Household Isolation Model for COVID-19: Context and Potential for HPC Acceleration

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1 Context and Importance

Non-pharmaceutical interventions (NPIs) are a key tool that we have to fight against COVID-19. While there are multiple models of most NPIs, to my knowledge there is only one that explicitly includes isolation at the household level, which is the influential study from Imperial College [3]. The modelling methodology for this study is individual-based simulation, which makes it slow and hard to run sensitivity analysis. The SPI-MO committee that coordinates modelling work in the UK regards it as important to have multiple models that investigate each question. Models are being developed at Lancaster University and the London School of Hygiene and Tropical Medicine (LSHTM), but this work is not completed. I have coded and disseminated a household model, but the feedback on this is that additional sensitivity analysis would be beneficial, and HPC would help with this.

The methodology involved is the use if self-consistent differential equations. These were first written down (as were many firsts in household modelling) by Frank Ball [1]. More recent developments, including numerical methods for these equations, include [4, 2, 5]. The important features of this approach is that it allows for the small, finite size of each household in which random effects are important and each pair can only participate in one infection event.

In the language of compartmental epidemic models, the dynamics are SEPIR (susceptible, latent, mildly symptomatic prodrome, symptomatic infectious, removed).

In general, within-household transmission needs to be scaled with household size and the Cauchemez model where transmission $\propto$ size$^{-\eta}$ is assumed.

The distribution of household sizes is realistic for the UK.

At present, an epidemic with no intervention is considered, then with three weeks of global / non-household-based interventions of varied efficacy brought in three weeks into the epidemic, as well as combination of different kinds of isolation:

1. Individual isolation, where a proportion of individuals stay at home when symptomatic.

2. Weak household isolation, where a proportion of households isolate when there is at least one symptomatic individual in the household.

3. Strong household isolation, where a proportion of households isolates from the first appearance of symptoms until 14 days after the end of all illness in the household.

The main model limitations that cannot be easily overcome in this framework are determinism outside the household, lack of other spatial / risk structure besides households, compartmental structure.

Another limitation where HPC methods could be very helpful is in systematic assessment of sensitivity of the results. There are two kinds of such sensitivity – the first is multi-core runs of different scenarios (lengths and types of non-household interventions, lengths and types of household isolation policies). The other is sensitivity to the underlying rate constants, which I think could be done by looking for the gradient of the outputs with

respect to the parameters, perhaps with autograd, in the first instance. There is also the possibility for hardware acceleration of the solution of the basic model, which heavily depends on linear algebra.

2 Formal model description

Let $Q_{n,s,e,p,i,\mathbf{f}}(t)$ be the proportion of households in the population at time t of size n, with s susceptibles, e exposed, p prodromal, and i symptomatic infectious individuals, and with vector of 'flags' $\mathbf{f}$ representing implementation of more complex interventions. The number of recovered individuals will be $n - s - e - p - i$ so we do not need to index this explicitly. We now consider how to model different intervention scenarios.

2.1 Baseline

In the absence of household-based interventions, we have

$$
\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t} Q_{n,s,e,p,i} = & - \left(s r_{s \to e}(t, \mathbf{Q}) + e r_{e \to p} + p r_{p \to i} + i r_{i \to \emptyset} + n^{-\eta} s p \tau_p + n^{-\eta} s i \tau_i \right) Q_{n,s,e,p,i} \\
& + (s+1) r_{s \to e}(t, \mathbf{Q}) Q_{n,s+1,e-1,p,i} + (e+1) r_{e \to p} Q_{n,s,e+1,p-1,i} \\
& + (p+1) r_{p \to i} Q_{n,s,e,p+1,i-1} + (i+1) r_{i \to \emptyset} Q_{n,s,e,p,i+1} \\
& + n^{-\eta}(s+1) p \tau_p Q_{n,s+1,e-1,p,i} + n^{-\eta}(s+1) i \tau_i Q_{n,s+1,e-1,p,i} \,,
\end{aligned}
\tag{1}
$$

where we take any Q with logically impossible indices just to equal 0, and the transmission into households is given by

$$
r_{s \to e}(t, \mathbf{Q}) = \Lambda(t) + \sum_{n=1}^{n_{\max}} \sum_{s=0}^{n} \sum_{e=0}^{(n-s)} \sum_{p=0}^{(n-s-e)} \sum_{i=0}^{(n-s-e-p)} \left(p \beta_p(t) + i \beta_i(t) \right) Q_{n,s,e,p,i} \,.
\tag{2}
$$

