# COVID-19 Vaccination Model

The model is developed by splitting the total population at time $t$, denoted by $N(t)$, into sub-populations of unvaccinated susceptible ($S_u(t)$), vaccinated susceptible ($S_v(t)$), exposed ($E(t)$), asymptomatically-infectious ($I_a(t)$), symptomatically-infectious ($I_s(t)$), hospitalized or self-isolated ($I_h(t)$) and recovered ($R(t)$) individuals. It is assumed that the vaccine is imperfect, so that breakthrough infection (i.e., the infection of vaccinated susceptible individuals) can occur (but at a reduced rate, compared to the infection of unvaccinated susceptible individuals). It is also assumed that the vaccine-induced immunity may not last a lifetime. The vaccination model is given by the following equations (where a dot represents differentiation with respect to time $t$):

$$
\begin{aligned}
\dot{S}_u &= \Pi + \omega_v S_v - \left(\frac{\beta_s I_s + \beta_a I_a + \beta_h I_h}{N}\right) S_u - (\mu + \xi_v) S_u, \\
\dot{S}_v &= \xi_v S_u \ - (1-\varepsilon_v)\left(\frac{\beta_s I_s + \beta_a I_a + \beta_h I_h}{N}\right) S_v - (\mu + \omega_v) S_v, \\
\\
\dot{E} &= \left(\frac{\beta_s I_s + \beta_a I_a + \beta_h I_h}{N}\right) S_u + (1-\varepsilon_v)\left(\frac{\beta_s I_s + \beta_a I_a + \beta_h I_h}{N}\right) S_v - (\mu + \sigma) E, \\
\dot{I}_s &= (1-r)\sigma E - (\mu + \phi_s + \gamma_s + \delta_s) I_s, \\
\dot{I}_a &= r\sigma E - (\mu + \gamma_a) I_a, \\
\dot{I}_h &= \phi_s I_s - (\mu + \gamma_h + \delta_h) I_h, \\
\dot{R} &= \gamma_s I_s + \gamma_a I_a + \gamma_h I_h - \mu R.
\end{aligned}
$$

Table 1: Description of the state variables of the model

| **State variable** | **Description** |
|---|---|
| $S_u$ | Population of unvaccinated susceptible individuals |
| $S_v$ | Population of vaccinated susceptible individuals |
| $E$ | Population of exposed (newly-infected) individuals |
| $I_a$ | Population of asymptomatically-infectious individuals |
| $I_s$ | Population of symptomatically-infectious individuals |
| $I_h$ | Population of hospitalized (or self-isolated) individuals |
| $R$ | Population of recovered individuals |

Table 2: Description of the parameters of the model.

| **Parameters** | **Description** |
|---|---|
| $\Pi$ | Recruitment (birth or immigration) rate into the population |
| $\mu$ | Natural mortality rate |
| $\xi_v$ | *Per capita* vaccination rate |
| $0 < \varepsilon_v \leq 1$ | Vaccine efficacy |
| $\omega$ | Vaccine waning rate |
| $\beta_a$ | Effective contact rate for asymptomatically-infectious individuals |
| $\beta_s$ | Effective contact rate for symptomatically-infectious individuals |
| $\beta_h$ | Effective contact rate for hospitalized (or self-isolated)individuals |
| $\sigma$ | Progression rate from exposed to symptomatic or asymptomatic class |
| $0 < r < 1$ | Proportion of exposed individuals who become asymptomatic after incubation |
| $\phi_s$ | Hospitalization rate for symptomatically-infectious individuals |
| $\gamma_a$ | Recovery rate for asymptomatically-infectious individuals |
| $\gamma_s$ | Recovery rate for symptomatically-infectious individuals |
| $\gamma_h$ | Recovery rate for hospitalized individuals |
| $\delta_h$ | Disease-induced mortality rate for hospitalized individuals |

