Endemic Disease Models

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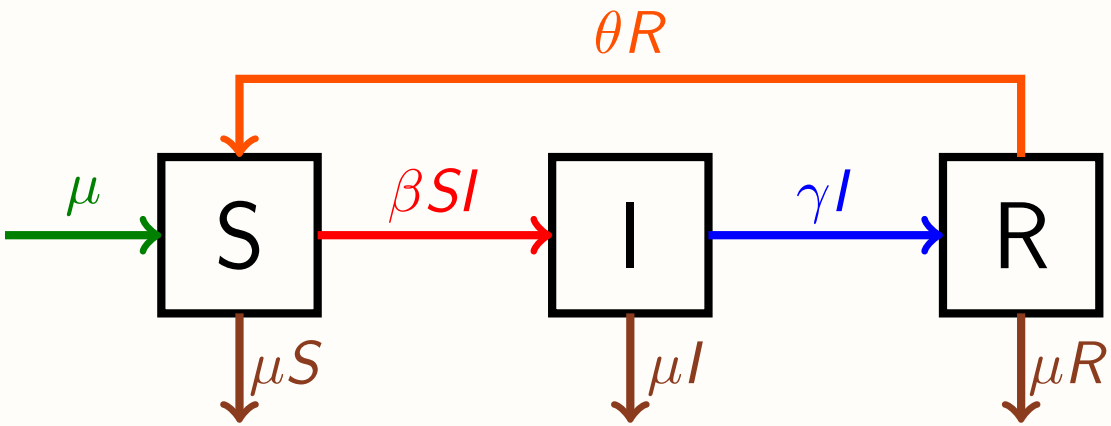
Endemic Disease Models

- Features common to all endemic disease models:
  - Population is partitioned into mutually exclusive classes.
  - Disease processes of transmission and recovery.
  - Demographic processes of birth and death.
- Standard SIR model classes:
  - (S)usceptible – can be infected.
  - (I)nfectious – can transmit infection.
  - (R)emoved – can no longer be infected or transmit.
- Demographic assumptions:
  - Natural deaths, sometimes disease-induced deaths.
  - Fixed birth rate.
    - reasonable simplification if disease mortality is small

The Fixed Population SIRS Model



transmission, recovery, birth, death, loss of immunity

$$\frac{dS}{dT} = \mu - \beta SI - \mu S + \theta R,$$

$$\frac{dI}{dT} = \beta SI - (\gamma + \mu)I.$$

$$N_0 = S + I + R.$$

Basic Reproduction Number

$$\frac{dI}{dT} = \beta SI - (\gamma + \mu)I.$$

$$N_0 = S + I + R.$$

- The basic reproduction number $\mathcal{R}_0$ is the expected number of secondary infections from one primary infective in a disease-free population.
  - transmission rate into a disease-free population is $\beta N_0 I$.
  - rate per I is βN_0.
  - time is $1/(\gamma + \mu)$.

$$\mathcal{R}_0 = \frac{\beta N_0}{\gamma + \mu}.$$

Other Dimensionless Parameters

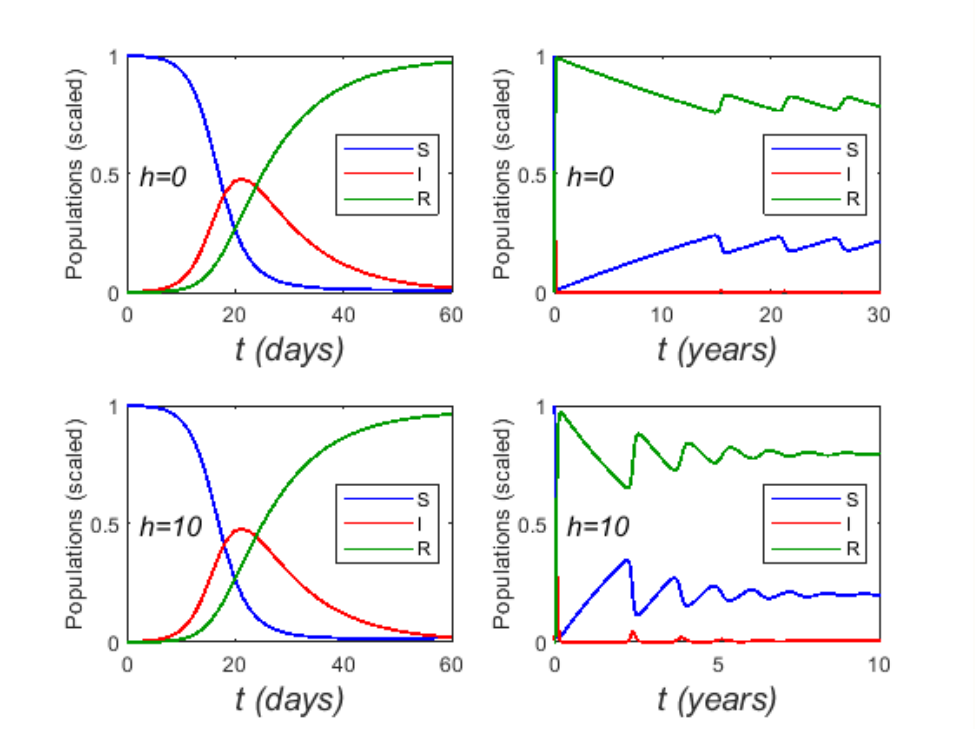
$$\frac{dS}{dT} = \mu - \beta SI - \mu S + \theta R,$$

