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Discussion Paper Contribution

M. Gabriela M. Gomes, Ibrahim Mohammed and Chris Robertson's contribution to the Discussion of 'Some statistical aspects of the Covid-19 Pandemic' by Wood et al.

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Abstract

This contribution to the discussion of (Wood et al., 2025) addresses 'Epidemic dynamic models' (Section 4).

In Section 4 of their paper (Wood et al., 2025), the authors address the omission of person-to-person variability in Covid-19 transmission models selected to inform policy (such as SEIR models). Modelling efforts incorporating unobserved individual variation in susceptibility and exposure to infection ((Gomes et al., 2022), akin frailty models established in survival analysis (e.g. Balan and Putter, 2020)), were excluded from policy research on the basis of supposed parameter identifiability issues. This contribution aims to refute the view that the frailty parameter is especially accountable for lack of identifiability in SEIR models.

For illustration, use the SEIR model with individual variation in susceptibility (Gomes et al., 2022; Wood et al., 2025)

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -c(t)R_0\gamma I S^{\lambda}, \qquad \frac{\mathrm{d}E}{\mathrm{d}t} = c(t)R_0\gamma I S^{\lambda} - \delta E, \qquad \frac{\mathrm{d}I}{\mathrm{d}t} = \delta E - \gamma I,$$

where S, E and I are susceptible, exposed and infectious population fractions (the remaining fraction R being recovered or removed), $\delta = 0.18$ per day, $\gamma = 0.25$ per day, $\lambda = 1 + \nu^2$ where ν is the coefficient of variation of individual susceptibility, R_0 is the basic reproduction number and $c(t)$ is a time-dependent multiplicative factor representing voluntary behaviour changes and compliance with NPIs (starting at 1 and, from $t = t_0$ onward, decreasing towards c_1 (Figure 1, bottom). The model with $R_0 = 3$, $\lambda = 3$, $t_0 = 15$ days and $c_1 = 0.3$, was run forward in time starting from two alternative sets of initial conditions to generate the coloured trajectories in Figure 1 (middle). For comparison, the scenario where $c(t) = 1$ is also included in Figure 1 (top).

To assess parameter identifiability, sets of synthetic data were generated with a stochastic version of the model and parameters R_0, ν, t_0 and c_1 were estimated by maximum likelihood. Simulated scenarios assumed $R_0 = 3$, $\nu = \sqrt{2}$, $t_0 = 15$ days, and $c_1 = 0.2$ or 0.3.

First, we fitted the model to data from a single epidemic curve generated with initial infectious fraction $I_1(0) = 2.4\text{e}{-4}$. The procedure was conducted 200 times and correlations between parameters were obtained from the Hessian matrix of the MLEs. We found strong positive correlations between ν and c_1: 0.87 when $c_1 = 0.2$ and 0.81 when $c_1 = 0.3$ (open circles in Figure 2 (left)). This is not surprising as both increasing ν and decreasing c_1 flatten the curve.

Second, we fitted the model to two concurrent epidemics (which might be occurring in different regions) assuming that the same parameters applied to both but initial conditions were different. The approach resulted in a marked reduction in $|\text{Corr}(\nu, c_1)|$ (dots in Figure 2 (left)). This outlines an inference approach, originally applied to Covid-19 in England and Scotland (Gomes et al., 2022), to overcome common challenges in the inference of unobserved individual variation from population data (Balan and Putter, 2020; Gomes et al., 2024).

Finally, we conducted a similar analysis with a version of a model that assumes no individual variation ($\lambda = 1$). In the single epidemic analysis we identified strong negative correlations between R_0 and t_0: -0.89 when $c_1 = 0.2$ and -0.92 when $c_1 = 0.3$ (open circles in Figure 2 (right)). Introducing a second epidemic in the analysis alleviated $|\text{Corr}(R_0, t_0)|$ (dots in Figure 2 (right)) much like in the scenario of $|\text{Corr}(\nu, c_1)|$ above. Therefore, the identifiability issues in SEIR models do not originate from the introduction of ν.

