Social Care Working Group chairs summary of role of shielding.

SAGE steer: *the question is about the extent to which interventions targeted towards protecting the more vulnerable individuals could be effective in this wave e.g. guidance or additional support to reduce contacts (not necessarily shielding in the sense of the programme that was in place in 2020, though that is obviously relevant past experience), and whether that would mean fewer measures affecting the whole of society might be needed (to get to broadly similar outcomes). Also useful to have a view on how it changes if applied to a wider cohort of people than the previous shielding programme e.g. unboosted over-40s.*

1) This note focuses on applicability of shielding to social care settings rather than general vulnerable population given threat posed by omicron variant. However, the model given in Annex B is illustrative of a more general population.
2) National lockdowns act to reduce numbers of cases/deaths in social care settings [see Figure 1, below, analysis of CQC mortality notifications, grey areas are national lockdown periods] so breaking network is critical and hard without major lockdown or effective vaccine.
3) Experience of past waves of infection in social care settings:
    a. The Wave 1 situation is hard to generalise due to lack of testing/surveillance though excess deaths suggests impact was very high [Morciano et al 2021, Excess mortality for care home residents during the first 23 weeks of the COVID-19 pandemic in England: a national cohort study (biomedcentral.com)]. During Wave 2, whilst better testing regimes and PPE were in place and eventually vaccine was available, the exposure in Wave 1 mitigated outbreaks due to prior immunity (homes affected in Wave 1 did not have large outbreaks in Wave 2 on the whole).
    b. In Wave 3 outbreaks are smaller and impact of past outbreaks less clear in data (we are now 2 years into a pandemic, a timescale close to the average residency in care home settings). Wave 2 to Wave 3 comparison suggests vaccine has quartered the number of homes affected by relatively large outbreaks once averaged over time but once in a home outbreaks arising have had about half the cases observed in Wave 2 (but about a quarter the deaths because of case fatality reduction from vaccine). This is suggestive that within home mixing and contacts are strong and/or probability of transmission remains high – so preventing ingress is important. Scaling by ¼ is roughly similar to estimated vaccine effectiveness and so suggests any impact from loss of VE due to omicron can be estimated.
    c. Case fatality ratio has been stable [Overton et al 2021, figure 2 below, arXiv submission pending] at around 13% in W3, dropping from 25% in Jan 2021 suggesting vaccination has reduced case fatality ratio by 50% in care home settings.
    d. Currently Cornwall, Devon and North Somerset are showing significant signs of growing case numbers (P1 and P2 data from 13th Dec) in care home settings. One home in NW has had a high omicron clinical attack ratio but low signs of severity but extrapolating from one outbreak is challenging.
4) Evaluation of specific interventions that may be considered part of shielding policy
    a. Evaluating specific interventions is challenging [SCWG: What are the appropriate mitigations to deploy in care homes in the context of the post vaccination risk landscape?, 26 May 2021 - GOV.UK (www.gov.uk)] due to the responsive nature of the pandemic.
    b. Vaccine staff and resident 2nd doses are high (95%+ coverage), booster programme has reached 82% of residents and 39% directly employed staff. Only 11% agency

staff are boosted. Vaccination has reduced mortality and morbidity in care home settings.

