Dynamics of the "problem-place" model of disease outbreaks

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Abstract

Disease transmission is not homogeneous: in any outbreak a small number of infected individuals are responsible for a disproportionately large number of subsequent infections. This is certainly the case in COVID-19, in which 20% of infections may cause as many as 85% of secondary infections[citation?]. However, our mechanistic understanding of this phenomenon – known as super-spreading – is limited[citations?].

Here we introduce and analyze a simple model of an outbreak with super-spreading via "problem-place" locations: disease spreads homogeneously throughout the population at a low rate, but spreads rampantly at certain locations (bars, restaurants, churches, etc.) that individuals visit daily with their own fixed probabilities.

Compared to homogeneous dynamics, outbreaks are less likely to happen but are accelerated when they do occur; causing larger outbreaks in some cases, but paradoxically smaller and less sever outbreaks in moderately to highly infectious diseases.

- 1 Introduction
- 2 Model
- 3 Analysis

3.1 Disease Extinction

Let X be a random variable that represents the number of infections caused by a single infected individual with riskyness ρ_i before recovering, and let $j = 1, \ldots, N$ index the susceptible population so that ρ_j is the riskyness of individual i.

Then

$$P(X = 0) = (1 - \rho_i)[(1 - \beta_c)^N] + \rho_i [\prod_j (1 - (\beta_c + \beta_r \rho_j))]$$

By assumption riskyness for each individual is drawn independently from one distribution, so in expectation (over riskyness values) this is:

$$E[P(X=0)] = E[(1-\rho_i)[(1-\beta_c)^N] + \rho_i [\prod_j (1-(\beta_c+\beta_r\rho_j))]]$$

$$= (1-E[\rho_i])[(1-\beta_c)^N] + E[\rho_i][\prod_j (1-(\beta_c+\beta_rE[\rho_j]))]]$$

$$= (1-\bar{\rho})[(1-\beta_c)^N] + \bar{\rho}[(1-(\beta_c+\beta_r\bar{\rho}))^N]$$

$$= (1-\bar{\rho})B(\beta_c, N, 0) + \bar{\rho}B(\beta_c+\bar{\rho}\beta_r, N, 0)$$

Where B(a,b,x) is the Binomial probability mass at x with parameters a and b.

Similarly, E[P(X) = x] is given by

$$(1-\bar{\rho})B(\beta_c, N, x) + \bar{\rho}B(\beta_c + \bar{\rho}\beta_r, N, x)$$

So

$$G_X(s) = P(X = 0) + P(X = 1)s + P(X = 2)s^2 + \dots$$

$$= [\bar{\rho}B_1(0) + (1 - \bar{\rho})B_2(0)] + [\bar{\rho}B_1(1) + (1 - \bar{\rho})B_2(1)]s + [\bar{\rho}B_1(2) + (1 - \bar{\rho})B_2(2)]s^2 + \dots$$

$$= \bar{\rho}G_{B_1}(s) + (1 - \bar{\rho})G_{B_2}(s)$$

$$= \bar{\rho}[(1 - \bar{\rho}\beta_r)(1 - \beta_c) + (1 - (1 - \bar{\rho}\beta_r)(1 - \beta_c)s]^N + (1 - \bar{\rho})[(1 - \beta_c) + \beta_c s]^N$$

$$\tau = \bar{\rho}[(1 - \bar{\rho}\beta_r)(1 - \beta_c) + (1 - (1 - \bar{\rho}\beta_r)(1 - \beta_c)\tau]^N + (1 - \bar{\rho})[(1 - \beta_c) + \beta_c\tau]^N$$

3.2 Outbreak Dynamics

3.2.1 Some initial definitions/conveniences

Initial equations:

$$\frac{\partial S(\rho,t)}{\partial t} = -\beta_c S(\rho,t) \int_0^1 I(u,t) du - \beta_r S(\rho,t) \rho \int_0^1 I(u,t) u du$$
$$\frac{\partial I(\rho,t)}{\partial t} = \beta_c S(\rho,t) \int_0^1 I(u,t) du + \beta_r S(\rho,t) \rho \int_0^1 I(u,t) u du - \gamma I(p,t)$$

