A probabilistic model of an epidemic

Mihir Arjunwadkar

Centre for Modeling and Simulation
Savitribai Phule Pune University

- Suppose that an epidemic sorts people in a population in 3 states: **S**usceptible, **I**nfected, **R**ecovered.
- The government needs predictions for the daily numbers

$$(S_t, I_t, R_t), t = 1, 2, \ldots$$

from the initial counts (S_0, I_0, R_0).

Modeling an epidemic as a probabilistic phenomenon

- Assume that nobody dies.

  So,
  $$N = S_t + I_t + R_t = \text{constant}$$
  independent of t.

Modeling an epidemic as a probabilistic phenomenon

- Assume that the population size N is large.

  So, we model the probability of being an

  - **S** at time t, $P_t(\mathbf{S}) \approx S_t/N$
  - **I** at time t, $P_t(\mathbf{I}) \approx I_t/N$
  - **R** at time t, $P_t(\mathbf{R}) \approx R_t/N$

Modeling an epidemic as a probabilistic phenomenon

- Assume that the population is well-mixed: Everybody interacts with everybody, everyday.

  Everyday

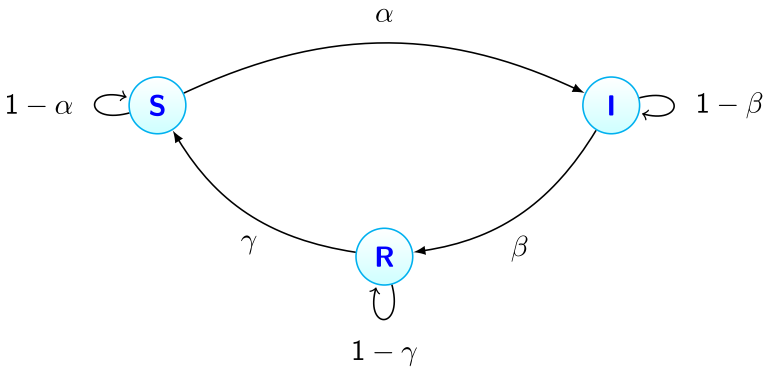
  - some of the **S** become **I** with probability α and some remain **S** with probability $1-\alpha$
  - some of the **I** become **R** with probability β and some remain **I** with probability $1-\beta$
  - some of the **R** become **S** with probability γ and some remain **R** with probability $1-\gamma$

  Interpretation

$$\begin{aligned}
\alpha &\equiv \text{probability of catching the infection} \\
\beta &\equiv \text{probability of recovering from the infection} \\
\gamma &\equiv \text{probability of losing immunity}
\end{aligned}$$

$0 \leq \alpha, \beta, \gamma \leq 1$ are the model parameters, independent of t.

Modeling an epidemic as a probabilistic phenomenon



$$
\begin{array}{c}
 \\ \mathbf{S} \\ \mathbf{I} \\ \mathbf{R}
\end{array}
\begin{array}{c}
\begin{array}{ccc} \quad\mathbf{S} \quad & \quad \mathbf{I} \quad & \quad \mathbf{R} \quad \end{array} \\
\begin{bmatrix} 1-\alpha & \alpha & 0 \\ 0 & 1-\beta & \beta \\ \gamma & 0 & 1-\gamma \end{bmatrix}.
\end{array}
$$

Modeling an epidemic as a probabilistic phenomenon

- Assume that tomorrow's numbers

  $$(S_{t+1}, I_{t+1}, R_{t+1})$$

  depend only on today's numbers

  $$(S_t, I_t, R_t)$$

  and not on the past

  $$(S_{t-1}, I_{t-1}, R_{t-1}), (S_{t-2}, I_{t-2}, R_{t-2}), \ldots, (S_0, I_0, R_0)$$

How state probabilities change

$$
\begin{array}{lcccccccc}
P_{t+1}(\mathbf{S}) & = & \gamma & \times & P_t(\mathbf{R}) & + & (1-\alpha) & \times & P_t(\mathbf{S}) \\
P_{t+1}(\mathbf{I}) & = & \alpha & \times & P_t(\mathbf{S}) & + & (1-\beta) & \times & P_t(\mathbf{I}) \\
P_{t+1}(\mathbf{R}) & = & \beta & \times & P_t(\mathbf{I}) & + & (1-\gamma) & \times & P_t(\mathbf{R})
\end{array}
$$

Try to interpret these equations in terms of proportions instead of probabilities ...

