Supplementary Information

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1 Closed form expressions for R_* for $n = 2, 3$

We consider only a single neighbourhood here. For households fixed at size 2, the expected number of infections within the primary household with a single initial infection is $1 + \beta/(\beta + \gamma)$. The expected cases an infectious individual produces outside of their own household is α/γ. Hence, the household reproduction number is simply

$$R_* = \left(1 + \frac{\beta}{\beta + \gamma}\right)\left(\frac{\alpha}{\gamma}\right).$$

For populations of households of size 3, the construction of R_* for a single neighbourhood becomes more complex:

$$\begin{aligned}R_* = \Bigg[&\frac{\gamma}{\beta+\gamma} + 2\frac{\beta}{\beta+\gamma}\frac{2\gamma}{\beta+2\gamma}\frac{\gamma}{\beta/2+\gamma} \\ &+3\left(\frac{\beta}{\beta+\gamma}\frac{\beta}{\beta+2\gamma} + \frac{\beta}{\beta+\gamma}\frac{2\gamma}{\beta+2\gamma}\frac{\beta/2}{\beta/2+\gamma}\right)\Bigg]\left(\frac{\alpha}{\gamma}\right).\end{aligned}$$

Here, the terms in square brackets represent the expected number of infections within the primary household. We calculate this by walking through each possible path of events within the household.

2 Closed form expressions for offspring distributions for $n = 1, 2$

For a single neighbourhood of households fixed to size 1, the probability mass function of secondary infections is

$$g(m) = \frac{\alpha^m \gamma}{(\alpha + \gamma)^{m+1}}.$$

This is simply the geometric distribution with parameter $\alpha/(\alpha + \gamma)$ [1].

Whereas for a single neighbourhood of households size 2, the probability mass function of secondary infections becomes

$$g(m) = \alpha^m \left[\frac{\gamma(\beta+\gamma)}{\beta}\frac{1}{(\alpha+\beta+\gamma)^{m+1}} + \gamma^2(m+1)\frac{1}{(\alpha+\gamma)^{m+2}} - \frac{\gamma^2}{\beta}\frac{1}{(\alpha+\gamma)^{m+1}}\right].$$

3 Multi-type branching process approximation for geometric offspring distribution

The probability generating functions are [2]

