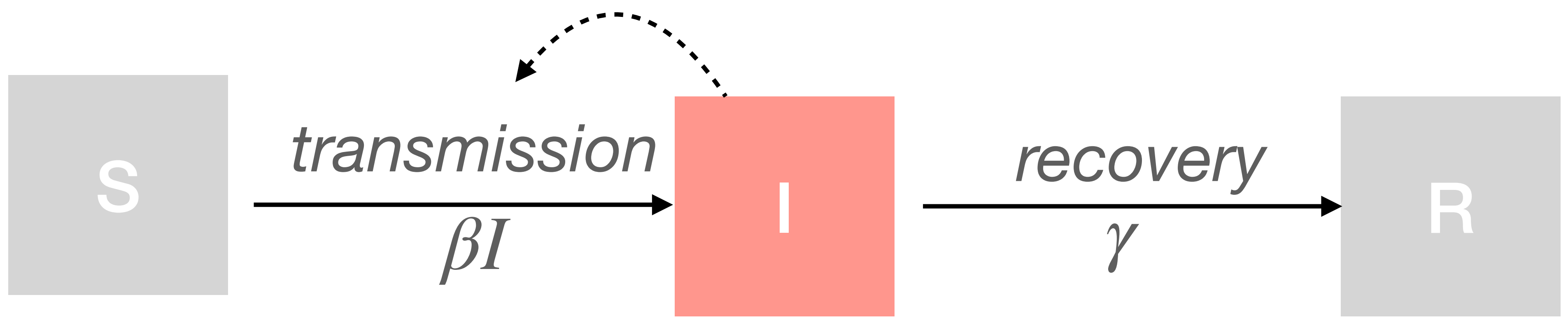
# Formal demography in research on infectious diseases

C. Jessica E. Metcalf

# Infectious diseases drive demography, and *vice versa*

The **S**usceptible **I**nfected **R**ecovered model:



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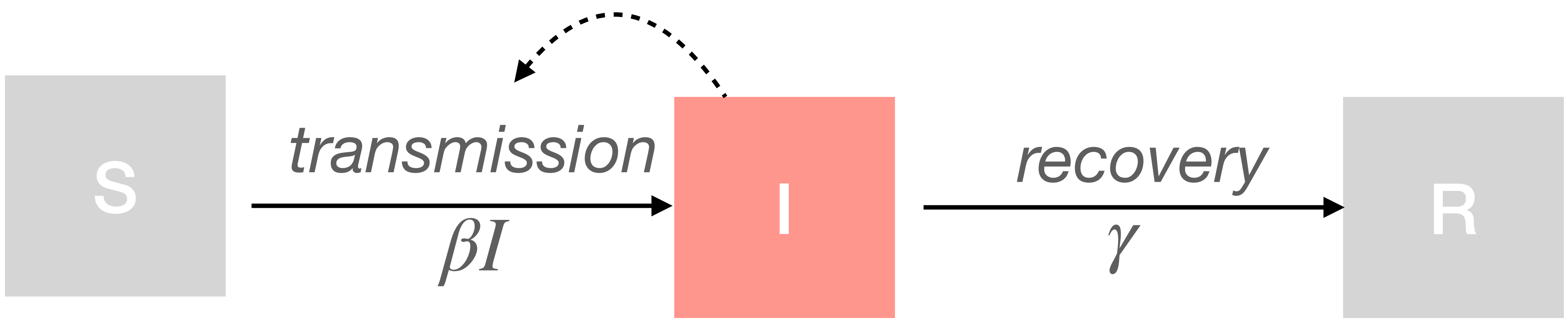
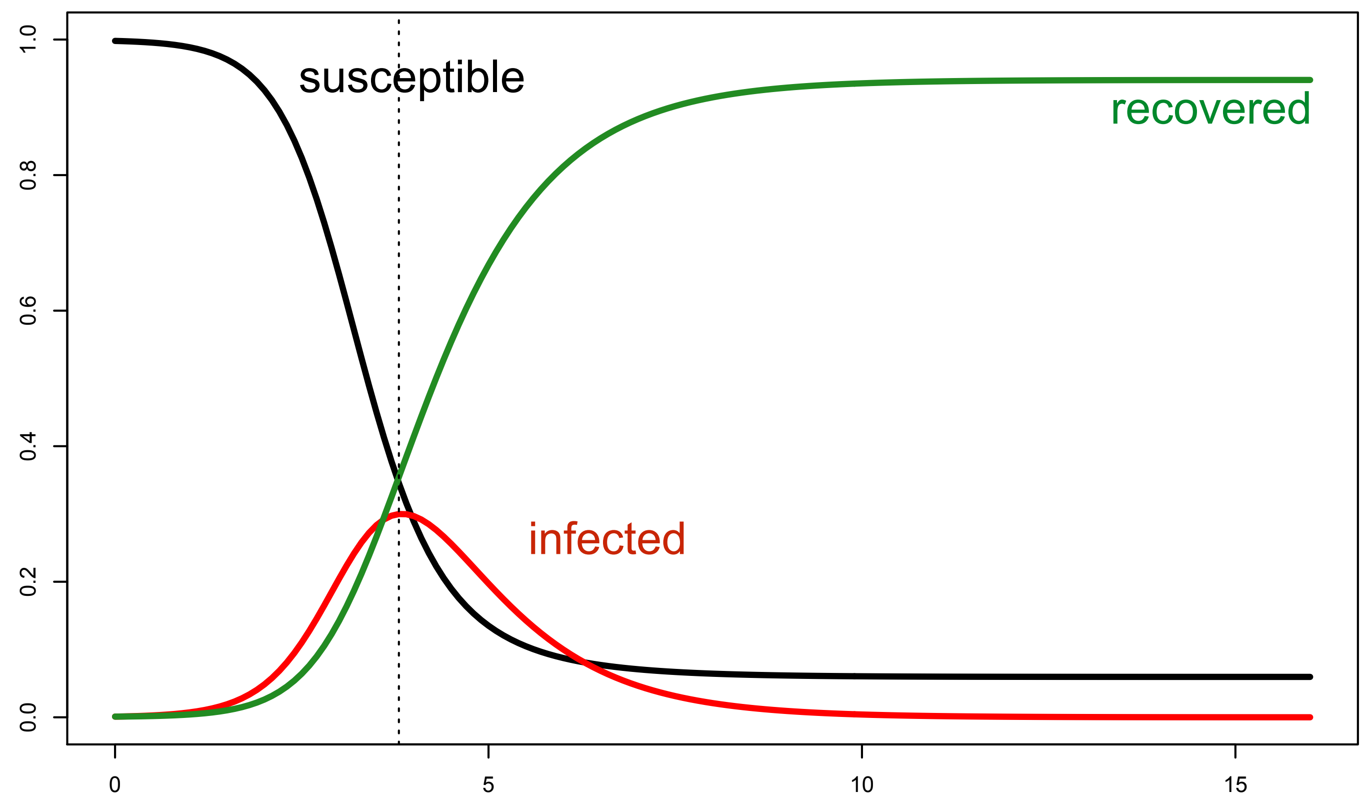



