

LIFE DATA EPIDEMIOLOGY

Lecture 3: SIR with demography

Leonardo Badia

leonardo.badia@unipd.it

SIR model

- Susceptible-Infected-Recovered model



- For a population of size N , we consider the amount of individuals in each state
 - equal to S , I , R , respectively. $S + I + R = N$
 - take $s = S/N$, $x = I/N$, $r = R/N$: $s + x + r = 1$

SIR model

- We can write the following equations

$$(1) \quad \frac{ds}{dt} = -\beta sx$$

$$(2) \quad \frac{dx}{dt} = \beta sx - \mu x$$

$$(3) \quad \frac{dr}{dt} = \mu x$$

from (1) + (3) we derived

$$s = s_0 e^{-R_0 r}$$

now, consider (2) and put
 $x = 1 - r - s = 1 - r - s_0 e^{-R_0 r}$

into: $dr / dt = \mu x$

we get: $dr / dt = \mu (1 - r - s_0 e^{-R_0 r})$

Solution of SIR model?

- Can we solve $dr / dt = \mu (1 - r - s_0 e^{-R_0 r})$?
 - In principle, we have r vs t ; thus we should find the trend of r over $t \rightarrow$ then, s and x
 - However, the equation is not solvable in closed-form (no primitive for the integral)

$$t = \frac{1}{\mu} \int_0^t \frac{dy}{1 - y - s_0 e^{-R_0 r}}$$

Solution of SIR model?

- If discretized time: (Euler's method)

$$\frac{dx}{dt} = \beta s x - \mu x$$

$$\frac{\Delta x}{\Delta t} = (\beta s - \mu) x$$

$$\Delta x = (\beta s - \mu) x \Delta t$$

- Starting from x_0 , we compute $x_1 = x_0 + \Delta x$,
 $x_1 = x_0 + \Delta x$, ... $x_k = x_{k-1} + \Delta x$
 - crude but useful method for simulations
 - constructively models dynamics (+noise?)
 - can lead to approximation errors

Epidemic curve

- Or (with another brutal approximation) we estimate the “epidemic curve,” roughly describing the number of newly identified cases per time unit – taken as dr / dt
- We start from $dr / dt = \mu (1 - r - s_0 e^{-R_0 r})$
 - key step: assume $R_0 r$ is **small** \rightarrow Taylor:
$$dr / dt = \mu [1 - r - s_0 (1 - R_0 r + R_0^2 r^2)]$$
 - a bit dirty... but this admits a primitive!

Epidemic curve

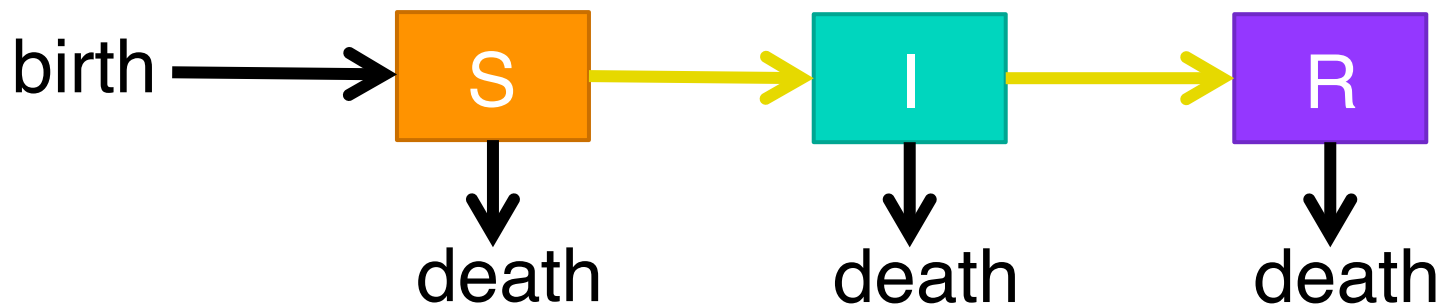
- Solve $dr / dt = \mu [1 - r - s_0 (1 - R_0 r + R_0^2 r^2)]$
- We get:
$$r = [s_0 R_0 - 1 + a \tanh(a \mu t / 2 - \phi)] / (R_0^2 s_0)$$
- where $a = [(s_0 R_0 - 1)^2 + 2s_0 x_0 R_0^2]^{1/2}$
and $\phi = \tanh^{-1} [(s_0 R_0 - 1)/a]$
- Finally, we derive to get:
$$dr / dt = \mu a^2 \operatorname{sech}^2(a \mu t / 2 - \phi) / (2s_0 R_0^2)$$