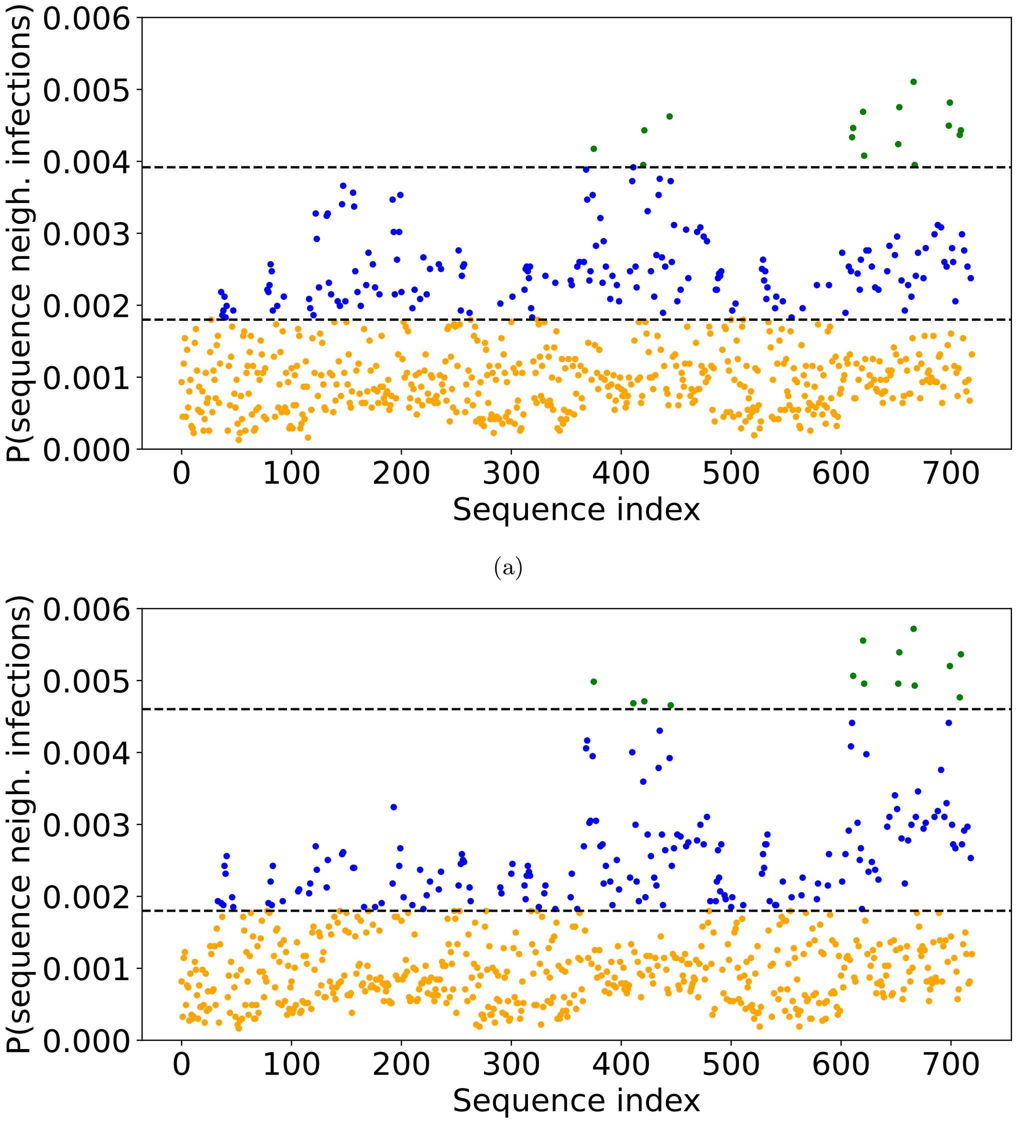
$$G_1(p_1, p_2) = \frac{1}{1 + R_*^{11}(1 - p_1) + R_*^{12}(1 - p_2)},$$
$$G_2(p_1, p_2) = \frac{1}{1 + R_*^{21}(1 - p_1) + R_*^{22}(1 - p_2)}.$$

4 Extra figures

References

[1] Joshua V Ross, Thomas House, and Matt J Keeling. Calculation of disease dynamics in a population of households. *PLoS One*, 5(3):e9666, 2010.