$$\frac{dS}{dt} = -\beta SI$$

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

$$\frac{dR}{dt} = \gamma I$$



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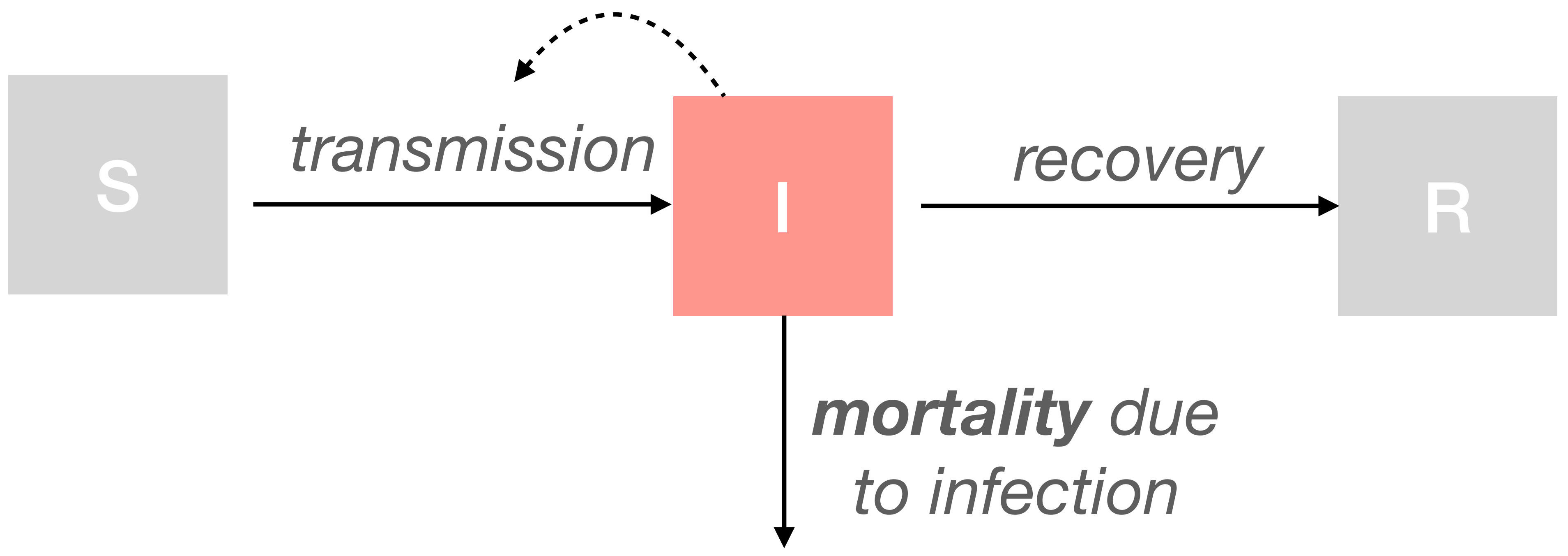


