

An SIR Disease with Vaccination and Immunity Loss

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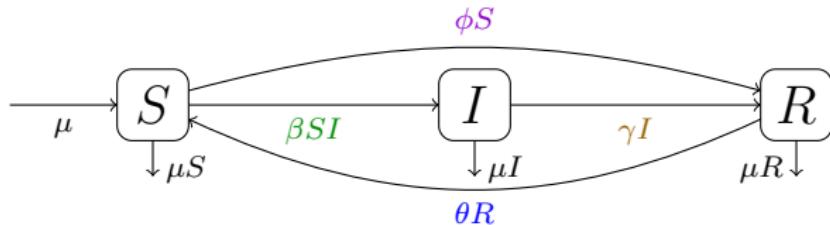
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Outline

1. Building the Model
2. Scaling the Model
3. Analyzing the Model
4. Visualizing the Model Results
5. Take-Home Messages

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An Initial Model



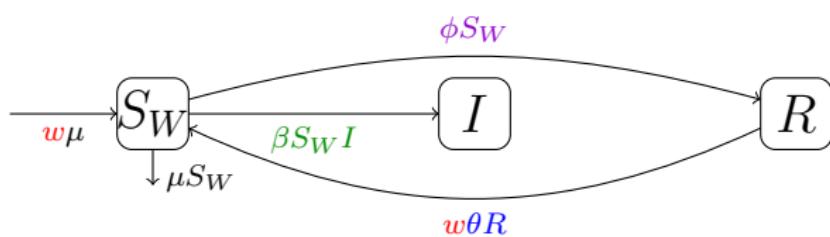
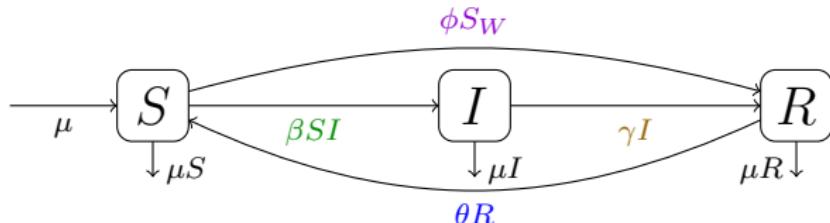
$$1 = S + I + R$$

$$\frac{dI}{dt} = -\mu I + \beta SI - \gamma I$$

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \phi S + \theta (1 - S - I)$$

- ▶ The vaccination assumption has a serious flaw!
 - It assumes everyone is willing to be vaccinated!
- ▶ Instead, assume that only a fraction w of people are willing.
 - The vaccination rate should be ϕS_W , not ϕS .
 - **But now we need a differential equation for S_W .**

A Corrected Model



$$\frac{dI}{dt} = -\mu I + \beta SI - \gamma I$$

$$\frac{dS}{dt} = \mu - \mu S - \beta SI - \phi S_W + \theta (1 - S - I)$$

$$\frac{dS_W}{dt} = w\mu - \mu S_W - \beta S_W I - \phi S_W + w\theta (1 - S - I)$$

1. Building the Model

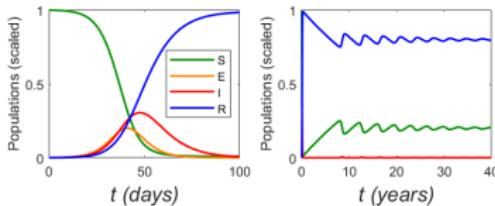
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Two Time Scales in Disease Models



- ▶ The fast time scale (days) shows the epidemic phase.
 - Infectious population fractions are significant.
 - Plots on the fast time scale show no clue to endemic behavior.
 - Demographic changes (birth, natural death, etc) are negligible.
- ▶ The slow time scale (years) shows the long-term behavior.
 - Infectious population fractions are very small.
 - On the slow scale, the epidemic behavior appears at $t = 0$.
 - Both demographic and disease processes are important.

