

Effect of compliance with Whole Household Isolation in the Covid-19 outbreak.

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Abstract

We develop a simple SEIDR model with two levels of population mixing: within- and between-households. We assume parameters given currently agreed point estimates from the SPI-M committee, and study the behaviour of the epidemic curve under different assumptions about people's compliance with Whole Household Isolation in response to detected cases. We find that even a 50% compliance with WHI may have a dramatic reduction effect on the size of the epidemic peak, helping to preserve NHS capacity. In our setup, we achieve a 40% reduction in peak height assuming 50% compliance, whilst having a comparatively minor effect on peak timing. We recommend, therefore, that WHI be re-considered as an intervention to slow the spread of Covid-19.

1 Introduction

In this investigation, we build on methods developed in [1] examining the behaviour of epidemics with two levels of mixing, i.e. within- and between-households. Here, we aim to investigate the likely effect of varying compliance to whole household isolation (WHI) measures. We take a necessarily theoretical approach to this, since we currently lack precise line-listing data at the household level. Our aim is to determine the sensitivity of transmission reduction (reduction in R_*) to the level of compliance with household isolation in response to a case within the household.

Caveat: This is an indicative study only. The model does not attempt to capture population heterogeneity beyond household grouping, and remains uncalibrated to the current epidemic due to the paucity of detailed case data available.

2 Model description

We assume a closed population of m individuals, where m is small and the “population” represents a household. We assume homogeneous mixing within the household.

We propose a Markov $S \rightarrow E \rightarrow I \rightarrow N \rightarrow R$ epidemic model with the states as follows:

- **S** Susceptible
- **E** Exposed - infected with the disease but not yet infectious.
- **I** Infectious - able to infect people but no symptoms.
- **D** Detected - still infectious but symptoms have appeared.
- **R** Removed - no longer infectious and immune to further infection.

The Detected state allows for individuals to continue to infect within their household even if they are quarantined from the general public.

We assume the following transitions. Once the individual becomes infected (enters state **E**) they transition through the states **I** and **N** before finishing in state **R**. The time spent in each state is exponentially distributed with:

- $E \rightarrow I$ - rate κ
- $I \rightarrow N$ - rate γ
- $D \rightarrow R$ - rate δ

New infections occur at rate: $S(\lambda I + \beta D)$, where S , I and D denote the total number of individuals in each of the respective states. Within a household, λ is the rate of infection between Infectious and Susceptible, and β is the rate of infection between Detected and susceptible. We assume that Infectious individuals exert a “global” infection rate α onto other individual *outside* the household. For Detected and isolated individuals, we assume this rate is $\omega\alpha$ such that $0 \leq \omega \leq 1$ denotes the percentage reduction in infection outside the household in response to isolation.

We further assume that:

- We assume individuals are grouped into households with sizes given by ONS 2019 household size estimates. This gives a mean household size of 2.4 individuals, and a distribution of household sizes 8197, 9609, 4287, 3881, 1254, 597thousand for households of size 1, 2, 3, 4, 5, 6+ respectively.
- Mixing between individuals and households is assumed to be frequency dependent, and therefore is invariant to overall population size.
- We assume a single introductory case to a household and no further infections from outside. This is a reasonable assumption in the early stages of an epidemic where global/chance contacts with the disease are rare.
- There is no contact behaviour change once the disease has been observed in the household.
- There is no change in the infection parameters whether or not an infectious individual (I) is isolated.
- All times in states are exponentially distributed according to the usual Markovian assumptions.

3 Analysis

We base our investigate around the concept of R_{star} as described by Ball et al. [1] (see appendix). R_* gives the mean number of infections outside the household infected by a typical household. The aim is to reduce $R_* > 1$ to control the epidemic in the normal way.

In all investigations below, we choose $\kappa = 4\text{day}^{-1}$, $\gamma = 2\text{day}^{-1}$, $\delta = 2\text{day}^{-1}$ in accordance with currently agreed transition rates. $\beta = \lambda = \alpha = 0.51\text{day}^{-1}$ to give $R_* = 2.7$ equivalent to a doubling time of 4.6 days as currently agreed by SPI-M. Furthermore, we conservatively assume $\omega = 0.2$ such that an isolated individual, if infectious, exerts 20% of the infection rate onto individuals outside the household compared to if they were not isolated. This accounts for practicalities such as needing to buy provisions.

3.1 Whole household-level isolation compliance

WHI compliance is defined as the propensity of individuals to self-isolate in response to the occurrence of one detected case in the household. We look at this in two ways, firstly in terms of individual compliance within a household (i.e. some or all of a single household comply), and secondly in terms of a proportion of households that comply fully versus those who do not comply at all.