Epidemic curve

- The epidemic curve given by
$$dr/dt = \mu a^2 \operatorname{sech}^2(a \mu t / 2 - \phi) / (2s_0 R_0^2)$$
is subject to many assumptions
- As we need $R_0 r$ to be small, it works only for lowly infective diseases and at small t
- We know numerical integration techniques
→ this approximation may be unnecessary

Expanding the SIR model

- The SIR model is essential but works only for closed populations (short time span)
- For epidemic dynamics over a long time horizon, we include “natural” birth/deaths
 - i.e. disease-unrelated (assumed non-lethal)



SIR model with demography

- The simplest choice of assumptions is
 - “natural” life-span: exponentially-distributed with average duration $1/\lambda$ years
 - “natural” demography is at a steady-state, so birth rate = overall death rate = λ
 - “natural” deaths independent of the disease thus their localized rate in classes S, I, R is equal to λs , λx , λr , respectively (in total, λ)

SIR model with demography

□ The model becomes

$$\frac{ds}{dt} = \lambda - \beta sx - \lambda s$$

□ Also re-compute parameter R_0 as

$$R_0 = \frac{\beta}{\lambda + \mu}$$

$$\frac{dx}{dt} = \beta sx - \mu x - \lambda x$$

$$\frac{dr}{dt} = \mu x - \lambda r$$

that keeps R_0 defined as $\mathbb{E}[\text{\#contagions created by first infected in a naive population}]$

SIR model with demography

- Immediate implications of these changes:
 - smaller R_0 : some infected die by “natural causes” before fully spreading the disease
 - recovered state is no longer absorbing
- We expect the final outcome can be
 - either the disease is fully eradicated
 - or there is an endemic equilibrium where some infected individuals are present

SIR+demography: applications

- The model can be used for several epidemiologic purposes
 - computing disease incidence at equilibrium
 - assessing stability of equilibria
 - identify oscillatory dynamics of disease
 - address therapies (such as vaccination) for complete eradication of the disease
- Feel free to think of these also in non-epidemiologic contexts!

SIR+demography: equilibrium

- To compute the equilibrium, we must set all the derivatives in the equations to 0
- If we set $dx/dt = 0$, $\rightarrow \beta s_{\infty} x_{\infty} - (\lambda + \mu) x_{\infty} = 0$
 - clearly, one possible solution is $x_{\infty} = 0$ representing a **disease-free equilibrium**
 - or, $s_{\infty} = (\lambda + \mu) / \beta$ that is equal to $1 / R_0$; this is an **endemic equilibrium** where $x_{\infty} = (R_0 - 1) \lambda / \beta$ (and $r_{\infty} = 1 - s_{\infty} - x_{\infty}$)

SIR+demography: equilibrium

- What is the right equilibrium?
 - since $x_\infty = (R_0 - 1) \lambda / \beta$, in the endemic case we need $R_0 > 1$; consistent with R_0 's role:
 $R_0 > 1 \rightarrow$ endemic $R_0 < 1 \rightarrow$ disease-free
- Stability of equilibria
 - disease-free eq: trivially stable if reached
 - endemic eq: also stable, although not as immediate to derive

SIR+demography: equilibrium

- For a system of n ordinary differential eqs:

$$\{ dA_i/dt = f_i(A_1, A_2, \dots, A_n), \quad i = 1, \dots, n$$

- equilibrium $(A_1^*, A_2^*, \dots, A_n^*)$ = solution of $\{ f_i(A_1, A_2, \dots, A_n) = 0$; stability = dynamics at $A_i = A_i^* + \varepsilon$

- Compute eigenvalues of Jacobian matrix $J =$

- ∂f_i^* is $\partial f_i(A_1^*, \dots, A_n^*)$

$$J = \begin{pmatrix} \frac{\partial f_1^*}{\partial A_1} & \dots & \frac{\partial f_1^*}{\partial A_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial f_n^*}{\partial A_1} & \dots & \frac{\partial f_n^*}{\partial A_n} \end{pmatrix}$$