c. Testing (both PCR and LFD) can be simulated in isolation to other interventions (Annex A modelling is agnostic of setting) but it is hard to get reliable measure of adherence and whether it will change with policy changes. In annex A, adherence is measured as number of LFDs matched to number of PCRs: this is pessimistic due to most missing tests likely being people not recording a negative result. More frequent testing could be worse if adherence drops with frequency. So monitoring adherence is critical part of policy effectiveness and ensuring that those tested trust the testing programme and are engaged in process. Staff are hard-working and have been operating for a long time under COVID pressures.
d. Daily contact testing for workers around the shielded, understandably works well with a critical mass of participation and quickly becomes ineffective when participation is patchy. Regular communication and support is vital – ideally with certification https://www.liverpool.ac.uk/coronavirus/research-and-analysis/covid-smart-pilot/.
e. PPE and other interventions are hard to measure/model and there has been a lack of trials, so any simulation would be predicated on assumptions made. It is noteworthy that the evidence shows infection risk is greater at home than at work for healthcare staff. Also there is evidence that staff-staff transmission occurs during breaks when PPE is not worn. It is critical that PPE is fitted correctly with appropriate training. [see The effectiveness of PPE in reducing the transmission of COVID-19 in health and social care settings: December 2021 update]
f. Ventilation is likely effective but likely challenging to implement given a) season and b) variety of housing stock used for care homes.
g. Limiting visitors and visiting out reduces ingress but has a large impact on general wellbeing and visitors are a relatively small fraction compared to staff (daily contact with staff but weekly contact with visitors, though essential care providers visit as often as staff in many situations). Those visiting in or out are advised to undertake regular LFD testing, and have negative LFD on the day of the visit. Those who are visiting are advised to have had their CV-19 vaccinations including booster if eligible and flu vaccine if eligible.. Pod visiting clearly safer but impact on wellbeing should be monitored. See SAGE papers S0584_Adverse_effects_of_social_isolation_and_loneliness_in_care_homes_during_COVID-19.pdf (publishing.service.gov.uk) and S0875_Social_Care_Working_Group_Consensus_statement_on_visitor_policies.pdf (publishing.service.gov.uk)
h. The hierarchy of control model suggests that the impact of a range of interventions will not be additive but instead support each other [SCWG: What are the appropriate mitigations to deploy in care homes in the context of the post vaccination risk landscape?, 26 May 2021 - GOV.UK (www.gov.uk)]. Interventions deployed target specific hazards and a holistic view is necessary. Modelling theory suggests that due to the non-linearity the total impact of interventions is often greater than the sum of the parts

5) Other considerations
   a. A simple model (2 age groups under and over 55's suggests that a policy needs to reduced contacts between groups by 80% to avert half of cases in older group (2.5 million cases still infected) if vaccine is all or nothing; if vaccine is leaky this would avoid ¾ of cases, but given a larger baseline epidemic size, a larger absolute number of cases would be infected (4 million) [Annex B]

b. Isolation of older people from each other is ineffective by itself, it is the additional reduction of contacts ***between*** age groups that is key. Any model is limited by spontaneous behavioural change.
c. If omicron has complete vaccine escape the situation could be worse than in W1 as social care staff recruitment and retention is an emerging issue. Staff wellbeing should be monitored.
d. Home care clients are less connected to community than a care home and due to size/nature of work less at risk of major outbreaks but are harder to monitor so signals of adverse outcomes may be lagged.
e. Staff in social care settings, whilst mandated to have vaccine, also have children so likely remain exposed to household cases whilst COVID-19 circulates in schools; late school holiday and incubation period mean this remains an issue over Christmas period. This connectivity to areas of high circulation is likely important if relaxation is continued elsewhere in system.
f. High staff absences from a community outbreak may impact on care for other needs. Social care staffing is optimised to minimise costs so there is little slack in system. Any intervention that reduces care time of staff would impact on outcomes to other conditions. So there is an opportunity cost to intervention that is hard to measure or equate to COVID infections.
g. Some residents/clients want to be protected and some want to see family. A care home is a home but with a social contract for all residents which is difficult to balance.

6) The lived experience of W1, W2 and W3 is that shielding is challenging and there is no precedent nationally for effective shielding of care home settings, though it may be workable in households. Impact assessment of omicron is dependent on vaccine effectiveness after boosting programme.