3.1.1 Individual compliance within a household

In order to investigate individual-within-household compliance to WHI, we introduce a parameter $0 \leq \eta \leq 1$ which represents the proportion of the household which self-isolate in response to the occurrence of the first detected case. η is interpreted such that

$\eta = 0$ Nobody in the household self-isolates apart from individuals who are symptomatic (i.e. equivalent to individual case isolation);

$\eta = 1$ Everybody in the household isolates immediately in response to 1 symptomatic case (i.e full household isolation);

$\eta = 0.5$ 50% of the household complies with household isolation after 1 symptomatic case.

Using the parameter values described above, Figure 1 presents the effect on R_* for various values of η . This analysis indicates that full compliance with whole-household isolation results in a 40% reduction in R_* from 2.7 to 1.6. The relationship between compliance level η and R_* is approximately linear over the support of η .

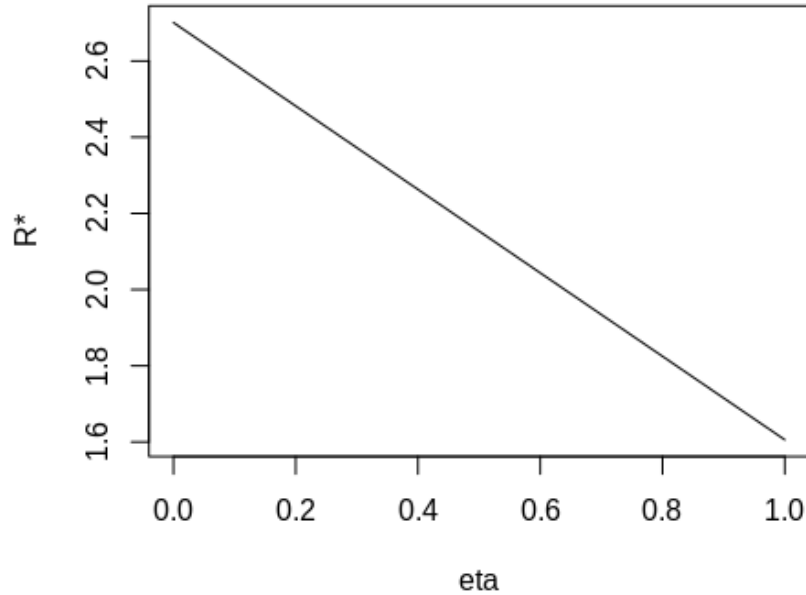


Figure 1: Individual-level WHI compliance. R_* as a function of individual-level compliance η .

3.1.2 Household-level Whole Household Isolation compliance

Having looked at how individual-level compliance with WHI affects R_* , we now look at compliance at the household level. Here, we assume that households fully comply ($\eta = 1$) with probability p or do not comply ($\eta = 0$) with probability $1 - p$. We vary p over its full support, again assuming our model transition rates as above.

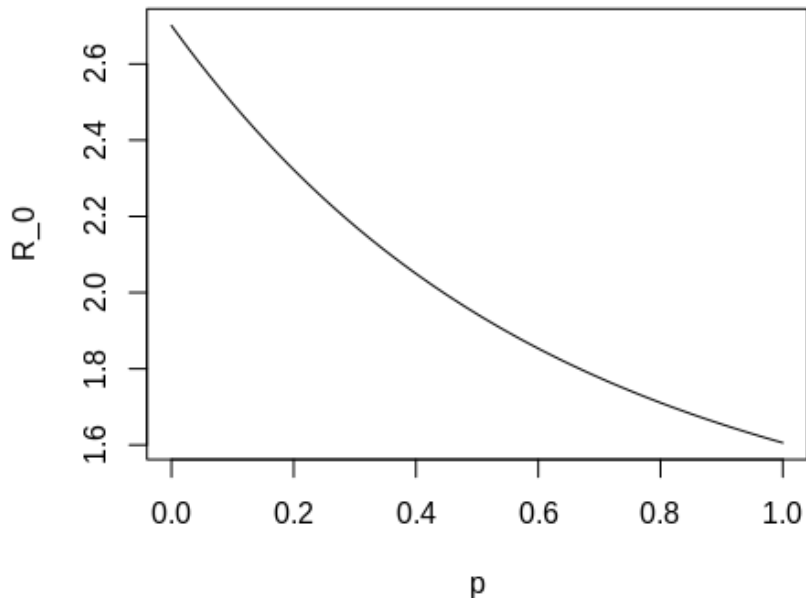


Figure 2: Household-level WHI compliance. R_* as a function of household-level compliance p .

3.2 Whole household isolation trigger level

In this section, we use our SEIDR household model to investigate how triggering WHI at different numbers of detected cases within a household affects R_* . Here, we used our model transition parameters as described above to calculate R_* assuming that WHI is applied after 1, 2, 3, 4, 5, and 6 symptomatic cases respectively. For simplicity, we assume that following the respective numbers of case detections households fully comply with WHI. Table 1 provides R_* values for varying trigger levels. Note that as our maximum household size is 6, the R_* for a trigger of 6 is equivalent to either individual case-isolation or no compliance with WHI, the two being mathematically equivalent.

