

Estimating probability of major epidemic from initial importation/spillover

Adam Kucharski, January 2014

Spillover transmission model The probability the infection will cause a major outbreak, P , is the average of the probabilities for each age group, weighted by the probability of exposure to the infection reservoir:

$$P = \sum_j \mathbb{P}(\text{causes major outbreak} \mid \text{starts in } j) \mathbb{P}(\text{starts in group } j) \quad (0.1)$$

$$= \sum_j z_j q_j \quad (0.2)$$

where q_j is the probability it starts in group j and z_j is the probability the infection fails to go extinct given that it starts in j .

Define generating function for a branching process:

$$g(\mathbf{s}) = \sum_{i=0}^{\infty} p_i s^i \quad (0.3)$$

Generic formulation with Poisson transmission [1]:

$$p_i = \frac{\lambda^i e^{-\lambda}}{i!} \quad (0.4)$$

$$g(\mathbf{s}) = \int_0^{\infty} e^{-\lambda(1-s)} f(\lambda) d\lambda \quad (0.5)$$

$f(\lambda)$ constant, equal to R_0 (i.e. Poisson offspring distribution):

$$g(\mathbf{s}) = e^{-R_0(1-s)} \quad (0.6)$$

$f(\lambda)$ exponentially distributed:

$$p_i = \frac{R_0^i e^{-R_0}}{i!} \quad (0.7)$$

$$g(\mathbf{s}) = \exp[-R_0(1-s)] \quad (0.8)$$

If assume fixed $f(\lambda)$, we can define Poisson offspring distribution for multiple groups [2]:

$$g_i(\mathbf{s}) = \exp\left(-\sum_j R_{ji}(1-s_j)\right). \quad (0.9)$$

If we assume $f(\lambda)$ is gamma distributed, offspring distribution is negative binomial:

$$g_i(\mathbf{s}) = \prod_j \left(1 + \frac{R_{ji}}{k}(1-s_j)\right)^{-k}. \quad (0.10)$$

We can find the probability of extinction given outbreak starts in group i , by solving $g_i(\mathbf{s}) = s_i$. Let the probability of extinction given an outbreak starting in group i by s_i^* . The probability the infection will cause an epidemic, z_i , is therefore $1 - s_i^*$.

References

- [1] Lloyd-Smith JO, Schreiber SJ, Kopp PE, Getz WM. Superspreading and the effect of individual variation on disease emergence. *Nature*. 2005;438(7066):355–9.
- [2] Yates A, Antia R, Regoes RR. How do pathogen evolution and host heterogeneity interact in disease emergence? *Proc Biol Sci*. 2006 Dec;273(1605):3075–83.