JAMA Guide to Statistics and Methods

Modeling Epidemics With Compartmental Models

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During epidemics, there is a critical need to understand both the likely number of infections and their time course to inform both public health and health care system responses. Approaches to forecasting the course of an epidemic vary and can include simulating the dynamics of disease transmission and recovery[1,2] or empirical fitting of data trends.[3] A common approach is to use epidemic compartmental models, such as the susceptible-infected-recovered (SIR) model.[1,2]

Why Is a SIR Model Used?

The SIR model aims to predict the number of individuals who are susceptible to infection, are actively infected, or have recovered from infection at any given time. This model was introduced in 1927, less than a decade after the 1918 influenza pandemic,[4] and its popularity may be due in part to its simplicity, which allows modelers to approximate disease behavior by estimating a small number of parameters.

Description of the SIR Model

In compartmental models, individuals within a closed population are separated into mutually exclusive groups, or *compartments*, based on their disease status. Each individual is considered to be in 1 compartment at a given time, but can move from one compartment to another based on the parameters of the model. The SIR model is one of the most basic compartmental models, named for its 3 compartments (susceptible, infected, and recovered). In this model, the assumed progression is for a susceptible individual to become infected through contact with another infected individual. Following a period as an infected individual, during which that person is assumed to be contagious, the individual advances to a noncontagious state, termed *recovery*, although that stage may include death or effective isolation.

In most modeled epidemics, all of a population begins in the susceptible compartment (**Figure**), which contains individuals who might become infected if exposed to the pathogen. This implies that no one has immunity to the disease at the beginning of the outbreak. The infected compartment is defined as individuals who have the ability to infect individuals in the susceptible compartment. As such, this compartment includes asymptomatic transmitters of the pathogen as well as hospitalized patients who require intensive levels of care. One simplification in the SIR model is that it does not consider the latent period following exposure, rather it assumes that newly infected individuals are immediately contagious.

The rate at which susceptible individuals become infected is dependent on the number of individuals in each of the susceptible and infected compartments. At the start of an outbreak, when there are few infected individuals, the disease spreads slowly. As more individuals become infected, they contribute to the spread and increase the rate of infection. An additional factor in calculating the rate of spread is the effective contact rate (β). This parameter accounts for the transmissibility of the disease as well as the mean number of contacts per individual. Community mitigation strategies, such as quarantining infected individuals, social distancing, and closing schools, reduce this value and therefore slow the spread. Although these interventions can alter the movement of individuals from the susceptible compartment to the infected compartment, the transition from the infected to the recovered compartment is solely dependent on the amount of time that an individual is contagious, captured in the rate of recovery (γ).

The term *recovered* in the SIR model can be misleading because the recovered compartment does not necessarily refer to an individual's clinical course of the disease, but instead represents individuals who are no longer contagious. Because compartmental models assume "closed" populations (without migration), individuals who have gained immunity to the disease and those who die of the disease are both included in this compartment.

The SIR model is defined by only 2 parameters: the effective contact rate (β), which affects the transition from the susceptible compartment to the infected compartment, and the rate of recovery (or mortality; γ), which affects the transition from the infected compartment to the recovered compartment. If the rate at which individuals become infected exceeds the rate at which infected individuals recover, there will be an accumulation of individuals in the infected compartment. The basic reproduction number R_0, the mean number of new infections caused by a single infected individual over the course of their illness, is the ratio between β and γ. A decrease in the effective contact rate β through community mitigation strategies decreases R_0, delaying and lowering the peak infection rate that occurs in the epidemic (ie, "flattening the curve"). However, to maintain the decrease in total infections, the decrease in R_0 generally must be sustained.

