Heterogeneity and Herd Immunity

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Based on

- "A mathematical model reveals the influence of population heterogeneity on herd immunity to SARS-CoV-2" by Ball, Britton, and Trapman (2020)
- Rick Durrett's notes

Herd Immunity

- Herd Immunity: What percentage of the population needs immunity to stop the spread of an epidemic?
- In the SIR model for a homogeneously mixing population, herd immunity is reached at $1 - 1/R_0$
- What do we do when the population is heterogeneous?

Ball, Britton, Trapman - Model 1

Age Groups

- 6 groups: 0-5, 6-12, 13-19, 20-39, 40-59 and 60+
- a_{jk} is the contact intensity from group j to group k
- π_j is the population fraction of group j
- $\pi_k a_{jk}$ is the entries of the contact matrix

$$\pi = (0.0725, 0.0866, 0.1124, 0.3323, 0.2267, .01695)$$

$$\begin{pmatrix}
2.2257 & 0.4136 & 0.2342 & 0.4539 & 0.2085 & 0.1506 \\
0.4139 & 3.6140 & 0.4251 & 0.4587 & 0.2712 & 0.1514 \\
0.2342 & 0.4257 & 2.9514 & 0.6682 & 0.4936 & 0.1972 \\
0.4539 & 0.4592 & 0.6676 & 0.9958 & 0.6510 & 0.3300 \\
0.2088 & 0.2706 & 0.4942 & 0.6508 & 0.8066 & 0.4341 \\
0.1507 & 0.1520 & 0.1968 & 0.3303 & 0.4344 & 0.7136
\end{pmatrix}$$

Ball, Britton, Trapman - Model 2

Activity Levels

- 3 groups per age group: low, normal, high
- low is half as social, high is twice as social
- low is 25% of the population, high is 25% of the population
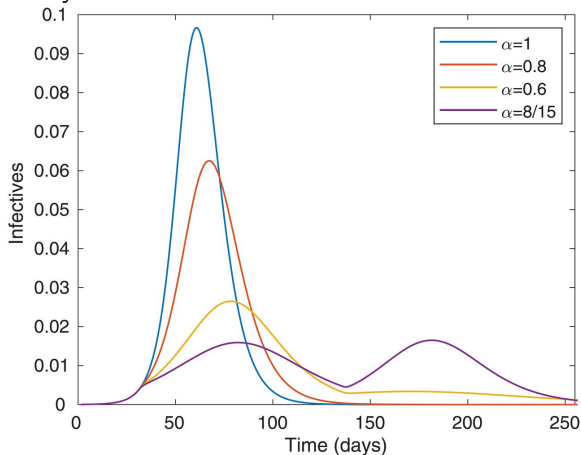
Example: Group j low to group k high is

$$a_{jk}(0.5 \times 2)(0.25\pi_k)$$

By combining the two layers, the model can be summed by an 18x18 matrix

Ball, Britton, Trapman - Herd Immunity

α is a reduction factor for contact intensities, represents preventative measures, which are removed day 130

herd immunity = number infected for smallest α with no wave 2

Ball, Britton, Trapman - Herd Immunity

Table 1. Disease-induced herd immunity level h_D and classical herd immunity level h_C for different population structures. Numbers correspond to percentages.

Population structure	$R_0 = 2.0$		$R_0 = 2.5$		$R_0 = 3.0$	
	h_D	h_C	h_D	h_C	h_D	h_C
Homogeneous	50.0	50.0	60.0	60.0	66.7	66.7
Age structure	46.0	50.0	55.8	60.0	62.5	66.7
Activity structure	37.7	50.0	46.3	60.0	52.5	66.7
Age and activity structure	34.6	50.0	43.0	60.0	49.1	66.7

Adding population structure decreases h_D

Ball, Britton, Trapman - Herd Immunity

Table 2. Final outcome fractions infected in different groups. These values assume that $R_0 = 2.5$ and preventive measures are put in place such that $\alpha = \alpha$, just barely reaching herd immunity for $R_0 = 2.5$. Population structure includes both age and activity. Numbers correspond to percentages.

Age group	Low activity	Average activity	High activity
0–5 years	17.6	32.1	53.9
6–12 years	25.8	44.9	69.7
13–19 years	31.4	52.9	77.8
20–39 years	27.4	47.2	72.1
40–59 years	22.8	40.3	64.4
≥60 years	14.6	27.0	46.7

- h_D is achieved from a certain distribution of immunity among the population groups.
- What happens if we change that distribution?

We now try some simpler models where we can compute herd immunity as a vector.

Simple Model 1: Two Groups

$$\begin{pmatrix} a_{11}\pi_1 & a_{12}\pi_2 \\ a_{21}\pi_1 & a_{22}\pi_2 \end{pmatrix}$$

Solving for eigenvalues gives

$$\lambda^2 - (a_{11}\pi_1 + a_{22}\pi_2)\lambda + \pi_1\pi_2 \det(a) = 0$$

Then the largest eigenvalue (R_0) is

$$\lambda_{max} = \frac{(a_{11}\pi_1 + a_{22}\pi_2) + \sqrt{(a_{11}\pi_1 + a_{22}\pi_2)^2 - 4\pi_1\pi_2 \det(a)}}{2}$$

so if we want $R_0 = \lambda_{max} = 1$, then

$$a_{11}\pi_1 + a_{22}\pi_2 < 2$$
$$\pi_2 = \frac{1 - a_{11}\pi_1}{a_{22} - det(a)\pi_1}$$

Maximize $\pi_1 + \pi_2$. This is tedious when more than 2 groups.

Simple Model 2: Activity Level

Let α_k be the activity level of group k. Just like in Ball, Britton, Trapman

$$b_j \alpha_j c_k \alpha_k \pi_k$$

Setting

$$v = (c_k \alpha_k \pi_k)^T$$
$$w = (b_j \alpha_j)$$

Our contact matrix is vw

- The matrix is rank 1, so only one nonzero eigenvalue
- $w(vw) = (w \cdot v)w$ so eigenvalue is $w \cdot v$ and left eigenvector is w

Simple Model 2: Activity Level - Example

Going back to Ball, Britton, Trapman

- 3 activity levels: low, normal, high
- $\alpha = (0.5, 1, 2)$
- $\pi = (0.25, 0.5, 0.25)$

$$v(\pi) = \beta(0.5 \times 0.25, 1 \times 0.5, 2 \times 0.25)^T$$

$$w = (0.5, 1, 2)/\gamma$$

Setting the eigenvalue $w \cdot v(\pi) = R_0 = 2.5$ and $\gamma = 0.2$, we find $\beta = .32$

Immunity in group j decreases π_j, so to find herd immunity, set $R_0 = 1$

$$1 = w \cdot v(\overline{\pi}) = \frac{.32}{0.2}(0.5^2 \overline{\pi_1} + \overline{\pi_2} + 2^2 \overline{\pi_3})$$

Setting $\overline{\pi} = (0.25, 0.5, 1/64)$, we can achieve herd immunity at
$1 - (0.25 + 0.5 + 1/64) \approx 0.233$

Conclusions

- Ball, Britton, Trapman calculated herd immunity $h_D = 0.463 > 0.233$ so achieving herd immunity is easier when you get to pick who becomes immune, rather than the virus.

- The activity model's contact matrix being rank 1 makes it easy to compute R_0 and herd immunity.

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THANK YOU!