SIR+demography: equilibrium

- For the SIR+demography model, this is:

$$J = \begin{pmatrix} -\beta x_{\infty} - \mu & -\beta s_{\infty} & 0 \\ \beta x_{\infty} & \beta s_{\infty} - (\lambda + \mu) & 0 \\ 0 & \mu & -\lambda \end{pmatrix}$$

- The characteristic polynomial in Λ is
 $(\beta x_{\infty} - \lambda - \Lambda)(\beta s_{\infty} - \lambda - \mu - \Lambda)(-\lambda - \Lambda) + \beta^2 s_{\infty} x_{\infty} (-\lambda - \Lambda)$

SIR+demography: equilibrium

- The characteristic polynomial in Λ is $(\beta x_\infty - \lambda - \Lambda)(\beta s_\infty - \lambda - \mu - \Lambda)(-\lambda - \Lambda) + \beta^2 s_\infty x_\infty (-\lambda - \Lambda)$
 - one root is surely $\Lambda_1 = -\lambda$ (always negative)
 - the others depend on which equilibrium we are talking about
- For disease-free equilibrium, $s_\infty = 1$, $x_\infty = 0$:
 - we are left with $(-\lambda - \Lambda)(\beta - \lambda - \mu - \Lambda) = 0$, that has solutions: $\Lambda_2 = -\lambda$ (same as Λ_1) and $\Lambda_3 = \beta - \lambda - \mu$
 - so, stability implies $\beta < \lambda + \mu$, i.e., $R_0 < 1$

SIR+demography: equilibrium

- For the endemic equilibrium, we just have some more complicated math. We set:

$$s_{\infty} = 1/R_0 \quad x_{\infty} = (R_0 - 1) \lambda / \beta$$

- Resulting in $\Lambda^2 + \lambda R_0 \Lambda + (\lambda + \mu) \lambda (R_0 - 1) = 0$.

- If $A = 1/[\lambda(R_0 - 1)]$, $G = 1/(\lambda + \mu)$:
$$\Lambda_{2,3} = -\frac{\lambda R_0}{2} \pm \frac{\sqrt{(\lambda R_0)^2 - \frac{4}{AG}}}{2}$$