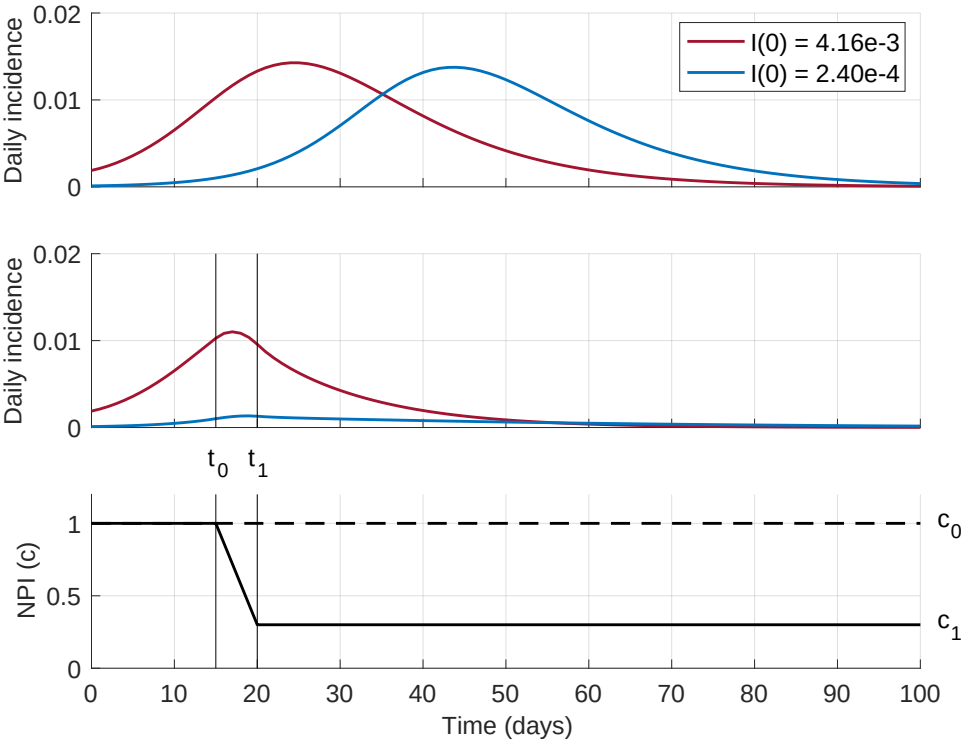

Fig. 1: Incidence trajectories generated by the SEIR model with individual variation in susceptibility. The two curves on top and middle panels correspond to different initial conditions (red $\sim$ 17 times higher prevalence than blue when $t = 0$). Bottom panel is the multiplicative factor for transmission due to voluntary behaviour change and NPI.

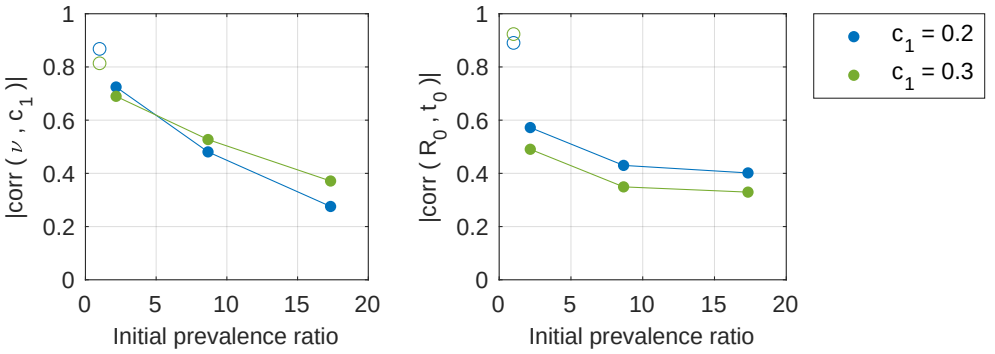

Fig. 2: Parameter correlations in the SEIR model. Pairwise correlations obtained from the Hessian of MLEs based on simulated data of a single epidemic (open circles) and two concurrent epidemics which differ in initial infectious prevalence (dots). The left panel accounts for individual variation in susceptibility represented by parameter λ (or ν) while the right panel assumes a homogeneous population by imposing $\lambda = 1$ (or $\nu = 0$).

Code availability

Code used for these analyses can be found at...

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