Model for Polio Transmission Dynamics

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1 Model Formulation

The models to be developed are based on splitting the total population of children in the community at time t, denoted by $N(t)$, into the mutually-exclusive compartments of unvaccinated susceptible children ($S(t)$), vaccinated susceptible children ($V(t)$), exposed (newly-infected) children ($E(t)$), symptomatically-infectious children ($I(t)$, children children due to the virus ($P(t)$) and recovered children ($R(t)$, so that

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

1.1 Model for Polio Virus Transmission Dynamics

$$\begin{aligned}
\frac{dS}{dt} &= \Pi(1-\phi) + \omega_v V - \beta S\frac{I}{N} - \mu S,\\
\frac{dV}{dt} &= \Pi\phi - (\omega_v + \mu)V,\\
\frac{dE}{dt} &= \beta S\frac{I}{N} - (\sigma + \mu)E,\\
\frac{dI}{dt} &= \sigma E - (\kappa + \gamma + \mu)I,\\
\frac{dP}{dt} &= \kappa I - \mu P,\\
\frac{dR}{dt} &= \gamma I - \mu R.
\end{aligned} \tag{1.1}$$

Main assumptions and simplifications

1. We only consider cohort vaccination: that is, we consider the proportion of infants and young children (under 5) who received all four doses. We do not include continuous (booster) vaccination for (much) older children
2. Vaccine offers perfect protection against acquisition of infection... but the protection can wane (at a rate ω_v)
3. Homogeneous mixing (every child is equally likely to mix with every other child in the community)
4. Polio-induced mortality is negligible (hence, neglected in the modeling)
5. Recovery induces permanent immunity against reinfection.

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

$$\mathbb{R}_V = \beta\left[\frac{\omega_v + \mu(1-\phi)}{\omega_v + \mu}\right]\left(\frac{\sigma}{\sigma+\mu}\right)\left(\frac{1}{\kappa+\gamma+\mu}\right). \tag{1.2}$$

Table 1: Description of state variables of the Polio model.

State variable	Description
S	Population of unvaccinated susceptible children
V	Population of vaccinated susceptible children
E	Population of exposed (recently-infected) children
I	Population of symptomatically-infectious children
P	Population of polio-paralysed children
R	Population of recovered children

Table 2: Description of the parameters of the model (1.1).

Parameter	Description
β	Effective contact rate
Π	Recruitment rate into the community (by birth or immigration)
ϕ	Fraction of infants/children vaccinated (cohort vaccination)
ω_v	Vaccine waning rate
σ	Progression rate from exposed to infectious class I
κ	Rate of polio-induced paralysis in children
γ	Recovery rate
μ	Natural mortality rate

Table 3: Parameter values of the model (1.1).

Parameter	Values
β	??? day^{-1}
Π	441 day^{-1}
ϕ	0.56 (dimensionless)
ω_v	0???
ψ	1/7 day^{-1}
σ	1/7 day^{-1}
κ	1/200 day^{-1}
γ	1/16 day^{-1}
μ	0.00001119 day^{-1}

In the absence of vaccination (i.e., if $\phi = \xi_v = \omega_v = V = 0$), the vaccination reproduction number ($\mathcal{R}_V$) reduces to the basic reproduction number (denoted by $\mathbb{R}_0$) given by

$$\mathbb{R}_0 = \beta \left(\frac{\sigma}{\sigma + \mu} \right) \left(\frac{1}{\kappa + \gamma + \mu} \right). \tag{1.3}$$

Define $f_v = \dfrac{\mu\phi}{\omega_v + \mu}$, the fraction of infants/children vaccinated at (disease-free) steady-state. The vaccination reproduction number can then be re-written (in terms of $\mathbb{R}_0$ and f_v) as:

$$\mathbb{R}_V = \mathbb{R}_0 \left(1 - f_v\right). \tag{1.4}$$

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 ($\mathbb{R}_V$) 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

$$f_v > \left(1 - \frac{1}{\mathbb{R}_0}\right). \tag{1.5}$$

Key Points on Parameter Estimation

(i) 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.

(ii) The effective contact rate (β) is estimated based on the value of the basic reproduction number ($\mathbb{R}_0$). The basic reproduction number of polio is typically estimated to lie in the range 5 to 7. So, it is plausible to take the average value of $\mathbb{R}_0$ for polio to be 6. Hence, you can estimate β as $\beta = (\gamma + \mu + \delta) * \mathbb{R}_0$ (with $\mathbb{R}_0 = 6$).