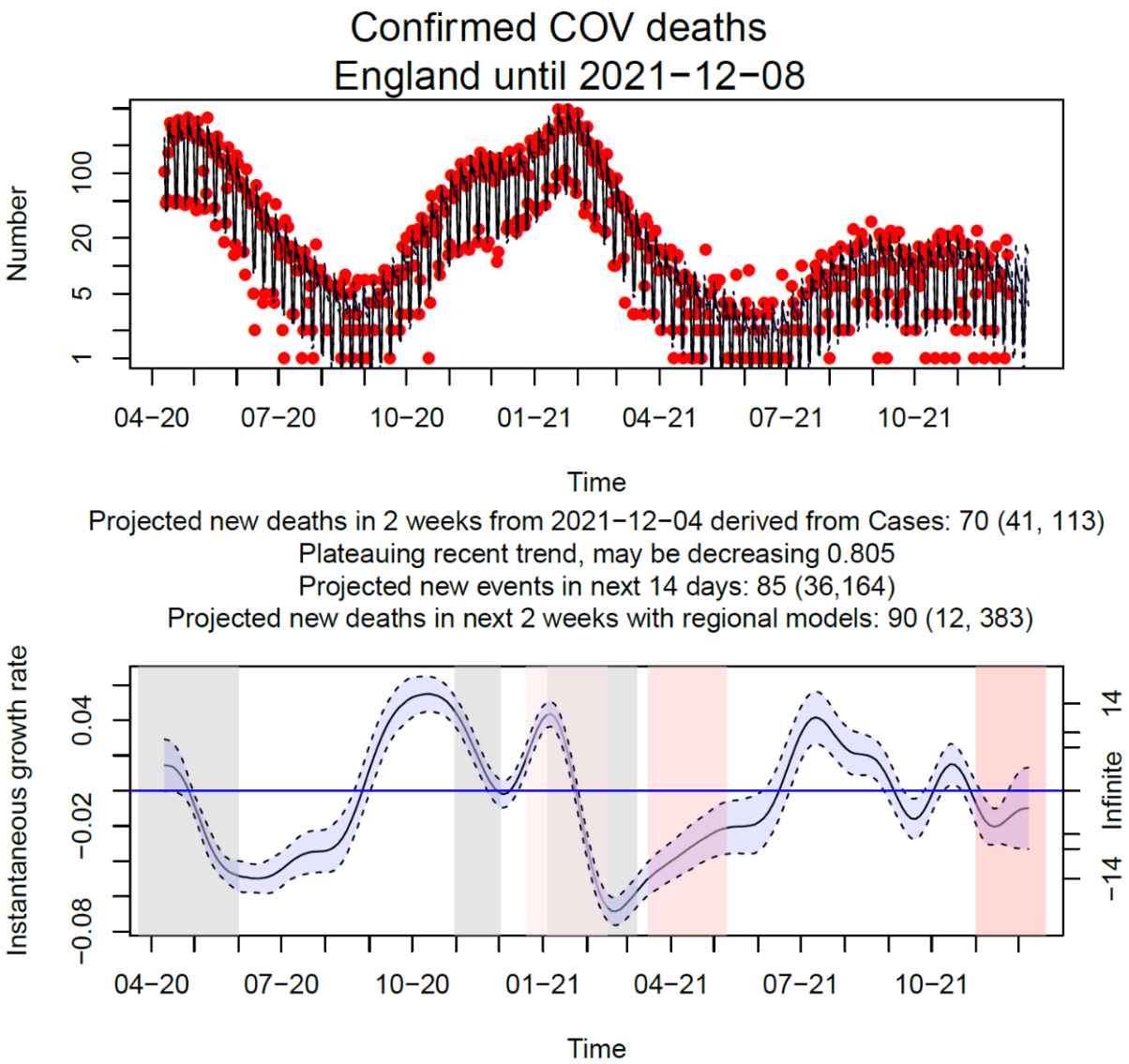

Figure 1) Top panel: Daily CQC death notifications confirmed as COVID-19 and GAM model fit. Lower panel: instantaneous growth rate of GAM spline (black line central estimate, blue region 95% CI, grey shade time periods of national lockdowns, pink shaded time periods of vaccine delivery to homes.

