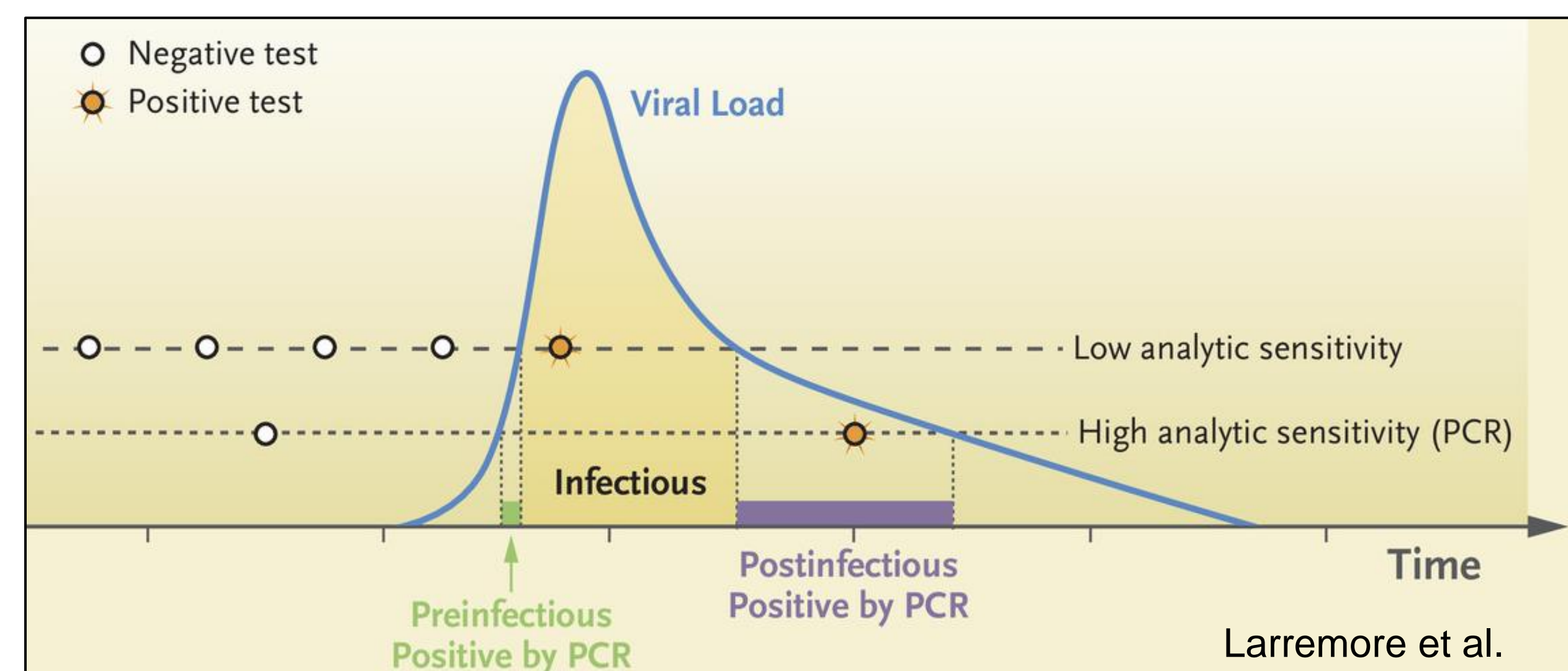


The effect of time-dependent infectiousness on epidemic dynamics

Nicholas W. Landry, Karen L. Stengel, University of Colorado Boulder

Background

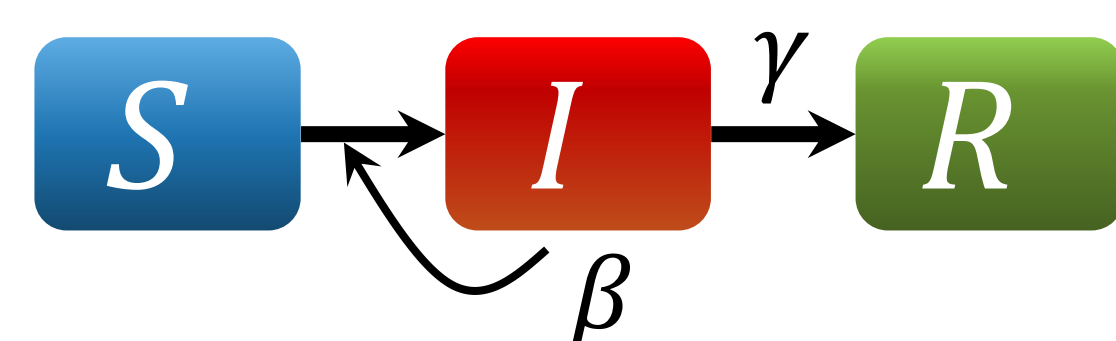
Infectiousness depends on viral load



- There is a **time-dependent rate of transmission** over the course of an illness, determined by your viral load
