Two levels of mixing

• Each individual $i$:

\[ p_G = \text{prob. to infect any other individual}, \]
\[ p_L = \text{prob. to infect any neighbor } \in \mathcal{N}(i); \]

*global* and *local* infections respectively.

• Local infections: households, schools, etc.;
  global: as before.

• Simplest example:

  $m$ groups, each of $n$ individuals.
  $N = mn$ is a total population size.
Two levels of mixing

Random graph framework

• Individuals are nodes in the graph.

• Directed arrow from individual $i$ to $j$ – if $i$ is infected he will infect $j$.

• Recall Reed-Frost epidemic: each time period any infected infects any susceptible w/prob. $p$; probability of an edge is $p$.

Situation is symmetric, so undirected graph.
Two levels of mixing

*Random graph framework*

- Partition an undirected graph into connected components.
- Simple Reed-Frost: $G(N, p)$.

For large $N$ this graph has a “giant” component iff $R_0 = Np > 1$; “giant” component will contain $Nz$ individuals, where $z$ is the largest root of

$$z = 1 - e^{-R_0z}.$$
Two levels of mixing

Random graph framework

• If $I_0 = 1$ then $\zeta$, prob. of large outbreak, is same as prob. that first infected individual belongs to the giant connected component, so equals $z$.

• If $I_0 = k$ then $\zeta(k) = 1 - (1 - \zeta)^k$. 
Two levels of mixing

Two models: small number of local contacts

- Fix size of household (or its distribution); partition households into connected components – doesn’t matter which household they come from.

- Individuals in same group (household) can both have a local, w/prob. $p_L$, and a global, $p_G$ contact. Actually same as allowing only local contacts $p'_L = 1 - (1 - p_L)(1 - p_G)$ within households.

- $\pi_k = \text{prob. that a randomly chosen individual belongs to component of size } k$.

- Component sizes are not independent (b/c of household dependance) but almost when $m$ is large.
Two levels of mixing

Two models: small number of local contacts

- Second model: “great circle” - individuals are located on a circle, each has two neighbors. (note: this defines components but not households.)

- \( p_L = \text{prob. of link between two neighbors} \)
  \( p_G = \text{prob. of link for any pair of individ’s.} \)

- \( \pi_k = k p_L^{k-1} (1 - p_L)^2 \) - belong to a component of size \( k \).
Two levels of mixing

*Clumped Reed-Frost*

- Both models above a special cases of *clumped Reed-Frost* model.

- Population consists of clumps, \( i^{th} \) has weight \( \omega_i \).

- \( 1 - e^{-c\omega_i\omega_j} \) = prob. of contact between \( i \) and \( j \).

- In the two original models: clumps are locally connected components; \( \omega_k = k \), where \( k \) is the size of component; \( p_G = 1 - e^{-c} \).
Two levels of mixing

*Size-biased distributions*

- $\pi_k$ - size biased distribution of clumps of size $k$. That is, prob. that a randomly chosen individual belongs to clump of size $k$.

- If $h_k$ is the prob. that a randomly chosen clump is of size $k$, then $\pi_k = kh_k / \sum_j jh_j$.

- $\mu_\pi = \mu_h + \sigma_h^2 / \mu_h$. 

Two levels of mixing

Clumped Reed-Frost

• As before we “compare” the clumped Reed-Frost to a branching process. Offsprings of a clump are clumps that it ties to. Approximation assumes that newly contacted clumps are STILL susceptible.

• For large $N$ number of clumps contacted by an individual is $\approx \text{Poisson}(N p G)$, so the g.f. is $g(z) = e^{N p G (z-1)}$.

• A number of clumps contacted by a given clump, i.e. the offspring distribution of the branching process, has a g.f. $G_{\pi}(e^{N p G (z-1)})$. 
Two levels of mixing

*Clumped Reed-Frost*

- It follows that a probability of a large outbreak is the largest solution $\zeta$ of
  \[
  1 - \zeta = G_\pi e^{-N_p G \zeta}
  \]
  and $\zeta > 0$ iff mean $= N_p G \mu \pi > 1$.

