Staff testing model/preventing introductions to congregate facilities/settings

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See google doc for additional background/ideas/outlining

Model framework and parameterization for SARS-CoV2

Building on previous work investigating the effects of non-pharmaceutical interventions [1] and testing [2] on the transmission of infectious diseases, we model individual contributions to infection through time from an infectiousness profile, β_t, generated from key biological parameters of the disease that determine the distribution of infectiousness over time. We model β_t using a triangle distribution with infectiousness beginning after the latent period, ending after the duration of the infectious period, and peaking at some point in between ($a = t_{latent}$, $b = t_{tot} = t_{infectious} + t_{latent}$, $c = t_{peak}$, and a<c<b).

The viral dynamics of SARS-CoV2 are challenging in terms of control efforts, as asymptomatic and presymptomatic transmission caused by high infectiousness in the absence of symptoms are common CITE, CITE. In terms of the infectiousness profile for SARS-CoV2, this means that peak infectiousness t_{peak} tends to coincide with the onset of symptoms (for cases that are symptomatic), but occurs after completion of the latent period (i.e. $t_{peak} \approx t_{incubation} > t_{latent}$). The expected number of new cases generated at time t is thus $r_t = \mathcal{R}\beta_t$, where $\mathcal{R}$ is the effective reproduction number interpreted as the expected number of cases generated by a new case over the duration of the infectious period. The model therefore assumes that new cases are most likely to be generated around the time of peak infectiousness, t_{peak}. Table X lists the distributions of $t_{incubation}$, t_{latent}, and $t_{infectious}$ used here.

In the presence of interventions that isolate infectious individuals prior to t_{tot}, e.g. through contact tracing, self-isolation following the onset of symptoms, or testing, the effect of isolation on $\mathcal{R}$ can be directly estimated from the time to isolation as $\mathcal{R}_{iso} = \mathcal{R}\big(1 - \int_{t_{iso}}^{t_{tot}} \beta_t dt\big)$, where t_{iso} is the time at which isolation occurs. Reducing $\mathcal{R}_{iso}$ via improved contact tracing or more frequent testing can thus be envisioned as removing a larger slice from the overall infectiousness triangle by reducing t_{iso}. The size of the slice removed is dependent on the shape of the overall triangle distribution, which is primarily determined by t_{tot} and t_{peak}, and the location of t_{iso} in relation to t_{peak}. For instance, if $t_{iso} > t_{peak}$, then the proportional reduction in $\mathcal{R}$ can be estimated as $\frac{2}{t_{infectious}(t_{tot} - t_{peak})} \int_{t_{iso}}^{t_{tot}} (t_{tot} - t) dt$. Other interventions that reduce $\mathcal{R}$ across all levels of infectiousness such as wearing a mask or reducing the contact rate between infectious and susceptible individuals can also be accommodated simply by multiplying $\mathcal{R}$ by a constant.

Analytic results: influence of testing frequency and delay on t_{iso} and $\mathcal{R}_{iso}$

Assuming testing is independent of symptoms, known contacts, and other reasons for explicitly seeking testing, we can estimate the probability of going t days without being tested from the testing frequency, f, as $(1 - f)^t$ and the probability that $t_{iso} \leq \tau$ as $\mathrm{P}(t_{iso} = \tau | f) = 1 - (1 - f)^\tau$, assuming isolation occurs immediately after testing. Given substantial turnaround times between testing and isolation, particularly when relying on PCR-based tests, we can also incorporate the delay between testing and isolation, d, as: $\mathrm{P}(t_{iso} = \tau | f, d) = 1 - \left(1 - \frac{1}{f^{-1} + d}\right)^\tau$, where f^{-1} is simply the average number of days between tests.

This allows for incorporation of the testing frequency and delay into estimation of $\mathcal{R}_{iso}$:

$$\mathbb{E}[\mathcal{R}_{iso}|\beta_t, f, d] = \mathcal{R} \int_{\tau=t_{latent}}^{t_{infectious}} \beta_\tau \left(1 - \frac{1}{f^{-1} + d}\right)^\tau d\tau$$