Smallpox infection fatality ratio as high as 20%

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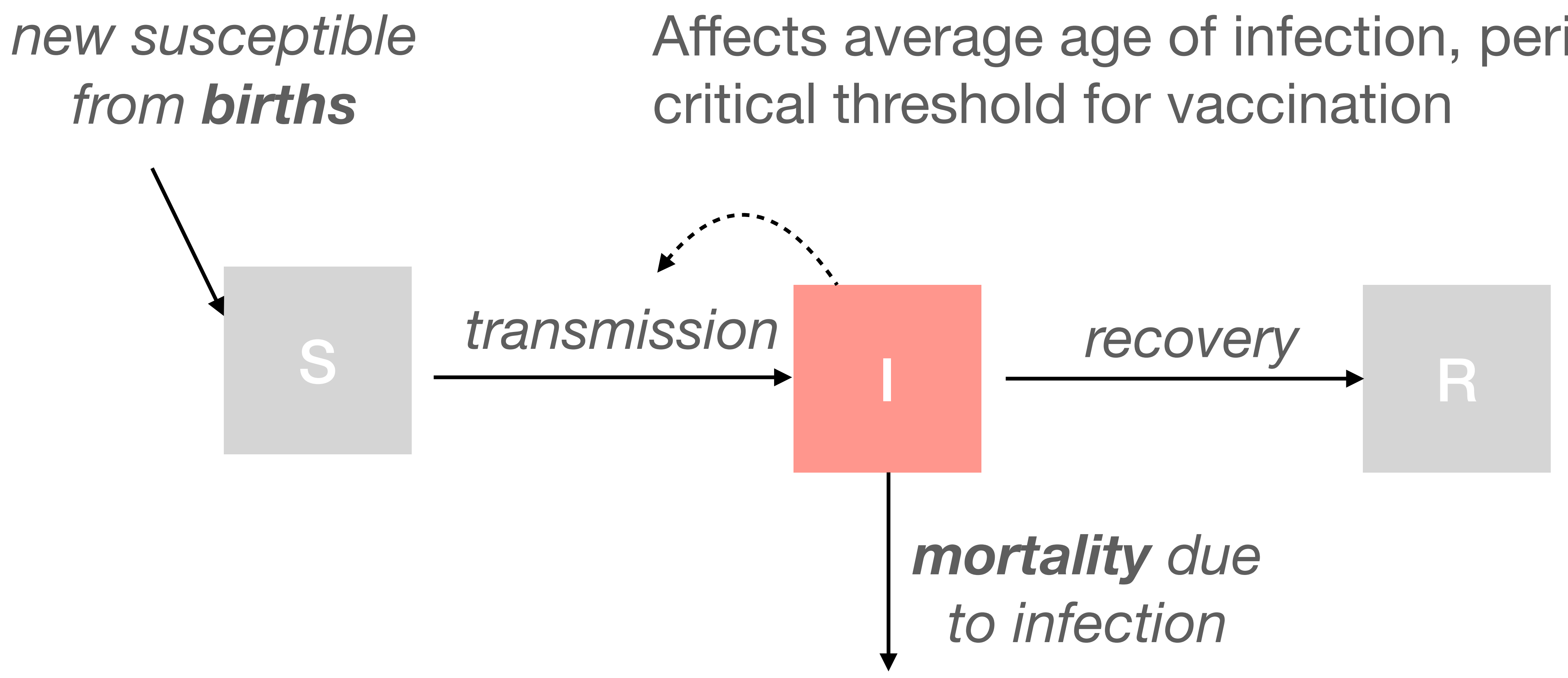


Affects average age of infection, periodicity, critical threshold for vaccination

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*new susceptible from* ***births***