Here Λ represents infections imported from outside the population of households, and the other terms represent between-household transmissions. We take a 'global' intervention as part of the baseline, in particular, we can model phenomena such a school closures that hold during a set of times $\mathcal{T}$ as

$$
\beta_x(t) = \begin{cases} (1 - \varepsilon) \beta_x(0) & \text{if } t \in \mathcal{T} \,, \\ \beta_x(0) & \text{otherwise,} \end{cases}
\tag{3}
$$

for $x \in \{p, i\}$. We call ε the **global reduction**. We will generally drop this t-indexing below, but it is present in all scenarios.

2.2 Individual isolation

We are then in a position to consider interventions. For individual isolation we assume that a fraction α_{I}, which we call the **compliance**, of symptomatic cases self-isolates and ceases transmission outside the household, but

$$
r_{s \to e}(t, \mathbf{Q}) = \Lambda(t) + \sum_{n=1}^{n_{\max}} \sum_{s=0}^{n} \sum_{e=0}^{(n-s)} \sum_{p=0}^{(n-s-e)} \sum_{i=0}^{(n-s-e-p)} \left(p \beta_p + (1 - \alpha_{\mathrm{I}}) i \beta_i \right) Q_{n,s,e,p,i} \,.
\tag{4}
$$

2.3 Weak household isolation

This corresponds to a situation where a fraction α_{W} of households isolate when there is at least one symptomatic case in the household. These households do not experience new infections, meaning that the dynamics

become

$$
\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}Q_{n,s,e,p,i} = & -\left(\left(1-\alpha_{\mathrm{W}}\mathbf{1}_{\{i>0\}}\right)sr_{s\to e}(t,\mathbf{Q}) + er_{e\to p} + pr_{p\to i} + ir_{i\to\emptyset} + n^{-\eta}sp\tau_p + n^{-\eta}si\tau_i\right)Q_{n,s,e,p,i} \\
& + \left(1-\alpha_{\mathrm{W}}\mathbf{1}_{\{i>0\}}\right)(s+1)r_{s\to e}(t,\mathbf{Q})Q_{n,s+1,e-1,p,i} + (e+1)r_{e\to p}Q_{n,s,e+1,p-1,i} \\
& + (p+1)r_{p\to i}Q_{n,s,e,p+1,i-1} + (i+1)r_{i\to\emptyset}Q_{n,s,e,p,i+1} \\
& + n^{-\eta}(s+1)p\tau_p Q_{n,s+1,e-1,p,i} + n^{-\eta}(s+1)i\tau_i Q_{n,s+1,e-1,p,i}\ ,
\end{aligned}
\tag{5}
$$

and also do not transmit outside, meaning that the rate of between-household transmission becomes

$$
r_{s\to e}(t,\mathbf{Q}) = \Lambda(t) + \sum_{n=1}^{n_{\max}}\sum_{s=0}^{n}\sum_{e=0}^{(n-s)}\sum_{p=0}^{(n-s-e)}\sum_{i=0}^{(n-s-e-p)}\left(1-\alpha_{\mathrm{W}}\mathbf{1}_{\{i>0\}}\right)\left(p\beta_p + i\beta_i\right)Q_{n,s,e,p,i}\ .
\tag{6}
$$

2.4   Strong household isolation

We now suppose that a fraction α_{S} of households start to isolate when there is at least one symptomatic case in the household, and stop isolation 14 days after the absence of symptoms in the household. This is modelled by having a flag $f=0$ if the household is not isolating and $f=1$ if it is. The dynamics become

