Evaluating at $S_0 \simeq N$ gives the familiar SIR $\mathcal{R}_0$ value, $\mathcal{R}_0^{SIR} = \frac{\beta}{r}$. If $\frac{\beta}{r} > 1$ the epidemic grows (if unchecked) as long as there is a sufficiently large fraction of susceptibles, $s_t = \frac{S_t}{N} > \frac{1}{\mathcal{R}_0^{SIR}}$. In contrast, if $\mathcal{R}_0^{SIR} < 1$ the epidemic would die out on its own.

I define the effective reproduction number $\mathcal{R}_t$ in the NSIR model analogously. Define

$$\sigma_{it}(G) \equiv \frac{\sum_{j \in C_G(i)} \mathbf{1}_{x_{jt}=I}}{\#C_G(i)},$$

corresponding to the agent i's probability of infection from one of her social contacts in graph G at time t. Using (1), in the (no-intervention) NSIR model we have,

$$\frac{d(I_t + E_t)}{dt} = p\beta I_t s_t + (1-p)\beta \sum_{i \in S_t} \sigma_{it}(G) - rI_t =$$

$$= rI_t \left(p\frac{\beta}{r}s_t + (1-p)\frac{\beta}{r}\frac{S_t}{I_t}\frac{\sum_{i \in S_t}\sigma_{it}(G)}{S_t} - 1 \right)$$

The number of infected agents (exposed plus infectious) would grow if the expression in the brackets is positive. Hence, for $s_t \simeq \frac{S_t}{N}$, define the NSIR model effective reproduction number $\mathcal{R}_t^{NSIR}$ as

$$\frac{\beta}{r}[p\frac{S_t}{N} + (1-p)\frac{S_t}{I_t}\frac{\sum_{i \in S_t}\sigma_{it}(G)}{S_t}] \tag{6}$$

At $p = 1$ this expression equals $\mathcal{R}_t^{SIR}$ but in general, including at $t = 0$, the NSIR model reproduction number $\mathcal{R}_t^{NSIR}$ differs from $\mathcal{R}_t^{SIR}$ and depends on the graph G. For example, [9] emphasize the importance of the ratio between the second and first moment of the degree distribution for the infection growth rate.

2.3.2 Population vs. network transmission. I next compare the reproduction numbers for the SIR model ($p = 1$) and the network-only transmission NSIR model ($p = 0$) for given values of I_t and S_t. Using (6), for $p = 0$ we have

$$\mathcal{R}_t^{NSIR} = \frac{\beta S_t}{rI_t}\frac{\sum_{i \in S_t}\sigma_{it}(G)}{S_t} \tag{7}$$

where

$$\frac{\sum_{i \in S_t}\sigma_{it}(G)}{S_t} \equiv \bar{\sigma}_t(G)$$

is the average chance of infection across all susceptible nodes $i \in S_t$ at time t, given the set $\mathcal{I}_t$ of infectious agents i with $x_{it} = I$. Comparing (5) and (7), observe that

$$\mathcal{R}_t^{NSIR} \gtreqless \mathcal{R}_t^{SIR} \Leftrightarrow \bar{\sigma}_t(G) \gtreqless \frac{I_t}{N} \tag{8}$$

Intuitively, the standard SIR model assumes a *uniform* chance of infection for each susceptible agent which is proportional to the population infection rate $\frac{I_t}{N}$. In contrast, in the network-augmented NSIR model an individual's chance of infection is *heterogeneous* and is a function of the social network G. The average time-t infection probability in the network, $\bar{\sigma}_t(G)$ determines the reproduction number $\mathcal{R}_t^{NSIR}$. For example, consider the first infection, $I_0 = 1$ of some agent i_0, at which $\mathcal{R}_0^{SIR} \simeq \frac{\beta}{r}$. In contrast, the value of the NSIR effective reproduction number