Mathematical Modeling Lecture 6

Population transfers: SIR dynamics, thresholds, and numerical conservation

Lecture notes

A closed population changes composition through infection and recovery. From explicit contact assumptions we derive the SIR equations, establish their feasible state space, analyze their threshold and orbit, and construct a numerical update that respects the population budget.

1 Population categories and contact assumptions

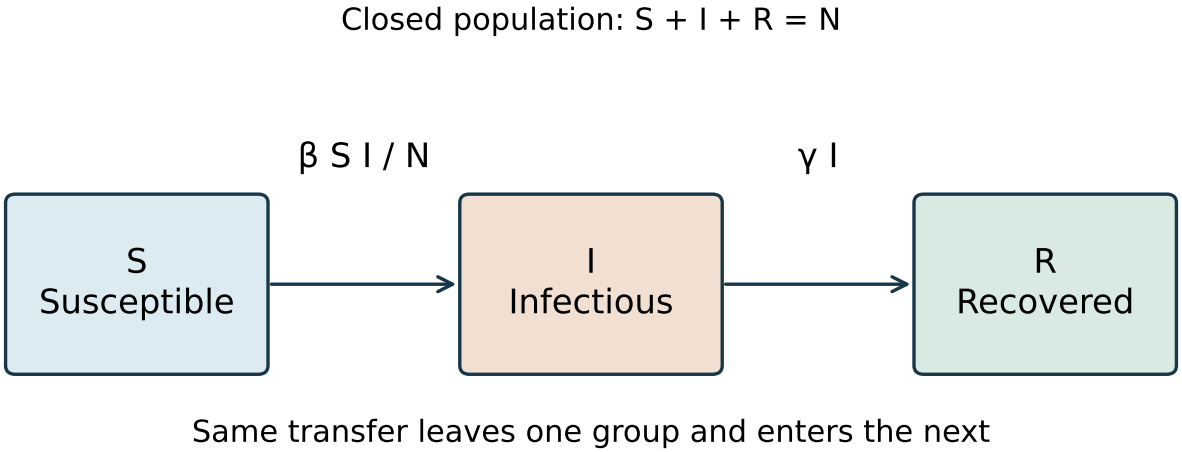
Slides for this section

Let $S(t)$, $I(t)$, and $R(t)$ denote susceptible, infectious, and recovered people. In this model recovery confers protection for the duration considered. The categories are disjoint and exhaust a closed population of size N: no births, deaths, migration, or return to susceptibility occur. We use continuous-valued group sizes as a deterministic population approximation. They need not be integers, and they are not claimed to be the exact expectations of an unspecified stochastic process.

Suppose a susceptible person makes potentially transmitting contacts at effective rate β, measured in day^{-1}. Homogeneous mixing replaces the probability that the contacted person is infectious by I/N. The per-susceptible infection hazard is therefore $\beta I/N$, and the population transfer rate is

$$J_{\text{inf}} = \beta \frac{SI}{N}.$$

A constant recovery hazard γ gives $J_{\text{rec}} = \gamma I$. Both fluxes have units of people per day. A constant hazard corresponds to an exponential residence-time model, not a common fixed infectious duration. The assumptions exclude latent stages, contact structure, and variation among individuals.



Original SIR schematic. Each transfer leaves one category and enters the next; recovered people remain inside the population and do not return to susceptibility in this model.

2 Conservation, positivity, and the SIR equations

Slides for this section

Infection transfers a person from S to I; recovery transfers one from I to R. Hence

$$\boxed{\dot{S} = -\beta SI/N, \quad \dot{I} = \beta SI/N - \gamma I, \quad \dot{R} = \gamma I.}$$

Adding the equations gives $\dot{S} + \dot{I} + \dot{R} = 0$, so the initial total remains N. Conservation reduces the number of independent states to two, although storing all three is convenient for auditing the numerical budget.

The feasible set is the simplex $\{(S, I, R) : S, I, R \geq 0,\ S + I + R = N\}$. At $S = 0$ or $I = 0$, the corresponding outward transfer vanishes; at $R = 0$, $\dot{R} = \gamma I \geq 0$. More explicitly,

$$S(t) = S_0 \exp\left(-\frac{\beta}{N}\int_0^t I(s)\ \mathrm{d}s\right), \qquad I(t) = I_0 \exp\left(\int_0^t [\beta S(s)/N - \gamma]\ \mathrm{d}s\right).$$

These expressions prove nonnegativity when the initial state is nonnegative. They also show that the deterministic model approaches an extinction limit continuously rather than removing the last infectious individual at a random time.