Scaling for the Endemic Phase

- ▶ Time is referred to the demographic time scale $1/\mu$.
- ▶ Infectious populations are rescaled via $I = \epsilon Y$.
 - *This is necessary so that all variables are $O(1)$ as $t \rightarrow \infty$.*
- ▶ Slow process parameters are referred to a slow time scale.
 - Loss of immunity is slow.
 - $1/\mu$ is the principal slow time scale (≈ 80 years).

$$h = \frac{\theta}{\mu} \quad .$$

- ▶ Fast process parameters are referred to a fast time scale.
 - Infection and vaccination are fast.
 - $1/(\gamma + \mu)$ is the principal fast time scale (≈ 2 weeks).

$$\textcolor{violet}{b} = \frac{\beta}{\gamma + \mu}, \quad \textcolor{blue}{v} = \frac{\phi}{\gamma + \mu}, \quad \epsilon = \frac{\mu}{\gamma + \mu} \ll 1.$$

Final Formulation

$$\epsilon Y' = (bS - 1)Y,$$

$$S' = (1 + h)(1 - S) - P - bSY + O(\epsilon),$$

$$\delta P' = w - P + wh(1 - S) + O(\epsilon),$$

$$P = \epsilon^{-1}vS_W \equiv \delta^{-1}S_W \quad (\delta = \epsilon/v).$$

- ▶ Infection and death for S_W can be neglected.

Base Parameter Values:

- ▶ $v \approx 0.5$: vaccination takes a mean of one month (so $\delta = 2\epsilon$)
- ▶ $2 \leq b \leq 10$: infectiousness is between influenza and Covid
- ▶ $0 \leq h \leq 80$: loss of immunity has a mean of 1 year to infinity

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Basic Reproduction Number

- ▶ The basic reproduction number \mathcal{R}_0 is the expected number of secondary infections from one primary infection in a population with no current disease.
- ▶ It matters because a new disease becomes epidemic and then endemic if $\mathcal{R}_0 > 1$.

Calculation

1. The definition is best for simple models:
 - \mathcal{R}_0 = infection rate divided by recovery rate.
2. \mathcal{R}_0 can be found from the stability criterion for the disease-free equilibrium.
3. There is a “next generation” method for complicated models.

Disease-Free Equilibrium (DFE)

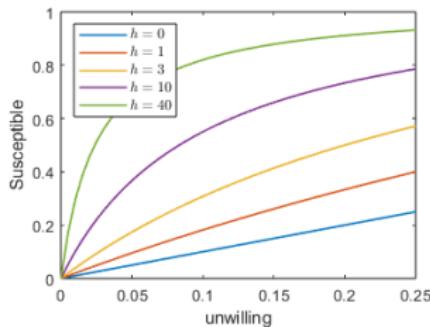
$$\epsilon Y' = (bS - 1)Y,$$

$$S' = (1 + h)(1 - S) - P - bSY,$$

$$\delta P' = w - P + wh(1 - S),$$

$$Y^* = 0 \rightarrow (1 + h)(1 - S^*) = P^* = w + wh(1 - S^*)$$

$$S^* = \frac{(1 + h)u}{1 + hu}, \quad u \equiv 1 - w.$$



Stability for the DFE

The Jacobian for the DFE is

$$J_{DFE} = \left(\begin{array}{cc|cc} \epsilon^{-1}(bS^* - 1) & 0 & 0 \\ -bS^* & -(1+h) & -1 \\ 0 & -\delta^{-1}wh & -\delta^{-1} \end{array} \right),$$

- ▶ Upper left block:
 - eigenvalue $\epsilon^{-1}(bS^* - 1)$
- ▶ Lower right block:
 - trace is negative
 - determinant is $\delta^{-1}(1 + h - hw) = \delta^{-1}(1 + hu) > 0$
- ▶ DFE stability (disease eradication) requires $bS^* < 1$.
 - $\mathcal{R}_0 = bS^* = \frac{b(1+h)u}{1+hu}$.

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Looking at Formulas

- ▶ Eradication requires $\mathcal{R}_0 < 1$, or

$$\frac{b(1+h)u}{1+hu} < 1$$

- ▶ There are various ways to write the result:

1. $b(1+h)u < 1 + hu$
2. $b < \frac{1+hu}{(1+h)u}$
3. $u < \frac{1}{b(1+h)-h}$, provided $b(1+h) > h$
4. $u < \frac{1}{b+(b-1)h}$, provided $b + (b - 1)h > 0$

- ▶ Which is best?

