Basic model for measles vaccination

The total population at time t, denoted by $N(t)$, is sub-divided into the disjoint compartments of susceptible ($S(t)$), successfully- vaccinated (i.e., those who received the two MMR doses) ($V(t)$), 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:

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

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 (i.e., the 1 to 6-year old cohort group that are targeted for vaccination) 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. Vaccinated individuals (i.e., those who received the two MMR doses) are fully protected against the acquisition of measles infection. Data shows that the two

doses of the MMR vaccine provides 97% protected efficacy in vaccinees.... so, it is reasonable to assume perfect protection (keeps the model simple(r)).

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

$$\mathcal{R}_V = (\beta)\left[\frac{\omega_V + \mu(1-p)}{\omega_V + \mu}\right]\left(\frac{\sigma}{\sigma+\mu}\right)\left(\frac{1}{\gamma+\mu+\delta}\right).$$

The *basic reproduction number* (i.e., the reproduction number in the absence of vaccination), denoted by $\mathbb{R}_0$ (obtained by setting $\omega_V = p = 0$ in $\mathcal{R}_V$), 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 fraction of the population is vaccinated.

The vaccination reproduction number can be re-written in terms of $\mathbb{R}_0$ as below:

$$\mathcal{R}_V = (1-m)\mathbb{R}_0,$$

where $m = \dfrac{p\mu}{\omega_V + \mu}$ is the overall fraction of individuals vaccinated at steady-state. Herd immunity is achieved if $m > 1 - \frac{1}{\mathbb{R}_0}$.

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

State variable	Description
$S(t)$	Population of susceptible individuals
$V(t)$	Population of successfully vaccinated 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	Birth rate
p	Proportion of individuals (1 to 6-year olds) vaccinated
β	Effective contact rate
μ	Natural death rate (i.e., $1/\mu$ is the average lifespan in the community)
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
ω_R	Rate of loss of natural (infection-acquired) immunity

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 measles to be 17, we can estimate β as $\beta = (\gamma + \mu + \delta) * \mathbb{R}_0$.

(c) The mortality rate for measles is generally low (between 100,000 to 150,000 deaths globally *per* year). Hence, it is probably plausible to set δ to zero.

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
p	0.60	Heffernan and Keeling, 2012
μ	$1/(78 * 365)$	Estimated from census data
β	$17 * (\gamma + \mu + \delta)$	Estimated
ω_V	$1/(10 * 365)$	Estimated (based on 10 years of protection)
σ	$1/10$	Estimated (incubation period is from 7 to 12 days)
γ	$1/7$	Heffernan and Keeling, 2012
δ	0	Estimated
ω_R	$1/(10 * 365)$	Estimated

Some Random Thoughts

1. Probably a good idea to set the vaccine proportion (p) as an input parameter. Let the players choose the vaccine coverage for their location (city, state, country etc.) But ensure that this is incorporated as a fraction in the app ($0 < p \leq 1$).

2. Note that β will be different for different regions or nations (since it is defined in terms of γ, μ and δ, which may vary between places). So, you probably do not need to incorporate the density-related heterogeneity we talked about yesterday.

3. Players to input the total size of the vaccinated cohort (i.e., the total population of 1 to 6-year olds) and average lifespan in their community. This will then be used to estimate Π and μ for their location.

4. Note that I set the vaccine waning rate (ω_V) and the waning rate of natural immunity (ω_R) to be the same.... I couldn't find an estimate for the latter (it may be good to check; but I think $\omega_V = \omega_R$ is reasonable).