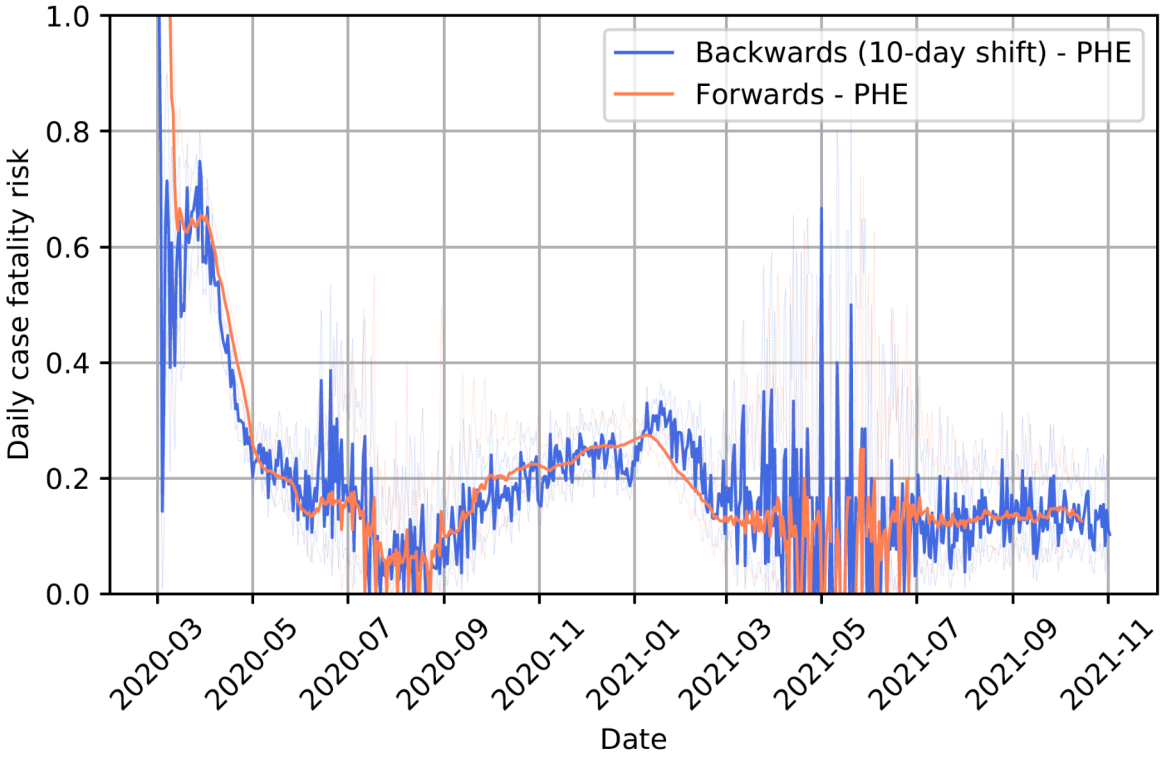

Figure 2: Modelled daily case fatality ratio over time. Since March 2013 this has been fairly consistent with period of large uncertainty due to small case numbers [See Overton 2021 for details of method and data used].

Annex A. **Modelling the impact of weekly PCR tests on potential SARS-CoV-2 transmission in high-risk work environments.**

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Executive Summary

- Using the latest data on LFD sensitivity vs. PCR-quantified viral load (from concurrent testing in social-care settings) has enabled us to re-evaluate previous models. This update suggests that **removing weekly PCR tests for staff (even if replacing with an extra LFD test) is likely to increase SARS-CoV-2 transmission** in these settings.
- Using "infectious days out of isolation" as a proxy for transmission risk, our analysis suggests that 2 LFDs per week, assuming no change in compliance, is likely to be approximately **64% as effective at reducing transmission** as the current intervention (2 LFDs and 1 concurrent PCR). In settings with 40% adherence to LFD testing, this reduced to only 43% as effective.
- The magnitude of the impact of testing is difficult to predict, since the sensitivity of PCR testing is uncertain, but our estimates suggest that the status quo leads to a total reduction in infectious days out of isolation (RPI – reduction in potential infectiousness) of **between 25% and 60% depending on the model of PCR testing and the adherence rate**.
- Stochastic modelling indicates that while testing can be an effective intervention, it is not sufficient alone to prevent introduction into the workplace, and so needs to be accompanied by other measures.

