Basic model for vaccination against seasonal influenza (or H1N1)

The total population at time t, denoted by $N(t)$, is sub-divided into the disjoint compartments of susceptible ($S(t)$), vaccinated ($V(t)$), newly-infected (i.e., latent/exposed) ($E(t)$), infectious ($I(t)$) and recovered ($R(t)$), so that

$$N(t) = S(t) + V(t) + E(t) + I(t) + R(t).$$

The model is given by the following equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Pi + \omega_v V - \beta \frac{SI}{N} - \xi_v S - \mu S, \\
\frac{dV}{dt} &= \xi_v S - \beta(1-\varepsilon_v)\frac{VI}{N} - \omega_v V - \mu V, \\
\frac{dE}{dt} &= \beta \frac{SI}{N} + \beta(1-\varepsilon_v)\frac{VI}{N} - (\sigma + \mu)E, \\
\frac{dI}{dt} &= \sigma E - (\gamma + \mu + \delta)I, \\
\frac{dR}{dt} &= \gamma I - \mu R.
\end{aligned} \tag{1}$$

The state variables and parameters of the model, as well as the baseline values of the parameters, are given in the tables below. The main assumptions made in the formulation of the model are:

1. Homogeneous-mixing (i.e., well-mixed population): every member of the community is equally likely to meet with (and acquire infection from) every other member of the community. In other words, the simple model does not account for heterogeneities such as age-related contact patterns, spatial and temporal heterogeneity etc.

2. Exponentially-distributed waiting time in each epidemiological compartment.

3. The vaccine does not offer perfect protection against infection. It offers partial protection, with efficacy $0 < \varepsilon_v < 1$, against acquisition of infection.

4. Continuous vaccination (no cohort/childhood vaccination).

The *vaccination reproduction number* (denoted by $\mathcal{R}_V$) of the influenza vaccination model is given by

$$\mathcal{R}_V = \mathbb{R}_0 \left(1 - \varepsilon_v f_v\right),$$

where $f_v = \dfrac{\xi_v}{\xi_v + \omega_v + \mu}$ is the overall fraction of susceptible individuals vaccinated at steady-state and $\mathbb{R}_0$ is the *basic reproduction number*, and is given by:

$$\mathbb{R}_0 = \beta \left(\frac{\sigma}{\sigma + \mu}\right) \left(\frac{1}{\gamma + \mu + \delta}\right).$$

The threshold quantity $\mathbb{R}_0$ is the average number of new cases generated by a typical (not atypical...such as a super-spreader) infected individuals if introduced in a completely susceptible population (i.e., no one is immunized or has immunity due to recovery from prior infection). On the other hand, the vaccination reproduction number ($\mathcal{R}_V$) is the average number of new cases generated by a typical infected individual introduced into a population where a certain proportion of the population is vaccinated.

Vaccine-induced herd immunity is achieved if

$$f_v > \frac{1}{\varepsilon_v}\left(1 - \frac{1}{\mathbb{R}_0}\right).$$

Table 1: Description of state variables and parameters of the model

State variable	Description
$S(t)$	Population of unvaccinated susceptible individuals
$V(t)$	Population of vaccinated susceptible individuals
$E(t)$	Population of newly-infected (latent/exposed) individuals
$I(t)$	Population of infectious (symptomatic) individuals
$R(t)$	Population of recovered individuals

Parameter	Description
Π	Recruitment rate (birth/immigration) into the population
ξ_v	Vaccination rate (continuous vaccination)
β	Effective contact rate
μ	Natural death rate (i.e., $1/\mu$ is the average lifespan in the community)
ε_v	Vaccine efficacy
ω_v	Vaccine waning rate
σ	Progression rate from E to the symptomatic class I (i.e., $1/\sigma$ is the incubation period)
γ	Recovery rate
δ	Disease-induced mortality rate

Key Points on Parameter Estimation

(a) The demographic parameters (Π and μ, for birth and natural death rate, respectively) are estimated based on census data. In particular, the estimated for μ is obtained from the fact that $1/\mu$ equals the average life span in the community. For the US, $1/\mu$ is approximately 78 years. Thus, $\mu \approx 1/(78 * 365)$ *per* day. Further, in the absence of disease, the total population is given by its equilibrium value Π/μ. For instance, if the total population of the cohort group is 1 million, then $\Pi/\mu = 1$ million. Since we already know what the value of μ is, we can then use this equation to obtain an estimate for Π.... giving $\Pi = \mu$ times 1 million. So, this is how the values of Π and μ should be estimated for each of the jurisdiction or country you are considering in the simulations.

(b) The effective contact rate (β) is estimated based on the value of the basic reproduction number ($\mathbb{R}_0$). Taking the average value of $\mathbb{R}_0$ for influenza to be 1.4, we can estimate β as $\beta = (\gamma + \mu + \delta) * \mathbb{R}_0$. **(You can also use an estimate of β from the literature)**

(c) The mortality rate for influenza is ..... **(there should be good estimates from the literature)**

Table 2: Estimated values for the parameters of the model

Parameter	Baseline value (*per* day)	Source
Π	μ times the total cohort population	Estimated from census data
μ	$1/(78 * 365)$	Estimated from census data
β	$1.4 * (\gamma + \mu + \delta)$	Estimated
ξ_v	????	Estimated (check literature)
ω_v	$1/(1 * 365)$	Estimated (based on 1 year or season of protection)
ε_v	0.3-0.6	Estimated (check literature)
σ	1/10	Estimated (incubation period is from 7 to 12 days)
γ	1/7	Estimated (check literature)
δ	???	Estimated (check literature)