15.5: The I Equation

We shall simplify the SI model further to an “I” model, the most basic epidemiological formulation. This can be done by considering a constant population, with births always matching deaths. To accomplish this, the birth term, \(b(S+I)\), can be made equal to the death term, \(\delta(S+I)\), giving

\[
\begin{align*}
\frac{dS}{dt} &= \delta(S+I) - \beta I \frac{S}{S+I} - \delta S \\
\frac{dI}{dt} &= \beta I \frac{S}{S+I} - \alpha I
\end{align*}
\]

However, since the total population—call it \(N\)—is constant, \(S\) is not needed in the equations at all. It is always equal to the total population \(N\) minus the number infected: \(S = N - I\). You can forget about the \(S\) equation and substitute \(S = N - I\) into the \(I\) equation. This gives

\[
\begin{align*}
\frac{dI}{dt} &= \beta I \frac{N-I}{N} - \alpha I
\end{align*}
\]

This is the beginning of the I model. It needs a little more work before proceeding with its analysis, but first some additional terminology:

- **Infection**: A term applied as soon as a pathogen has taken hold in a host.
- **Disease**: A term often applied when an infection starts producing symptoms in a host.
- **Incidence**: The number of new infections or cases of disease appearing in a population per time unit. Often expressed as a fraction of the total population.
- **Prevalence**: The total number of infections or cases of disease existing in a population. Often expressed as a fraction of the total population.
With this terminology in mind, let us put the I model into the form of prevalence, as a fraction of the entire population. In this case, prevalence is just \( p = I/N \). Start where we left off, with

\[
\frac{1}{I} \frac{dI}{dt} = \beta \left( 1 - \frac{I}{N} \right) - \alpha
\]

multiply through by \( I \),

\[
\frac{dI}{dt} = \beta I(1 - \frac{I}{N}) - \alpha I
\]

divide through by \( N \),

\[
\frac{d}{dt} \left( \frac{I}{N} \right) = \beta I(1 - \frac{I}{N}) - \alpha I
\]

substitute prevalence

\[
\frac{dp}{dt} = \beta p(1-p) - \alpha p
\]

and, finally, divide through by \( p \),

\[
\frac{1}{p} \frac{dp}{dt} = \beta (1-v-p) - \alpha
\]

Now think about the \( (1-p) \) term. This “one minus the prevalence” represents the fraction of the population that is susceptible to the disease. But some fraction of the population may have natural immunity to the disease, and another may have been successfully vaccinated against the disease. Let us call this fraction \( v \) and subtract it too from the fraction that is susceptible, finally giving

\[
\frac{1}{p} \frac{dp}{dt} = \beta (1-v-p) - \alpha
\]

Whew, that is the final I model—the starting place for analysis!

You will see in an upcoming chapter that Equation \( \ref{15.5.12} \) is identical to a model of habitat destruction in which plants are isomorphic to “infections” of the landscape, and that habitat destruction, which “protects” the landscape from infection by plants, is isomorphic to vaccination.

Here is the equation with term-by-term explanations:

\[
\frac{1}{p} \frac{dp}{dt} = \beta (1-v-p) - \alpha
\]

\( \frac{dp}{dt} \Rightarrow \) Relative growth in prevalence under conditions prevailing at time \( t \)

\( \beta \Rightarrow \) Number of new infections induced by each infected individual in each time unit in a completely uninfected population.

\( v \Rightarrow \) Probability of encountering an individual who cannot be infected.

\( p \Rightarrow \) Probability of encountering an infected individual.
\(\alpha\) Fraction of infected individuals lost per time unit.

Keep in mind that this is a constant-population approximation. Whenever an individual dies of the disease, a new susceptible individual enters the population.