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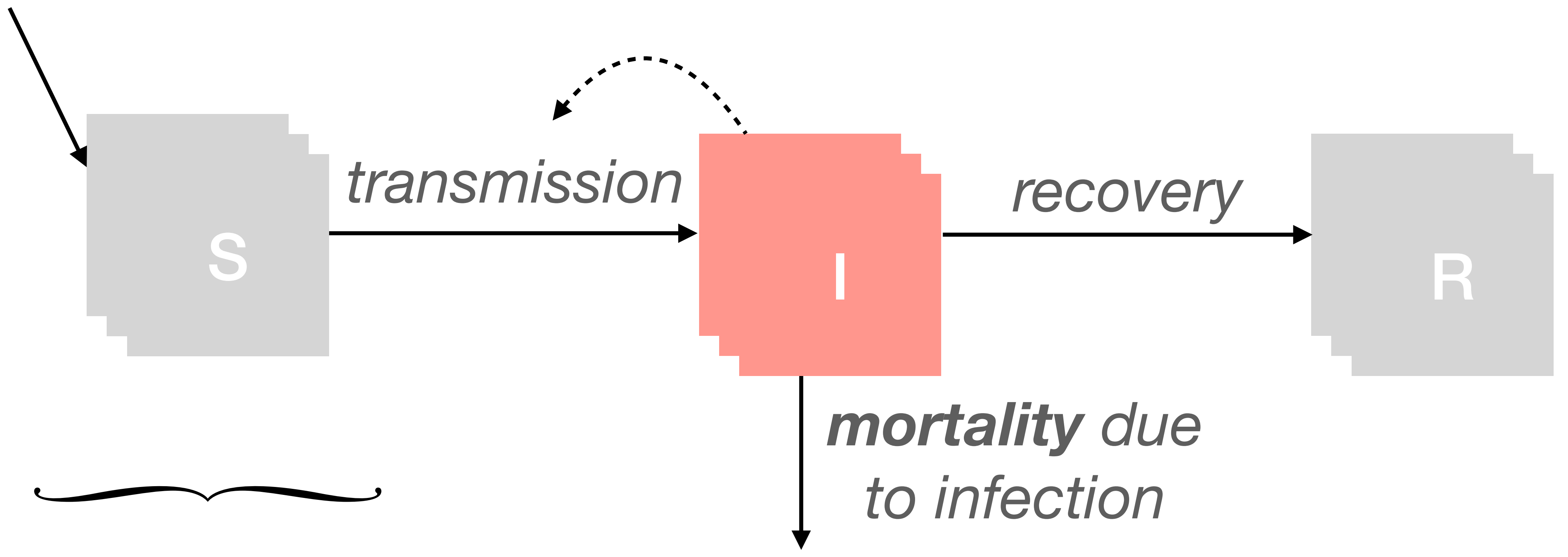


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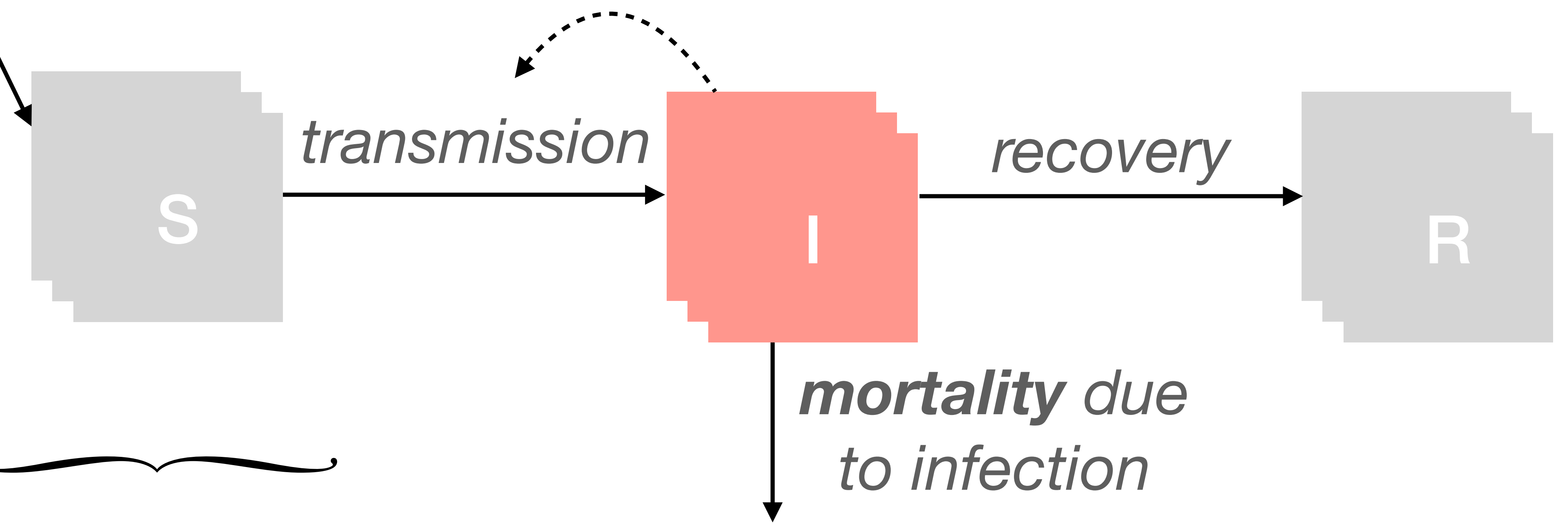


