

The SIR dynamic model of infectious disease transmission from the viewpoint of a chemical engineer

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Abstract

The classical Susceptible-Infectious-Recovered (SIR) mathematical model of the dynamics of infectious disease transmission resembles a dynamic model of a batch reactor carrying out an auto-catalytic reaction with catalyst deactivation.

Mathematical models of the dynamics of infectious disease [1,2] are useful for forecasting epidemics, assessing intervention strategies, and inferring properties of diseases.

In compartmental epidemic models [3], each member of the population is categorized based on their disease status and (possibly) attributes. Because we can make reasonable assumptions about the *rates* at which people are infected and recover, a set of differential equations describe the flow of individuals to and from the compartments as the population mixes, the disease is spread/contracted, and infected individuals progress through the stages of the disease. In this article, we highlight the analogy between compartmental epidemic models and dynamic models of chemical reactions.

In the classic SIR model of an epidemic [2, 4, 5], each member of the population belongs to one of three compartments: Susceptible, Infectious, or Recovered. Fig. 1 depicts the flow of individuals through compartments, assuming that the disease confers immunity to re-infection after recovery.

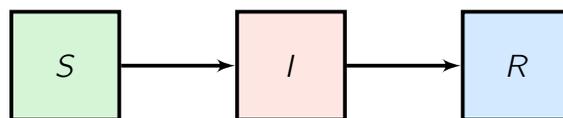


Figure 1: The SIR model. The boxes represent the set of Susceptible, Infectious, and Recovered individuals. The arrows represent flow from one compartment to another.

Susceptible folks can contract the disease if they come into contact with an infectious individual. Once infected, they move into the infectious compartment, assuming zero delay between infection

and the ability to transmit the disease. This is analogous to an irreversible auto-catalytic chemical reaction [6, 7] between a reactant S and catalyst I:



Infectious individuals eventually recover from the disease, entering the recovered compartment, and then cannot transmit the disease or contract it again. This is analogous to a reaction where the catalyst I irreversibly degrades or converts to a deactivated form R:



So, the SIR model of an epidemic is analogous to an auto-catalytic reaction with catalyst deactivation. An infectious individual (the catalyst I) (i) converts susceptibles (the reactant S) into more infectious individuals (more catalyst) and (ii) recovers (deactivates) with time.

Mathematically, the SIR model [4, 5] is equivalent to a dynamic model of a well-mixed batch reactor carrying out the two homogeneous reactions {1} and {2}. Let [S], [I], and [R] denote the fraction of the population in the susceptible, infectious, and recovered compartments, respectively. Invoking the law of mass action to model the rate at which susceptible and infectious individuals “react”, as in a bimolecular reaction, and positing that infectious individuals “decay” (recover) with first-order kinetics:

$$\frac{d[S]}{dt} = -\alpha[S][I] \quad (1)$$

$$\frac{d[I]}{dt} = \alpha[S][I] - \gamma[I] \quad (2)$$

$$\frac{d[R]}{dt} = \gamma[I]. \quad (3)$$

The inverse of the first-order rate constant $\gamma > 0$ is the average time period that an individual with the disease is infectious¹ [8]. The second-order rate constant $\alpha > 0$ encapsulates both the degree of mixing between susceptible and infectious individuals (frequency of contacts) and the contagiousness of the disease (the probability of transmission conditioned upon contact). While γ could be estimated independently from studies on the duration of infectiousness, α could be identified by fitting differential eqns. 1-3 to epidemic time series data (case counts) [9], much like identifying a reaction rate constant from concentration time series [10]. As in a closed batch reactor, the SIR model neglects immigration and emigration. By also assuming births and deaths (from causes other than the disease²) are negligible over the time scale of the epidemic, $[S] + [I] + [R] = 1$, seen by adding eqns. 1-3.

In the SIR model, what happens if we introduce a *single* infectious individual into a population of entirely susceptible individuals? This is akin to introducing our deactivating auto-catalyst into a batch of

¹The probabilistic implication of differential eqn. 2 for a single infected individual is that their time period of infectiousness is an exponentially distributed random variable with mean γ^{-1} [3].

²The SIR model accounts for disease-induced deaths by including them in the R category, assuming the deceased cannot transmit the disease.

