

# Supplementary Text: The spatial resolution of epidemic peaks

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## S1 Simplification of the next generation matrix

Under certain circumstances, we can find a simple expression for  $R_0$  from the next generation matrix. The derivation is similar to the simplification of  $R_0$  for the multi-city epidemic model described in Ref. [1]. For this we need the following theorems:

**Theorem S1.1** *Let  $B$  be a  $n$  by  $n$  matrix with transpose  $C = B^T$ . Then  $B$  and  $C$  have the same eigenvalues. (Standard result).*

**Theorem S1.2** *Let  $B$  be a  $n$  by  $n$  matrix with entries  $b_{ij}$  and spectral radius  $\rho(B)$ . Then:*

$$\min(\sum_j b_{ij}) \leq \rho(B) \leq \max(\sum_j b_{ij}).$$

*i.e.  $\rho(B)$  is bounded by the limits of the row sums of  $B$ , (standard result, see for example [2]).*

**Corollary S1.3** *Using Theorems 0.1 and 0.2, it is therefore true that for a matrix  $B$  with entries  $b_{ij}$  and spectral radius  $\rho(B)$ ,  $\rho(B)$  is bounded by the column sums of  $B$ :*

$$\min(\sum_i b_{ij}) \leq \rho(B) \leq \max(\sum_i b_{ij}).$$

**Proof** By Theorem 0.1 it is true that for the matrices  $C$  and  $B$  where  $C = B^T$ , the spectral radius of  $C$  and  $B$  is the same:  $\rho(C) = \rho(B)$ .

By Theorem 0.2 it is true that the spectral radius of matrix  $C$  is bounded by the limits of the row sums of matrix  $C$ :

$$\min(\sum_j c_{ij}) \leq \rho(C) \leq \max(\sum_j c_{ij}). \quad (\text{S1})$$

As  $C = B^T$  the row sums of matrix  $C$  are equivalent to the column sums of matrix  $B$ :  $\min(\sum_j c_{ij}) = \min(\sum_i b_{ij})$ .

Therefore it follows that Eqn. S1 may be equivalently written:

$$\min(\sum_i b_{ij}) \leq \rho(B) \leq \max(\sum_i b_{ij}).$$

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Therefore, we calculate the column sums for the Next Generation Matrix defined as:

$$G_{ij} = N_i T \beta \sum_{k=1}^D \frac{m_{ik} m_{jk}}{\sum_{p=1}^D m_{pk} N_p} \quad (\text{S2})$$

where  $T$  was the time spent infected (which depended on recovery rate  $r$  such that  $T = \frac{1}{r}$ , same for all pixels),  $N_i$  was the number of individuals in pixel  $i$ , infectious contacts were made with other individuals present in the pixel with rate  $\beta$  and  $m$  was the mobility matrix defined earlier. We let  $\sum_{k=1}^D m_{ki} N_k = N_i^N$ , the total number of individuals in pixel  $i$  at any time (where  $m_{ki}$  is the probability that for an individual from pixel  $k$ , given that the individual made a contact, this contact was with an individual from pixel  $i$ ). Recall that  $\sum_{k=1}^D m_{jk} = 1$ . Then summing the  $j$ th column of the next generation matrix gives:

$$\begin{aligned} \sum_{i=1}^D G_{ij} &= G_{1j} + G_{2j} + \dots + G_{Dj} \\ &= N_1 T \beta \frac{m_{11} m_{j1}}{N_1^N} + \dots + N_1 T \beta \frac{m_{1D} m_{jD}}{N_D^N} \\ &\quad + N_2 T \beta \frac{m_{21} m_{j1}}{N_1^N} + \dots + N_2 T \beta \frac{m_{2D} m_{jD}}{N_D^N} \\ &\quad + \dots \\ &\quad + N_D T \beta \frac{m_{D1} m_{j1}}{N_1^N} + \dots + N_D T \beta \frac{m_{DD} m_{jD}}{N_D^N} \\ &= \beta T m_{j1} \left( \frac{m_{11} N_1 + \dots + m_{D1} N_D}{N_1^N} \right) \\ &\quad + \dots \\ &\quad + \beta T m_{jD} \left( \frac{m_{1D} N_1 + \dots + m_{DD} N_D}{N_D^N} \right) \\ &= \beta T (m_{j1} + \dots + m_{jD}) \\ &= \beta T \end{aligned} \quad (\text{S3})$$

This holds for all columns  $j$  of  $G$ . Therefore using Corollary S1.3 it follows that  $\rho(G) = \beta T$ . This holds for all values of  $s_d$  and  $\gamma$  in the mobility matrix  $m$  and for any resolution (any number of pixels over the same region).