WHI trigger level	R_*
1	1.61
2	2.06
3	2.37
4	2.58
5	2.67
6	2.70

Table 1: WHI triggering level versus R_* .

3.3 Effect of household isolation on epidemic curve

To investigate the effect of household isolation on the epidemic curve, we simulated from the Lancaster Covid-10 population model. This is a SEIR metapopulation model, where we assume the following rates $E \rightarrow I = 0.25\text{day}^{-1}$, $I \rightarrow R = 0.25\text{day}^{-1}$ based on currently agreed values. We optimised our basic disease transmission rate β to give a global R_0 equal to R_* given by Figure 1 for compliance values $\eta = 0, 0.5, 1$. We acknowledge that equating R_0 in the Lancaster Covid-19 model to R_* in our household model is an

approximation. However, we do not expect this approximation to appreciably affect the qualitative findings from our study.

In Figure 3, we find that even 50% compliance with WHI results in a drop in epidemic peak by 40%, and pushes the peak epidemic time back by approximately 1.5 months. Full compliance, in our model, results in a broad epidemic curve which may last well into next year, across the winter 'flu' season. The whole-population attack rates is also profoundly affected by WHI, as shown in Table 2 indicating that as compliance increases, the final size of the epidemic also decreases.

We also find that the reduction in transmission also decreases synchrony between different areas in the UK, as show particularly clearly in the $\eta = 0.5$ and $\eta = 1$ curves which are not monotonic in their second-order behaviour (that is, the curves appear “lumpy” in response to epidemic curves in different regions).

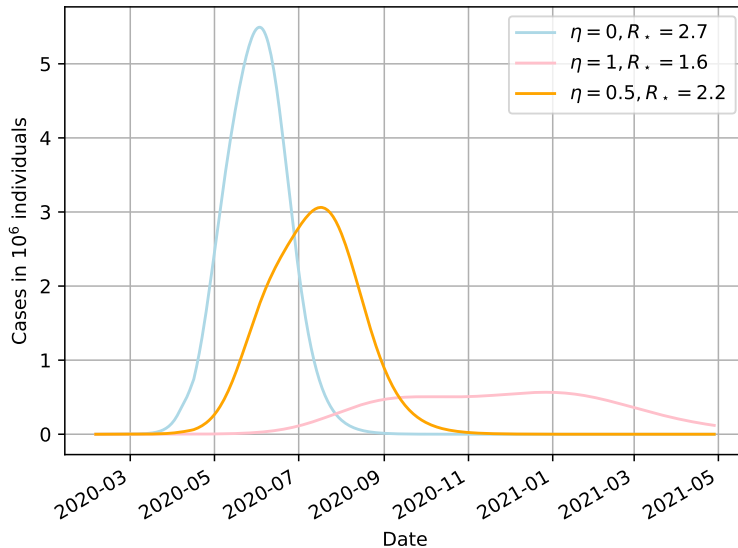


Figure 3: Predicted curves for number of infected (E+I) individuals from the Lancaster Covid-19 model set for $R_0 \approx R_*$ values equivalent to setting individual level WHI compliance $\eta = 0, 0.5, 1$.

η	R_*	Attack rate
0.0	2.7	75%
0.5	2.2	61%
1.0	1.6	31%

Table 2: Whole-population attack rates (proportion of population infected by the end of the epidemic) for varying values of η , the individual-level WHI compliance parameter.

4 Conclusion

Initially, Whole Household Isolation was dismissed as a suitable intervention to slow the spread of Covid-19 in the UK, based on concern that households would not comply with the intervention advice. In this brief paper, we have used a mathematical approach to address the issue of partial compliance. We find that even 50% compliance with Whole Household Isolation is enough to reduce the size of the epidemic curve by 40% , pushing the epidemic curve back by approximately 1.5 months. If compliance were to be 100%, then we

might expect a far longer and lower epidemic curve which would stretch over the winter. Encouragingly, the R_* that gives this drop in epidemic peak size is between the R_* found for triggering (fully compliant) WHI after the occurrence of 2 and 3 cases respectively within the household. Thus we might expect a degree of tolerance in the intervention to people not reacting to the first case in their household.

The analysis here is subject to many caveats, not least that it has not been formally calibrated to reliable UK case data. If these data become available, then the model will be recalibrated. Beyond this, it is a necessarily simple model which does not account for the effects of age and space on contact rate between individuals. However, it does provide a useful insight into the benefits of even imperfect compliance with WHI, and we would expect that population heterogeneity in contact rate would act to enhance its effectiveness as an intervention. We therefore recommend that WHI should be re-considered as an intervention to manage the spread of Covid-19 in the UK.

References

- [1] F Ball, D Mollison, and G Scalia-Tomba. Epidemics with two levels of mixing. *The Annals of Applied Probability*, 7:46–89, 1997.