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

June 7, 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 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. Form the cohort Eq.

$$\mathbf{I}' = -V\mathbf{I}, \tag{1}$$

with the vector of initial condition $\mathbf{I}(0)$ where $\mathbf{I}_i(0)$ be the number of infected individuals initially in compartment i, and $I(\tau)$ is the number of these initially infected individuals remaining in the infected compartments after τ time units. Note that as van den Driessche and Watmough (2002) set their formulation, "the (i, j) entry of F is the rate at which infected individuals in compartment j produce new infections in compartment i". Matrix V is the flow matrix in which the (i, j) entry is the the rate of transfering infected individuals from compartment j into compartment i, with positive (negative) means transfering out (into) a compartment. The (j, k) entry of V^{-1} is the average length of time an infected individual introduced into compartment k spends in compartment j during its lifetime, assuming that the population remains near the DFE and barring reinfection. Note that V is a non-singular M-matrix and is, therefore, invertible and all of its eigenvalues have positive real parts (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

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

The kernel will be

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

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.

Step 3. Calculating the next-generation vector $\mathbf{G}$ is ([**Ali:** *feels odd here, help!* $\mathbf{G}$ *here is a vector with elements of the eigenvalues of the (van den Driessche and Watmough, 2002)'s next-generation matrix* FV^{-1}*. Also check Heesterbeek work what he calls this*])

$$\mathbf{G} = FV^{-1}\mathbf{I}(0) = \int_0^\infty \mathbf{K}(\tau)d\tau. \tag{4}$$

Note that $\mathcal{R}_0$ would be the dominant element of $\mathbf{G}$.

Note 1. The following notes/points are to be considered in moving from one framework to another, namely, cohort framework (Champredon et al., 2018) and comartmental framework (van den Driessche and Watmough, 2002);

1. In the compartment framework, steps 2 and 3 are combined.

2. If the initial condition $\mathbf{I}(0)$ of the cohort Eq. (2) (in the cohort framework) is chosen as the normalized principal eigenvector of the next-generation matrix FV^{-1} corresponding to $\mathcal{R}_0$ (in compartmental framework), the next generation vector $\mathbf{G}$ (4) would be

$$\mathbf{G} = FV^{-1}\mathbf{I}(0) = \mathcal{R}_0\mathbf{I}(0). \tag{5}$$

Thus, in this case inorder to collapse $\mathbf{G}$ to $\mathcal{R}_0$, when $\mathbf{I}(0)$ is the normalized initial distribution of infected individuals, i.e., $\|\mathbf{I}(0)\| = 1$, it follows that $\mathbf{I}(0)^t \cdot \mathbf{G} = \mathcal{R}_0$, where the row vector $\mathbf{I}(0)^t$ is the transpose of $\mathbf{I}(0)$.

3 Examples

Example 1. Simple SIR model; The model is

$$\dot{S} = -\beta\, S\, I/N, \quad \dot{I} = \beta\, S\, I/N - \gamma\, I, \quad \dot{R} = \gamma\, I. \tag{6}$$

Where $F = \beta$ and $V = \gamma$, thus $V^{-1} = 1/\gamma$. The next-generation matrix $G = FV^{-1} = \beta/\gamma$ which results in $\mathcal{R}_0 = \beta/\gamma$ in the compartment framework. The cohort analogy of the simple SIR model is via the cohort Eq. with the following steps.

Step 1; The cohort Eq. $I' = -\gamma I$ with the initial condition $I(0) = 1$. Thus, the solution is $I(\tau) = \exp(-\gamma\tau)$.

Step 2; The intrinsic infectiousness kernel is given by integrating the cohort Eq. and solving for its time evolution. Thus, $K(\tau) = F\, I(\tau) = \beta \exp(-\gamma\tau)$.

Step 3; The next-generation vector would be

$$G = FV^{-1} = \int_0^\infty K(\tau)\, d\tau = \beta/\gamma.$$

This gives $\mathcal{R}_0 = \beta/\gamma$.

Example 2. Simple SEIR model; The simplest form of a SEIR model without vital rates is

$$\dot{S} = -\beta\, S\, I/N, \quad \dot{E} = \beta\, S\, I/N - \sigma\, E, \quad \dot{I} = \sigma\, E - \gamma\, I, \quad \dot{R} = \gamma\, I. \tag{7}$$

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

$$F = \beta \begin{bmatrix} 0 & 1 \\ 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \sigma & 0 \\ -\sigma & \gamma \end{bmatrix}, \quad \text{thus} \quad V^{-1} = \frac{1}{\sigma\,\gamma} \begin{bmatrix} \gamma & 0 \\ \sigma & \sigma \end{bmatrix}. \tag{8}$$

Note that matrix F determines the rate of new infections and their source. Specifically, here $F_{12} = \beta$, that is the rate of new infections in compartment E is β and it is originated from compartment I. Also note that matrix V determines the flow 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

$$\mathbf{I}' = -V\,\mathbf{I}, \quad \text{where} \quad \mathbf{I}(\tau) = \begin{bmatrix} E(\tau) \\ I(\tau) \end{bmatrix}, \quad \mathbf{I}(0) = \begin{bmatrix} 1 \\ 0 \end{bmatrix}. \tag{9}$$

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

$$\mathbf{I}(\tau) = \begin{bmatrix} E(\tau) \\ I(\tau) \end{bmatrix} = \frac{\sigma}{\gamma - \sigma} \Big(\exp(-\sigma\,\tau) \begin{bmatrix} \gamma/\sigma - 1 \\ 1 \end{bmatrix} - \exp(-\gamma\,\tau) \begin{bmatrix} 0 \\ 1 \end{bmatrix} \Big). \tag{10}$$