3 Growth threshold and the infectious peak

Slides for this section

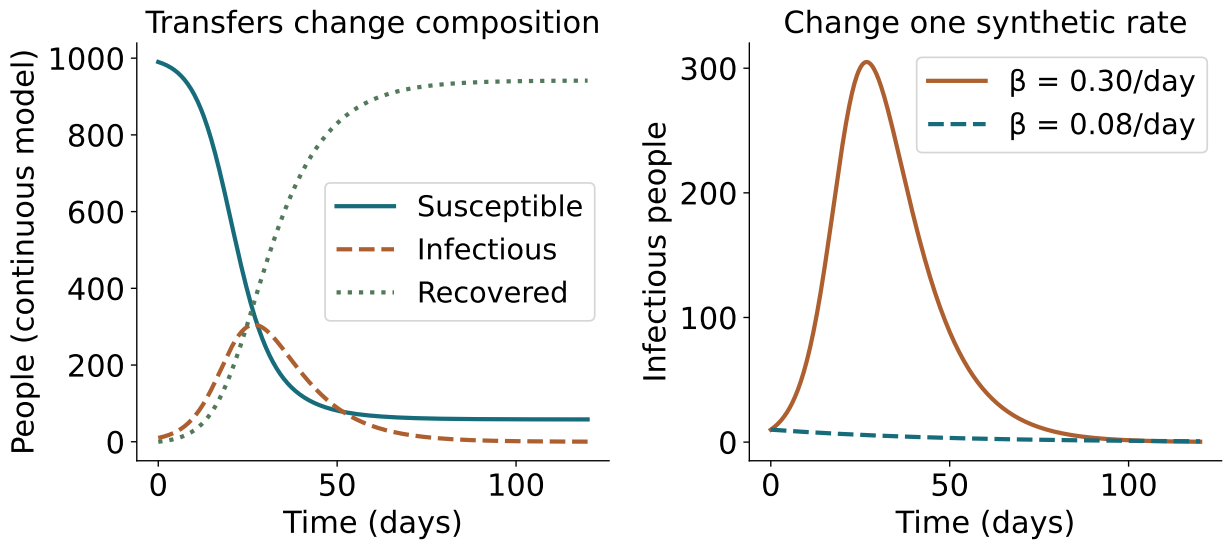
For $I > 0$, divide its equation by I:

$$\frac{\dot{I}}{I} = \beta\frac{S}{N} - \gamma.$$

When $\gamma > 0$, define $\mathcal{R}_0 = \beta/\gamma$ and the susceptible-dependent ratio $\mathcal{R}_{\text{eff}}(t) = \mathcal{R}_0 S(t)/N$. Infectious prevalence grows when $\mathcal{R}_{\text{eff}} > 1$ and declines when it is below one. These are model parameters and a model threshold; no real intervention effect is estimated here.

For $N = 1000$, $(S_0, I_0, R_0) = (990, 10, 0)$, $\beta = 0.3\,\text{day}^{-1}$, and $\gamma = 0.1\,\text{day}^{-1}$, the initial per-infectious growth rate is $0.297 - 0.1 = 0.197\,\text{day}^{-1}$. Thus $\dot{I}(0) = 1.97$ people per day. While S remains close to S_0, $I(t) \simeq I_0 e^{0.197t}$ is a local early-time approximation, not a full-outbreak solution.

Since S decreases, the positive-infection trajectory reaches its interior peak when $S = N\gamma/\beta$, if it starts above that threshold. It need not exhaust susceptibility. With only β changed to $0.08\,\text{day}^{-1}$, the initial rate is $0.0792 - 0.1 = -0.0208\,\text{day}^{-1}$, and it cannot later turn positive because S cannot increase.



Synthetic Euler trajectories at 0.1 day per step. Baseline N = 1000, initial (990, 10, 0), $\beta = 0.3$/day and $\gamma = 0.1$/day. The comparison changes only β to 0.08/day.

4 An invariant and the final-size relation

Slides for this section

For constant positive β, γ, and while $S, I > 0$, divide the infectious equation by the susceptible equation:

$$\frac{\mathrm{d}I}{\mathrm{d}S} = -1 + \frac{\gamma N}{\beta S}.$$

Integration between the initial state and the current state gives a dimensionally meaningful logarithm,

$$\boxed{I - I_0 = -(S - S_0) + \frac{\gamma N}{\beta} \log \frac{S}{S_0}.}$$

This relation describes the orbit in the (S, I) plane without solving for time. It supplies an independent analytic comparison for a numerical trajectory; Euler preserves the population total exactly but generally does not preserve this nonlinear invariant exactly.