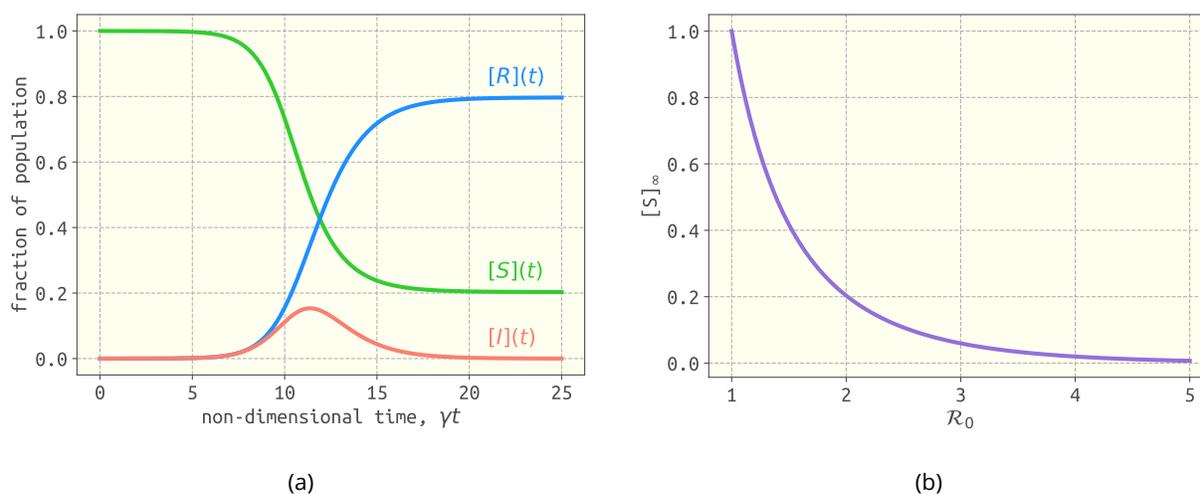


Figure 2: Numerical results for the SIR model. (a) Simulation of the SIR model in eqns. 1-3 for $\mathcal{R}_0 = 2.0$. Initial conditions: $[I](t = 0) = 1/100000$, $[S](t = 0) = 99999/100000$, and $[R](t = 0) = 0$. (b) The fraction of the population that remains susceptible (never infected) at the end of the SIR epidemic, $[S]_\infty$, as a function of the basic reproductive number \mathcal{R}_0 , computed via eqn. 4.

reactant. Intuitively, if the catalyst has a sufficiently high activity and/or remains active long enough, it will initiate a reaction (an epidemic). To the contrary, if the catalyst has a low activity and/or quickly deactivates, it will not initiate a reaction. The activity and longevity of the catalyst are embedded in α and γ , respectively. Indeed, the qualitative outcome of introducing an infectious individual into a population of susceptible folks depends on the (dimensionless) basic reproductive number $\mathcal{R}_0 := \alpha/\gamma$, a property of both the disease and the population. See Appendix. If $\mathcal{R}_0 < 1$, the infectious recover quickly, the disease is not easily transmitted, and/or the mixing of susceptibles and infectious is not vigorous. Consequently, an epidemic will not ensue. If $\mathcal{R}_0 > 1$, the infectious are infectious for a long period of time, the disease is easily transmitted, and/or the mixing of susceptibles and infectious is vigorous. Consequently, the single infectious individual propagates the disease and starts an epidemic. Fig. 2a shows a simulation of SIR model dynamics for $\mathcal{R}_0 = 2$. The solution to the non-linear, coupled set of differential eqns. 1-3 must be obtained numerically [8].

An SIR model epidemic (case $\mathcal{R}_0 > 1$) does not result in *every* susceptible member of the population being infected, even after an infinite amount of time (see Fig. 2a). As the disease propagates, the concentration of susceptible individuals decreases, causing the rate of disease propagation to diminish; in conjunction with the infectious folks recovering, this causes the epidemic to die out before the entire population is infected. From a chemical engineer's standpoint, the reaction begins to die out ($\frac{d[I]}{dt} < 0$) when the concentration of the reactant, $[S]$, becomes so low that any given catalyst molecule I is expected to deactivate before it can convert a reactant molecule S into another catalyst molecule to replace itself. i.e., an SIR epidemic dies out not because the population is depleted of susceptible folks, but rather because it is depleted of infectious folks [5]. The fraction of the reactant consumed (fraction of susceptibles infected) at the end of the reaction (epidemic) depends on both the activity and longevity of the catalyst (frequency of S-I contact, contagiousness of the disease,

time period of infectiousness; all of which are embedded in \mathcal{R}_0). By the end of the epidemic, the fraction of the population that will not have been infected, $[S]_\infty := \lim_{t \rightarrow \infty} [S](t)$, is related to the basic reproductive number (see Appendix):

$$\log[S]_\infty = ([S]_\infty - 1)\mathcal{R}_0. \quad (4)$$

Fig. 2b shows $[S]_\infty$ as a function of the basic reproductive number; as \mathcal{R}_0 increases from one, more of the population will be infected over the course of the epidemic.

The mechanism by which a vaccination program provides herd immunity to a population is mathematically similar to the time in Fig. 2a when the epidemic begins to die off: owing to a sufficiently small concentration of susceptible folks (achieved by vaccination or, as is the case in Fig. 2a, by a fraction of the population having been infected and now immune), the infectious recover faster than they spread the disease to the susceptible folks to replace themselves [11]. A simple way to model vaccination in the SIR model is to allow flow in Fig. 1 from the S category directly to the R category when a vaccine that confers complete immunity is administered to susceptible folks [9, 12, 13]. A chemical engineering view of herd immunity is the reduction of the concentration of the reactant S.