- Most epidemic simulations assume the transmission rate is constant

Model

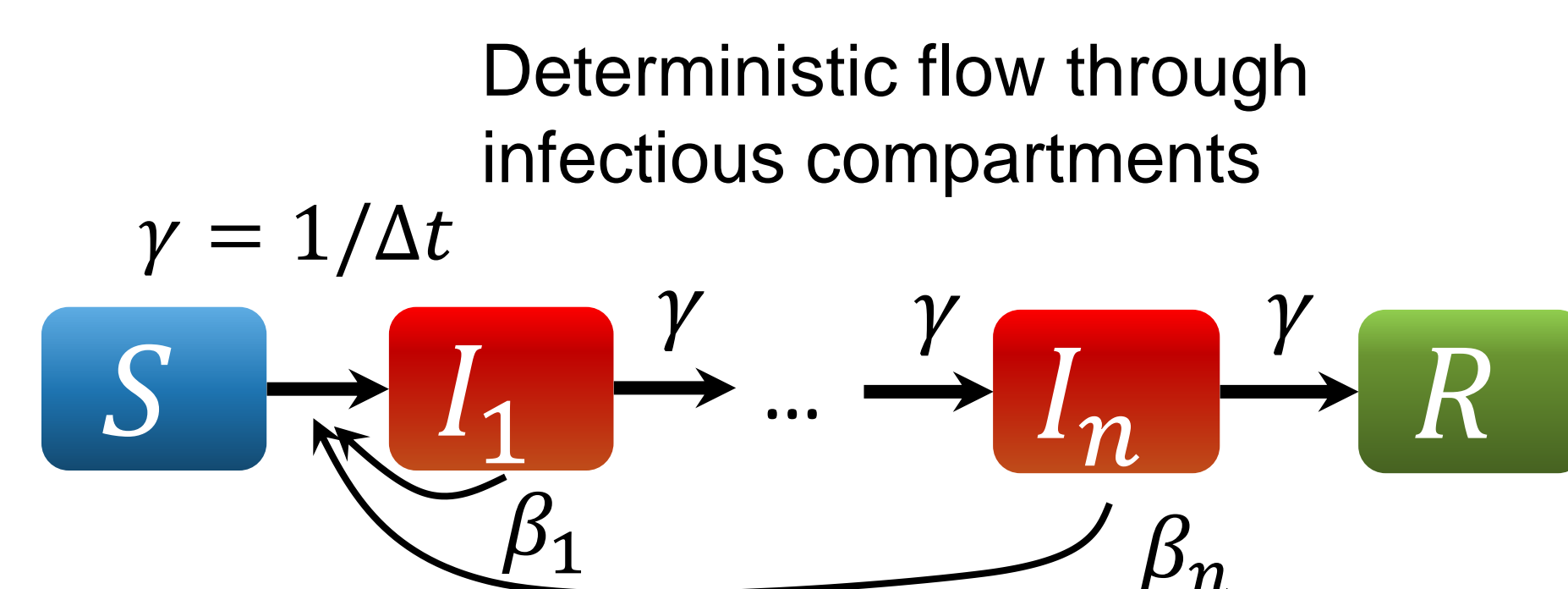
We start from the SIR model



Assume instead of a constant rate of infection, that $\beta_i(\tau)$ is the infection rate of node i that has been infected for a time τ

