

1 The model

The model schematic for SEIR epidemiology is shown in Figure 1 [1]. Based on this schematic, the basic population compartment evolution equations for each n age classes are [2]:

$$\frac{dS_i}{dT} = \Lambda N_i - \beta S_i \sum_{j=1}^n C_{ij} \frac{I_j^s}{N_j} - \alpha \beta S_i \sum_{j=1}^n C_{ij} \frac{I_j^a}{N_j} - \mu_i^n S_i, \quad (1)$$

$$\frac{dE_i}{dT} = \beta S_i \sum_{j=1}^n C_{ij} \frac{I_j^s}{N_j} + \alpha \beta S_i \sum_{j=1}^n C_{ij} \frac{I_j^a}{N_j} - \kappa_i E_i - \mu_i^n E_i, \quad (2)$$

$$\frac{dI_i^s}{dT} = \rho_i \kappa_i E_i - \gamma_i I_i^s - \mu_i^d I_i^s, \quad (3)$$

$$\frac{dI_i^a}{dT} = (1 - \rho_i) \kappa_i E_i - \gamma_i I_i^a - \mu_i^d I_i^a, \quad (4)$$

$$\frac{dR_i}{dT} = \gamma_i I_i^s + \gamma_i I_i^a - \mu_i^n R_i. \quad (5)$$

Here, Λ is the birth rate in the population and μ_i^n and μ_i^d are the age-classified mortality rate in the normal and infectious population fractions respectively. All other symbols are explained in Figure 1. Finally, the net population dynamics is given by the equation

$$\frac{dN_i}{dT} = \Lambda N_i - \mu_i^n (S_i + E_i + R_i) - \mu_i^d (I_i^s + I_i^a). \quad (6)$$

The effects of lockdown for a finite period can be parameterized by weighting the contact matrix coefficients with a box-function $b(t)$: $C_{ij}^{\text{lockdown}} = b(t) C_{ij}^{\text{normal}}$ [3].

The contact matrix idea provides a mathematical framework to characterize the rate of random interactions between different demographic groups in the population [4, 5]. The specific formulation used here assumes interactions between individuals from demographic groups i and j within a population to be a homogeneous Poisson process with rate parameter C_{ij} [2]. The data for contact matrices was obtained from the supplementary material of [5]. The advantage of the contact matrix formulation is that diverse responses of different α demographic groups in the population to mitigation efforts can be parameterized through the weight matrices W_{ij}^α [4, 5].

2 Calculating R_0

One question of importance in these models is the estimation of R_0 . For such structured models, the only way to calculate these is through the construction of the next generation matrix [6]. Following the convention in [6], I construct the ‘Transmission matrix’ T and the ‘Transition matrix’ Σ for the age structured model in the case where the disease parameters $\alpha, \beta, \rho, \gamma$, and κ are all age-structured into column vectors. The infective subset for n age classes is a $3n$ long vector $\mathbf{x} = [E_1, E_2, \dots, E_n, I_1^s, I_2^s, \dots, I_n^s, I_1^a, I_2^a, \dots, I_n^a]$. The definition of T and Σ are derived from a linearization of the system of ODEs about the ‘disease free equilibrium’ (DFE) state $\mathbf{x} = [N_1, N_2, \dots, N_n, 0, \dots, 0]$ as follows:

$$\dot{\mathbf{x}} = (T + \Sigma)\mathbf{x}, \quad (7)$$

where both T and Σ are $3n \times 3n$ matrices. For the age-structured SEIR model, transmission implies those cases which are being introduced fresh from S to any of the three infected compartments (see [6] for a formal definition). Therefore, in our case:

$$T = \begin{pmatrix} \mathbf{0}_n & \beta C_{ij} \frac{N_i}{N_j} & \alpha \beta C_{ij} \frac{N_i}{N_j} \\ \mathbf{0}_n & \mathbf{0}_n & \mathbf{0}_n \\ \mathbf{0}_n & \mathbf{0}_n & \mathbf{0}_n \end{pmatrix}, \quad (8)$$

