

Supplementary Materials: Modeling the 2013 Zika outbreak in French Polynesia: Intervention Strategies

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1. Basic Reproduction Number

The basic reproduction number (R_0) for a disease is defined as the average number of new cases of an infection caused by one infected individual during their infectious period in a completely susceptible population [1]. The basic reproduction number for multi category compartmental models can be calculated using the Next Generation Matrix (NGM) [2]. The next generation matrix, K , introduced in [3] relates the numbers of newly infected individuals in the various categories in consecutive generations [4]. The element K_{ij} of the matrix K represents the number of new cases in state i caused by a new born individual in state j . A generation is defined by number of individuals infected by the previous generation. Figure S1 shows a basic example for the next generation matrix and its use in the calculation of R_0 .

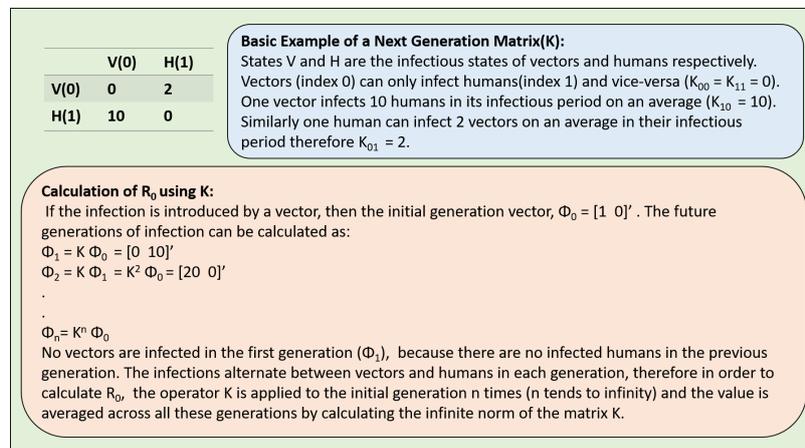


Figure S1. Next Generation Matrix Example

Construction of NGM

The process of constructing the NGM for a heterogeneous epidemiological system is described in detail in [2]. The steps involve:

1. Linearize the infected subsystem to get the Jacobian matrix, J .
2. Decompose the Jacobian matrix into T and Σ , where T is the transmission part and Σ is the transition matrix, such that $J = T + \Sigma$. T represents the birth of new infections and Σ represents all other transitions (recovery, mortality etc). T_{ij} is the rate at which individuals in state i give rise to individuals in state j and $-\Sigma_{ij}^{-1}$ represents the time an individual in state j will spend in state i in their future life.
3. Compute K as $-T\Sigma^{-1}$

Calculation of Reproduction Number

K can be viewed as an iterative linear operator which when applied to the current generation results in the infections in the new generation. In case of vector-borne diseases or other diseases

$$\begin{aligned}
 \frac{\partial E_H}{\partial t} &= \beta_{VH} I_V - \alpha_H E_H \\
 \frac{\partial I_H}{\partial t} &= \alpha_H E_H - \gamma I_H \\
 \frac{\partial E_V}{\partial t} &= \beta_{HV} \frac{N_V}{N_H} I_H - (\mu_{A_h} + \rho_{A_h}) E_V - \alpha_V E_V \\
 \frac{\partial I_V}{\partial t} &= \alpha_V E_V - (\mu_{A_h} + \rho_{A_h}) I_V
 \end{aligned}
 \tag{1}$$

The infected subsystem

involving heterogeneous populations, infections in one kind of population happen in alternate generations. Figure S1 exemplifies this phenomenon. If ϕ_i denotes the i^{th} infection generation then,

$$\begin{aligned}
 \phi_1 &= K\phi_0 \\
 \phi_n &= K^n\phi_0
 \end{aligned}$$

Then, the basic reproduction number R_0 for the infection is defined as the $\frac{1}{n^{th}}$ power of the growth of K in n generations (geometric mean across n generations) as n grows to infinity, $R_0 = \lim_{n \rightarrow \infty} (|K^n|)^{\frac{1}{n}}$ which is also equal to its spectral radius or its largest eigenvalue[4].

For the transmission system defined by equations 1 and equation 2, the infected subsystem consists of 4 categories $\{E_H, I_H, E_V, I_V\}$. Since R_0 is calculated when the entire population is susceptible, $\therefore S_H = N_H$ and $S_V = N_V$ which leads to linear system of ODEs:

$$\begin{aligned}
 T &= \begin{bmatrix} 0 & 0 & 0 & \beta_{VH} \\ 0 & 0 & 0 & 0 \\ 0 & \beta_{HV} \frac{N_V}{N_H} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \\
 \Sigma &= \begin{bmatrix} -\alpha_H & 0 & 0 & 0 \\ \alpha_H & -\gamma & 0 & 0 \\ 0 & 0 & -(\mu_{A_h} + \rho_{A_h} + \alpha_V) & 0 \\ 0 & 0 & \alpha_V & -(\mu_{A_h} + \rho_{A_h}) \end{bmatrix} \\
 -\Sigma^{-1} &= \begin{bmatrix} \frac{1}{\alpha_H} & 0 & 0 & 0 \\ \frac{1}{\gamma} & \frac{1}{\gamma} & 0 & 0 \\ 0 & 0 & \frac{1}{(\mu_{A_h} + \rho_{A_h} + \alpha_V)} & 0 \\ 0 & 0 & \frac{\alpha_V}{(\mu_{A_h} + \rho_{A_h})(\mu_{A_h} + \rho_{A_h} + \alpha_V)} & \frac{1}{(\mu_{A_h} + \rho_{A_h})} \end{bmatrix}
 \end{aligned}
 \tag{2}$$

The transmission matrix(T) and the transition matrix (Σ) for the system

R_0 is calculated as the largest eigenvalue of the matrix $K = -T\Sigma^{-1}$. Estimates for the basic reproduction number R_0 ranged from 1.56-2.95 (95% CI: 2.0767-2.2026).

References

1. Heffernan, J.; Smith, R.; Wahl, L. Perspectives on the basic reproductive ratio. *J R Soc Interface* **2005**, *2*, doi:10.1098/rsif.2005.00425.
2. Deikmann, O.; Heesterbeek, J.; Roberts, M. The construction of next-generation matrices for compartmental epidemic models. *J R Soc Interface* **2010**, *7*, 873–885. doi:10.1098/rsif.2009.0386.
3. Deikmann, O.; Heesterbeek, J.; Roberts, M. On the definition and the computation of the basic reproduction ratio r_0 in models for infectious diseases in heterogeneous populations. *Journal of Mathematical Biology* **1990**, *28*, 365–383. doi: 10.1007/BF00178324.
4. Deikmann, O.; Heesterbeek, J. *Mathematical epidemiology of infectious diseases: Model building, analysis and interpretation*; John Wiley, 2003.