$$\frac{dI}{dT} = \beta SI - (\gamma + \mu)I.$$

- h is the mean losses of immunity in a lifespan;
- ϵ is disease duration/lifespan.

$$h = \frac{\theta}{\mu}, \quad \epsilon = \frac{(\gamma + \mu)^{-1}}{\mu^{-1}} = \frac{\mu}{\gamma + \mu} \approx 0.0005 \ll 1$$

Typical Model Behavior



- Lifelong immunity ($h = 0$) leads to a classic childhood disease (top).
- Reinfection ($h > 0$) changes the pattern after the initial outbreak (bottom).
- Note that i is small after the initial outbreak.

Dimensionless Version of the Model

$$\frac{dS}{dT} = \mu - \beta SI - \mu S + \theta R,$$

$$\frac{dI}{dT} = \beta SI - (\gamma + \mu)I.$$

- Let

$$S = Ns, \quad I = \epsilon N y, \quad \frac{d}{dT} = \mu \frac{d}{dt}.$$

$$s' = (1 + h)(1 - s) - \mathcal{R}_0 sy - O(\epsilon),$$

$$y' = \epsilon^{-1}(\mathcal{R}_0 sy - y).$$

- ϵ is a time scale parameter:
  - Equilibrium points depend only on the disease parameters $\mathcal{R}_0$ and h.

Basic Plan for Equilibrium Analysis

- Long-term behavior is determined by equilibrium analysis.
  - An equilibrium x^* is asymptotically stable if

$$\exists \delta > 0 \text{ s.t. } \lim_{t \to \infty} x = x^* \text{ whenever } \|x(0) - x^*\| < \delta.$$

- Procedure for equilibrium analysis:
  1. Find the *Jacobian* matrix.
  2. Find the equilibria.
  3. Linearize the system at each equilibrium by evaluating the Jacobian there.
  4. Use eigenvalues or the *Routh-Hurwitz conditions* to determine stability.

Equilibria and the *Jacobian*

$$s' = (1+h)(1-s) - \mathcal{R}_0 sy,$$
$$y' = \epsilon^{-1}(\mathcal{R}_0 sy - y).$$

$$J = \left(\frac{\partial x_i'}{\partial x_j}\right) = \begin{pmatrix} -(1+h+\mathcal{R}_0 y) & -\mathcal{R}_0 s \\ \epsilon^{-1}\mathcal{R}_0 y & \epsilon^{-1}(\mathcal{R}_0 s - 1) \end{pmatrix}.$$

- Disease-free equilibrium: $y = 0, \quad s = 1$
- Endemic-disease equilibrium (requires $\mathcal{R}_0 > 1$):

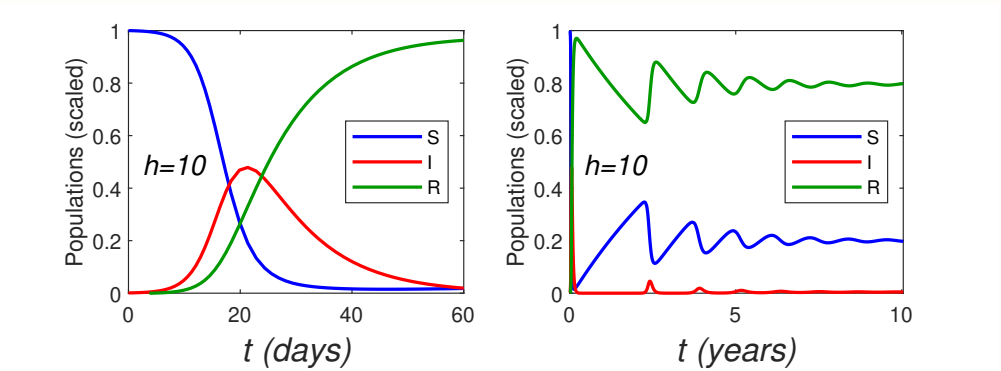
$$s = s^* = \mathcal{R}_0^{-1}, \quad y^* = (1+h)(1-\mathcal{R}_0^{-1}).$$

$$J_{DFE} = \begin{pmatrix} -(1+h) & -\mathcal{R}_0 \\ 0 & \epsilon^{-1}(\mathcal{R}_0 - 1) \end{pmatrix}; \quad J_{EDE} = \begin{pmatrix} -(1+\mathcal{R}_0 y^*) & -1 \\ \epsilon^{-1}\mathcal{R}_0 y^* & 0 \end{pmatrix}$$