## S2 Final epidemic size

We showed in the main text that the final epidemic size (the final cumulative attack rate) for a population was the same at all resolutions and all mobilities we considered (as long as for all pixels,  $i$  and  $j$ ,  $m_{ij} > 0$ ). Here we demonstrate how this is an outcome of the particular way our model was defined. The derivation is based on those in Refs. [3, 4].

Our SIR meta-population model can be defined as a system of differential equations as follows:

$$\begin{aligned} \frac{dS_i}{dt} &= -\lambda_i S_i \\ \frac{dI_i}{dt} &= \lambda_i S_i - r I_i \\ \frac{dR_i}{dt} &= \gamma I_i, \end{aligned} \quad (\text{S4})$$

where  $r$  is the recovery rate and  $\lambda_i$  is the force of infection in pixel  $i$ :

$$\lambda_i = \beta \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} I_l}{\sum_{p=1}^D m_{pj} N_p}. \quad (\text{S5})$$

$D$  is the total number of pixels,  $m$  is the mobility model and  $N_i$  is the total number of individuals in pixel  $i$ . Transmission occurs during a contact between an infected and a susceptible individual at a rate  $\beta$ .

Then it is straightforward to show that a final equilibrium exists, we represent this equilibrium as  $S_i(\infty)$ ,  $I_i(\infty)$  and  $R_i(\infty)$  and we can show that  $I_i(\infty) = 0$  and  $S_i(\infty) + R_i(\infty) = N_i$ .

We have shown earlier that  $R_0$  for the system is constant and  $R_0 = \beta T$ , where  $T = \frac{1}{r}$ , the mean infectious period.

In each pixel  $i$  the fraction who did not get infected is  $\sigma_i = \frac{S_i(\infty)}{S_i(0)}$ , so the final epidemic size in each pixel is  $x_i = N_i(1 - \sigma_i)$  (recall that  $N_i$  is the total population in pixel  $i$ ). Then the total final epidemic size in the whole population is

$$Z = \frac{\sum_i^D x_i}{\sum_i^D N_i} = \frac{\sum_i^D N_i(1 - \sigma_i)}{\sum_i^D N_i}. \quad (\text{S6})$$

We divide  $\frac{dS_i}{dt}$  (Eqn. (S4)) by  $S_i$  and integrate between 0 and  $\infty$ , then we have:

$$\begin{aligned} \int_0^\infty \frac{dS_i}{S_i} dt &= \int_0^\infty -\lambda_i dt \\ &= - \int_0^\infty \beta \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} I_l}{\sum_{p=1}^D m_{pj} N_p} dt \\ &= -\beta \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} \int_0^\infty I_l dt}{\sum_{p=1}^D m_{pj} N_p} \end{aligned} \quad (\text{S7})$$

and we note that:

$$\begin{aligned} \int_0^\infty \frac{dR_i}{dt} dt &= \int_0^\infty r I_i dt \\ R_i(\infty) - R_i(0) &= r \int_0^\infty I_i dt \\ \text{therefore} \\ \int_0^\infty I_i dt &= \frac{R_i(\infty) - R_i(0)}{r} \\ &= \frac{N_i(1 - \sigma_i)}{r} \end{aligned} \quad (\text{S8})$$

as  $R_i(\infty) - R_i(0) = N_i(1 - \sigma_i)$ , the final epidemic size in pixel  $i$ . Therefore,

$$\int_0^\infty \frac{dS_i}{S_i} dt = -\beta \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} \frac{N_l(1 - \sigma_l)}{r}}{\sum_{p=1}^D m_{pj} N_p} \quad (\text{S9})$$

and as it is also true that:

$$\begin{aligned} \int_0^\infty \frac{dS_i}{S_i} dt &= \log\left(\frac{S_i(\infty)}{S_i(0)}\right) \\ &= \log(\sigma_i). \end{aligned} \quad (\text{S10})$$

we can write (recalling that  $\frac{1}{r} = T$ ):

$$\log(\sigma_i) = -\beta T \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} N_l (1 - \sigma_l)}{\sum_{p=1}^D m_{pj} N_p} \quad (\text{S11})$$

equivalently, as  $x_i = N_i(1 - \sigma_i)$ :

$$x_i = N_i \left[ 1 - \exp \left( -\beta T \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} x_l}{\sum_{p=1}^D m_{pj} N_p} \right) \right]. \quad (\text{S12})$$