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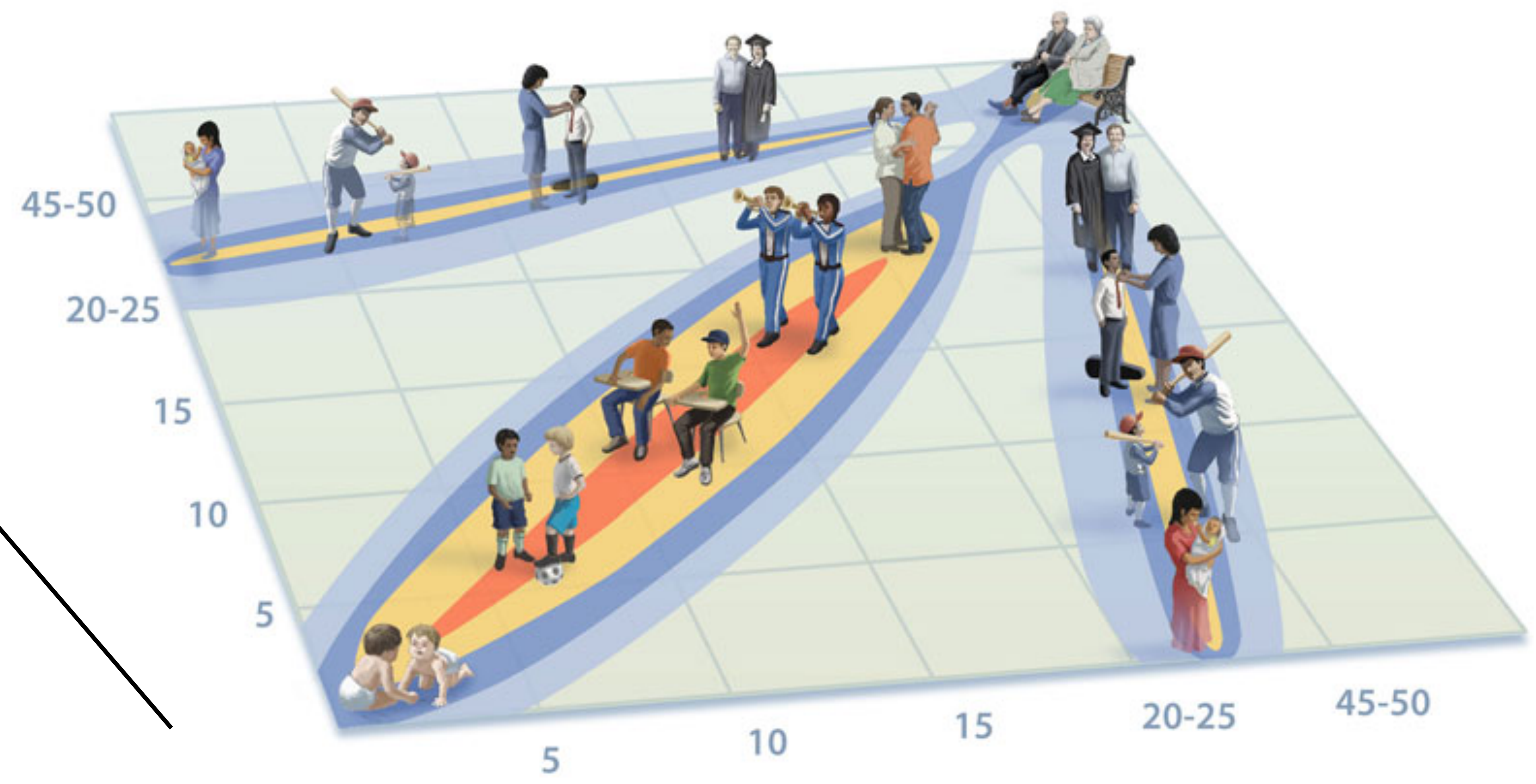
Contact patterns
Susceptibility
Transmission
Morbidity or mortality