Methods

Model 1: Population average model

Model 1 is a population-average model used to predict the impact of different testing strategies in a previous SCWG document [citation]. It used published data on PCR and LFD sensitivity, infectiousness, and symptom onset, to estimate the relative reduction in total infectivity (i.e. integrated over time) for different testing regimes relative to the case with no testing but symptomatic isolation. This model **does not use** sensitivity data from LFD testing in social care settings (unlike model 2) and so the relative impact of LFDs compared to PCR is less reliable in this model.

Parameters and assumptions:

Epidemiological parameter	**Value/Distribution**	**Source/notes**
Symptom Onset Time τ_s	Gamma (mean 4.84 and s.d. 2.6 days)	[10]
Symptomatic fraction P_s	0.5	[8, 11] Note older people may have atypical presentation and this is not considered.
Infectiousness $f(t)$	Weibull (mean 5 s.d. 1.92 days)	[4] A function of days since infected t
Test positive probability for PCR $P_{PCR}(t)$ and LFD $P_{LFD}(t)$	Empirical distribution (see supplementary section S1).	[5] A function of days since infected t. See figure S1.

Delay from PCR test to receipt of result τ_D	42.8 hours	Median observed in high-risk settings [6].
Adherence with LFD testing	70% or 40%	Average observed in care and prison settings respectively.
Adherence with PCR testing	100%	Assumed (mandated at workplace).
Adherence with symptomatic isolation	100%	Assumed.
Isolation period τ_I	10 days	Current guidelines

Table 1: Parameters for model 1.

A key assumption of the model is that an individual has 0 (effective) infectiousness while isolated – this may over-estimate the impact of testing on transmission in the workplace if staff are still contacting other staff or residents outside of work while isolating (e.g. via shared households). The model then calculated the expected value of the total infectiousness under each testing scenario.

Limitations

- Uses population average estimates, so is not representative of individuals and does not account for variation between people.
- While vaccines and variants have broadly been shown not to impact on peak viral load or infectiousness [7], there is some evidence that they affect the average prodromal period, which may alter the results. There is also very little evidence available on the Omicron variant.
- There is no information about shift pattens and how these relate to test timings. This may have an impact on their role in reducing workplace infection risk.

Model 2: Viral-load model

Model 2 accounts for the fact that individuals have different viral load trajectories, and therefore their infectiousness and test positive probabilities are likely to be different to the population average, and highly correlated within each individual. This model **does use** the observed sensitivity data from LFD testing in social care settings and so the relative impact of LFDs compared to PCR is more reliable in this model. However, due to extra complexity of this model we are less confident in the absolute magnitude of the impact of testing predicted.

Parameters and assumptions:

Epidemiological parameter	**Value/Distribution**	**Source/notes**
Peak Viral Load $V_{\max}$	Normal (mean 7.5 and s.d. 1.2 $\log_{10}$ copies/ml).	[7]
Viral load parameter V_0	2.6 $\log_{10}$ copies/ml	Equivalent to Ct = 40 in[7], note we use a lower threshold for modelling PCR.