For convenience, we introduce the following shorthands for the "moments" of $I(\rho)$ and $S(\rho)$:

$$\bar{S} := \int_0^1 S(\rho) d\rho \qquad \qquad \bar{I} := \int_0^1 I(\rho) d\rho$$

$$\hat{S} := \int_0^1 S(\rho) \rho d\rho \qquad \qquad \hat{I} := \int_0^1 I(\rho) \rho d\rho$$

$$\hat{S} := \int_0^1 S(\rho) \rho^2 d\rho \qquad \qquad \hat{I} := \int_0^1 I(\rho) \rho^2 d\rho$$

$$\vdots \qquad \qquad \vdots$$

$$S := \int_0^1 S(\rho) \rho^n d\rho \qquad \qquad I := \int_0^1 I(\rho) \rho^n d\rho$$

Now we can more concicely write the initial equations:

$$\begin{split} \frac{\partial S(\rho,t)}{\partial t} &= -\beta_c S(\rho,t) \bar{I} - \beta_r S(\rho,t) \rho \hat{I} \\ \frac{\partial I(\rho,t)}{\partial t} &= \beta_c S(\rho,t) \bar{I} + \beta_r S(\rho,t) \rho \hat{I} - \gamma I(p,t) \end{split}$$

Finally, notice that $S(\rho)$ and $I(\rho)$ are defined over $\rho \in [0,1]$, and that these give the population at a given risk level. We can equivalently think of how risk is distributed over the S and I populations:

We introduce ρ_S and ρ_I : these are random variables drawn from the distributions of risk in the S and I populations, respectively. The means of these variables are:

$$\bar{\rho}_S = \frac{\int_0^1 S(\rho)\rho d\rho}{\int_0^1 S(\rho)d\rho} = \frac{\hat{S}}{\bar{S}}$$
$$\bar{\rho}_I = \frac{\int_0^1 I(\rho)\rho d\rho}{\int_0^1 I(\rho)d\rho} = \frac{\hat{I}}{\bar{I}}$$

(This is just setting up interpretable variables for the terms $\frac{\hat{S}}{S}$ and $\frac{\hat{I}}{I}$, which start to pop up in a bunch of places.)

3.2.2 Moments equations

First we have a general result relating the "moments" of S and I.

Suppose we want to know how the total susceptible population is changing. We can integrate $\frac{\partial S}{\partial t}$ over ρ :

$$\begin{split} \frac{d\bar{S}}{dt} &= \int_0^1 \frac{\partial S(\rho)}{\partial t} d\rho = \int_0^1 (-\beta_c S(\rho) \bar{I} - \beta_r S(\rho) \rho \hat{I}) d\rho \\ &= -\beta_c (\int_0^1 S(\rho) d\rho) \bar{I} - \beta_r (\int_0^1 S(\rho) \rho d\rho) \hat{I} \\ &= -\beta_c \bar{S} \bar{I} - \beta_r \hat{S} \hat{I} \end{split}$$

Similary, we can find that:

$$\frac{d\bar{I}}{dt} = \int_0^1 \frac{\partial I(\rho)}{\partial t} d\rho = \beta_c \bar{S}\bar{I} + \beta_r \hat{S}\hat{I} - \gamma \bar{I}$$

If we want to see how the first moments are changing, we follow a similar method:

$$\begin{split} \frac{d\hat{S}}{dt} &= \int_0^1 \frac{\partial S(\rho)}{\partial t} \rho d\rho = \int_0^1 (-\beta_c S(\rho) \bar{I} - \beta_r S(\rho) \rho \hat{I}) \rho d\rho \\ &= -\beta_c (\int_0^1 S(\rho) \rho d\rho) \bar{I} - \beta_r (\int_0^1 S(\rho) \rho^2 d\rho) \hat{I} \\ &= -\beta_c \hat{S} \bar{I} - \beta_r \hat{S} \hat{I} \end{split}$$

And for any general moment:

$$\frac{dS}{dt} = -\beta_c S \bar{I} - \beta_r S \rho \hat{I} - \gamma I \qquad (1)$$

3.2.3 Basic Reproduction Number

In the homogeneous SIR model, the basic reproduction number (number of secondary infections per infection) is:

$$R(t) = \frac{S\beta}{\gamma}$$

In this model, we can derive a similar form for the expected number of secondary infections per infection by dividing $\frac{d\bar{S}}{dt}$ by \hat{I} (current number of infected individuals) then multiplying by the mean duration of an infection $\frac{1}{\gamma}$.

$$R(t) = -\frac{d\bar{S}}{dt} \frac{1}{\gamma \bar{I}}$$

$$= \frac{1}{\gamma} \beta_c \bar{S} \frac{\bar{I}}{\bar{I}} + \frac{1}{\gamma} \beta_r \hat{S} \frac{\hat{I}}{\bar{I}}$$

$$= \frac{1}{\gamma} \bar{S} \left(\beta_c + \beta_r \frac{\hat{S}}{\bar{S}} \frac{\hat{I}}{\bar{I}} \right)$$

$$= \frac{1}{\gamma} \bar{S} \left(\beta_c + \beta_r \bar{\rho}_S \bar{\rho}_I \right)$$

This gives a nicely analogous result, where the homogenous β is replaced by what we can think of as an effective β : $(\beta_c + \beta_r \bar{\rho}_I \bar{\rho}_S)$, which is a straightforward function of both β terms and the mean riskiness in both populations.

