

# 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  $\tau$  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.* Form 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  $\tau$ .

*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.