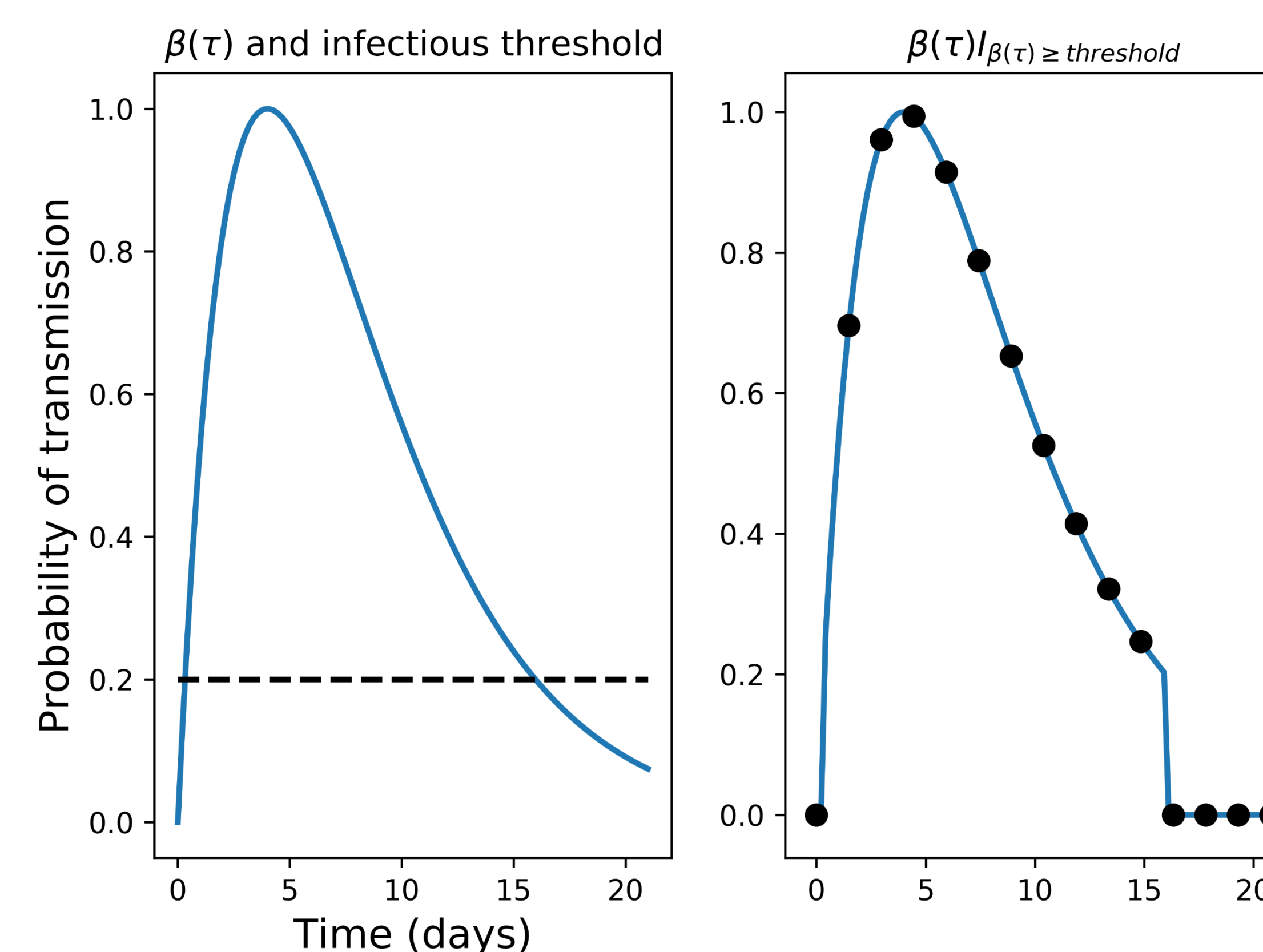
Assume that $\beta_j(\tau) = \beta(\tau), \forall j$

We divide the infected state into n discrete infectious states and denote them $\beta(\tau_i) = \beta_i$, where $\tau_i = i\Delta\tau$



Theory

An example of a viral load function (rescaled gamma distribution)



We can write the model as a mean-field system of ODEs for the fully-mixed case:

$$\frac{dS}{dt} = -\frac{S}{N} \sum_{i=1}^n \beta_i I_i$$

$$\frac{dI_1}{dt} = -\frac{I_1}{\Delta\tau} + \frac{S}{N} \sum_{i=1}^n \beta_i I_i$$