avg age at infection

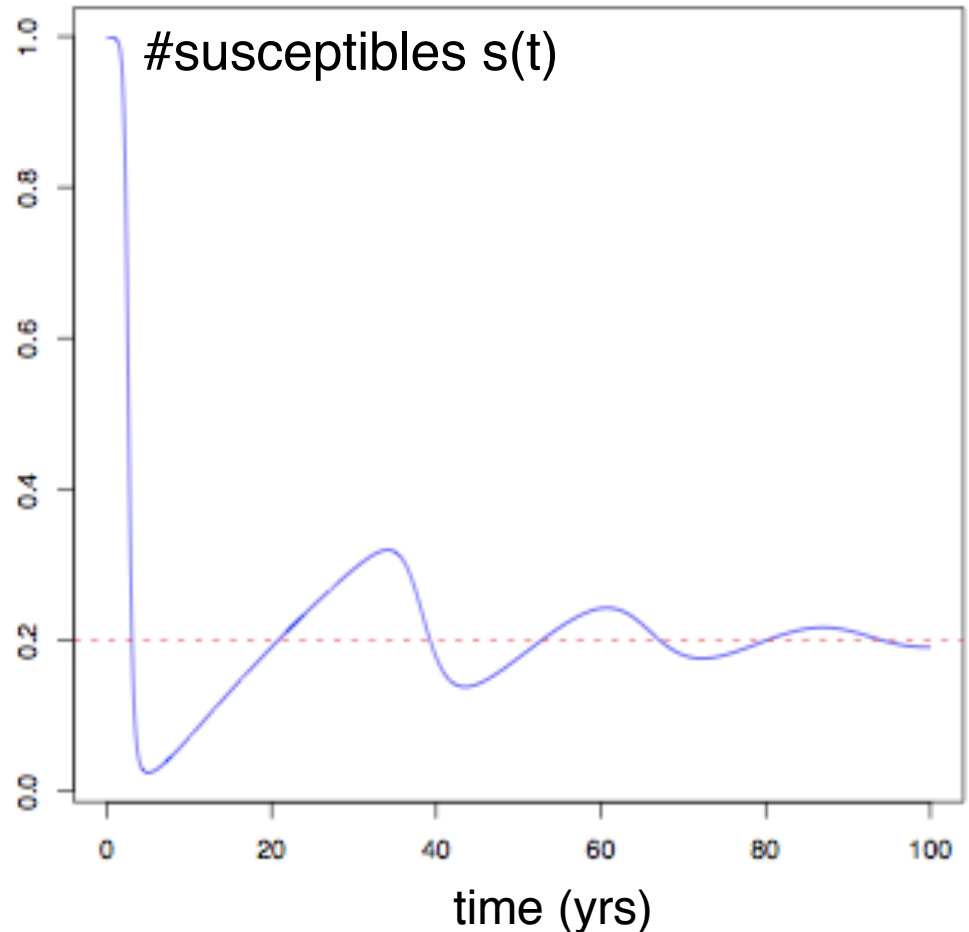
duration of the disease

SIR+demography: equilibrium

- The endemic equilibrium has $\Lambda_1 = -\lambda$ and
$$\Lambda_{2,3} = -\frac{\lambda R_0}{2} \pm \frac{\sqrt{(\lambda R_0)^2 - \frac{4}{AG}}}{2}$$
- Λ_2 and Λ_3 real part < 0 , so stable equilibrium
- term inside square root is typically negative so $\Lambda_{2,3} = a \pm j b$, with $a < 0 \rightarrow$ endemic equilibrium is reached with oscillatory dynamics (dampened oscillations)

SIR+demography: equilibrium

- $\lambda=1/70$, $\beta=5.0$
 $\mu=1.0$, $R_0=5.0$
- Same descent of standard SIR model for $s(t)$; but after it oscillations to endemic eq.
 $s_\infty = 1/R_0$



SIR+demography: equilibrium

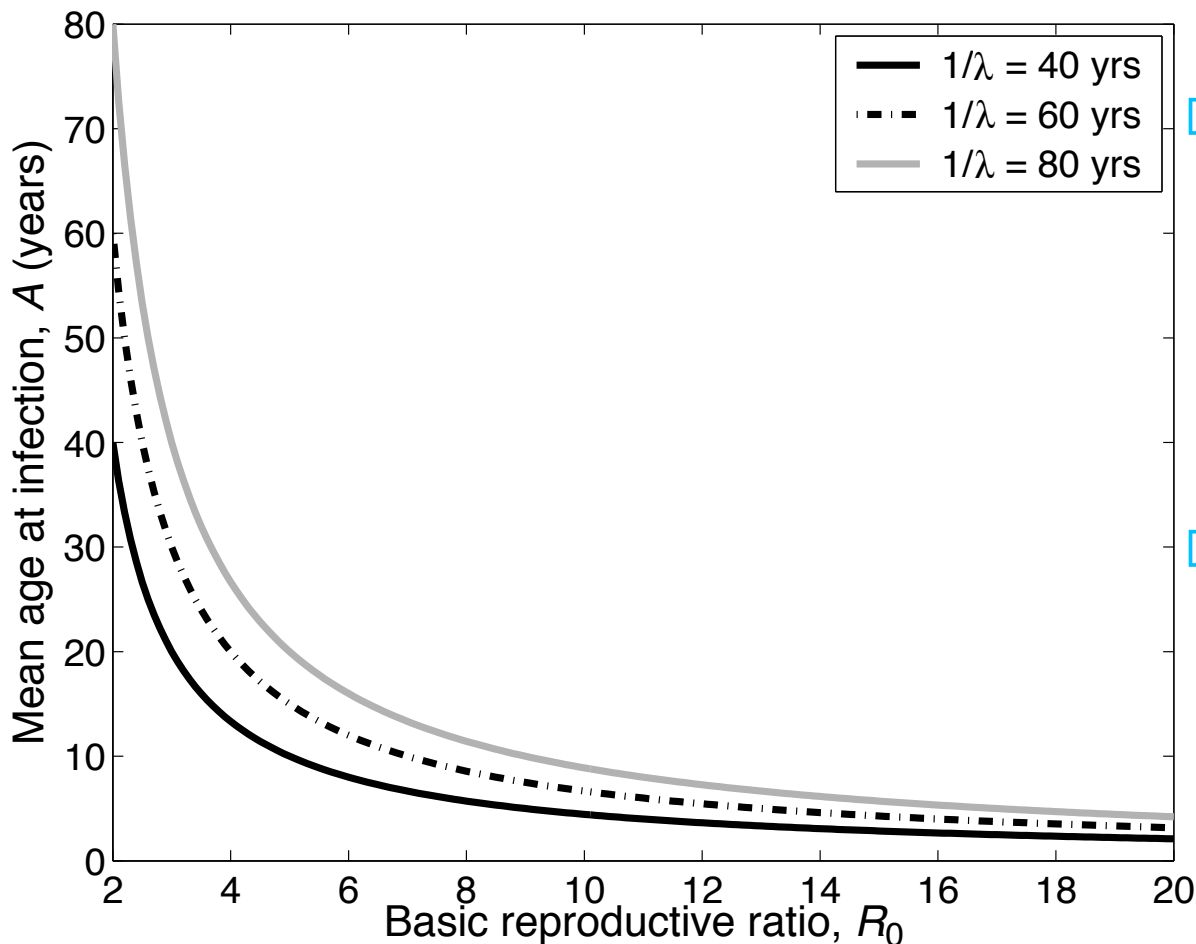
- Assume $\Lambda_{2,3} = a \pm j b$ are the last two eigenvalues for the endemic equilibrium
- then, the oscillations towards the endemic equilibrium can be seen as superpositions of an exponential decay with parameter a (hence, becoming 37% at time $1/a$)
- and oscillations with period $2\pi / b$

