

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].

References

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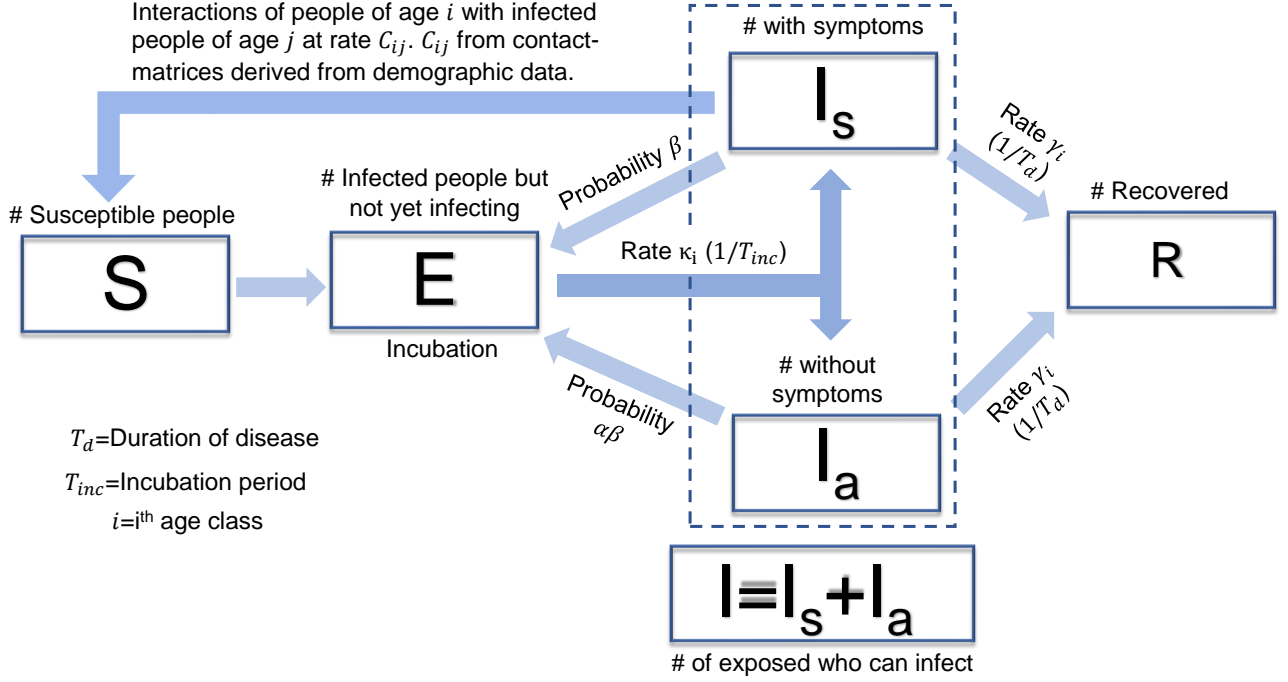


Figure 1: The age classified SEIR model. The model divides the population into 4 compartments: people susceptible to infection (S), people infected but not yet infecting (exposed, E), people who are now infecting (I) (further subdivided into symptomatic, I_s , and asymptomatic, I_a , compartments) and 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.