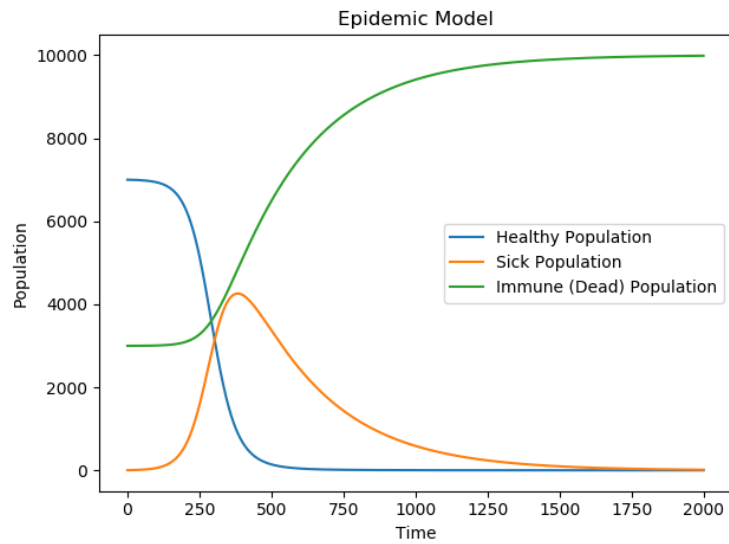


Figure 7: Disease spread through a population with an immunized subset.



Parameter	Description	Value
$\Psi_H$	Infection rate of high-risk susceptible individuals	1.2
$\delta_I$	Disease-induced death rate of infected individuals	0.10
$\delta_H$	Disease-induced death rate of hospitalized individuals	0.5
$\theta_I$	Recovery rate of infected individuals	0.1
$\theta_H$	Recovery rate of hospitalized individuals	0.2
$\alpha$	Rate at which latent individuals become infectious	0.1
$\tau$	Hospitalization rate for infected individuals	0.16
$\Pi$	Recruitment rate	1.7
$p$	Fraction of the individuals at high-risk	0.2
$\beta$	Transmission rate of disease	Estimated
$\frac{1}{\mu}$	Average life of human	63

Table 1: Parameters for Ebola outbreak model.

hospitalization, the abundance of high risk individuals etc. It would be nearly impossible to model such a scenario without measured parameters, so to do so we will use equations and parameters used to model the 2014 ebola virus outbreak in Sierra Leone and Liberia (Khan, et al. 2015) <sup>2</sup>.

$$\begin{aligned}
\dot{S}_L &= \Pi(1 - p) - \lambda S_L - \mu S_L \\
\dot{S}_H &= \Pi p - \Psi_H S_H - \mu S_H \\
\dot{E} &= \lambda(S_L + \Psi_H S_H) - (\alpha + \mu)E \\
\dot{I} &= \alpha E - (\tau + \theta_I + \delta_I + \mu)I \\
\dot{H} &= \tau I - (\theta_H + \delta_H + \mu)H \\
\dot{R} &= \theta_I I + \theta_H H - \mu R
\end{aligned}$$

In these equations,  $S_L$  are the number of low-risk individuals,  $S_H$  are the number of high-risk individuals,  $E$  are the number of exposed individuals,  $I$  are infected individuals,  $H$  are hospitalized and  $R$  are recovered.  $\lambda$  is known as the force of the disease and is given by

$$\lambda = \beta \frac{(I + \eta H)}{N}$$

The coefficients are described in Table 1.

$\beta$  is the contact rate, and is estimated case-by-case. For the 2014 Sierra Leone Ebola outbreak, it was measured to be .344 (Khan et al. 2015). Integrating the equations with the given constants yields the results shown in Figure 8. Perhaps most interesting is the rapid increase in exposed individuals. This emphasizes how a disease can run out of control, especially in underdeveloped

<sup>2</sup>Khan A, Naveed M, Dur-E-Ahmad M, Imran M. Estimating the basic reproductive ratio for the Ebola outbreak in Liberia and Sierra Leone. *Infect Dis Poverty*. 2015;4:13. Published 2015 Feb 24. doi:10.1186/s40249-015-0043-3

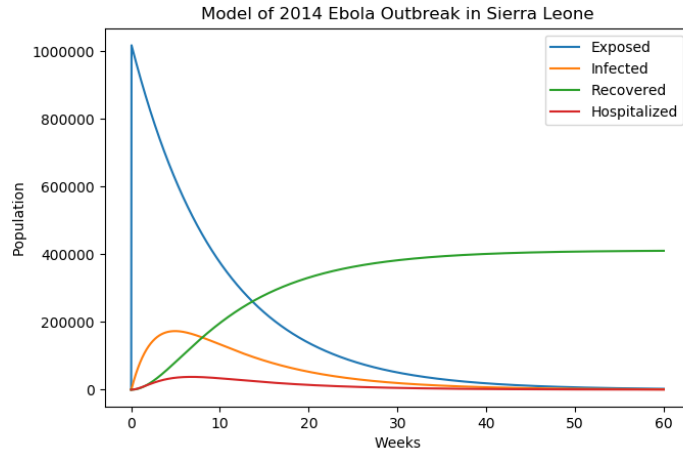


Figure 8: Model of the 2014 Sierra Leone Ebola outbreak.

countries that lack the infrastructure and education to prevent the rapid spread of the disease. Appropriately, hospital admittance lags behind both exposed and sick individuals. Although this model certainly still has flaws, it is much better at modeling an actual epidemic.