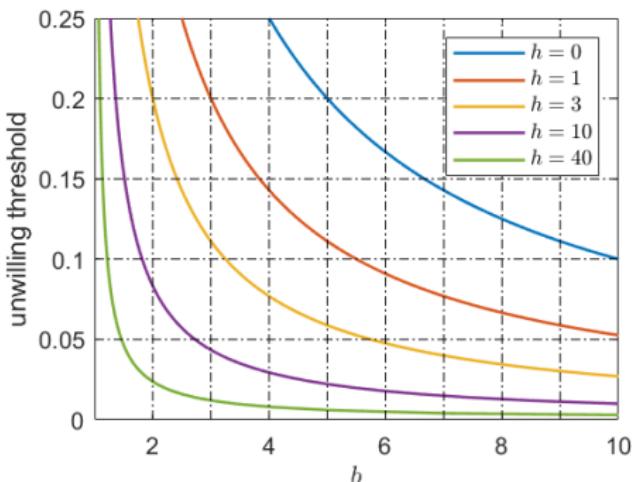
- 2, 3, and 4 are solved for a single variable.
- 2 does not require a range restriction.
- The range restriction in 4 is more clearly assessed than the one in 3.

Designing Plots

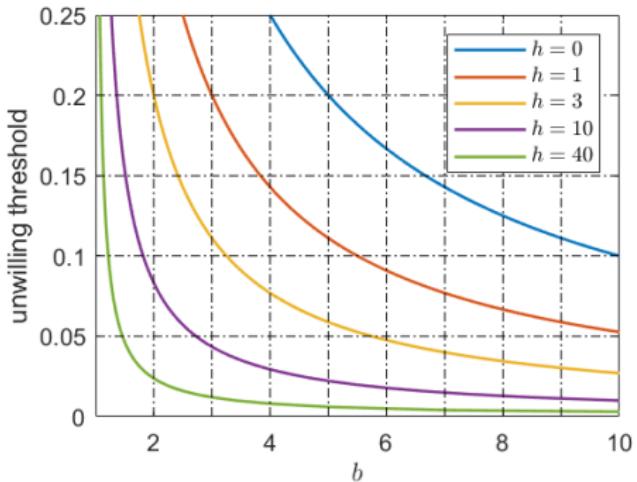
- ▶ Think of the key result as having the form $f(b, h, u) = 0$.
 - This avoids bias in identifying the roles of the variables.
- ▶ To plot an equation in 3 variables:
 1. Fix 'variable 1' to be a constant.
 2. Assign the other variables to x and y axes.
 3. Choose a range for one axis variable.
 4. Calculate values of the other axis variable.
 5. Plot the curve.
 - You can calculate x from y if more convenient than y from x .
 6. Repeat with several values of variable 1.
 - 'Variable1 = const' marks a curve rather than an axis value.
 - The plot shows how variable 1 affects the result for the y variable as a function of the x variable.
 7. The axis limits should conform to meaningful ranges.

Visualizing the Results

- ▶ Plot minimum u for eradication as a function of infectivity b .
 1. Choose h to mark curves.
 2. Choose values of u and calculate b .
 - Avoids negative results.
 3. Use ranges $1 \leq b \leq 10$, $0 < u \leq 0.25$
 4. Reasonable h are from 0 to 80.
 - We want roughly even spacing for the curves, not the values.



Interpreting Plots



- ▶ One specific conclusion:
 - With $< 20\%$ unwillingness, we can just eradicate diseases with
 - (a) $b = 5, h = 0$, (b) $b = 3, h = 1$, (c) $b = 2, h = 3$
- ▶ Some general conclusions:
 1. Faster loss of immunity makes eradication more difficult.
 2. Greater infectivity makes eradication more difficult.
 3. It is extremely difficult to eradicate diseases with fast loss of immunity, even if they are not very contagious.

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Take-Home Messages

1. Be careful that the model assumptions are a good compromise between realistic and simple.
 - o ‘Everyone gets vaccinated’ is usually a bad assumption.
2. Scaling and paying attention to small-order terms simplifies the analysis with only minimal quantitative error.
3. Choose analysis tasks that address fundamental questions about the model.
4. The goal is not a solution formula; it is one or more graphs whose interpretation answers the fundamental questions.
 - o Good graph design is essential.