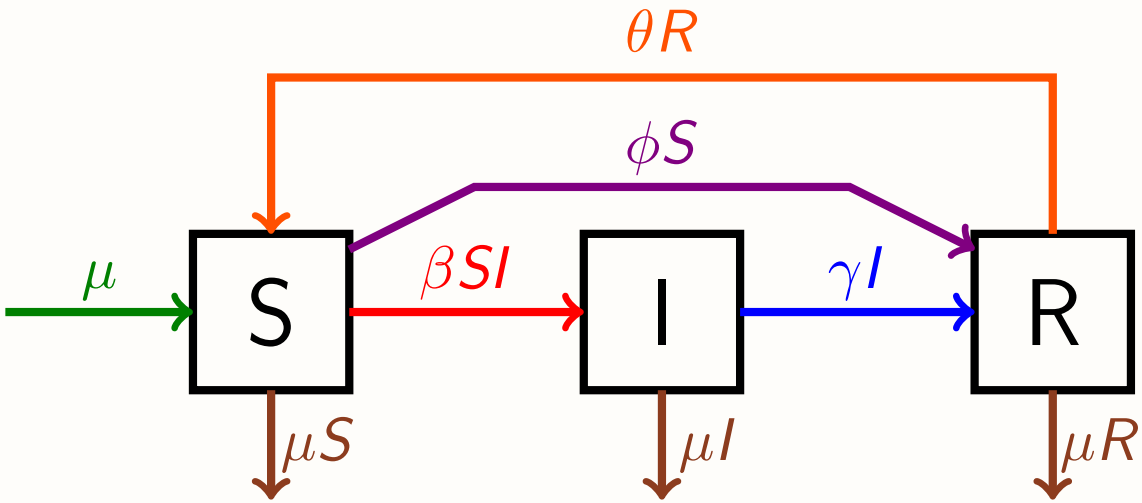
Stability Results

$$J_{DFE} = \begin{pmatrix} -(1+h) & -\mathcal{R}_0 \\ 0 & \epsilon^{-1}(\mathcal{R}_0 - 1) \end{pmatrix}; \quad J_{EDE} = \begin{pmatrix} -(1+\mathcal{R}_0 y^*) & -1 \\ \epsilon^{-1}\mathcal{R}_0 y^* & 0 \end{pmatrix}$$

- The eigenvalues for J_{DFE} are $-(1+h)$ and $\epsilon^{-1}(\mathcal{R}_0 - 1)$.
  - The DFE is stable if $\mathcal{R}_0 < 1$.
- The trace and determinant for J_{EDE} are $-(1+\mathcal{R}_0 y^*) < 0$ and $\epsilon^{-1}\mathcal{R}_0 y^* > 0$.
  - The EDE is stable if it exists ($\mathcal{R}_0 > 1$). [*R-H conditions*]



The SIRS Model with fixed birth and vaccination



transmission, recovery, birth, death, vaccination, loss of immunity

- What is wrong with this implementation of vaccination?

Adding Vaccination to Epidemiology Models

- Standard treatment of vaccination:
  - Spontaneous transition process (rate proportional to population)
  - **Applied to the entire susceptible class.**
- Flaws in the standard treatment:
  - Limitations of supply and distribution.
  - **Significant vaccine non-acceptance.**
- In an endemic disease model, supply and distribution should not matter, but **non-acceptance should be important.**