Time for viral load to grow from V_0 to $V_{\max}$: τ_{peak}	Gamma (mean 3.5 and s.d. 2.2 days)	[8]
Time from infection to V_0 viral load: τ_{onset}	$0.38 \times \tau_{peak}$	Assumed. Results in mean time to peak viral load matching symptom onset.
Time for viral load to decay from $V_{\max}$ to V_0: τ_{decay}	Gamma If symptomatic: mean 10.5 and s.d. 5.9 days If asymptomatic: mean 6.7 and s.d. 4.7 days	For all individuals in [7], the best fit distribution had shape parameter 2.4 and inverse scale parameter 0.3. Means for symptomatic and asymptomatics were reported in [7], but s.d. used assumption that both distributions had scale parameter 0.3.
Symptom Onset Time τ_s	Gamma (mean 4.84 and s.d. 2.6 days), truncated to the range $\tau_{onset} + \tau_{peak} - 2 \leq \tau_s \leq \tau_{onset} + \tau_{peak} + 2$	[1] Truncation added based on observation of peak viral load occurring within 2 days of symptom onset [8,9].
Symptomatic fraction P_s	0.5	[2,3] Note older people may have atypical presentation and this is not considered.
Infectious viral load threshold V_{inf}	6 $\log_{10}$ copies/ml	[11] See figure S2.
Test positive probability for PCR $P_{PCR}(V(t))$	0 if $V(t) < 1$ $\log_{10}$ copies/ml $0.95e^{-4.41(V-1.93)^2}$ if $V(t) \geq 1$ $\log_{10}$ copies/ml	1 $\log_{10}$ copies/ml is our assumed Ct=40 threshold [6]. Sensitivity for Ct<40 is from [11], with a cap at 95% to account for bad swabs. See figure S3.
Test positive probability for LFD $P_{LFD}(V(t))$	$0.004P_{PCR}(V(t))$ if $V(t) \leq 2$ $0.025P_{PCR}(V(t))$ if $2 < V(t) \leq 3$ $0.087P_{PCR}(V(t))$ if $3 < V(t) \leq 4$ $0.162P_{PCR}(V(t))$ if $4 < V(t) \leq 5$ $0.414P_{PCR}(V(t))$ if $5 < V(t) \leq 6$ $0.651P_{PCR}(V(t))$ if $6 < V(t) \leq 7$ $0.80P_{PCR}(V(t))$ if $V(t) > 7$	[6]. All values of $V(t)$ in $\log_{10}$ copies/ml. See figure S3.
Alternative test positive probability for LFD (Oct 2021 values) $P_{LFD2}(V(t))$	$0.032P_{PCR}(V(t))$ if $V(t) \leq 4$ $0.255P_{PCR}(V(t))$ if $4 < V(t) \leq 6$ $0.477P_{PCR}(V(t))$ if $V(t) > 6$	[6]. All values of $V(t)$ in $\log_{10}$ copies/ml. See figure S3.
Delay from PCR test to receipt of result τ_D	Gamma (mean 45 and s.d. 17.3 days)	Estimated from [6]. See figure S3.

Adherence with LFD testing	70% or 40%	Average observed in care and prison settings respectively [6].
Adherence with PCR testing	100%	Assumed (mandated at workplace).
Adherence with symptomatic isolation	100%	Assumed.
Isolation period τ_I	10 days	Current guidelines

Table 2: Parameters for model 2.

For each individual, a piecewise linear (in $\log_{10}$ copies/ml) viral load trajectory is randomly drawn using the parameters $V_{\max}$, τ_{onset}, τ_{peak}, and τ_{decay} in table 2. People are assumed infectious on days where their viral load exceeds V_{inf}, for which they are assigned an "infectiousness" value of 1. If their viral load transitions from $V < V_{\text{inf}}$ to $V > V_{\text{inf}}$ over the course of the day, their "infectiousness" value on that day is taken as the fraction of the day they are infectious. Thus, in this model, "total infectious days" is used as a proxy for infectiousness.

Since we simulate using a timestep of 1 day, symptomatic isolation is assumed to begin on the nearest whole number day to onset time. Similarly, for positive PCRs, isolation begins on the nearest whole number day from the test result. For positive LFDs, people isolate on the day they perform their test (so it is assumed to be taken at the start of the day, before any workplace exposure). All positive LFD tests are immediately followed by a confirmatory PCR, the result of which has the same viral-load dependent probability as any other PCR test.

We generated 100,000 viral load trajectories and simulated all testing scenarios once for each individual. We the calculated each person's total infectious potential (their total number of infectious days) for each scenario.

Limitations

- Data on viral load trajectories is sourced from a sample that is not representative of the wider population (professional athletes). However, fig S6 compares this to a model based on an alternate dataset and shows very similar results.
- The viral load model is not mechanistic, and so some viral load trajectories may be unrealistic.
- While vaccines and variants have broadly been shown to not impact on peak viral load or infectiousness [7], there is some evidence that they influence the growth and decay rates in the viral load trajectories, potentially altering the results.
- There is no information about shift pattens and how these relate to test timings. This may have an impact on their role in reducing workplace infection risk.