Average age at 1st infection

- The average age at 1st infection A is important and also easy to characterize
 - why is it equal to $1/[\lambda(R_0 - 1)]$?
 - at equilibrium, individuals are born in class S and stay there a time $A = 1/(\text{exit rate})$
 - said exit rate is equal to βx_∞
(also called the strength of infection)
 - at endemic equilibrium, $x_\infty = (R_0 - 1) \lambda / \beta$

Average age at 1st infection

- Strong dependence on R_0 , weaker on λ



- $A = \frac{1}{[\lambda(R_0 - 1)]}$
natural lifespan
 $(R_0 - 1)$

- Practical way to estimate parameters from data!

Another parametrization

- Anderson&May propose to rewrite the model in terms of **force of infection**
 - denoted here as $\varphi = \beta x$ (also a function of t)
 - consider just equations (1) and (2)

$$\frac{ds}{dt} = \lambda - (\varphi + \lambda)s$$
$$\frac{dx}{dt} = \varphi \left(s - \frac{\mu + \lambda}{\beta} \right)$$

1/R₀

$$\frac{ds}{dt} = \lambda - (\varphi + \lambda)s$$
$$\frac{d\varphi}{dt} = (\mu + \lambda)\varphi (sR_0 - 1)$$

multiply by $\beta = (\lambda + \mu)R_0$

Early growth

- Use A&M version to better understand the initial evolution of the epidemics
 - so, assume a very small x_0 is spreading a disease over a population of $s_0 \approx 1$
- The last equation of A&M becomes
$$d\varphi = (\lambda + \mu) \varphi (R_0 - 1) dt$$
 - but $\lambda \ll \mu$; close to $t=0$, we even neglect λ
(usual procedure) $\rightarrow \varphi = \varphi_0 e^{Ft}$
 - where $F = \mu (R_0 - 1)$ and $\varphi_0 = \beta x_0$

Early growth

- So early growth of strength of infection ϕ and number of infected I is exponential
 - this explain the rapid increase of x over t
 - clearly, this holds true until $s \approx 1$, because after that we replace R_0 with $s R_0$ (lower)
 - we reach the point where s is so low that $s R_0$ is becomes < 1 , we start decreasing
- The initial growth of an epidemics can also serve to give a good estimate of R_0

Five values affected by R_0

- The importance of R_0 :
 - it is the threshold parameter, determining whether or not the disease spreads (>1)
 - $1-1/R_0$ is also the critical vaccination share
 - the **initial** increase rate of an epidemics (exponential growth) is related to R_0-1
 - $>e^{-R_0}$ is the **final** fraction of individuals affected at some point by the disease
 - R_0 gives s at endemic equilibrium ($= 1/R_0$)