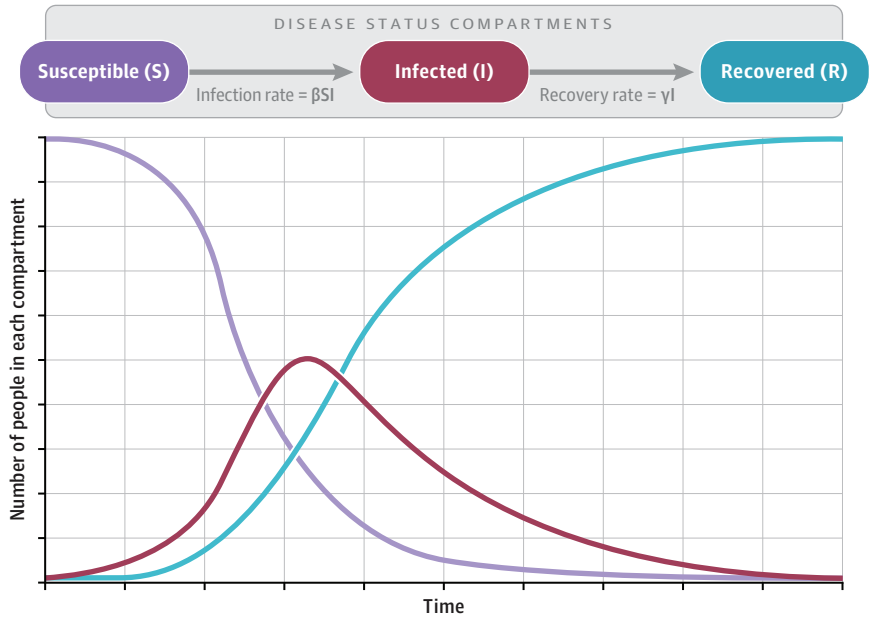
What Are the Limitations of SIR Models?

The simplicity of the SIR model makes it easy to compute, but also likely oversimplifies complex disease processes. The model does not, for example, incorporate the latent period between when an individual is exposed to a disease and when that individual becomes infected and contagious. In the context of coronavirus disease 2019 (COVID-19), this corresponds to the time it takes for severe acute respiratory syndrome coronavirus 2 to replicate in a newly infected individual and reach levels sufficient for transmission. Extensions of the SIR model, such as the SEIR model ("E" denotes exposed but not yet contagious), account for this parameter, but additional extensions of the model would be necessary to, for example, model the time-dependent introduction of community mitigation strategies.

The SIR model also makes several simplifying assumptions about the population. It assumes homogeneous mixing of the population, meaning that all individuals in the population are assumed to have an equal probability of coming in contact with one another. This does not reflect human social structures, in which the majority of contact occurs within limited networks. The SIR model also assumes a closed population with no migration, births, or deaths from causes other than the epidemic.

In addition, the parameters in a traditional SIR model do not allow for quantification of uncertainty in model parameters. The parameter inputs are point estimates, which are single values reflecting

Figure. Epidemic Trajectory Predicted by a Susceptible-Infected-Recovered Model



This model is based on the rates over time of persons moving from the susceptible compartment to the infected compartment to the recovered compartment. The rate of infection is equal to β times the number of individuals in the susceptible and infected compartments, and the rate of recovery is equal to γ times the number of individuals in the infected compartment.

the modeler's best guess. A common strategy in predicting the course of an epidemic is to calculate the SIR model over a few possible values for each parameter. The result is a range of future trajectories, but this strategy does not formally quantify the uncertainty in the predictions. More complex models use distributions for each parameter instead of a point estimate to characterize the probability of various future trajectories.[5] If the parameters are not known with any precision, these more complex models will demonstrate the uncertainty in projections. The actual effect of social distancing, for example, is often unknown. It is also possible, in more complex adaptations of the SIR compartmental framework, to incorporate observed data formally so that parameter values are estimated from the incoming data.[5]

How Should SIR Models Be Interpreted?

The SIR model is one of several types of models that can be used to model an infectious disease epidemic. During the COVID-19 pandemic, the results of SIR models have been compared with those of other modeling approaches.[6] For example, some groups have used network transmission models, which use information about connectivity between individuals and groups within a population to spatially model disease transmission.[7] Alternative models that are not based on the biologic mechanisms of disease have also been developed, such as the Institute for Health Metrics and Evaluation's COVID-19 pandemic model, which is based on fitting curves to empirically observed data.[3] When different modeling approaches produce qualitatively different results, it may be due to critical differences in underlying assumptions, making it imperative to determine which assumptions are more likely to be valid. Alternatively, differing results may indicate that the supporting data are simply insufficient to draw a reliable conclusion. Although no model can perfectly predict the future, a good model provides an approximation that is accurate enough to be useful for informing public policy.

ARTICLE INFORMATION

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Published Online: May 27, 2020. doi:10.1001/jama.2020.8420

Conflict of Interest Disclosures: None reported.

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