$$
\begin{aligned}
\frac{\mathrm{d}}{\mathrm{d}t}Q_{n,s,e,p,i,f} = & -\left(\mathbf{1}_{\{f=0\}}sr_{s\to e}(t,\mathbf{Q}) + er_{e\to p} + pr_{p\to i} + ir_{i\to\emptyset} + n^{-\eta}sp\tau_p + n^{-\eta}si\tau_i + \mathbf{1}_{\{f=1\}}\sigma\right)Q_{n,s,e,p,i,f} \\
& + \mathbf{1}_{\{f=0\}}(s+1)r_{s\to e}(t,\mathbf{Q})Q_{n,s+1,e-1,p,i,f} + (e+1)r_{e\to p}Q_{n,s,e+1,p-1,i,f} \\
& + (1-\mathbf{1}_{\{f=1\&i=1\&s+e+p=n-1\}}\alpha_{\mathrm{S}})(p+1)r_{p\to i}Q_{n,s,e,p+1,i-1,f} + (i+1)r_{i\to\emptyset}Q_{n,s,e,p,i+1,f} \\
& + n^{-\eta}(s+1)p\tau_p Q_{n,s+1,e-1,p,i,f} + n^{-\eta}(s+1)i\tau_i Q_{n,s+1,e-1,p,i,f} \\
& + \mathbf{1}_{\{f=0\}}\sigma Q_{n,s,e,p,i,1} + \mathbf{1}_{\{f=1\&i=1\&s+e+p=n-1\}}\alpha_{\mathrm{S}}(p+1)r_{p\to i}Q_{n,s,e,p+1,i-1,0}\ ,
\end{aligned}
\tag{7}
$$

with between-household term

$$
r_{s\to e}(t,\mathbf{Q}) = \Lambda(t) + \sum_{n=1}^{n_{\max}}\sum_{s=0}^{n}\sum_{e=0}^{(n-s)}\sum_{p=0}^{(n-s-e)}\sum_{i=0}^{(n-s-e-p)}\left(p\beta_p + i\beta_i\right)Q_{n,s,e,p,i,0}\ .
\tag{8}
$$

References

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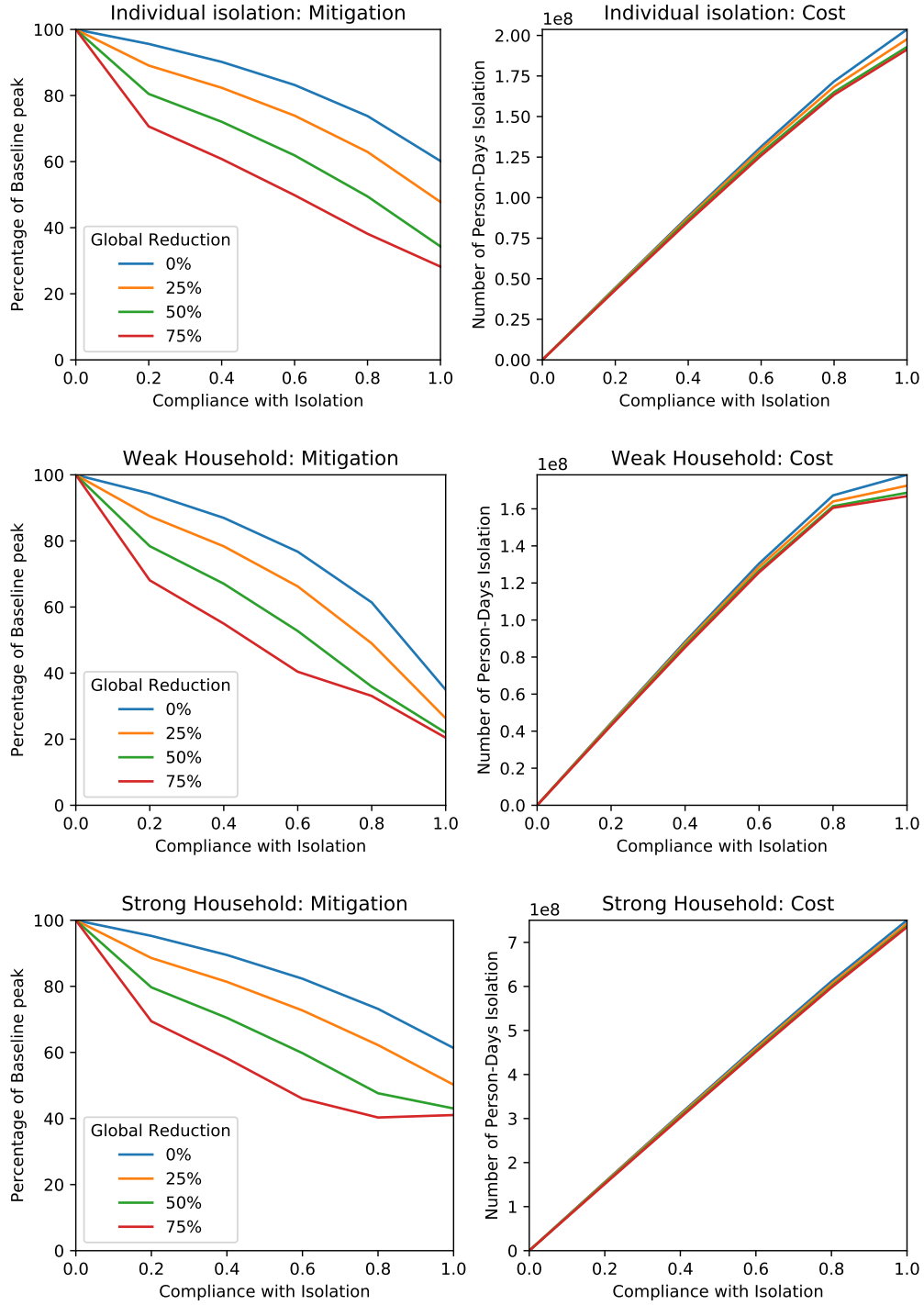
Figures