At an interior peak, substitute $S_p = N\gamma/\beta$ to obtain

$$I_p = I_0 + S_0 - S_p + S_p \log(S_p/S_0).$$

If $I(t) \to 0$, the final susceptible count satisfies

$$\log \frac{S_\infty}{S_0} = -\frac{\beta}{\gamma N}(R_\infty - R_0), \qquad R_\infty = N - S_\infty.$$

This is an implicit equation, not a declaration that all susceptible people are eventually infected. The calculation is an analytical extension of the synthetic constant-parameter model. It does not turn its assumptions into empirical evidence.

5 A conservative Euler step and its restrictions

Slides for this section

Evaluate the two flows once at the start of an interval of length h and reuse them with opposite signs:

$$\begin{aligned} S_{n+1} &= S_n - h\beta S_n I_n/N, \\ I_{n+1} &= I_n + h\beta S_n I_n/N - h\gamma I_n, \\ R_{n+1} &= R_n + h\gamma I_n. \end{aligned}$$

The sum is unchanged by exact arithmetic. For the stated initial state and a one-day step, infection transfers 2.97 people and recovery transfers 1 person. The updated state is $(987.03, 11.97, 1)$ and sums to 1000.

The separate donor restrictions $h\beta I_n/N \le 1$ and $h\gamma \le 1$ ensure nonnegative updates. A sufficient uniform choice is

$$h \max(\beta, \gamma) \le 1,$$

because $I_n/N \le 1$. Indeed $S_{n+1} = S_n(1 - h\beta I_n/N)$ and $I_{n+1} = I_n(1-h\gamma) + h\beta S_n I_n/N$ are then sums of nonnegative terms. This is an admissibility bound, not an accuracy estimate. The demonstration uses $h = 0.1$ day and checks smaller steps. Two half-steps recompute the flows at the intermediate state, so they need not equal one full step.

6 Numerical evidence and model discrepancy

Slides for this section

The original companion supplies two controlled scenarios, not a forecast fitted to observations. Check the population residual $S + I + R - N$, minimum group size, monotonic decrease of S, and monotonic increase of R. In the constant-parameter case, also compare the numerical (S, I) trajectory with the orbit relation. Evaluate errors at common physical times when comparing time steps.

A curve can conserve N exactly and still have an inaccurate peak height or peak time. Conversely, differences between observations and a converged solution may reflect omitted heterogeneity, observation processes, or changing parameters. Report the initial state, time unit, step, and the definition of the measured outcome before interpreting a comparison.

The reading introduces discrete epidemic models and their threshold reasoning. This companion uses a continuous-time SIR model with frequency-dependent incidence. Discrete infection probabilities and continuous hazards are related through a time interval; their numerical values must not be substituted for one another without conversion. A more detailed model requires a particular new mechanism and evidence, rather than additional compartments for their own sake.

Exercises

MM06-E1. Transfer the same people twice

Use N = 500, initial (S, I, R) = (480, 20, 0), $\beta = 0.25$/day, $\gamma = 0.1$/day and step h = 0.5 day.
a Compute the infection and recovery flows.

b Compute the two transfers and the next state.

c Check the total and explain the source of approximation.

MM06-E2. Predict growth without running a simulation

Use $\beta = 0.3$/day and $\gamma = 0.1$/day with $I > 0$.
a Compare recruitment and recovery when $S/N = 0.9$. Does I initially grow?

b Repeat for $S/N = 0.2$.

c Find the susceptible fraction at balance and explain why I can decline before S reaches zero.

MM06-E3. Diagnose a smooth but wrong update

At a step start, (S, I, R) = (900, 90, 10). The calculated infection transfer is 9 people and the recovery transfer is 18.
a Write the correct next state.

b A program instead returns (891, 82, 28). What invariant fails, by how much?

c Propose a repair and a separate accuracy check; explain why both are needed.

MM06-E4. State what a scenario establishes

Two runs differ only in β. Both use synthetic parameters and the same closed-population assumptions.
a Name two limiting-case tests and their expected outcomes.

b Name an independent observation and an observation-process issue needed for real validation.

c Explain why a lower synthetic curve alone does not quantify the effect of a real intervention.

References

Zan Ahmad, Fall 2024 HEART syllabus. PDF pages 1–2.

Hoppensteadt and Peskin, Modeling and Simulation in Medicine and the Life Sciences, second edition. Printed pages 300–304; PDF pages 311–315 in the supplied copy.