# Basic SEIR

SEIR

The SEIR model is a compartmental model commonly used in epidemiology to understand the spread of infectious diseases within a population. The acronym SEIR stands for Susceptible, Exposed, Infectious, and Recovered. Each of these compartments represents a different stage of the disease transmission. The model is an extension of the simpler SIR (Susceptible-Infectious-Recovered) model by adding an "Exposed" compartment to account for the latency period between exposure to the virus and the onset of infectiousness.

Model Description
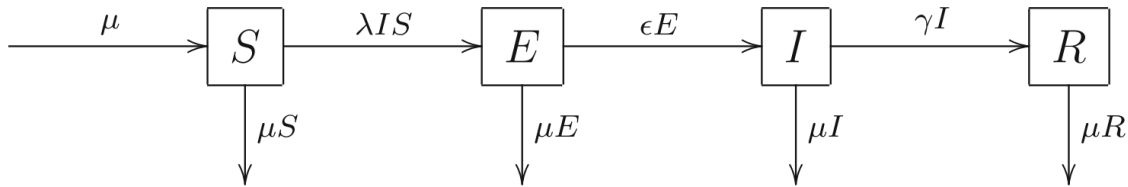
Meaning of Parameters in the model:

$$\text{nature birth/death rate } = 1/\mu$$
$$\text{contact rate} = \lambda$$
$$\text{mean latency period} = 1/\epsilon$$
$$\text{mean infectious period} = 1/\gamma$$

SEIR system(ordinary differential equation):

$$\frac{dS}{dt} = S' = \mu - \lambda IS - \mu S$$

$$\frac{dE}{dt} = E' = \lambda IS - (\epsilon + \mu)E$$

$$\frac{dI}{dt} = I' = \epsilon E - (\gamma + \mu)I$$

$$\frac{dR}{dt} = R' = \gamma I - \mu R$$

The S,E,I, and R denote the subpopulations that are susceptible, exposed, infectious, and recovered, respectively. They are functions of t and we assume the conservation of the total population: $S(t) + E(t) + I(t) + R(t) = 1$.

Therefore, substitute $R(t) = 1 - S(t) - E(t) - I(t)$ into the system, then we get:

$$S' = \mu - \lambda IS - \mu S$$
$$E' = \lambda IS - (\epsilon + \mu)E$$
$$I' = \epsilon E - (\gamma + \mu)I$$

The natural feasible region of system is: $\mathbb{R}^3_+ = \{(S, E, I) \mid S \geq 0, E \geq 0, I \geq 0\}$. The initial conditions in the bounded region we consider: $\Gamma = \{(S, E, I) \in \mathbb{R}^3_+ \mid S + E + I \leq 1\}$.

Equilibria

The Equilibrium point will satisfy:

$$\mu - \lambda IS - \mu S = 0$$
$$\lambda IS - (\epsilon + \mu)E = 0$$
$$\epsilon E - (\gamma + \mu)I = 0$$

Solving the equation set, one solution, the disease-free equilibrium $P_0 = (1, 0, 0)$ always exits. Another solution, endemic equilibrium $P^* = (S^*, E^*, I^*)$ satisfies:

$$S^* = \frac{(\epsilon + \mu)(\gamma + \mu)}{\lambda \epsilon}$$
$$E^* = \frac{\gamma + \mu}{\epsilon} I^*$$
$$I^* = \frac{\mu(1 - S^*)}{\lambda S^*}$$

The equilibrium P^* doesn't always belong to the feasible region Γ and its interior $\overset{\circ}{\Gamma}$. The relations: $0 \leq S^*, E^*, I^* \leq 1$ have to be satisfied:

$$P^* \in \overset{\circ}{\Gamma} \iff S^* < 1 \iff \frac{\lambda \epsilon}{(\epsilon + \mu)(\gamma + \mu)} > 1$$

Therefore, we can use the $\mathcal{R}_0$, which is basic reproduction number of model to determine the Equilibrium:

$$\mathcal{R}_0 = \frac{\lambda \epsilon}{(\epsilon + \mu)(\gamma + \mu)}$$

If $\mathcal{R}_0 \leq 1$, then system has only the disease-free equilibrium $P_0 = (1, 0, 0)$ in Γ.