How state probabilities change

Looking at the structure of the equations, we can arrange them nicely into a matrix form:

$$(P_{t+1}(\mathbf{S})\ P_{t+1}(\mathbf{I})\ P_{t+1}(\mathbf{R})) = (P_t(\mathbf{S})\ P_t(\mathbf{I})\ P_t(\mathbf{R})) \begin{bmatrix} 1-\alpha & \alpha & 0 \\ 0 & 1-\beta & \beta \\ \gamma & 0 & 1-\gamma \end{bmatrix}$$

Observations

- Each row of the matrix sums to 1.
- $P_t(\mathbf{S}) + P_t(\mathbf{I}) + P_t(\mathbf{R}) = 1$ for each t.

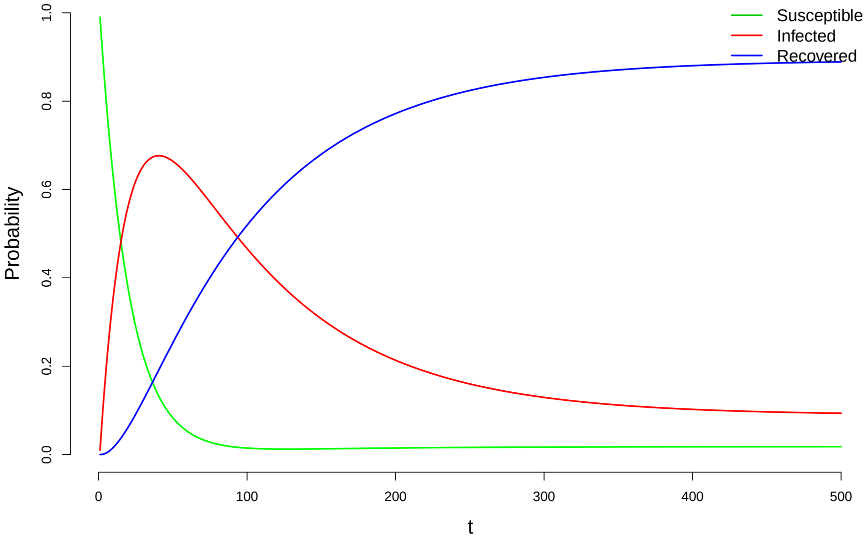
Try to

- interpret these observations
- generalize the above equation for $t+2, t+3, \ldots$

How state probabilities change

```
# model parameters
alpha <- 0.05  # prob per time step of catching infection
beta  <- 0.01  # prob per time step of recovering from infection
gamma <- 0.001 # prob per time step of losing immunity

# Markov / adjacency matrix
P <- matrix( 0, nrow = 3, ncol = 3,
                dimnames = list( c( 'S', 'I', 'R' ), c( 'S', 'I', 'R' ) ) )

P['S','I'] <-     alpha
P['S','S'] <- 1 - alpha

P['I','R'] <-     beta
P['I','I'] <- 1 - beta

P['R','S'] <-     gamma
P['R','R'] <- 1 - gamma

stopifnot( all( rowSums( P ) == 1 ) ) # each row should sum to 1

# total time steps
n <- 500

# matrix to store the evolution of the PMF over the state space
p <- matrix( 0, nrow = n, ncol = 3, dimnames = list( NULL, c('S','I','R') ) )

# initial probability distribution
p[1,] <- c( 0.99, 0.01, 0 )

# time evolution of the PMF over the state space
for ( i in 2:n ) p[i,] <- p[i-1,] %*% P
```

How state probabilities change



Probabilities $P_t(\mathbf{S}), P_t(\mathbf{I}), P_t(\mathbf{R})$ appear to stabilize to t-independent values; say (a, b, c). This implies

$$\begin{array}{ccccccccc} a & = & \gamma & \times & b & + & (1-\alpha) & \times & a \\ b & = & \alpha & \times & a & + & (1-\beta) & \times & b \\ c & = & \beta & \times & c & + & (1-\gamma) & \times & c \end{array}$$

Solving for (a, b, c), we get

$$\begin{aligned} a &= \frac{1}{\alpha}\left(\frac{1}{\gamma}+\frac{1}{\beta}+\frac{1}{\alpha}\right)^{-1} \\ b &= \frac{\alpha}{\beta}a \\ c &= \frac{\alpha}{\gamma}a \end{aligned}$$

Activities during lockdown

- Get COVID19 or other epidemic data from any source
- Guess the parameter values for this model by trial-and-error
- Make a prediction about when the infection will reach its peak
- Incorporate lockdown in the evolution
- Gauge how well the model describes / fits to real data
- Think about how the model may be made more realistic
- Compare this model with similar agent-based and ODE models