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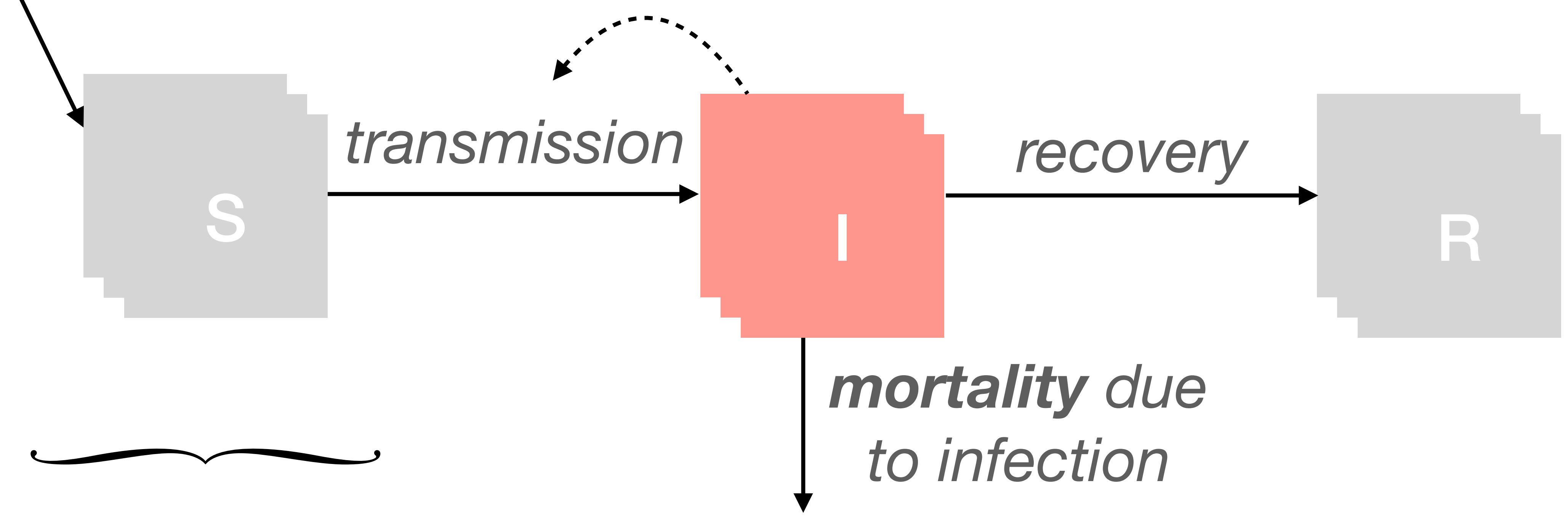


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$$A_{a,t} = \begin{pmatrix} 1-d_a & 0 & 0 & 0 & 0 \\ d_a & 1-\varphi_a(\mathbf{n}(t))(1-v_a) & 0 & 0 & 0 \\ 0 & \varphi_a(\mathbf{n}(t))(1-v_a) & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & v_a & 0 & 0 & 1 \end{pmatrix}.$$

$$\mathbf{A}(\mathbf{n}(t)) = \begin{pmatrix} s_1(1-u_1)\mathbf{A}_1 & 0 & 0 & \cdots & 0 \\ s_1u_1\mathbf{A}_1 & s_2(1-u_2)\mathbf{A}_2 & 0 & \cdots & 0 \\ 0 & s_2u_2\mathbf{A}_2 & s_3(1-u_3)\mathbf{A}_3 & \cdots & 0 \\ 0 & 0 & s_3u_3\mathbf{A}_3 & \cdots & 0 \\ \cdots & \cdots & \cdots & \cdots & 0 \\ 0 & 0 & 0 & \cdots & .s_zA_z \end{pmatrix}$$

Applied questions, e.g., critical threshold for introduction of Rubella-Containing-Vaccine

Metcalf et al. 2012 *Theoretical Population Biology*

# Classic demographic principles are essential to dissecting spread

$R_0$: number of new infections per infected individual in a completely susceptible population

Combine with the serial interval to obtain the speed of spread.

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$R_0$=2

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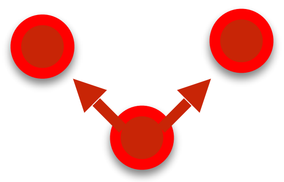

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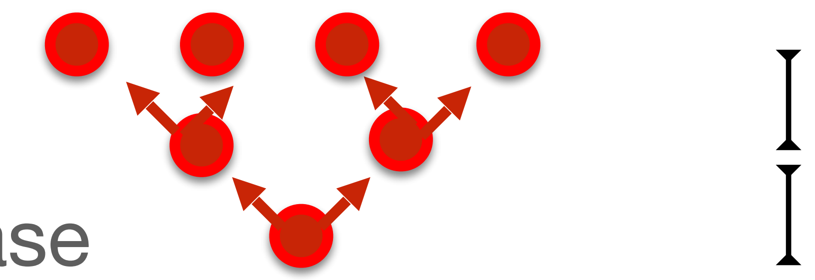