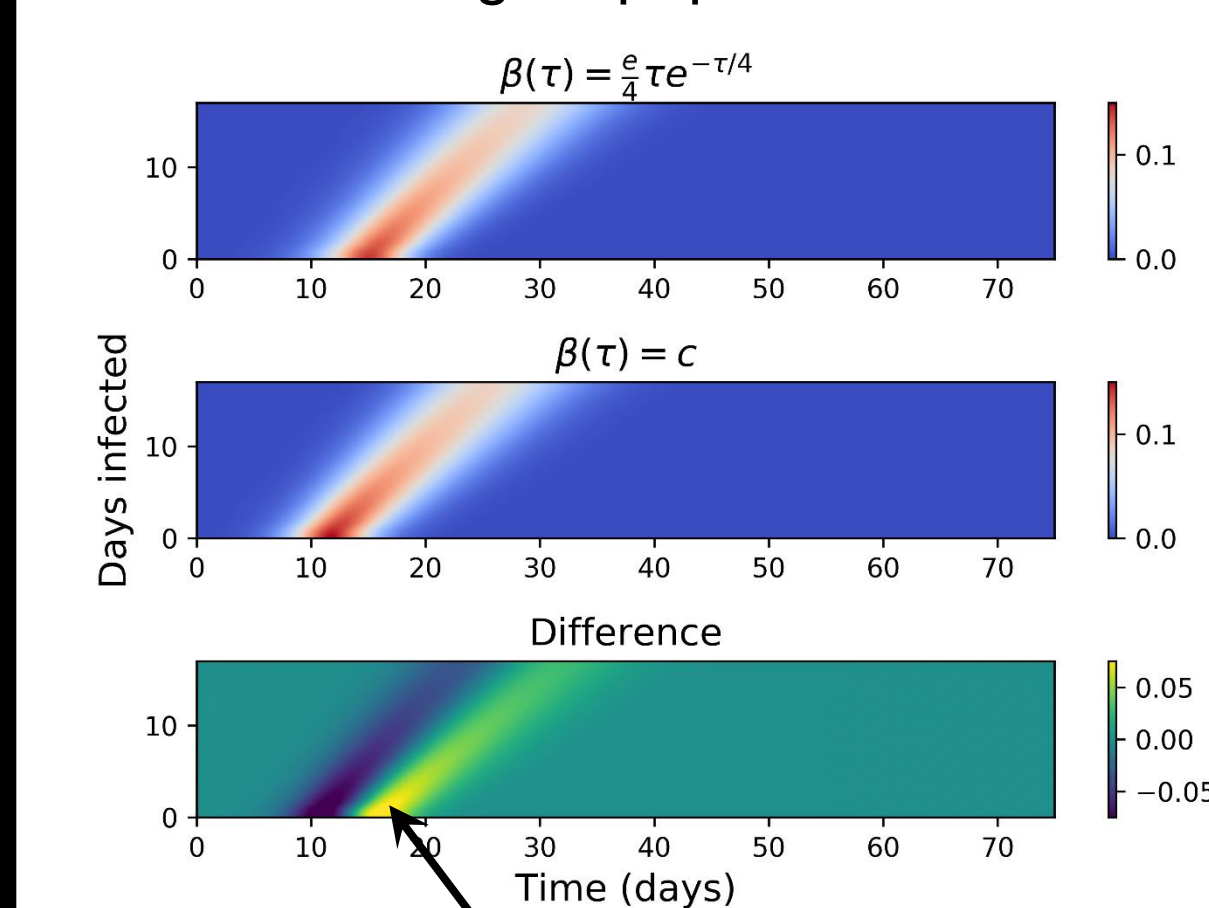
$$\frac{dI_i}{dt} = \frac{I_{i-1} - I_i}{\Delta\tau}, i = 2 \dots n$$