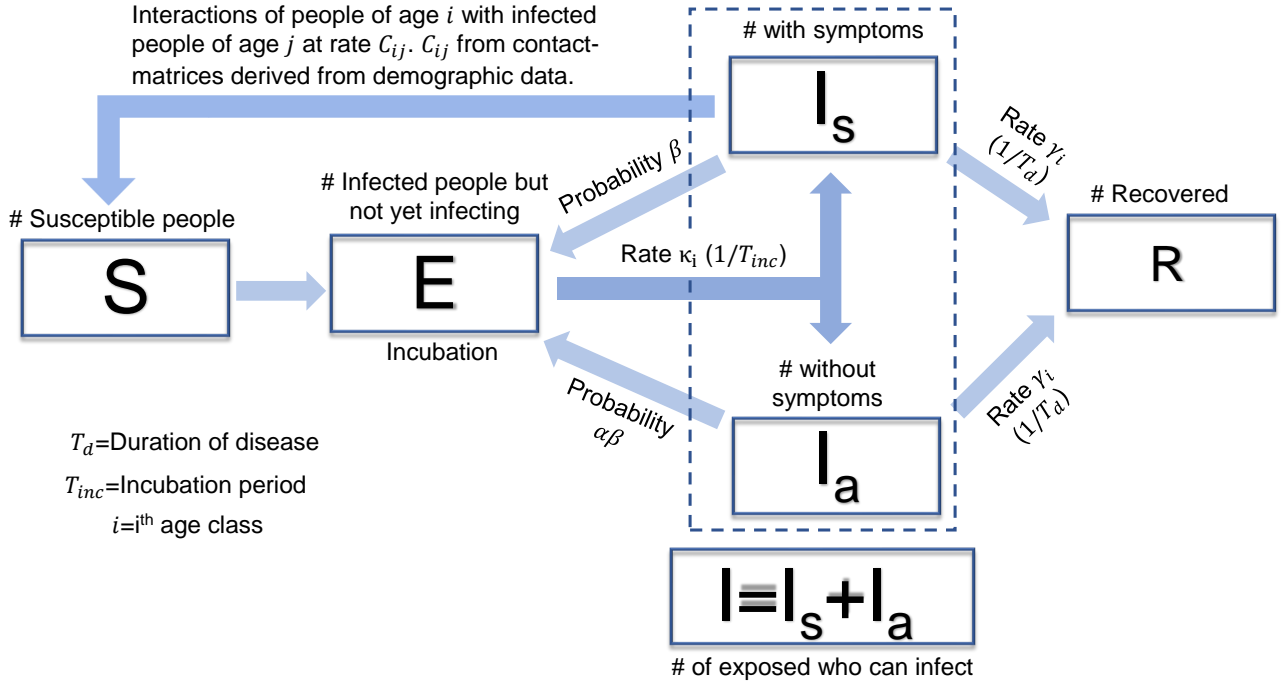


Figure 1: The age classified SEIR model. The model divides the population into 4 compartments: people susceptible to infection (S), people infected but not yet infecting (exposed, E), people who are now infecting (I) (further subdivided into symptomatic, I_s , and asymptomatic, I_a , compartments) and people who have recovered (R). The probabilities of infection acquired from symptomatic individuals, β , and asymptomatic individuals, $\alpha\beta$, are considered properties of the virus. The probability that an exposed person becomes symptomatic, ρ_i (or remains asymptomatic with probability $1 - \rho_i$) is considered age-dependent. The rate of interaction between S and I is defined by contact-matrices which provide the mean Poisson rates of age-group i to age-group j interaction. The general contact-matrix C_{ij} is further divided into interactions at school, home, work and other locations – $C_{ij} = W_{ij}^s C_{ij}^s + W_{ij}^w C_{ij}^w + W_{ij}^h C_{ij}^h + W_{ij}^o C_{ij}^o$ where the prefactor matrices W^α strictly diagonal weight matrices due to mitigation policies like school closure and social distancing in the α environment.

where each block in T is an $n \times n$ matrix. The transitions are defined when populations in one of the infective compartment transition to another infective compartment (again, see [6] for a formal definition). Therefore, for the present case, Σ is:

$$\Sigma = \begin{pmatrix} -\mathbf{diag}(\kappa_i + \mu_i) & \mathbf{0}_n & \mathbf{0}_n \\ -\mathbf{diag}(\rho_i \kappa_i) & -\mathbf{diag}(\gamma_i + \mu_i) & \mathbf{0}_n \\ -\mathbf{diag}\{(1 - \rho_i) \kappa_i\} & \mathbf{0}_n & -\mathbf{diag}(\gamma_i + \mu_i) \end{pmatrix}, \quad (9)$$

where $\mathbf{diag}(v)$ for a vector v_i implies a diagonal matrix of rank equal to the vector's dimension with diagonal entries equal to the components v_i . The R_0 value for this model is then (Section 3.2 in [6]):

$$R_0 = \rho(-T\Sigma^{-1}), \quad (10)$$

where $\rho(A)$ denotes the spectral norm of the matrix A .

References

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