Results

We simulate 6 scenarios in total:
(a) No testing
(b) Daily LFDs + 1 weekly PCR
(c) Daily LFDs (no PCR)
(d) Status Quo (2 LFDs + 1 concurrent PCR per week)
(e) 3 LFDs per week.
(f) 2 LFDs per week + 1 (randomly timed) fortnightly PCR

(g) 2 LFDs per week + 1 concurrent fortnightly PCR
(h) 2 LFDs per week

According to model 1, the status quo (2 LFDs and 1 PCR per week) Is predicted to reduce infectious potential by ~35% vs. no testing. 3 LFDs per week are predicted to perform similarly with adherence at 70%, however 2 LFDs per week are predicted to only reduce infectious potential by around ~25%. At lower adherence (40%) the LFD only options are considerably worse, with 2 LFDs only performing half as well as the status quo.

Model 2 predicts much higher effectiveness overall, primarily because PCR sensitivity is predicted to be higher in this model and also because there is greater correlation, at an individual level, between test sensitivity and infectiousness. Model 2 predicts a greater discrepancy between the Status Quo and LFD-only options. This model uses data on real-life sensitivity vs. PCR, so the relative sensitivity of LFD vs. PCR is more realistic than model 1. The results of the two models are compared in figure 1.

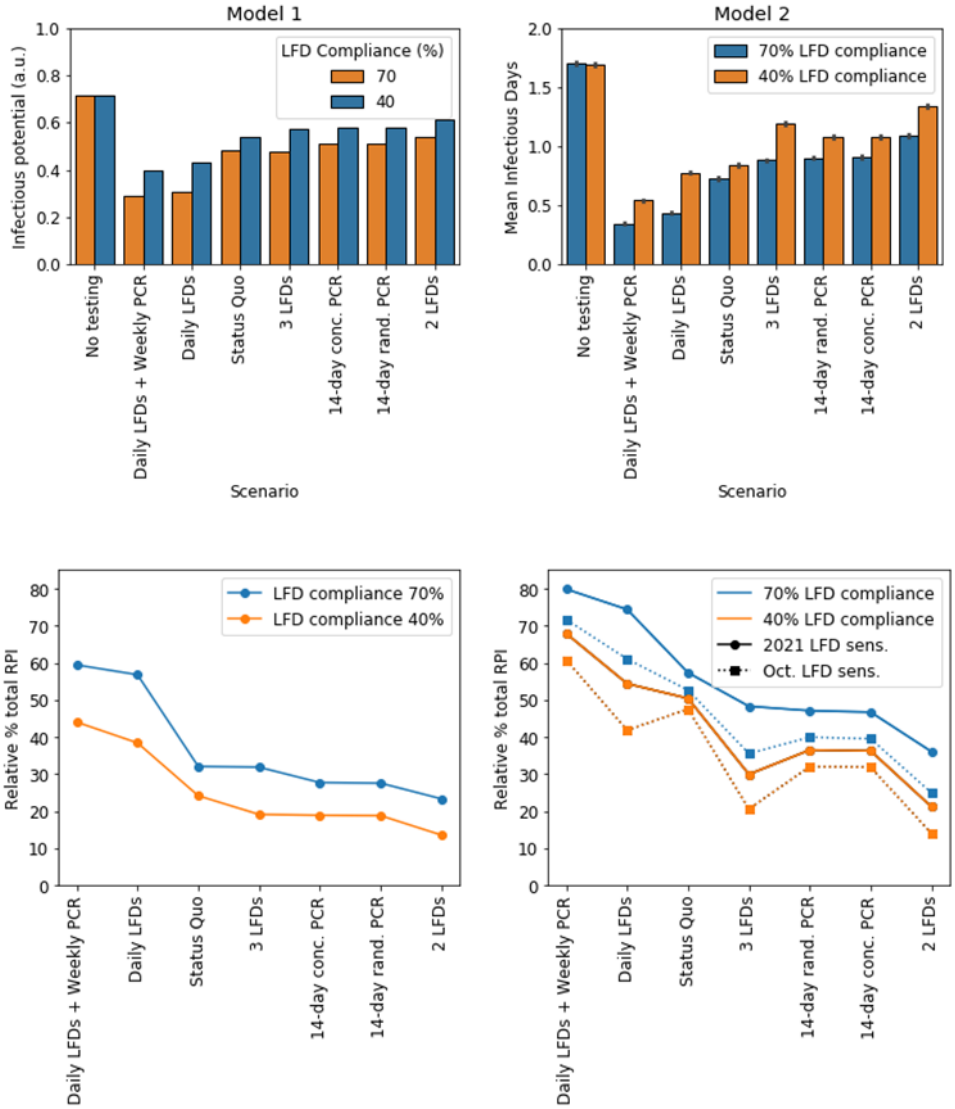

Figure 3: Top-Left: Model 1 (population average model) predictions for the potential infectiousness (1 is benchmark infectiousness with no symptom isolation) under 7 different testing scenarios (scenarios (b)-(h) respectively). Bottom-left: Model 1 results plotted as relative reduction compared to "no testing" case. Top-Right: Updated model 2 predictions for the same testing scenarios using LFD sensitivity data from all 2021. The bars show the mean number of infectious days for each scenario. Bottom-left: Model 2 results plotted as relative reduction in infectious days (at the population level)