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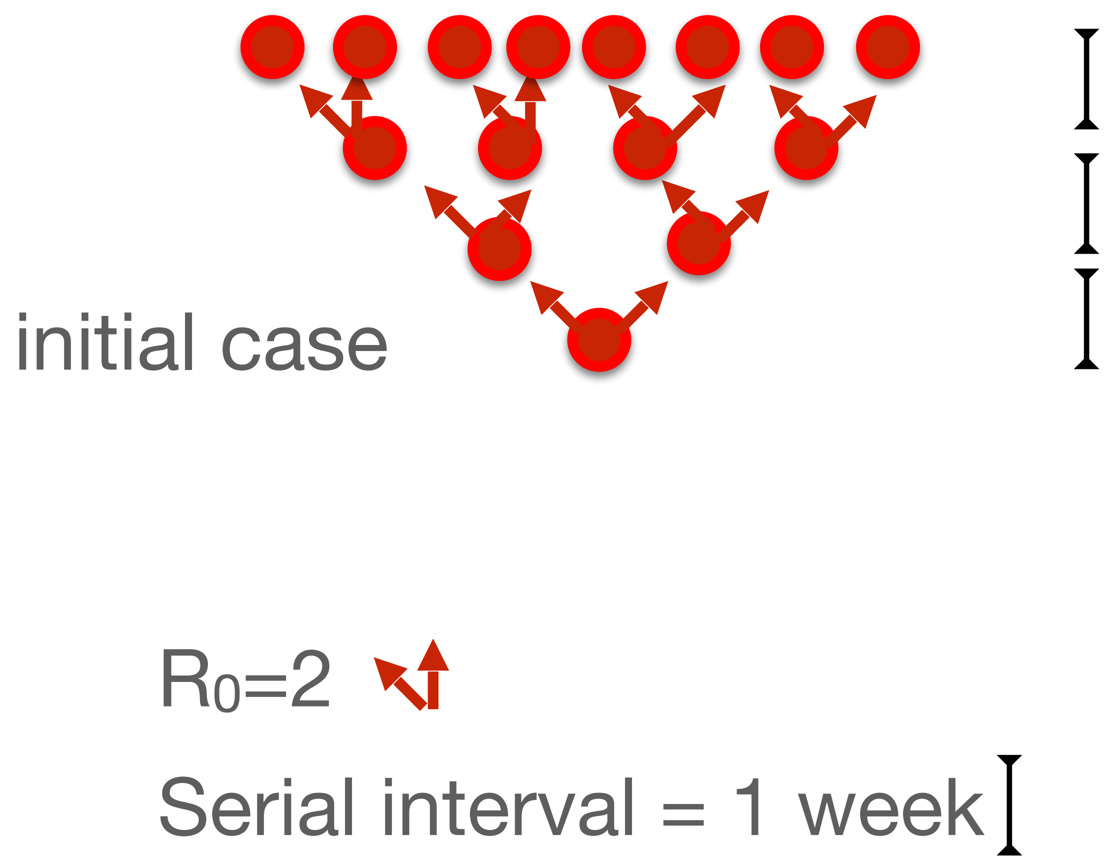

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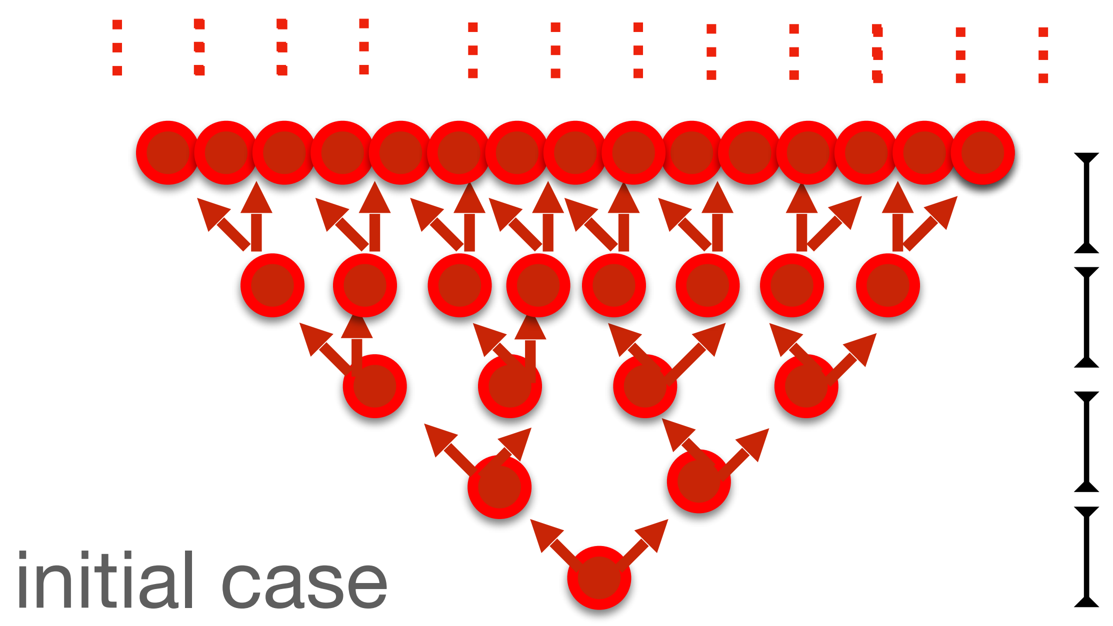