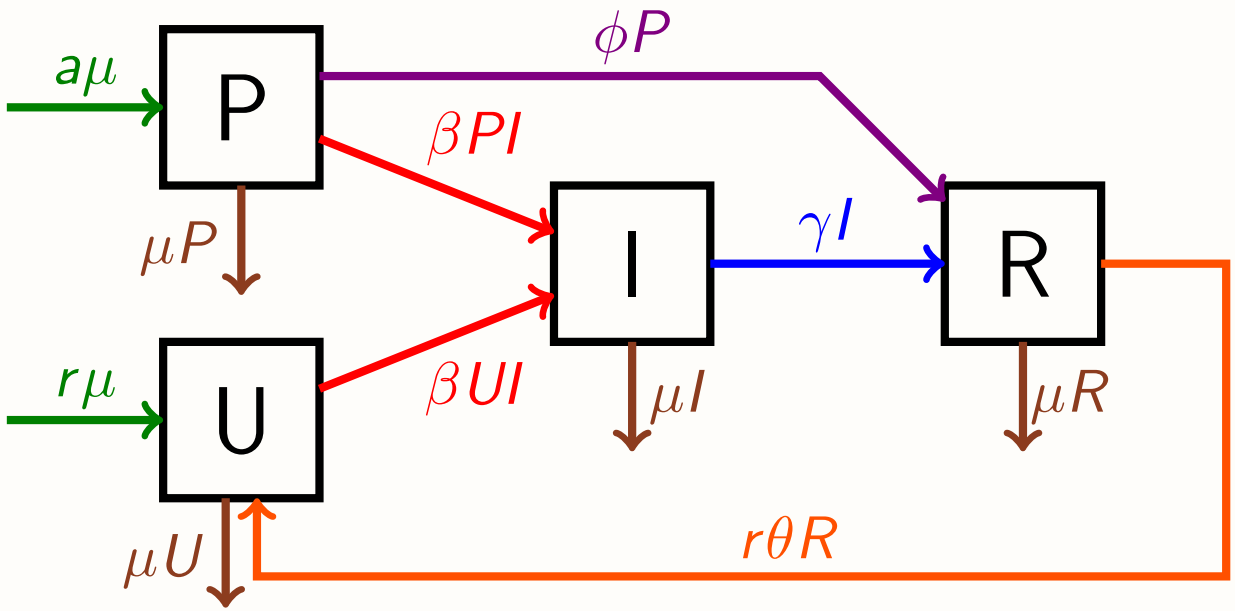
Investigating the Impact of Vaccine Non-Acceptance

- Requirements:
  1. Demographic processes of birth and natural death.
  2. Vaccination.
  3. Vaccine non-acceptance.
  4. Loss of immunity.

- Class Structure:
  - Start with SIR.
  - Partition S into (P)revaccinated and (U)nprotected subclasses.

- Principal Input Parameters:
  - $\mathcal{R}_0$ in the absence of vaccination.
  - Non-acceptance fraction (r).
  - Vaccination rate (ϕ).
  - Loss of immunity rate (θ).

The PUIRU Model



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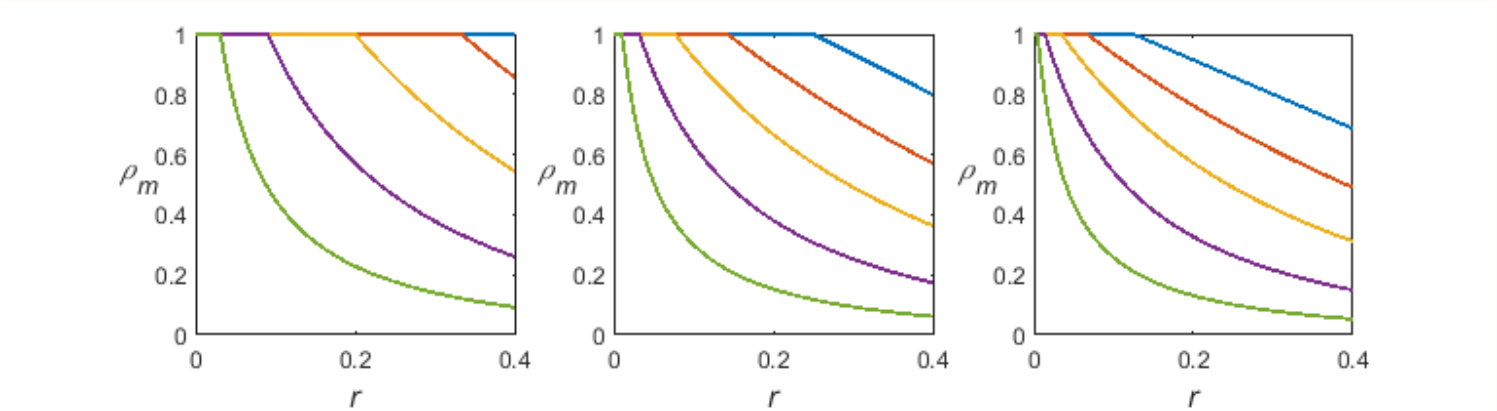
Vaccine Impact

- Let ρ_m be the maximum fraction of infections prevented by vaccination (take $\phi \to \infty$).
- $\mathcal{R}_0 = 2, 4, 8$ for left, center, and right.
- $h = 0, 1, 3, 9, 30$ from top to bottom.



- Non-acceptance makes a big difference.
  - Especially for diseases with short-lived immunity.

Opportunities for Research

- The PUIRU model is only recently published.
  - There is a lot of scope for model improvement.
  - There are potential applications to different disease assumptions.