Model specification

Following the approach outline in *Mathematics of Epidemics on Networks* by Miller *et al* we begin with a network of potentially infectious contacts given by degree distribution p_k. The probability generating function (pgf) is the primary tool used and it is given by $\Psi(x) = \sum_k x^k p_k$. Examples of what can be derived with the pgf include the mean degree $\langle k \rangle = \sum_k k p_k = \Psi'(1)$. In chapter 6 if p is the percolation probability then what is given is a necessary threshold condition for an outbreak to occur

$$p\frac{\langle k^2 - k \rangle}{\langle k \rangle} = p\frac{\Psi''(1)}{\Psi'(1)} = p\langle k_{ex} \rangle > 1 \tag{1}$$

where $\langle k_{ex} \rangle$ is the mean excess degree. From this we can infer that $p\langle k_e x \rangle$ is the population R_0. We define $\mathcal{P}$ as the probability of a major outbreak and $\mathcal{A}$ as the attack rate or expected final proportion of the population that gets sick. The texts shows that

$$\mathcal{P} = \mathcal{A} = 1 - \Psi(\alpha) \tag{2}$$

where α is the smallest positive value which solves the self-consistent equation

$$\alpha = f(\alpha) = 1 - p + p\frac{\Psi'(\alpha)}{\langle k \rangle}$$

The equation f and the existence of fixed points α follows from standard branching process theory. It turns out $\alpha = 1$ is always a fixed point, but $\alpha = 1$ would give $\mathcal{P} = 0$. The condition that there exists an $0 < \alpha < 1$ that satisfies the necessary conditions can be shown equivalent to the conditions given in Eq. (1).

One discussion about how to approach symptomatic versus asymptomatic was to write $p = \rho\beta_A + (1 - \rho)\beta_S$ where ρ is the proportion of infected people who are asymptomatic and β_A, β_S are the probabilities of transmitting along an existing contact link for asymptomatic and symptomatic persons respectively.

1 Poisson example

If the degree distribution of the contact network is distributed $Poisson(\lambda)$ then we are considering an Erdös-Reyni network. It follows that $\langle k \rangle = \lambda$, $\langle k^2 - k \rangle = \lambda^2$, and $\Psi(x) = \Psi'(x) = \exp(\lambda(x - 1))$. The threshold equation then becomes

$$(\rho\beta_A + (1 - \rho)\beta_S)\lambda > 1$$

From the threshold equation one can make a rough approximation of the necessary measure of social distancing required to prevent an outbreak, that is one would require

$$\lambda < \frac{1}{\rho\beta_A + (1 - \rho)\beta_S}$$

This is giving an upper bound on the average number of contacts the population can have to prevent an outbreak, and lowering λ to the necessary level is analogous to social distancing. If the number of contacts cannot be reduced below the threshold value $\lambda_c = (\rho \beta_A + (1-\rho)\beta_S)^{-1}$ then there is still a positive probability of outbreak and as above we have

$$\mathcal{P} = \mathcal{A} = 1 - \exp(\lambda(\alpha - 1))$$

where α is found numerically from the branching process equation

$$\alpha = 1 - (\rho\beta_A + (1-\rho)\beta_S) + (\rho\beta_A + (1-\rho)\beta_S)\frac{\exp(\lambda(\alpha-1))}{\lambda}$$

Natural explorations within this framework are to try and estimate ρ, β_A, β_S and then find λ_c that would prevent an outbreak and $\mathcal{P}$ if λ_c cannot be achieved. If we are able to estimate one parameter accurately or find reasonable assumptions defining a functional relationship between β_A and β_S then we can give contour plots or heat maps of λ_c and $\mathcal{P}$.

2   Other approaches

There are a couple other of possibilities that we discussed as analytic approaches as well:

The first is to assume that there is an additional parameter in the transmission probability that is related to social distancing, then the percolation probability would be $q(\rho\beta_A + (1-\rho)\beta_S)$ where $q < 1$ simultaneously represent the product of what percentage of reduction in transmission probability occurs via social distancing and what proportion of the population is complying. This would be an alternative approach to simply finding λ_c above.