Now, with the condition that  $m_{ij} > 0$  for all  $i, j$  (i.e. there is always some contact between every pixel), then if the total final epidemic size is non-zero, then the final epidemic size in each pixel,  $x_i$  or  $(1 - \sigma_i)$ , is also non-zero [3]. To see this, let an arbitrary pixel  $i$  have no infection, so  $\sigma_i = 1$ , then Eqn. (S11) implies that

$$\beta T \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} N_l (1 - \sigma_l)}{\sum_{p=1}^D m_{pj} N_p} = -\log(\sigma_i) = \log(1) = 0. \quad (\text{S13})$$

But, as  $m_{ij} > 0$ , then for the left hand side to be zero it must be that  $(1 - \sigma_l) = 0$  for all  $l$ , so no pixel has infection. Therefore, if  $Z > 0$  then  $x_i > 0$  for all pixels  $i$ .

Now, we focus on the RHS of Eqn. (S11). Note that the matrix  $m$  (mobility) is a positive, right stochastic matrix, as its rows sum to 1. Therefore,  $\rho(m) = 1$  (by definition of a stochastic matrix, and using Corollary S1.3).

We can simplify the RHS as follows (recall that  $\sum_{p=1}^D m_{pj} N_p = N_j^N$ ):

$$\begin{aligned} & -\beta T \sum_{j=1}^D m_{ij} \frac{\sum_{l=1}^D m_{lj} N_l (1 - \sigma_l)}{\sum_{p=1}^D m_{pj} N_p} \\ &= -\beta T \sum_{l=1}^D \sum_{j=1}^D \frac{m_{ij} m_{lj} N_l (1 - \sigma_l)}{N_j^N} \\ &= -\beta T \sum_{l=1}^D (1 - \sigma_l) \left[ \frac{m_{i1} m_{l1} N_l}{N_1^N} + \dots + \frac{m_{iD} m_{lD} N_l}{N_D^N} \right] \\ &= -\beta T \left[ (1 - \sigma_1) \left( \frac{m_{i1} m_{11} N_1}{N_1^N} + \dots + \frac{m_{iD} m_{1D} N_1}{N_D^N} \right) + \dots \right. \\ & \quad \left. + (1 - \sigma_D) \left( \frac{m_{i1} m_{D1} N_D}{N_1^N} + \dots + \frac{m_{iD} m_{DD} N_D}{N_D^N} \right) \right] \end{aligned} \quad (\text{S14})$$

Therefore, let  $C$  be a  $D \times D$  matrix, with entries  $C_{ij} = -\beta T \sum_{l=1}^D \frac{m_{ij} m_{lj} N_l}{N_j^N}$ , then the RHS of Eqn. (S11) is the  $i$ th row of matrix  $C$  multiplied by  $(\mathbf{1} - \sigma)$ , which is a vector of length  $D$  with entries  $(1 - \sigma_j)$ .

Note that the matrix  $C$  is mathematically similar to  $R$ , the next generation matrix (defined in Eqn. (S2)); this means that there exists a matrix  $\Delta$ , such that  $C = \Delta^{-1} R \Delta$ . In this case,  $\Delta$  is the  $D \times D$  matrix with the number of individuals in each pixel,  $N_i$ , on its diagonal. As  $C$  and  $R$  are similar, they have the same spectral radius:  $\rho(C) = \rho(R) = R_0 = \beta T$ . We note that the row sums of  $C$  are all equal to  $\beta T$ , the proof is similar to that for the column sums of  $R$  in the next generation matrix simplification (i.e. note that  $\sum_{j=1}^D \sum_{l=1}^D \frac{m_{ij} m_{lj} N_l}{N_j^N} = 1$ ).

Then, as all rows are equal, transmission in each patch is equal (to  $\beta T$ ) and so, as in [3], the final fraction infected is given implicitly by  $F = 1 - \exp(-R_0 F)$ . With  $R_0 = 1.8$  as in the main text, this can be solved numerically to give  $F = 0.73243$ , as we saw from the simulations.

## References

- [1] Arino J, Van den Driessche P (2003) A multi-city epidemic model. *Mathematical Population Studies* 10: 175–193.
- [2] Cohen J (1979) Random evolutions and the spectral radius of a non-negative matrix. In: *Mathematical Proceedings of the Cambridge Philosophical Society*. Cambridge Univ Press, volume 86, pp. 345–350.
- [3] Ma J, Earn D (2006) Generality of the final size formula for an epidemic of a newly invading infectious disease. *Bulletin of Mathematical Biology* 68: 679–702.
- [4] Andreasen V (2011) The final size of an epidemic and its relation to the basic reproduction number. *Bulletin of Mathematical Biology* 73: 2305–2321.