TITLE

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Abstract

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Introduction

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Models and Methods

Data. We use daily confirmed case data $\mathbf{X} = (X_1, \ldots, X_T)$ from several different countries. These incidence data summarize the number of individuals X_t tested positive for SARS-CoV-2 RNA (using RT-qPCR) at each day t. Data was retrieved from REFS for the following regions: Wuhan, China; Austria; ....

SEIR model. We model SARS-CoV-2 infection dynamics by following the number of susceptible S, exposed E, reported infected I_r, and unreported infected I_u individuals in a population of size N. This model distinguishes between reported and unreported infected individuals: the reported infected are those that have enough symptoms to eventually be tested and thus appear in daily case reports, to which we fit the model.

Susceptible (S) individuals become exposed due to contact with reported or unreported infected individuals (I_r or I_u) at a rate β_t or $\mu\beta_t$. The parameter $0 < \mu < 1$ represents the decreased transmission rate from unreported infected individuals, who are often subclinical or even asymptomatic. The transmission rate $\beta_t \geq 0$ may change over time t due to behavioral changes of both susceptible and infected individuals. Exposed individuals, after an average incubation period of Z days, become reported infected with probability α_t or unreported infected with probability $(1 - \alpha_t)$. The reporting rate $0 < \alpha_t < 1$ may also change over time due to changes in human behavior. Infected individuals remain infectious for an average period of D days, after which they either recover, or becomes ill enough to be quarantined. They therefore no longer infect other individuals, and therefore the model does not track their frequency. The model is described by the following equations:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta_t S \frac{I_p}{N} - \mu\beta_t S \frac{I_s}{N} \\
\frac{dE}{dt} &= \beta_t S \frac{I_p}{N} + \mu\beta_t S \frac{I_s}{N} - \frac{E}{Z} \\
\frac{dI_r}{dt} &= \alpha_t \frac{E}{Z} - \frac{I_r}{D} \\
\frac{dI_u}{dt} &= (1 - \alpha_t)\frac{E}{Z} - \frac{I_r}{D}.
\end{aligned} \tag{1}$$

This model is inspired by Li et al. (2020) and Pei & Shaman (2020), who used a similar model with multiple regions and constant transmission β and reporting rate α to infer COVID-19 dynamics in China and the continental US, respectively.

Likelihood function. The *expected* number of new reported infected individuals on day t is

$$Y_t = \alpha_t E(t)/Z.$$

We define $\tilde{Y}_t$ to be the cumulative expected number of reported infected individuals up to day t,

$$\tilde{Y}_t = \sum_{i=1}^{t} Y_i$$

As mentioned above, X_t is the number of confirmed cases in day t. Then,

$$\tilde{X}_t = \sum_{i=1}^{t} X_i$$

is the cumulative number of confirmed cases until day t (with $X_0 = 0$). We assume that reported infected individuals yet to be confirmed, i.e. individuals in $\tilde{Y}_t$, are confirmed and therefore appear in

the daily case report of day t with probability p_t, which may change over time (note that t is a specific date, and not the elapsed time since infection). Therefore, we assume that the number of confirmed cases in day t is binomially distributed,

$$X_t \sim Bin\big(n_t, p_t\big),$$

where n_t is the *realized* number of reported infected individuals yet to appear in daily reports by day t. Given $\tilde{X}_{t-1}$, we assume n_t is Poisson distributed,

$$\big(n_t \mid \tilde{X}_{t-1}\big) \sim Poi\Big(\tilde{Y}_t - \tilde{X}_{t-1}\Big), \quad n_1 \sim Poi(Y_1).$$

Therefore, $\big(X_t \mid \tilde{X}_{t-1}\big)$ is a binomial conditioned on a Poisson, which reduces to a Poisson with

$$\big(X_t \mid \tilde{X}_{t-1}\big) \sim Poi\Big(\big(\tilde{Y}_t - \tilde{X}_{t-1}\big)p_t\Big), \quad X_1 \sim Poi(Y_1 p_1). \tag{2}$$

Therefore, for given vector θ of model parameters

$$\theta = \Big(Z, D, \mu, \{\beta_t\}, \{\alpha_t\}, \{p_t\}, S(0), E(0), I_r(0), I_u(0)\Big),$$

which also includes the initial conditions (state at $t = 0$), it is possible to compute the expected number of exposed $\{E(t)\}_{t=1}^{T}$ and number of new infections $\{Y_t\}_{t=1}^{T}$ for each day. Then, since $\tilde{X}_{t-1}$ is a function of $X_1, \ldots, X_{t-1}$, we can use Eq. (2) to write the probability of the confirmed case data $\mathbf{X} = (X_1, \ldots, X_T)$ as

$$\mathbb{L}(\theta \mid \mathbf{X}) = P(\mathbf{X} \mid \theta) = P(X_1 \mid \theta)P(X_2 \mid X_1, \theta) \cdots P(X_T \mid X_1, \ldots X_{T-1}, \theta). \tag{3}$$

This defines our *likelihood function* for the parameter vector θ given the data $\mathbf{X}$.

NPI model. To model non-pharmaceutical interventions (NPIs), we set the start of the NPIs to day τ and define

$$\beta_t = \begin{cases} \beta, & t < \tau \\ \beta\lambda, & t \geq \tau \end{cases}, \quad \alpha_t = \begin{cases} \alpha_1, & t < \tau \\ \alpha_2, & t \geq \tau \end{cases}, \quad p_t = \begin{cases} 1/9, & t < \tau \\ 1/6, & t \geq \tau \end{cases},$$

where $0 < \lambda < 1$. The values for p_t follow Li et al. (2020), who estimated the average time between infection and reporting in Wuhan, China, at 9 days before the start of NPIs (Jan 23, 2020) and 6 days after start of NPIs. The parameter τ is then part of the parameter vector θ.

Model fitting. To fit our model (Eq. (1)) to the data $\mathbf{X}$ and estimate the model parameters θ, we apply a Bayesian inference approach. We define the following flat priors on the model parameters $P(\theta)$:

$$\begin{aligned} Z &\sim Uniform(2, 5) \\ D &\sim Uniform(2, 5) \\ \mu &\sim Uniform(0.2, 1) \\ \beta &\sim Uniform(0.8, 1.5) \\ \lambda &\sim Uniform(0, 1) \\ \alpha_1, \alpha_2 &\sim Uniform(0.02, 1) \\ E(0) &\sim Uniform(0, 3000) \\ I_u(0) &\sim Uniform(0, 3000) \\ \tau &\sim Uniform(1, T-1), \end{aligned} \tag{4}$$

where T is the number of days in the data $\mathbf{X}$. Most priors follow Li et al. (2020), except λ, which is used to enforce that the transmission rates are lower after the start of the NPIs ($\beta_{t\geq\tau} < \beta_{t<\tau}$). The posterior distribution on the model parameters $P(\theta \mid \mathbf{X})$ is then estimated using an affine-invariant ensemble sampler for Markov chain Monte Carlo (MCMC) implemented in the `emcee` Python package (Foreman-Mackey et al. 2013).

Results

Discussion

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Acknowledgements

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