Another possibility is to have a λ_A, λ_S, which is to say the expected number of possible transmissible contacts is different between asymptomatic and symptomatic people as a result of behavioral difference. The degree distribution would then be given by $\rho p_{k,A} + (1-\rho)p_{k,S}$. If we assume the same transmission probability per contact no matter infection type, β, this would yield the threshold expression

$$\beta\frac{\rho\lambda_A^2 + (1-\rho)\lambda_S^2}{\rho\lambda_A + (1-\rho)\lambda_S} > 1$$

In this model we could again consider social distancing by finding necessary changes in λ_A, λ_S or by adding a social distancing parameter in the transmission probability.

The last thing discussed thus far is consider if all people have a Poisson number of contacts but the average number of contacts for each person varies according to a Gamma distribution which gives the contact network as Negative Binomial. We could then apply the approach of considering different infectivity depending on symptomatic or not and vary the proportion of symptomatic person, exactly as above. For social distancing we could alter the parameters on the Gamma distribution or again introduce a social distancing term in the transmission probability.

3 Sym vs Asym changes degree distribution

This is the second point in the "other approaches" above and I believe what was discussed on Saturday and how Blake did his simulation. Using the notation we've settled on for the presentation we assume asymptomatic persons have contacts distribute according to distribution $Poiss(c_A)$ and similarly symptomatic persons contact distribution is $Poiss(c_S)$. We further assume that no matter type each person transmits with the same probability β and we let ν be the proportion of asymptomatic people. We first need to calculate the population mean degree and the population mean excess degree. We define the probability generating function as

$$\psi(x) = \sum_k x^k (\nu p_{k,A} + (1-\nu) p_{k,S})$$

where $p_{k,I}$ are the appropriate probabilities from a distribution $Poisson(c_I)$ with $I = A, S$. Omitting the details of the calculation and using what is known about Poisson PGFs we have

$$c = \psi'(1) = \nu \sum_k k p_{k,A} + (1-\nu) \sum_k k p_{k,S} = \nu c_A + (1-\nu) c_S$$

Now, to compute the mean excess degree we use a known formula (see *e.g.* Newman's book, the section on PGF's for excess degree: pg. 450 in edition 1) to find

$$c_{ex} = \frac{\psi''(1)}{\psi'(1)} = \frac{1}{\nu c_A + (1-\nu) c_S} \sum_k (k^2 - k)(\nu p_{k,A} + (1-\nu) p_{k,S}) = \frac{\nu c_A^2 + (1-\nu) c_S^2}{\nu c_A + (1-\nu) c_S}$$

The computations follow again from knowing the appropriate facts about a Poisson distribution's mean, variance and PGF. This expression immediately shows us that $c \neq c_{ex}$. Using Eq. (**??**) we thus find in this modeling approach that

$$R_0 = \beta c_{ex} = \beta \frac{\nu c_A^2 + (1-\nu) c_S^2}{\nu c_A + (1-\nu) c_S}$$

The outbreak probability is also likely to be different and will certainly have a different form. In this case we have

$$\mathcal{P} = 1 - \psi(\alpha) = 1 - \nu \exp(c_A(\alpha - 1)) - (1-\nu) \exp(c_S(\alpha - 1))$$

where again *alpha* is the smallest fixed point of the branching process equation. That is, α solves

$$\alpha = 1 - \beta + \beta \frac{\psi'(\alpha)}{c}$$
$$= 1 - \beta + \beta \frac{\nu c_A \exp(c_A(\alpha - 1)) + (1-\nu) c_S \exp(c_S(\alpha - 1))}{\nu c_A + (1-\nu) c_S}$$

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$$\beta_S = \gamma\beta_A, \quad \gamma \in (0,1)$$
$$\implies R_0 = c(\nu\beta_A + (1-\nu)\beta_S)$$
$$R_0 > 1$$
$$\implies c_{crit} = (\nu\beta_A + (1-\nu)\beta_S)^{-1}$$
$$R_A = \frac{\nu}{\nu + (1-\nu)\gamma}$$
$$R_S = \frac{(1-\nu)\gamma}{\nu + (1-\nu)\gamma}$$
$$R_0 = R_A + R_S$$
$$\beta_S \propto \beta_A$$
$$\mathcal{P} = 1 - \psi(\alpha)$$
$$\psi(z)$$
$$\alpha$$
$$\alpha = 1 - p + p\frac{\psi'(\alpha)}{c}$$