- Basic reproductive ratio for epidemic among clumps is then $R_* = \mu N_p G = \mu R_G$, where $R_G = N_p G$.

- As before, prob. of a large outbreak is the same as the prob. that an individual belongs to a giant connected component. The size of this component is the same as the final size of the epidemic.
Two levels of mixing

*Clumped Reed-Frost*

- Let $\zeta_k = \text{prob. that a clump of size } k \text{ is infected.}$

- Number of links from each individual to the "giant" clump is $\text{Poisson}(\zeta NP_G) \Rightarrow$

  prob. of no links is $e^{-kNP_G\zeta}$.

- $\zeta_k = 1 - e^{-kNP_G\zeta}$.
Two levels of mixing

Large households

• Large number, $m$, of large households of size $n$.

• Here, households themselves might have a large epidemic with $R_L = np_L$.

• If $R_L \leq 1$ then households consist of clumps of size $O(1)$ in $n$.

• So, same consideration as in small household case apply. $R_* = \mu R_G = \mu N p_G$, where $\mu$ is the mean clump size.

• $\mu = O(1) \Rightarrow$ need $p_G = O(1/N)$ to get a global epidemic.
Two levels of mixing

*Large households*

- If $R_L > 1$ then within households have large connected components, say $n z_h$.

- Here, giant to giant epidemic has threshold at $R_* = m(n z_h)^2 p_G = n N p_G z_h^2$. Others don’t affect the epidemic much.

- $z_h = O(1)$, so need only $p_G = O(1/N n)$ to get a large epidemic!

- In all cases, the local contacts have an amplifying effect on global epidemic. But for large household this undergoes a phase transition from $O(1)$ to $O(n)$ as we go through the local threshold $R_L = 1$. 
Two levels of mixing

Vaccination Strategies

- In homogeneously mixing population, the minimum proportion $\nu$ need to vaccinate is such that $R'_G = (1 - \nu)R_G \leq 1$, that is $\nu \geq 1 - 1/R_G$.

- Two levels of mixing $R_* = \mu R_G$.

- If simply vaccinate pro rata, then as above $R'_G = (1 - \nu)R_G$ but the effect on $\mu$ will depend on the distribution of vaccination among the population.
Two levels of mixing

Vaccination Strategies

• Suppose we vaccinate whole households. Then $\mu$ is not affected and $R'_* = (1 - \nu)R_*$.

• However, if we vaccinate proportions within groups, we can reduce $\mu$ and thus reduce $R_*'$ even further.

• Effects can be dramatic!
Two levels of mixing

Vaccination Strategies: Example.

• Suppose groups are of size $n = 1,000$, and $R_G = 1$.

• Suppose also $p_L = .003$ so $R_L = np_L = 3$, then from g.f. can get $z_h \approx .95$.

• $\mu = nz_h \times z_h$ and $R_* = \mu R_G \approx 900$.

• Consider vaccination strategies $\nu = 80\%$.

• Note that $R'_G = .2 \times R_G = .2$ for any strategy.
Two levels of mixing

\textit{Vaccination Strategies: Example.}

- If we vaccinate whole groups then \( R'_* = \mu R'_G = 900 \times .2 = 180 \) \textit{far above 1}.

- Suppose we vaccinate 80\% of each group instead, then \( R'_L = .2 \times 3 = .6 \), and mean clump size is \( \mu' \approx 1/(1-.6) = 2.5 \) (can get from approximating branching process).

- So, \( R'_* = \mu'R'_G \approx 2.5 \times .2 = .5 \) \textit{below the threshold}.

- This is very sensitive to properly carried out vaccination. If just 1\% of groups is vaccinated below 50\% then \( R'_* > 1! \)