If $\mathcal{R}_0 > 1$, then system has two equilibrium: the disease-free equilibrium P_0 and a unique endemic equilibrium $P^* = (S^*, E^*, I^*)$.

Local Stability Analysis

Consider the Jacobian matrix of system at $P_0 = (1, 0, 0)$ is

$$J(P_0) = \begin{bmatrix} -\mu & 0 & -\lambda \\ 0 & -\epsilon - \mu & \lambda \\ 0 & \epsilon & -\gamma - \mu \end{bmatrix}$$

The characteristic equation $\det(pI_{3\times3} - J(P_0)) = 0$ is a cubic equation:

$$(p + \mu)\left[p^2 + (\epsilon + \gamma + 2\mu)p + (\epsilon + \mu)(\gamma + \mu) - \lambda\epsilon\right] = 0$$

Therefore, the three eigenvalues satisfy:

$$p_1 = -\mu < 0$$
$$p_2 + p_3 = -(\epsilon + \gamma + 2\mu) < 0$$
$$p_2 p_3 = (\epsilon + \mu)(\gamma + \mu) - \lambda\epsilon) = (\epsilon + \mu)(\gamma + \mu)(1 - \mathcal{R}_0)$$

Through the Stability Analysis by Linearization, we can get that P_0 is asymptotically stable.

For the condition: $\mathcal{R}_0 > 1$ so that $P^* \in \overset{\circ}{\Gamma}$. The Jacobian matrix at P^* is

$$J(P^*) = \begin{bmatrix} -\lambda I^* - \mu & 0 & -\lambda S^* \\ \lambda I^* & -\epsilon - \mu & \lambda S^* \\ 0 & \epsilon & -\gamma - \mu \end{bmatrix}$$

Using the Routh–Hurwitz conditions, P^* is asymptotically stable.

Therefore, the conclusion is that:

If $\mathcal{R}_0 < 1$, then the disease-free equilibrium $P_0 = (1, 0, 0)$ is locally asymptotically stable in Γ.

If $\mathcal{R}_0 > 1$, then the disease-free equilibrium P_0 becomes unstable and the endemic equilibrium P^* is asymptotically stable.

The Global Stability

The disease-free equilibrium $P_0 = (1, 0, 0)$ of the system is globally asymptotically stable in Γ if $\mathcal{R}_0 \leq 1$. (Lyapunov function)

Suppose that $\mathcal{R}_0 > 1$. Then the unique endemic equilibrium P^* is globally asymptotically stable in the interior of Γ.

Examples

From the analysis, the key point of the stability and equilibrium of the basic SEIR model is basic reproduction number $\mathcal{R}_0$:

$$\mathcal{R}_0 = \frac{\lambda\epsilon}{(\epsilon + \mu)(\gamma + \mu)}$$

We fix these parameters: $\mu = 1/365/76, \epsilon = 1/7, \gamma = 1/14$ because they are related with the type of disease and region. We get the estimated parameter $\lambda = 3 \times \gamma = 2.99773$, and calculate the $\mathcal{R}_0 = 2.99773 \geq 1$, which will be stable at endemic equilibrium $P^* = (S^*, E^*, I^*)$, whatever the values of the initial value.(should be in the interior feasible region Γ)

Then we give some examples to change the value of λ, you can also determine the value through several slide bars.

Examples 1

We choose the parameter: $\lambda = \gamma$, then $\mathcal{R}_0 = 0.9992434 \le 1$, system will be stable at disease-free equilibrium: $P_0 = (1, 0, 0)$.

Examples 2

We choose the parameter: $\lambda = 0.999$, then $\mathcal{R}_0 = 13.97542 \ge 1$, system will be stable at endemic equilibrium $P^* = (S^*, E^*, I^*)$.

Examples 3

We choose the parameter: $\lambda = 0.001$, then $\mathcal{R}_0 = 0.01398941 \le 1$, system will be stable at disease-free equilibrium $P_0 = (1, 0, 0)$.

Reference

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