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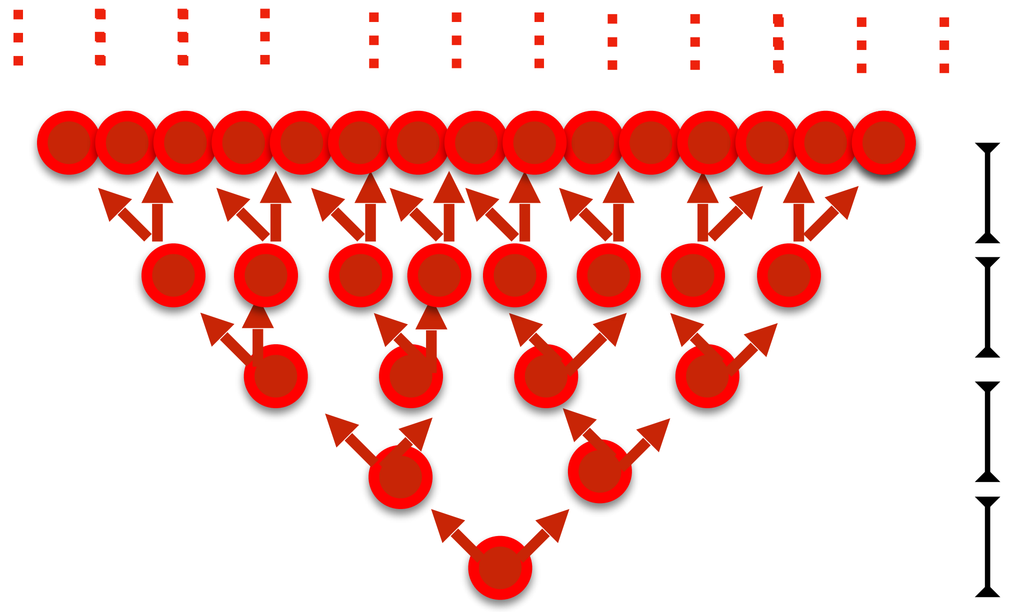

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Serial interval = 1 week

*r*: exponential growth rate, or how fast an epidemic grows at the population level

# Strength vs. speed in novel variants

Infection kernel: secondary infections from ind. infected $\tau$ time units ago

Euler-Lotka equation: $$1 = \int K(\tau) exp(-r\tau) d\tau$$

exponential growth rate

Park et al. MedRxiv

# Strength vs. speed in novel variants

reproductive number

If the infection kernel *K* does not change over time:

$$K(\tau) = Rg(\tau)$$

intrinsic generation interval distribution, integrates to 1

Park et al. MedRxiv

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generation interval distribution

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If generation interval is Gamma-distributed: $$R \approx (1 + \kappa r \bar{G})^{1/\kappa}$$

squared coefficient of variation

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Wildtype: $$R_{wt} \approx (1 + \kappa r_{wt} \bar{G}_{wt})^{1/\kappa}$$

Variant: $$R_{var} \approx (1 + \kappa r_{var} \bar{G}_{var})^{1/\kappa}$$

Relative strength: $$\rho = R_{var} / R_{wt}$$

Relative speed: $$\delta = r_{var} - r_{wt}$$

$$\rho = \left(\frac{1 + \kappa(r_{wt} + \delta)\bar{G}_{var}}{1 + \kappa_{wt}\bar{G}_{wt}}\right)^{1/\kappa}$$

Park et al. MedRxiv

# Formal demography and infectious disease

The latter affects the former, but also, vice versa.

Capturing details of transmission across (st)age can importantly shaped applied conclusions

Unpick growth rates (for new variants, to understand control) requires careful application of fundamental principles.

For all these reasons, we need models the encompass demography and transmissoin.

# References


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## Thank you


**C. Jessica E. Metcalf**
cmetcalf@princeton.edu
@CJEMetcalf


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https://eebcovid19.princeton.edu/