The SIR model is a very simple compartmental model, but it can be extended by (i) introducing additional compartments and (ii) allowing the parameters, e.g., γ and α to vary with time. As an example of (i), a Q compartment for Quarantined infectious individuals accounts for the reduced contacts of susceptible folks with infectious individuals that are quarantined [3]. As another example, age-structured compartmental models partition the S and I compartments into age groups to account for different mixing patterns, infectiousness, and susceptibility among different age groups [3]. As an example of (ii), social distancing initiatives can reduce the mixing of infectious and susceptible individuals, decreasing α [14].

Finally, compartmental models are not the only class of epidemic models. In the early stages of an epidemic and for small populations, it is important to account for the stochastic nature of human interaction and disease transmission. Stochastic epidemic models aim to describe the probabilistic distribution of outcomes [15, 16], e.g., the distribution of $[S]_\infty$. This is analogous to the need for stochastic models of chemical reaction dynamics when the reactants are not abundant, such as in a biological cell [17, 18]. Other models account for the spatial heterogeneity of the epidemic in a discrete [19, 20] or continuous [9] manner and allow for more detail in the interactions/mixing within a population [21, 22]. Modeling the spatial movement of susceptible and infectious individuals as a diffusive process results in reaction-diffusion equations, also familiar to chemical engineers [9].

In summary, an undergraduate student in chemical engineering is equipped to understand compartmental dynamic models of epidemics by making an analogy between disease transmission and chemical reactions.

the appendix

Consider introducing one infectious individual into a population comprised of $N - 1$ susceptible folks. The initial conditions here are:

$$[S](t = 0) = \frac{N - 1}{N} \quad (5)$$

$$[I](t = 0) = 1/N \quad (6)$$

$$[R](t = 0) = 0 \quad (7)$$

If N is large, $[S](t = 0) \approx 1$.

A: the basic reproductive number, \mathcal{R}_0 .

Qualitatively, if $\frac{d[I]}{dt}|_{t=0} > 0$, the disease will propagate, and an epidemic will ensue; if $\frac{d[I]}{dt}|_{t=0} < 0$, the infectious individual will recover before he/she transmits the disease to others [23]. According to eqn. 2 and our initial conditions, under the approximation of large N ,

$$\left. \frac{d[I]}{dt} \right|_{t=0} \approx \frac{1}{N}(\alpha - \gamma). \quad (8)$$

and it is apparent that the number of infectious individuals increases if $\alpha - \gamma > 0$ and decreases if $\alpha - \gamma < 0$. Consequently, the (dimensionless) basic reproductive number $\mathcal{R}_0 := \alpha/\gamma$ determines if an epidemic ensues upon introducing an infectious individual into the population of susceptible folks ($\mathcal{R}_0 > 1$) or not ($\mathcal{R}_0 < 1$).

B: the fraction of the population that were never infected after the epidemic ends, $[S]_\infty$.

After the epidemic ends (as $t \rightarrow \infty$), how many susceptibles will be left? Our derivation follows Ref. [24], but see Ref. [3] for a different derivation.

Adding differential eqns. 1 and 2:

$$\frac{d[S]}{dt} + \frac{d[I]}{dt} = -\gamma[I]. \quad (9)$$

Integrating this from $t = 0$ to $t \rightarrow \infty$:

$$\int_0^\infty \left(\frac{d[S]}{dt} + \frac{d[I]}{dt} \right) dt = - \int_0^\infty \gamma[I] dt. \quad (10)$$

The initial and final values of $[S]$ and $[I]$ appear from the left-hand side. The right-hand side can be written in terms of $[S]$ by solving differential eqn. 1 for $[I]$:

$$\lim_{t \rightarrow \infty} ([S](t) + [I](t)) - ([S](0) + [I](0)) = \frac{\gamma}{\alpha} \int_0^\infty \frac{1}{[S]} \frac{d[S]}{dt} dt. \quad (11)$$

$$= \frac{1}{\mathcal{R}_0} \log[S] \Big|_{t=0}^\infty \quad (12)$$

At the end of the epidemic, all infectious will have recovered, so $[I](t \rightarrow \infty) = 0$. Considering that all of the population was initially susceptible or infectious ($[S](0) + [I](0) = 1$) and approximating $[S](0) \approx 1$, we arrive at:

$$[S]_{\infty} - 1 = \frac{1}{\mathcal{R}_0} \log[S]_{\infty}, \quad (13)$$

which is equivalent to eqn. 4.

C: simulating the SIR model in Julia

Code in the Julia language to simulate the SIR model, via the DifferentialEquations.jl [25] package, is below.

```

R0 = 2.0    # basic reproductive number
N  = 100000 # population size

# right-hand side of the ODE, viewed as:
# du/dt = f = f(u, p, t)
# where u := [S, I, R]
function update_f!(f, u, p, t)
    # for clarity, unpack vector u
    s = u[1]
    i = u[2]
    r = u[3]
    # update f
    f[1] = -R0 * s * i
    f[2] =  R0 * s * i - i
    f[3] = i
end

# initial condition
u0 = [(N-1)/N; 1/N; 0.0]

# define the ODE problem
time_span = (0.0, 25.0)
prob = ODEProblem(update_f!, u0, time_span)

# numerically solve ODE
sol = solve(prob)

# obtain numerical approximation to the solution at e.g. t = 10
sol(10.0)

```

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