Table 3: Parameter values of the model

| **Parameter** | **Value** |
|---|---|
| $\Pi$ | $1.2 \times 10^4$/day |
| $\mu$ | $1/(79 \times 365)$/day |
| $\xi_v$ | Variable |
| $\varepsilon_v$ | 0.95 (for Pfizer or Moderna) and 0.7 for AstraZeneca |
| $\omega$ | 0/day |
| $\beta_s$ | 0.224334/day |
| $\beta_a$ | $1.5 \times \beta_s$/day |
| $\beta_h$ | $0.5 \times \beta_s$/day |
| $\sigma$ | 1/12/day |
| $r$ | 0.8 |
| $\phi_s$ | 1/6/day |
| $\gamma_s$ | 1/10/day |
| $\gamma_a$ | 1/5/day |
| $\gamma_h$ | 1/8/day |
| $\delta_h$ | 0.009505/day |

The model has a unique disease-free equilibrium given by:

$$\mathcal{E}_{0V} = (S_u^*,\, S_v^*,\, E^*,\, I_s^*,\, I_a^*,\, I_h^*,\, R^*) = \left( \frac{\Lambda(\mu + \omega_v)}{\mu(\mu + \xi_v + \omega_v)},\, \frac{\Pi \xi_v}{\mu(\mu + \xi + \omega_v)},\, 0,\, 0,\, 0, 0, 0 \right).$$

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

$$\mathcal{R}_{cv} = \mathcal{R}_0 \left(1 - \varepsilon_v f_v\right), \tag{0.1}$$

where, $f_v = \frac{\xi_v}{\mu+\xi_v+\omega_v}$ is the fraction of individuals vaccinated at the disease-free steady-state.

In the absence of vaccination, the threshold quantity $\mathcal{R}_{cv}$ reduces to the basic reproduction number ($\mathcal{R}_0$), given by:

$$\mathcal{R}_0 = \mathcal{R}_{cv}|_{\xi_v = S_v^* = 0} = \frac{\sigma}{\mu+\sigma}\left[\frac{r\beta_a}{\mu+\gamma_a} + \frac{(1-r)\beta_s}{(\mu+\phi_s+\gamma_s+\delta_s)} + \frac{(1-r)\beta_h\phi_s}{(\mu+\phi_s+\gamma_s+\delta_s)(\mu+\gamma_h+\delta_h)}\right]. \tag{0.2}$$

## Herd Immunity Threshold

It should be mentioned that, for vaccine-preventable diseases, not all susceptible individuals can be immunized when a vaccine is available. For instance people with underlying health conditions, or females who are pregnant or people who opt out of vaccination for various reasons (traditional or other reasons) may not be vaccinated. In particular, vaccinating people in the first two categories may worsen their condition. The notion of *herd immunity* is used to determine the minimum proportion of the community-wide immunity that is needed to ensure that those that cannot be immunized can also be protected from acquiring infection. In other words, herd immunity is associated with the indirect protection members of a community receive when a large percentage of the population has become immune to the infectious disease due to natural recovery from prior infection or vaccination [**?**]. Sweden adopted the first option, of allowing people to acquire infection and (hopefully) recover. This has not proven to be successful to date. Vaccination remains the safest and fastest way to achieve herd immunity for vaccine-preventable diseases.

To compute the herd immunity threshold associated with the vaccination model, we set the expression for the reproduction number, $\mathcal{R}_{cv}$, to one and solve for $f_v$. This gives

$$f_v = \frac{1}{\varepsilon_v}\left(1 - \frac{1}{\mathcal{R}_0}\right) = f_v^c. \tag{0.3}$$

It follows from (0.1) and (0.3) that $\mathcal{R}_{cv} < (>)1$ if $f_v > (<) f_v^c$. Further, $\mathcal{R}_{cv} = 1$ whenever $f_v = f_v^c$. This shows that vaccination will effectively control the pandemic if $f_v > f_v^c$ (i.e., if enough members of the community have been vaccinated to ensure $f_v > f_v^c$). Vaccination will not eliminate the disease if $f_v < f_v^c$ (the disease will persist in the population in this case). This result can be summarized as follows:

**A perfect anti-COVID-19 vaccine (i.e., a vaccine with $\varepsilon_v = 1$) can lead to the elimination of the pandemic if $f_v > f_v^c$ (i.e., if $\mathcal{R}_{cv} < 1$). If $f_v < f_v^c$ (i.e., if $\mathcal{R}_{cv} > 1$), then the disease will persist in the population.**