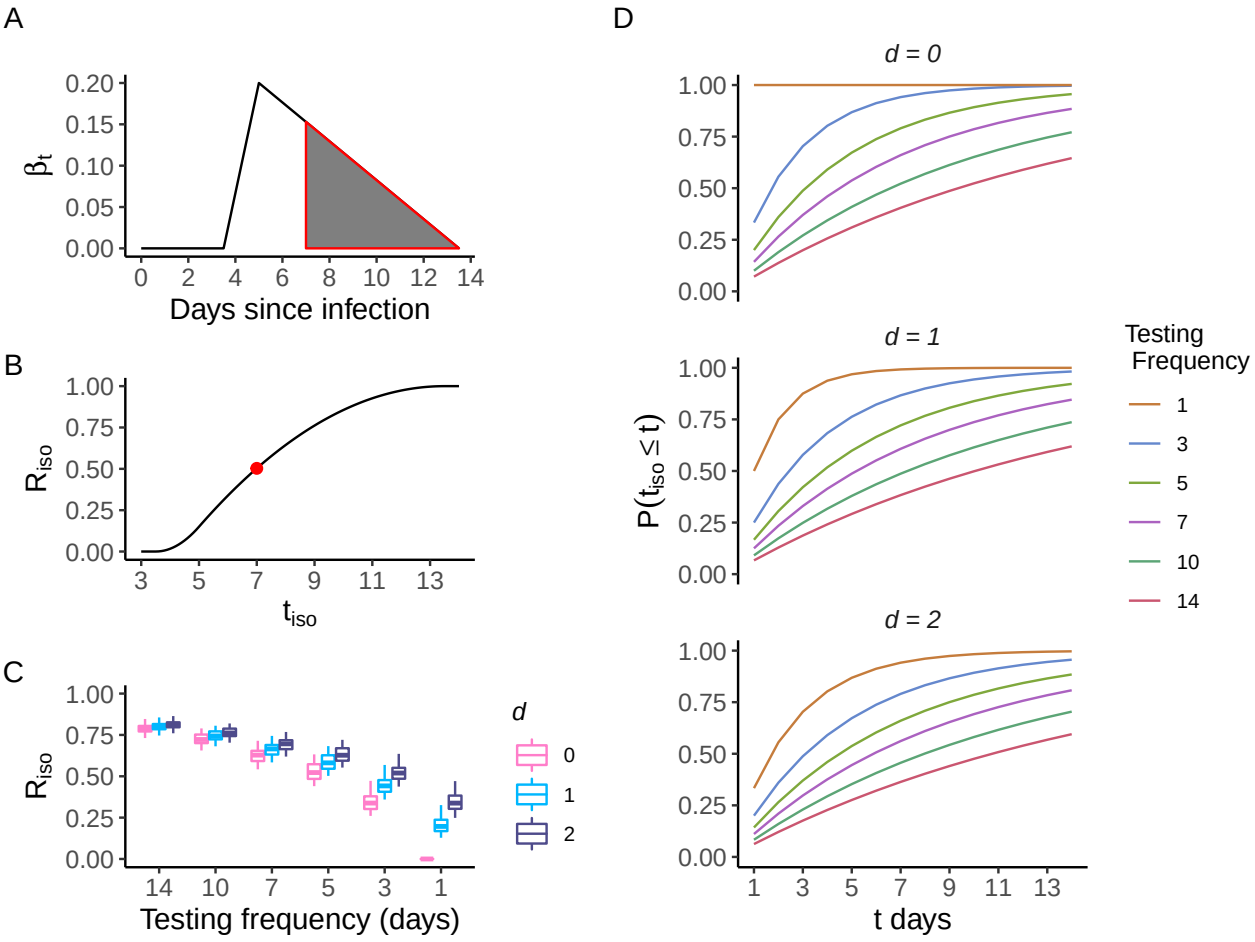

Figure 1: **Model framework and analytic results.** A) Example infectiousness profile for $\mathcal{R} = 1$, $t_{latent} = 3.5$, $t_{peak} = 5$, $t_{infectious} = 10$, with shaded area demonstrating infectiousness slice removed if $t_{iso} = 7$, leading to $\mathcal{R}_{iso} = 0.5$. B) $\mathcal{R}_{iso}$ as a function of t_{iso} with same parameters as in A and point indicating scenario depicted in A. C) Violin plots showing distributions of $\mathbb{E}[\mathcal{R}_{iso}|\beta_t, f, d]$ as a function of testing frequency, f, and test delay, d, incorporating uncertainty in t_{latent}, t_{peak}, and $t_{infectious}$ by drawing $n = 100$ parameter sets for each, with baseline $\mathcal{R} = 1$. Points indicate median values of $\mathbb{E}[\mathcal{R}_{iso}|\beta_t, f, d]$. D) Relationship between testing frequency, f, test delay, d, and probability isolation occurs by day t, i.e. $t_{iso} \leq t$.