$$\frac{dR}{dt} = \frac{I_n}{\Delta\tau}$$

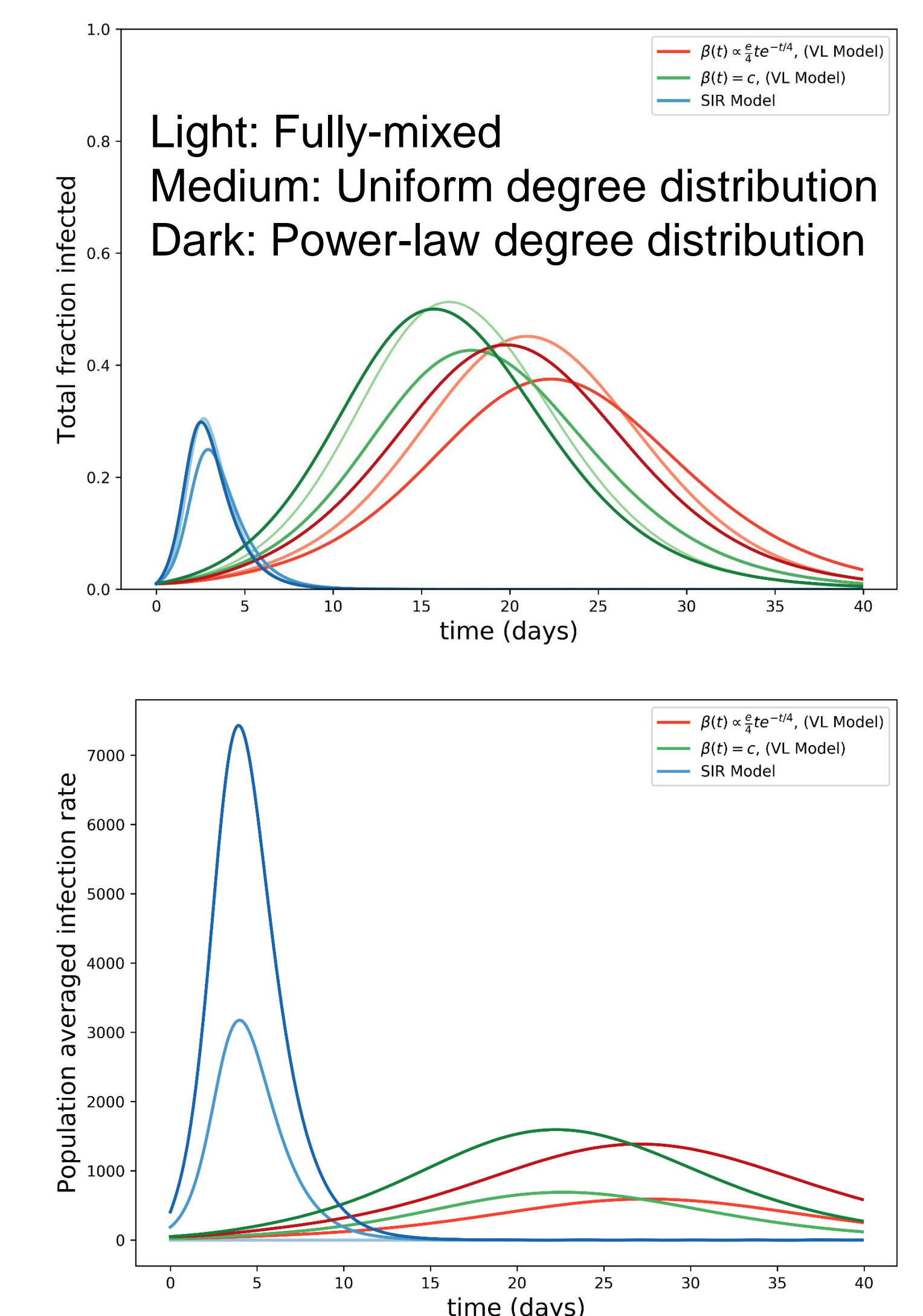
- Linearize as $x' = Ax$
- Express A as a sum of *infectious transmissions* and *non-infectious transitions*
- Use *Next Generation Matrix Theory* to derive the reproductive number
- As $\Delta\tau \rightarrow 0$, $R_0 = \int_{\tau_0}^{\tau_f} \beta(\tau) d\tau$ for the fully mixed case and $R_0 = \rho(P) \int_{\tau_0}^{\tau_f} \beta(\tau) d\tau$ for the category-based mixing case

Simulations

How an infection travels through a population



An infection rate function with an *exposure* period has delayed dynamics relative to a constant infection rate



Conclusions

- The reproductive number is only affected by the *exposure* of an individual and mixing effects and transmission effects are independent.
- Can write as the *transport equation* with boundary conditions capturing the infection.

References

- *Inferring high-resolution human mixing patterns for disease modeling* by Mistry et al.
- *The construction of next-generation matrices for compartmental epidemic models* by Diekmann et al.
- *Rethinking Covid-19 Test Sensitivity — A Strategy for Containment* by Mina et al.

Manuscript in preparation!