

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

May 19, 2021

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 susceptibles 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.

$$\mathbf{I}' = -V\mathbf{I}, \quad (1)$$

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

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

The kernel will be

$$\mathbf{K}(\tau) = F\mathbf{I}(\tau), \quad (3)$$

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 .

step 3 Calculating \mathbf{R} by integrating kernel $\mathbf{K}(\tau)$. Note that \mathcal{R}_0 would be the non-negative element of \mathbf{R} .

Note that in the compartment framework (van den Driessche and Watmough, 2002), steps 2 and 3 are combined.

3 Examples

3.1 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*; \mathcal{R}_0 will be the integration of the kernel. That is $\mathcal{R}_0 = \beta/\gamma$.

3.2 Simple SEIR model

The simplest form of a SEIR model without vital rates is

$$\dot{S} = -\beta SI/N, \quad \dot{E} = \beta SI/N - \sigma E, \quad \dot{I} = \sigma E - \gamma I, \quad \dot{R} = \gamma I. \quad (4)$$

We know that $\mathcal{R}_0 = \beta/\gamma$ from next generation method where

$$F = \beta \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \sigma & 0 \\ -\sigma & \gamma \end{bmatrix}, \quad \text{thus} \quad V^{-1} = \frac{1}{\sigma\gamma} \begin{bmatrix} \gamma & 0 \\ \sigma & \sigma \end{bmatrix}. \quad (5)$$

In the context of the cohort framework we show that the same \mathcal{R}_0 can be calculated by following the three steps.

Step 1; The cohort equation with the initial condition (in matrix form) is

$$\mathbf{I}' = -V \mathbf{I}, \quad \text{where} \quad \mathbf{I}(\tau) = \begin{bmatrix} E(\tau) \\ I(\tau) \end{bmatrix}, \quad \mathbf{I}(0) = \begin{bmatrix} 1 \\ 0 \end{bmatrix}. \quad (6)$$

Solving for $I(\tau)$ by finding the eigenvalues and eigenvectors of the above linear system results in

$$\mathbf{I}(\tau) = \begin{bmatrix} E(\tau) \\ I(\tau) \end{bmatrix} = c_1 \exp(-\sigma\tau) \begin{bmatrix} \gamma/\sigma - 1 \\ 1 \end{bmatrix} - c_1 \exp(-\gamma\tau) \begin{bmatrix} 0 \\ 1 \end{bmatrix}, \quad (7)$$

where

$$c_1 = \frac{\sigma}{\gamma - \sigma}.$$

Step 2; The kernel is

$$\mathbf{K}(\tau) = F\mathbf{I}(\tau) = c_1 \exp(-\sigma\tau) \begin{bmatrix} \beta \\ 0 \end{bmatrix} - c_1 \exp(-\gamma\tau) \begin{bmatrix} \beta \\ 0 \end{bmatrix}. \quad (8)$$

Step 3; The basic reproduction number \mathcal{R}_0 is given by integrating the non-zero element of the kernel as follows.

$$\mathcal{R}_0 = \int_0^\infty \mathbf{K}_1(\tau) d\tau = \beta c_1(1/\sigma - 1/\gamma) = \beta/\gamma. \quad (9)$$

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.