We then would like to know how $\bar{\rho}_S$ and $\bar{\rho}_I$ are changing. We'd expect $\bar{\rho}_S$ (mean riskiness of the susceptible population) to monotonically decrease, as more risk-taking- susceptible individuals are more likely to be infected. We'd expect $\bar{\rho}_I$ to behave almost like a chemostat as higher-risk- individuals flow in, and all individuals flow out at a rate of γ . It should increase initially, and eventually decrease after the mean of riskiness decreases sufficiently in the susceptible population.

3.2.4 $\bar{\rho}_S$

Fortunately, we can find explicit expressions for $\frac{d}{dt}\bar{\rho}_S$ and $\frac{d}{dt}\bar{\rho}_I$.

Start with $\frac{d\bar{\rho}_{S}}{dt}$, and differentiate:

$$\frac{d}{dt}\bar{\rho}_{S} = \frac{d}{dt} \begin{pmatrix} \hat{S} \\ \bar{S} \end{pmatrix}
= \frac{\frac{d}{dt}\hat{S}\bar{S} - \hat{S}\frac{d}{dt}\bar{S}}{\bar{S}^{2}}
= \frac{1}{\bar{S}} \left(-\beta_{c}\hat{S}\bar{I} - \beta_{r}\hat{S}\hat{I} \right) - \frac{\hat{S}}{\bar{S}^{2}} \left(-\beta_{c}\bar{S}\bar{I} - \beta_{r}\hat{S}\hat{I} \right)
= -\beta_{c}\frac{\hat{S}}{\bar{S}}\bar{I} - \beta_{r}\frac{\hat{S}}{\bar{S}}\hat{I} + \beta_{c}\frac{\hat{S}}{\bar{S}}\bar{I} + \beta_{r}\left(\frac{\hat{S}}{\bar{S}}\right)^{2}
= -\beta_{r}\frac{\hat{S}}{\bar{S}}\hat{I} + \beta_{r}\left(\frac{\hat{S}}{\bar{S}}\right)^{2}
= -\beta_{r}\hat{I}\left(\frac{\hat{S}}{\bar{S}} - \left(\frac{\hat{S}}{\bar{S}}\right)^{2}\right)$$

Here, notice $\hat{\hat{S}}$ sums ρ^2 over [0,1] and so $\frac{\hat{\hat{S}}}{\hat{S}}$ we can write as $E[\rho_S^2]$. And similarly $\frac{\hat{\hat{S}}}{\hat{S}} = E[\rho_S]$ so

$$\frac{\hat{\hat{S}}}{\bar{S}} - \left(\frac{\hat{S}}{\bar{S}}\right)^2 = E[\rho_S^2] - E[\rho_S]^2$$

which is the variance of the riskiness of the susceptible population $Var(\rho_S)$. This allows us to rewrite the equation as:

$$\frac{d}{dt}\bar{\rho}_S = -\beta_r \hat{I} \text{Var}(\rho_s)$$

or

$$\frac{d}{dt}\bar{\rho}_S = -\beta_r \bar{I}\bar{\rho}_I \text{Var}(\rho_s)$$

This confirms that ρ_S decreases monotonically (as long as there is some infected population with nonzero mean riskiness), and further shows that it decreases proportionally to the variance of the distribution of riskiness in the S population.

3.2.5 $\bar{
ho}_I$

$$\frac{d}{dt}\bar{\rho}_{I} = \frac{d}{dt} \begin{pmatrix} \hat{I} \\ \bar{I} \end{pmatrix}
= \frac{\frac{d}{dt}(\hat{I})\bar{I} - \hat{I}\frac{d}{dt}(\bar{I})}{\bar{I}^{2}}
=
= \bar{S} \left[\beta_{c}(\bar{\rho}_{S} - \bar{\rho}_{I}) + \beta_{r}\bar{\rho}_{S}\bar{\rho}_{I}((\bar{\rho}_{S} + \frac{\mathrm{Var}(\rho_{S})}{\bar{\rho}_{S}}) - \bar{\rho}_{I})) \right]$$