Supplemental materials for 'Review of mathematical models of HSV-2 vaccination: Implications for vaccine development'

Newton model reproduction

Because Newton et al. (2000) only reported on reductions in prevalence associated with vaccination, and also because the model was fairly straight-forward to implement exactly as the authors had done, we reproduced their model in R using the deSolve package to solve the differential equations. The differential equations are:

$$
\frac{dS}{dt} = -\mu S - \tau \kappa S - \beta S (\rho_H I_H + \rho_M I_M + \rho_L I_L)(1 - VE_I) + \mu N
$$

\n
$$
\frac{dE}{dt} = -\mu E - \nu_1 E + \beta S (\rho_H I_H + \rho_M I_M + \rho_L I_L)(1 - VE_I)
$$

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$$
\frac{dI_H}{dt} = -\mu I_H + \nu_1 E - \nu_2 I_H
$$

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$$
\frac{dI_M}{dt} = -\mu I_M - \nu_4 I_M + \nu_3 I_L
$$

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$$
\frac{dI_L}{dt} = -\mu I_L + \nu_4 I_M + \nu_2 I_H - \nu_3 I_L
$$

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$$
\frac{dV}{dt} = -\mu V + \tau \kappa S
$$

and the associated parameter symbols, descriptions, and values used in their manuscript and here are:

Under a prophylactic vaccine, Newton $et al. (2000)$ assume sterilizing immunity vaccine effects, where susceptible individuals who are vaccinated enter a vaccinated compartment, and are no longer able to be infected. Under this scenario, κ takes a non-zero value, and determines the rate of vaccination.

Under a therapeutic vaccine, Newton *et al.* (2000) assume all currently and infected individuals have reduced infectivity, determined by VE_I .

Initial conditions are such that, from a total stable population size of 10000, 9500 are S, 1 is E, 2 are I_H , 470 are I_L , and 27 are I_R . Under either vaccination scenario, the model is ran from its initial conditions for 20 years before vaccination begins.

Vaccine impact is calculated by comparing the incidence rate in each vaccination scenario to the incidence rate in the null scenario 10 years after vaccination began.

Figure S1

Figure S2

Comparison of incremental vaccine impact in Freeman et al. when a single feature is not present 10 years after vaccination began. Vaccine impact is defined as the incidence rate reduction 10 years after vaccination began. Scenarios defined along the y-axis are compared to a base-scenario that had the greatest vaccine impact in which all four features (i.e. catch-up vaccination, susceptibility effects, vaccination of both sexes, and breakthrough effects) are present. Each ratio is compared assuming the same level of coverage (color in the figure), vaccine efficacy (shape), and duration of conferred vaccine effects (left versus right panel). Lack of catch-up vaccination has the strongest detrimental effect, since vaccine impact is about 60% lower without it.

Table S1

Table 1: Characteristics and predictions of HSV-2 vaccine modeling literature scenarios. Biological vaccine effects in parentheses reflect vaccines with somecombination of susceptibility (S) , infectiousness (I) , and pathogenicity (P) effects. Multiple scenarios per article are possible when an article considered different scenarios defined by the type(s) of biological vaccine effects being conferred. Articles are organized by vaccine design (prophylactic, prophylactic with breakthrough effects, and therapeutic) and within these categories by increasing magnitude of impact. 1-sex models do not differentiate between males and females; 2-sex models represent females and males separately, allowing for vaccination of one or both sexes. Bounds represent upper and lower predictions either based on ranges from all the samples generated (Schwartz), or upper and lower estimates when only two data points were predicted (Garnett, Alsallaq,Freeman, Newton). [∗]Vaccine increased duration of symptomatic period compared to unvaccinated