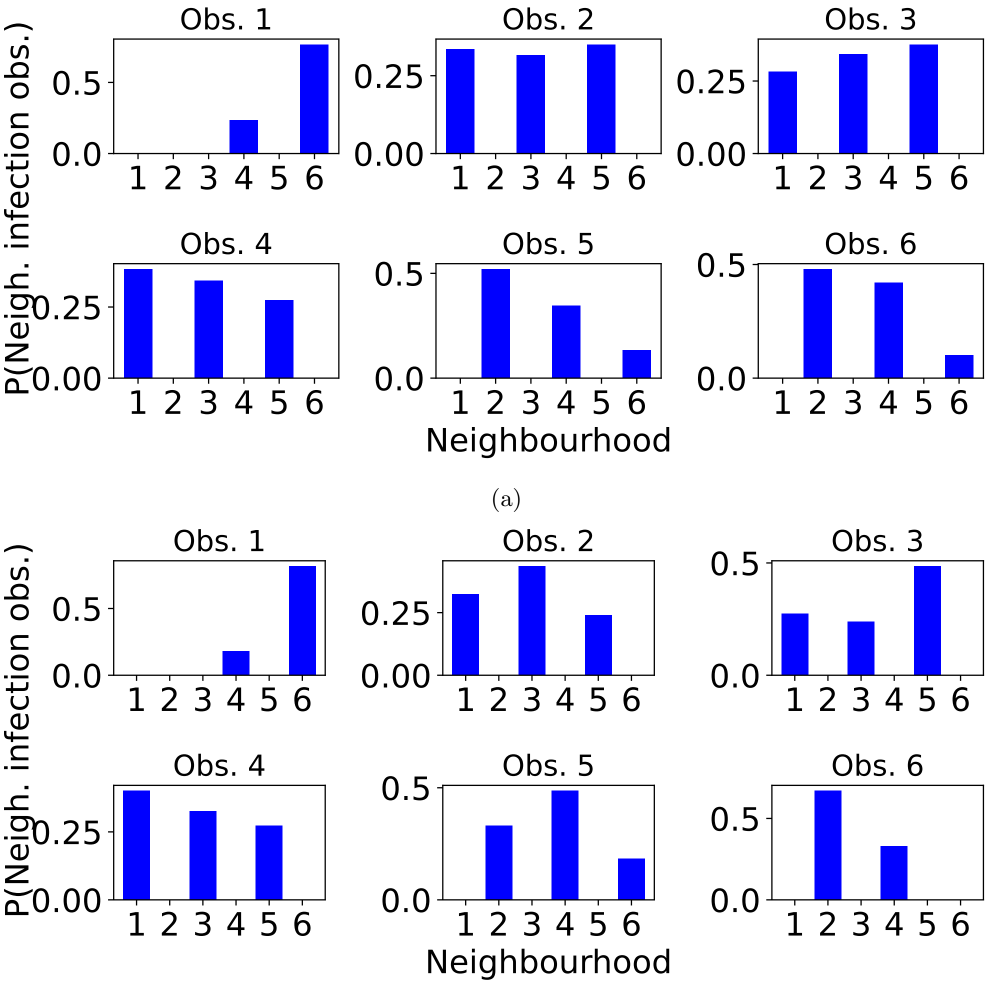
[2] Alun L Lloyd, Ji Zhang, and A Morgan Root. Stochasticity and heterogeneity in host–vector models. *J R Soc Interface*, 4(16):851–863, 2007.



(a)

(b)

Figure 1: Probability an outbreak is observed through given sequences of neighbourhoods. There are 720 possible sequences of 6 neighbourhoods. Each point in the scatter plot corresponds to a unique sequence and shows the proportion of outbreaks in which the outbreak was observed in that sequence of neighbourhoods. Calculated from $50,000$ Gillespie SSA trials with those that did not result in significant outbreaks discarded. Initially a single individual was infected in a randomly chosen neighbourhood. $\nu = 3$ and r is assigned a value from the distribution $U[0, 0.1]$ (neighbourhoods 1,3,5) or $U[0.4, 0.5]$ (neighbourhoods 2,4,6). Clustering on Figure 9 in the main text was performed with Python using the 'sklearn.cluster' library and indicated by colour-coding the points. We show the same same cut-offs here for comparison. Points above the first dashed black line correspond to sequences that occurred in the top 6.9% of trials. Those above the second black line occurred in $\geq 0.18\%$ of outbreaks. (a) $\nu = 1$ and (b) $\nu = 5$.



(a)

(b)

Figure 2: The probability a neighbourhood infection is observed in each neighbourhood. r takes value from either the distribution $U[0, 0.1]$ (neighbourhoods 1,3,5) or $U[0.4, 0.5]$ (neighbourhoods 2,4,6). $50,000$ realisations of Gillespie SSA were used with those not resulting in outbreaks being discarded. Of the remainder, only the top 6.9% of trials were used to construct this figure. From top left to bottom right the plots correspond to the 1^{st}, 2^{nd}, 3^{rd}, …, 6^{th} neighbourhood infection to be observed in the sequence of neighbourhood infections. (a) $\nu = 1$ and (b) $\nu = 5$.