Figure 1: Results of different strategies on the peak height, and also social cost of those interventions as person-days in isolation.
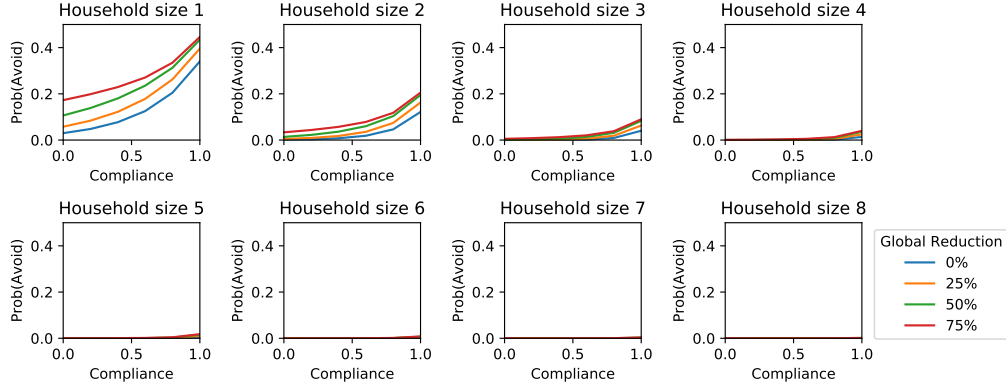
3 Figures – Vulnerable Individuals

Figure 2: Probability of escape by household size for individual isolation.
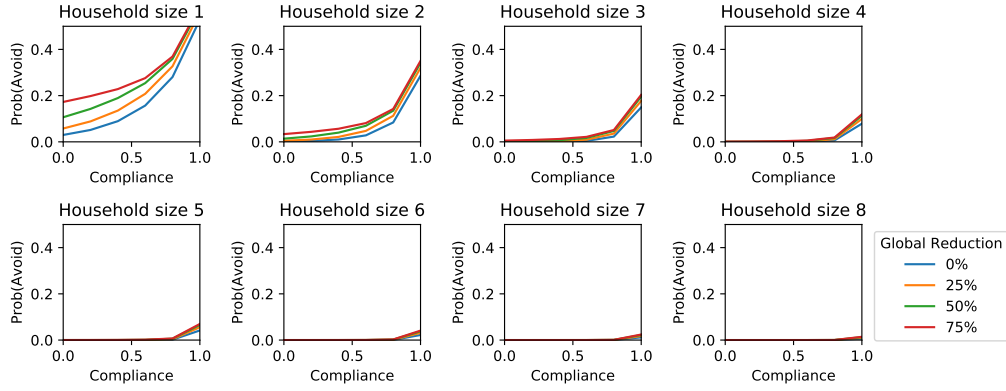
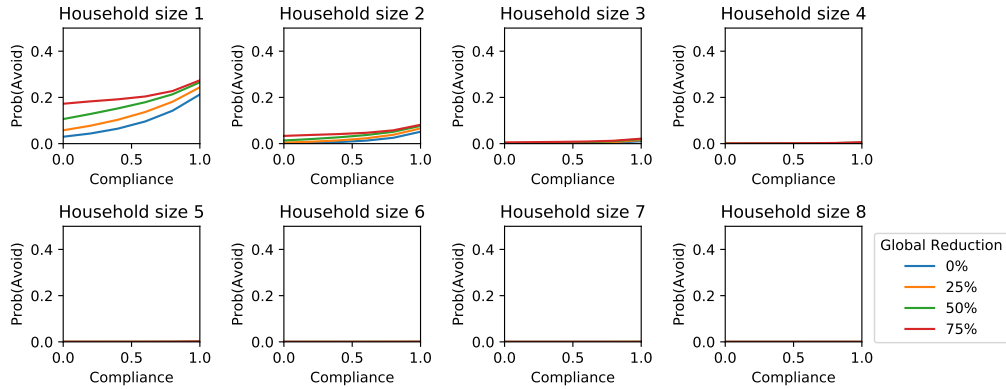Figure 3: Probability of escape by household size for weak household isolation.

