The analogy of the cohort-equations paradigm to the compartmental epidemic models

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1 Vision

1. 2 frameworks of van den Driessche and Watmough (2002), I call it compartment framework, and Champredon et al. (2018), I call it cohort framework, can be tied together and a mechanistic approach to go from one framework to another can be constructed.

2. Having the cohort framework enables one to study the strength-like and speed-like interventions. For example in our SIR model with testing and isolation, testing susciptables is a strength-like intervention and testing the infecteds' is a speed-like intervention. [**TODO:** *more context is required here.*]

2 Math foundation

Notation; we use I' for the cohort-framework of $dI/d\tau$, where τ is in the infection-time scale and $\dot{I}$ for the compartment-framework of dI/dt.

The matrix form of the cohort framework consists of the following 3 steps.

step 1 write the cohort Eq.

$$I' = -VI, \tag{1}$$

with the proper initial condition $I(0)$, where the n-by-n matrix V is the flow matrix of leaving infected compartments in van den Driessche and Watmough (2002).

step 2 finding the intrinsic infectiousness kernel by integrating the cohort Eq. and solving for its time evolution, thus the solution would be

$$I(\tau) = \exp(-V\tau)I(0). \tag{2}$$

The kernel will be

$$K(\tau) = FI(\tau), \tag{3}$$

where F is the matrix of new infections in the compartment framework. Note that the n-by-n matrix $\exp(-V\tau)$ is the probability of being infected and stay infectious at time τ, where $\exp(-V\tau) = \sum_{n=0}^{\infty} \tau^n(-V)^n/n!$.

step 3 Calculating R by integrating kernel $K(\tau)$.

Note that in the comartment framework, steps 2 and 3 are combined.

3 examples

Example 1, the simple SIR; The cohort analogy of a simple SIR compartmental model where $\dot{I} = \beta SI/N - \gamma I$. The cohort framework is via the cohort Eq. with the following steps step 1: write the cohort Eq. $I' = -\gamma I$ with the initial condition $I(0) = 1$,

step 2: finding the intrinsic infectiousness kernel by integrating the cohort Eq. and solving for its time evolution, thus $k(\tau) = \beta \exp(-\gamma\tau)$.

step 3: R will be the integration of the kernel. That is $R = \beta/\gamma$.

Example 2, the SIR model with testing; In the context of our SIR model with testing, $I^T = [I_u, I_n, I_p, I_c]$ where T is the transposed operator. And the solution is given by $I(\tau) = \exp(-V\tau)I(0)$ where $I(0) = [1, 0, 0, 0]$.

References

Champredon, D., Dushoff, J., and Earn, D. J. (2018). Equivalence of the erlang-distributed seir epidemic model and the renewal equation. *SIAM Journal on Applied Mathematics*, 78(6):3258–3278.

van den Driessche, P. and Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, 180(1-2):29–48.