

Supplementary Information Text S1.

Making only small changes to the notation of Kendall (1948; ref. [10] in the main text), the variance in the size of the outbreak at time t is given by the formula

$$(S1) \quad V = \beta_0 \int_0^t \{ \bar{n}_\tau + 2Cov(n_\tau, X_\tau) \} d\tau,$$

where \bar{n}_t is the average number of infected individuals at time t and Cov is the covariance between the number of infectious individuals at t and the total size of the outbreak at t . Of course, for outbreaks that are eventually controlled, the number of infected individuals and covariance will both be brought to zero and the total outbreak size will converge on a finite quantity. Thus, practically speaking, eqn S1 need not be integrated to infinity but just to a large time t_{large} longer than the duration of the typical outbreak. Now, working “backward”, S1 in turn depends on the following quantities: the covariance

$$(S2) \quad Cov = \bar{n}_t \beta_0 \int_0^t \{ 1 + V(n_\tau) / \bar{n}_\tau \} d\tau$$

depending on the variance in the number of infectious individuals at t ,

$$(S3) \quad V(n_t) = e^{-2\rho(t)} \int_0^t e^{\rho(\tau)} \{ \beta_0 + \gamma(\tau) \} d\tau,$$

where

$$(S4) \quad \rho(t) = \int_0^t \{ \gamma(\tau) - \beta_0 \} d\tau.$$

The average total outbreak size is given by

$$(S5) \quad M = 1 + \beta_0 \int_0^\infty e^{-\rho(\tau)} d\tau.$$

As above, M converges at a time $t < \infty$ when infectious individuals are removed from the population.

For the model with removals given by $\gamma(t) = \gamma_1 I(t \leq t^*) + \gamma_2 I(t > t^*)$, the solution to S1 was computed in MATLAB 7.0.1 R14 (MathWorks, Inc., Natick, Massachusetts) using recursive adaptive Simpson quadrature (function `quad`) for the integral in eqn S3 and the trapezoidal rule (function `trapz`) with step size $\tau=0.1$ for the integrals in eqns S1 and S2.