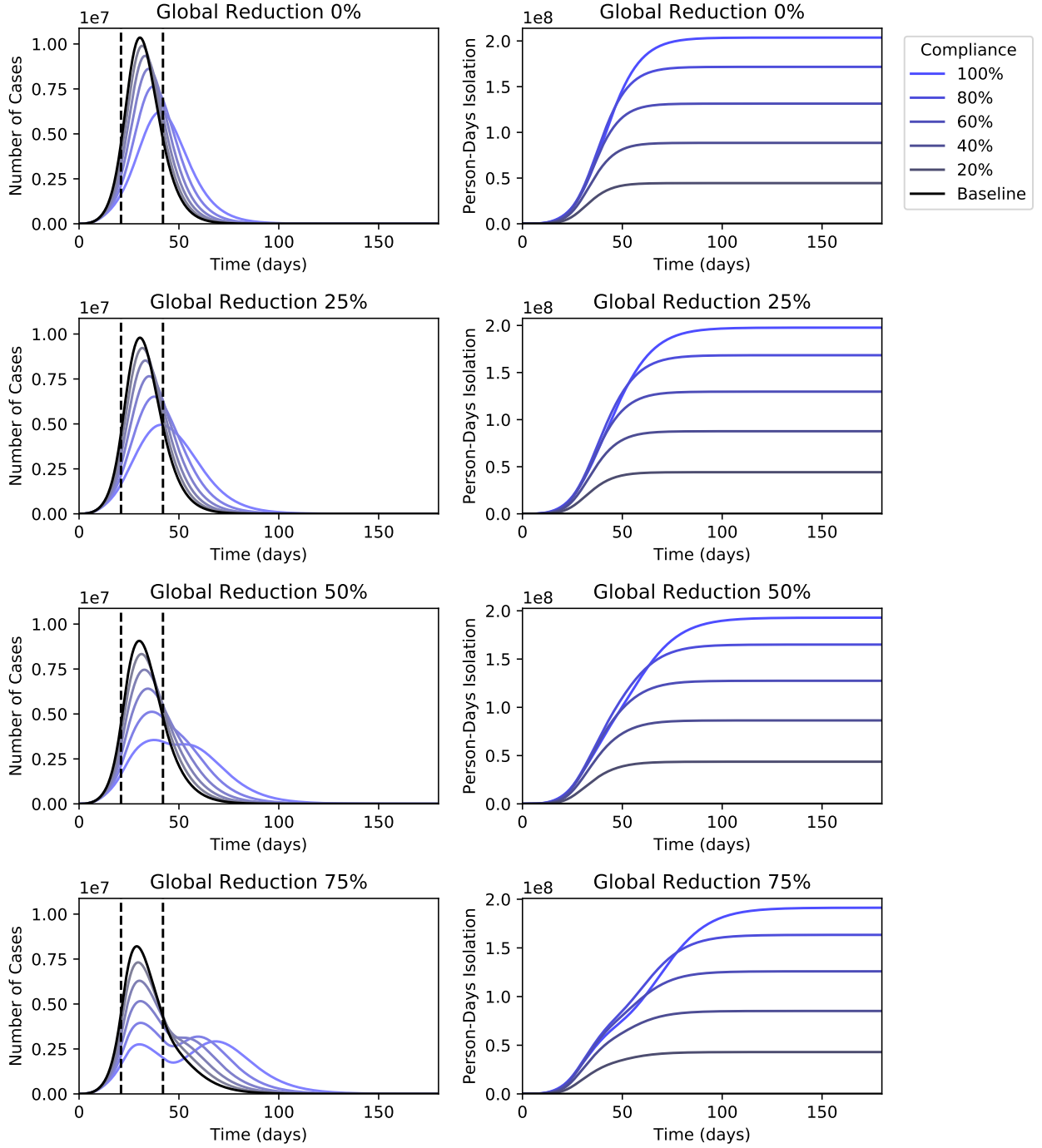Figure 4: Probability of escape by household size for strong household isolation.