Step 2; The kernel is

$$\mathbf{K}(\tau) = F\mathbf{I}(\tau) = \frac{\sigma}{\gamma - \sigma} \Big(\exp(-\sigma\,\tau) \begin{bmatrix} \beta \\ 0 \end{bmatrix} - \exp(-\gamma\,\tau) \begin{bmatrix} \beta \\ 0 \end{bmatrix} \Big). \tag{11}$$

Step 3; The next-generation vector is

$$\mathbf{G} = \int_0^\infty \mathbf{K}(\tau) d\tau = \beta\, \frac{\sigma}{\gamma - \sigma} \Big(\begin{bmatrix} 1/\sigma - 1/\gamma \\ 0 \end{bmatrix} \Big) = \begin{bmatrix} \beta/\gamma \\ 0 \end{bmatrix}. \tag{12}$$

Note that, $\mathcal{R}_0 = \mathbf{I}(0)^t \cdot \mathbf{G} = \beta/\gamma$.

Example 3. SIR with testing and isolation; The model can be summarized in the form of following matrices.

$$F = \beta/N_0 \begin{bmatrix} S_{\mathrm{u}}^* \\ (1-\theta_{\mathrm{w}})S_{\mathrm{n}}^* \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} 1, & 1-\theta_{\mathrm{w}}, & 1-\theta_{\mathrm{w}}, & 1-\theta_{\mathrm{c}} \end{bmatrix}, \text{and} \tag{13}$$

$$V = \begin{bmatrix} \hat{F}_I + \gamma & -\omega & 0 & 0 \\ 0 & \omega+\gamma & 0 & 0 \\ -\hat{F}_I & 0 & \omega+\gamma & 0 \\ 0 & 0 & -\omega & \gamma \end{bmatrix}. \tag{14}$$

Let the test be perfectly sensative, that is $p_I = 1$.

Step 1; The cohort Eq. is

$$\mathbf{I}' = -V\,\mathbf{I}, \quad \text{where} \quad \mathbf{I}(\tau) = \begin{bmatrix} I_{\mathrm{u}}(\tau) \\ I_n(\tau) \\ I_p(\tau) \\ I_c(\tau) \end{bmatrix}, \quad \mathbf{I}(0) = \begin{bmatrix} \frac{S_{\mathrm{u}}^*}{(1-\theta_{\mathrm{w}})S_{\mathrm{n}}^*} \\ 1 \\ 0 \\ 0 \end{bmatrix}. \tag{15}$$

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

$$\mathbf{I}(\tau) = \begin{bmatrix} \frac{F_I-\omega}{\omega}\mathrm{e}^{-(F_I+\gamma)\tau} & 0 & 0 & \frac{-1}{F_I}\mathrm{e}^{-(\omega+\gamma)\tau} \\ 0 & 0 & 0 & \frac{F_I-\omega}{-F_I\omega}\mathrm{e}^{-(\omega+\gamma)\tau} \\ \frac{-F_I}{\omega}\mathrm{e}^{-(F_I+\gamma)\tau} & 0 & -\mathrm{e}^{-(\omega+\gamma)\tau} & (\frac{1}{\omega}-\tau)\mathrm{e}^{-(\omega+\gamma)\tau} \\ \mathrm{e}^{-(F_I+\gamma)\tau} & \mathrm{e}^{-\gamma\tau} & \mathrm{e}^{-(\omega+\gamma)\tau} & \tau\mathrm{e}^{-(\omega+\gamma)\tau} \end{bmatrix} \mathbf{c}, \tag{16}$$

where

$$\mathbf{c} = \begin{bmatrix} -\frac{\omega\,((-\omega\,\theta_w+F_I)S_{\mathrm{u}}+\omega\,\theta_w-\omega)}{(F_I-\omega)^2(-1+\theta_w)S_{\mathrm{n}}} \\ \frac{-S_{\mathrm{u}}\,\theta_w-1+\theta_w}{(-1+\theta_w)S_{\mathrm{n}}} \\ -\frac{F_I\,((-\omega-F_I\,\theta_w+2\,\omega\,\theta_w)S_{\mathrm{u}}-F_I+F_I\,\theta_w+2\,\omega-2\,\omega\,\theta_w)}{(F_I-\omega)^2(-1+\theta_w)S_{\mathrm{n}}} \\ -\frac{F_I\,\omega}{F_I-\omega} \end{bmatrix}. \tag{17}$$

Step 2; The kernel is

$$\mathbf{K}(\tau) = F\mathbf{I}(\tau) \tag{18}$$

Step 3; The next-generation vector is $\mathbf{G}$ as follows.

$$\mathbf{G} = \int_0^\infty \mathbf{K}(\tau)d\tau \tag{19}$$

$$= \mathcal{R}_0\,\mathbf{I}(0), \tag{20}$$

where $\mathcal{R}_0$ is calculated in the previous work.

4 Ideas-Unknowns

- Collapsing the vectorized kernek $\mathbf{K}(\tau)$ into a scalar function of time.

- We have 3 cases; (i) the general case where each box in $\mathbf{I}$ been pulled into others boxes of $\mathbf{I}$ (ii) simple case where we have 1 group eg. linear chain (iii) intermediate case where we have more than 1 entry point into $\mathbf{I}$ but mediated through a unitary FoI like SIR with testing.

- SIR with testing;

- Linear Algebra refreshing: `https://see.stanford.edu/materials/lsoeldsee263/11-eig.pdf`

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.