# <span id="page-0-0"></span>Lotka-Volterra equations in Superinfection

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The most simple Lotka-Volterra model is a set of first order ordinary differential equations used to describe predator-prey dynamics:

$$
\dot{x} = \alpha x - \beta xy
$$

$$
\dot{y} = -\delta y + \gamma xy
$$

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#### <span id="page-2-0"></span>Equilibria of Basic Lotka-Volterra Model

The system has the following equilibria:

$$
\bar{x} = 0, \qquad \bar{y} = 0 \tag{1}
$$

$$
\bar{x} = \frac{\delta}{\gamma}, \qquad \bar{y} = \frac{\alpha}{\beta} \tag{2}
$$

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### <span id="page-3-0"></span>Solutions to Basic Lotka-Volterra Model



Figure: A phase portrait of the Predator-Prey Lotka-Volterra Equations. Note the periodic orbits surrounding a critical point.



Figure: Solutions to the Lotka-Volterra Equations with red representing predators, blue representing prey. The parameters used here are[:](#page-2-0)  $x_0 = 8$  $x_0 = 8$  $x_0 = 8$ ,  $y_0 = 12$  $y_0 = 12$ ,  $\alpha = 20$ , and  $\alpha$  =  $\frac{1}{20}$ [Lotka-Volterra equations in Superinfection](#page-0-0)

# <span id="page-4-0"></span>Logistic Equation

Basic Logistic Equation modelling population growth

$$
\dot{y}(t) = ry(t)\bigg(1 - \frac{y(t)}{K}\bigg)
$$



Figure: A phase portrait of the Logistic Population Model. The parameters are  $r = \frac{1}{2}$  and  $K = 10$ . Note the change in concavity at  $\frac{K}{2} = 5$ .

# Competitive Lotka-Volterra Equation

This is the competitive Lotka-Volterra Model describing population dynamics between two species in an environment with a carrying capacity, K.

$$
\dot{y}_1(t) = r_1 y_1 \left( \frac{K_1 - y_1 - a_{12} y_2}{K_1} \right) \tag{3}
$$

$$
\dot{y}_2(t) = r_2 y_2 \left( \frac{K_2 - y_2 - a_{21} y_1}{K_2} \right) \tag{4}
$$

The generalized Lotka-Volterra Equation has since been used to describe more complex evolutionary systems and dynamics across a theoretically infinite amount of species.

$$
\frac{dy_i}{dt}=y_i(r_i+\sum_{j=1}^n y_i b_{ij}),\ i=1,\ldots,n.
$$
 (5)

### Basic Model of Infection

This is the basic model of infection with a single virus within a population split into infected and susceptible

$$
\frac{dx}{dt} = k - ux - \beta xy \tag{6}
$$

$$
\frac{dy}{dt} = y(\beta x - u - v) \tag{7}
$$

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### Competitive Model of Infection

This is the competitive model of infection with multiple viruses within a population split into infected and susceptible

$$
\frac{dx}{dt} = k - ux - x(\beta_1 y_1 + \beta_2 y_2)
$$
 (8)

$$
\frac{dy_1}{dt} = y_1(\beta_1 x - u - v_1) \tag{9}
$$

$$
\frac{dy_2}{dt} = y_2(\beta_2 x - u - v_2)
$$
 (10)

### The Basic Model of Superinfection

Superinfection is the scenario in which an already-infected host is infected with a second virus strain. It can be represented with the following ODE system:

$$
\dot{x} = k - ux + x \sum_{i=1}^{n} \beta_i y_i
$$

$$
\dot{y} = y_i \left( \beta_i x - u - v_i + s\beta_i \sum_{j=1}^{i-1} -s \sum_{j=i+1}^{n} \beta_i y_j \right)
$$

# Reproductive Ratio in Superinfection

The reproductive ratio is the number of new cases generated if a single infected individual should enter a susceptible population.

$$
R_0=\frac{akv_i}{u(c+v_i)(u+v_i)}
$$

This gives us that optimal virulence is:

$$
v_{opt} = \sqrt{cu}
$$

# An Analytical Model of Superinfection

If we assume  $k = ux + uy + \sum_{i=1}^{n} v_i y_i$  and  $x + y = 1$ , we have

$$
\dot{y} = y_i \left( \beta_i (1 - y) - u - v_i + s \left( \beta_i \sum_{j=1}^{i-1} y_i - \sum_{j=i+1}^n \beta_i y_i \right) \right), \qquad i = 1, 2, ..., n
$$
\n(11)

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### An Analytical Model of Superinfection Cont.

This can be rewritten as a Generalized Lotka-Volterra Equation of the form

$$
\dot{y}=y_i\bigg(R_i+\sum_{j=1}^n A_{ij}y_j\bigg), \quad i=1,2,\ldots,n
$$

Where  $R_i = \beta_i - v_i - u_i$  and

$$
A = -\begin{bmatrix} \beta_i & \beta_1 + s\beta_2 & \beta_1 + s\beta_3 & \dots & \beta_1 + s\beta_n \\ \beta_2(1-s) & \beta_2 & \beta_2 + s\beta_3 & \dots & \beta_2 + s\beta_n \\ \beta_3(1-s) & \beta_3(1-s) & \beta_3 & \dots & \beta_3 + s\beta_n \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ n(1-s) & \beta_n(1-s) & \beta_n(1-s) & \dots & \beta_n \end{bmatrix}
$$

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### Competitive Lotka-Volterra Equation in Virology

If we set all infection rates to be equivalent, so  $\beta_i = \beta$ , we see that

$$
\dot{y}_i = y_i \beta \left( 1 - y - \frac{v_i + u}{\beta} + s \left( \sum_{j=1}^{i-1} y_{ij} - \sum_{j-i+1}^n y_j \right) \right)
$$

(This is a competitive Lotka-Volterra equation). Additionally, the matrix A becomes  $A = \lceil$  $\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array} \\ \end{array} \end{array} \end{array}$  $1 + s + s + s + s + s + s + s + s$  $1 - s$  1  $1 + s$  ...  $1 + s$  $1 - s$  1 - s 1 ... 1 + s . . . . . . . . . . . . . . .  $1 - s$   $1 - s$   $1 - s$  ... 1 1  $\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array} \\ \begin{array}{c} \end{array} \end{array} \end{array} \end{array}$ 

# <span id="page-14-0"></span>Equilibrium of the Model

If we set  $f_i = 1 - \frac{ {\sf v}_i + {\sf u}}{\beta} - (1-s) {\sf y} - 2 {\sf s} \sum_{j=i+1}^n {\sf y}_j$  then the model can be rewritten as

$$
\dot{y}=y_i\beta(f_i-sy_i)
$$

So, the equilibria can be seen to require that either  $y_n = 0$  or  $y_n = \frac{f_n}{s}$ . Through this, we can define  $y_n$  recursively as:

$$
y_n=\max\{0,f_n/s\}
$$

Hofbauer and Sigmund show that this is the only equilibrium.