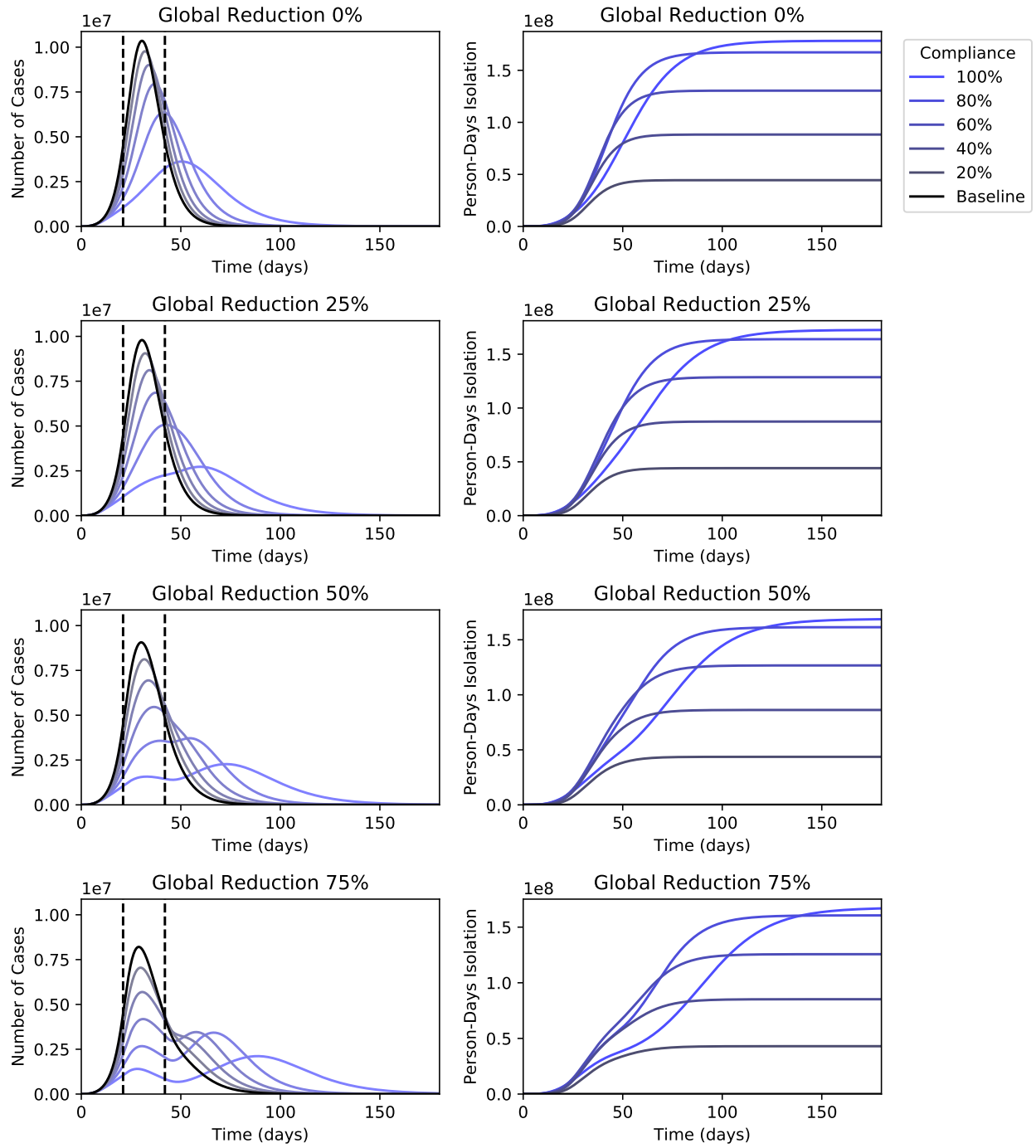Figure 5: Temporal behaviour for individual isolation.
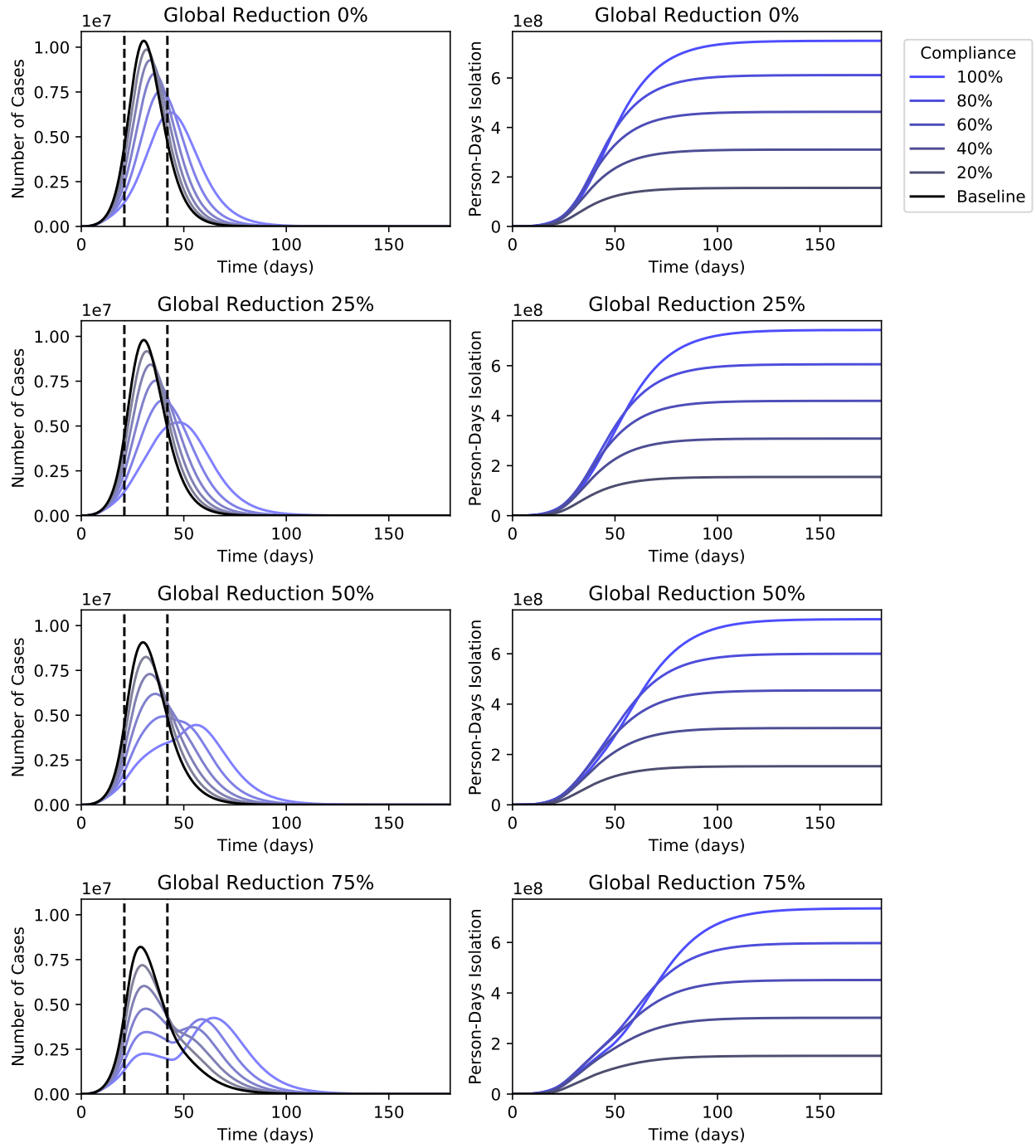
Figure 6: Temporal behaviour for weak household isolation.

Figure 7: Temporal behaviour for strong household isolation.