

Infectious Disease Models

Srijit Bhattacharjee

SEIRD Model Equations

$$\frac{dS}{dt} = -\beta SI,$$

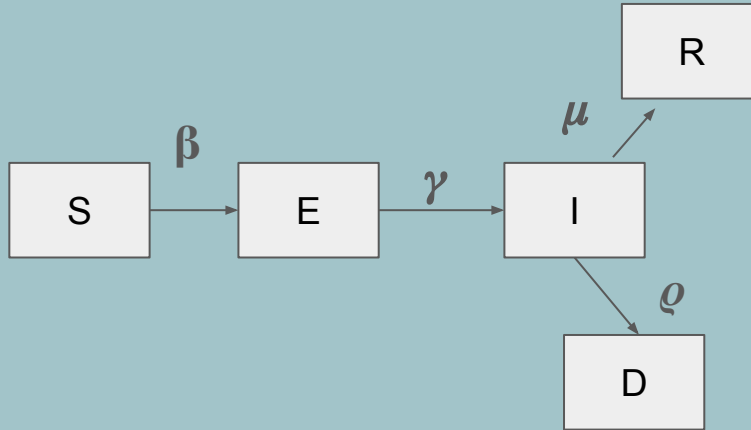
$$\frac{dE}{dt} = \beta SI - \gamma E,$$

$$\frac{dI}{dt} = \gamma E - \rho I - \mu I,$$

$$\frac{dR}{dt} = \mu I,$$

$$\frac{dD}{dt} = \rho I$$

SEIRD Model flow



Parameters and other Definitions

Infection Rate (transmission rate) (β): The average number of susceptible individuals infected by one infectious individual (per contact per unit of time).

Recovery Rate (μ): The infectious period is defined as the number of days an infected person remains infectious or can infect another person. The recovery rate is defined as the inverse of infectious period.

Incubation rate (γ): Incubation/latent period is the number of days after which a person develops symptoms after being exposed to an infected. Incubation rate is calculated by taking inverse of mean incubation period.

Mortality Rate (ρ): The mortality rate is calculated as number of individuals died on a given period of time divided by the total infected in that period.

Serial Interval (T) : The *generation time* (GT) use to be the sum of (average) incubation period and (average) infectious period. Serial Interval is the time lag between the onset of symptoms of an infector and the infectee. In few cases the GT is taken equal to the serial interval for estimating reproductive ratio.

Doubling Time: Doubling time is defined as time period in which the cumulative infection doubles. Sometimes used as a proxy for GT.

Simple estimation Method of R_0 from initial Epidemic Trajectory

Assume *prevalence* is the *cumulative incidence* at a given time.

Initial growth of epidemic follows an exponential curve:

$$I(t) = I(0) e^{rt}, \text{ r is the growth rate.}$$

r is estimated by regression analysis. $\text{Log } I(t) = \text{Log } I(0) + rt$; ($Y = a + bX$)

r is the slope of the regression line.

Relation between r and R_0

If T is the serial interval of the disease, then within T time an infected will on average infects R_0 individuals and 1 removed because within T time the primary infected is assumed to be removed.

Total change in prevalence within T is $R_0 - 1$

$$r = (R_0 - 1) / T$$

$$T_d = \ln 2 / r$$

$$R_0 = r \times T + 1$$

This estimation process doesn't include error or uncertainty in the data or in the method itself.