Justification for ϕ and calculation of its value from empirical estimates.

To derive an SIR model that doesn't allow movement of sick individuals, we begin with a basic susceptible/infectious/recovered epidemiological model. We modify this model by partitioning the infectious class into 3 compartments: pre-symptomatic (P), asymptomatic (A), and symptomatic (H), such that $P + A + H = I$.

The model with these three compartments plus the susceptible (S) and recovered (R) classes, applied to two populations ($i = A,B$; $i \neq j$) is

$$\begin{aligned}
\frac{dS_i}{dt} &= -\frac{S_i}{N_i}\left(\beta_P P_i + \beta_A A_i + \beta_H H_i\right) - \mu S_i + \mu S_j \\
\frac{dP_i}{dt} &= \frac{S_i}{N_i}\left(\beta_P P_i + \beta_A A_i + \beta_H H_i\right) - \delta P_i - \mu P_i + \mu P_j \\
\frac{dA_i}{dt} &= (1-p)\delta P_i - \gamma_A A_i - \mu A_i + \mu A_j \\
\frac{dH_i}{dt} &= p\delta P_i - \gamma_H H_i - \mu H_i \\
\frac{dR_i}{dt} &= \gamma_A A_i + \gamma_H H_i - \mu R_i + \mu R_j
\end{aligned} \qquad . \qquad (1)$$

The model works as follows. Individuals in the pre-symptomatic, asymptomatic, and symptomatic classes each infect susceptible individuals at class-specific rates, β_P, β_A, and β_H. Every individual, once acquiring the disease, begins in the pre-symptomatic class (P). They stay in that class for $1/\delta$ days. Upon leaving the pre-symptomatic class, individuals either develop symptoms with probability p, or do not with probability $1 - p$, and join the asymptomatic class. Those in the asymptomatic class recover after $1/\gamma_A$ days and those in the symptomatic class recover after $1/\gamma_H$ days or die at rate μ.

All individuals in the population, except symptomatic individuals, move between populations.

The model given by equation (1) can be approximated by an SIR model under the assumption that the distribution of pre-symptomatic, asymptomatic, and symptomatic individuals within the infectious class is constant. Mathematically, this means that P_i/I_i, A_i/I_i, and H_i/I_i are constant over time. This won't be generally true, but as serves as a simplifying assumption to account for differential movement while still keeping the model simple.

With a constant distribution of infectious classes, equation (1) above can be rewritten in the SIR model as follows

$$\frac{dS_i}{dt} = -\frac{S_i I_i}{N_i}\beta - mS_i + mS_j$$

$$\frac{dI_i}{dt} = \frac{S_i I_i}{N_i}\beta - \gamma I_i - m\frac{H_i}{I_i}I_i - m\left(\frac{P_i}{I_i}+\frac{A_i}{I_i}\right)I_i + m\left(\frac{P_j}{I_j}+\frac{A_j}{I_j}\right)I_j \qquad (2)$$

$$\frac{dR_i}{dt} = \gamma I_i - mR_i + mR_j$$

where $\beta = \left(\beta_P \frac{P_i}{I_i} + \beta_A \frac{A_i}{I_i} + \beta_H \frac{H_i}{I_i}\right)$ and $\gamma = \left(\gamma_A \frac{A_i}{I_i} + \gamma_H \frac{H_i}{I_i}\right)$ are the transmission and recovery rates of the total infectious class. Note that these are weighted averages across the distribution of infectious individuals. Again, provided that this distribution is constant, β and γ are constant.

Now define $\phi = A_i/I_i + P_i/I_i$, the fraction of infectious individuals that don't have symptoms and so move between populations. Since $P_i + A_i + H_i = I_i$, it follows that $H_i/I_i = 1 - \phi$. Using these in equation (2) above yields

$$\frac{dS_i}{dt} = -\frac{S_i I_i}{N_i}\beta - mS_i + mS_j$$

$$\frac{dI_i}{dt} = \frac{S_i I_i}{N_i}\beta - \gamma I_i - m(1-f)I_i - mfI_i + mfI_j,$$

$$\frac{dR_i}{dt} = \gamma I_i - mR_i + mR_j$$

which is the constant parameter version of the model.

To find a value for ϕ, we approximate the distribution of infectious individuals (P/I, A/I, H/I) as the expected fraction of time each contributes to the entire infectious duration. The total infectious duration is composed of three times 1) the pre-symptomatic duration, $1/\delta$, 2) the average asymptomatic duration, conditional on being asymptomatic, $(1 - p)/\gamma_A$, and 3) the average symptomatic duration, conditional on developing symptoms, $p/(\gamma_H + \mu)$. The sum total of these is the expected total infectious duration, $1/\delta + (1 - p)/\gamma_A + p/(\gamma_H + \mu)$. The expected proportion of the total infectious durations attributable to each class is thus

$$\frac{P}{I} \approx \frac{\delta^{-1}}{\delta^{-1} + (1-p)\gamma_A^{-1} + p(\gamma_H + \mu)^{-1}}$$

$$\frac{A}{I} \approx \frac{(1-p)\gamma_A^{-1}}{\delta^{-1} + (1-p)\gamma_A^{-1} + p(\gamma_H + \mu)^{-1}}.$$

$$\frac{H}{I} \approx \frac{p(\gamma_H + \mu)^{-1}}{\delta^{-1} + (1-p)\gamma_A^{-1} + p(\gamma_H + \mu)^{-1}}$$

Plugging these into the definition ϕ yields

$$f = \frac{\delta^{-1} + (1-p)\gamma_A^{-1}}{\delta^{-1} + (1-p)\gamma_A^{-1} + p(\gamma_H + \mu)^{-1}}. \qquad (3)$$

Moghadas et al. (2020) have the following average estimates: δ^{-1} = 2.3 days, γ_A^{-1} = 5 days, and γ_H^{-1} = 3.2 days. They have age-specific values for p, so we take the simple average of the age-specific probabilities, which yields p = 0.3. We also take $\mu = 0.04$ days^{-1} from Gatto et al. (2020). Plugging these values into equation (3) yields $\phi = 0.872$, which is the value we use for numerical results.

References

Gatto, M., E. Bertuzzo, L. Mari, S. Miccoli, L. Carraro, R. Casagrandi, and A. Rinaldo. 2020. Spread and dynamics of the COVID-19 epidemic in Italy: Effects of emergency containment measures. Proceedings of the National Academy of Sciences of the United States of America **117**:10484-10491.

Moghadas, S. M., M. C. Fitzpatrick, P. Sah, A. Pandey, A. Shoukat, B. H. Singer, and A. P. Galvani. 2020. The implications of silent transmission for the control of COVID-19 outbreaks. Proceedings of the National Academy of Sciences of the United States of America **117**:17513-17515.