compared to "no testing" case. We have also added the case of lower LFD sensitivity, as observed in Oct 2021 (see supplementary figure S3).

Model 2 also predicts the wide range of infectiousness potentials predicted for individuals in the model, shown by the violin and box plots in figure 2. This indicates that while testing can have a significant impact on reducing transmission, it cannot prevent highly infectious people entering the workplace entirely. Supplementary figure S2 also shows the impact on the fraction of people infectious out of isolation as a function of days since infected. This helps to visualise how testing shortens the effective infectious period via isolation measures.

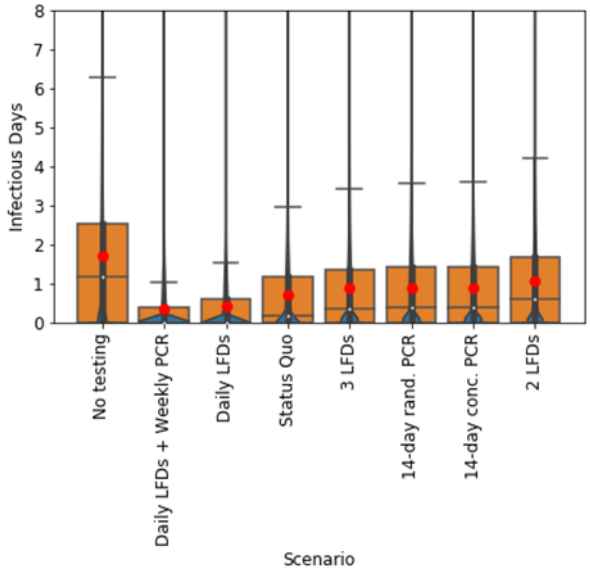

Figure 4: Violin and box-and-whisker plots of the distribution of total (non-isolated) infectious days predicted for each scenario. The white dot and middle line of the box indicates the median, while the red dot indicates the mean. Note that the tails (representing very rare events) of the violin distribution extend beyond the y-axis limit, which has been truncated here for visibility.

One potential drawback of increased staff testing frequency is that there will be more false positive tests resulting in unnecessary staff isolation. The absolute impact of this is highly dependent on the specificity of the test being used. Government estimates suggest that LFDs have 99.9% - 99.97% specificity. Figure 5 shows the number of false isolations per new infection that could be expected at different incidence rates for different specificity values. This assumes that the chance of receiving a false positive test in a given week is $1 - S^N$ where S is the specificity and N is the number of tests taken that week. Therefore, the number of false positive isolation per infection is $(1 - S^N)(1 - I)/I$ where I is the weekly incidence.

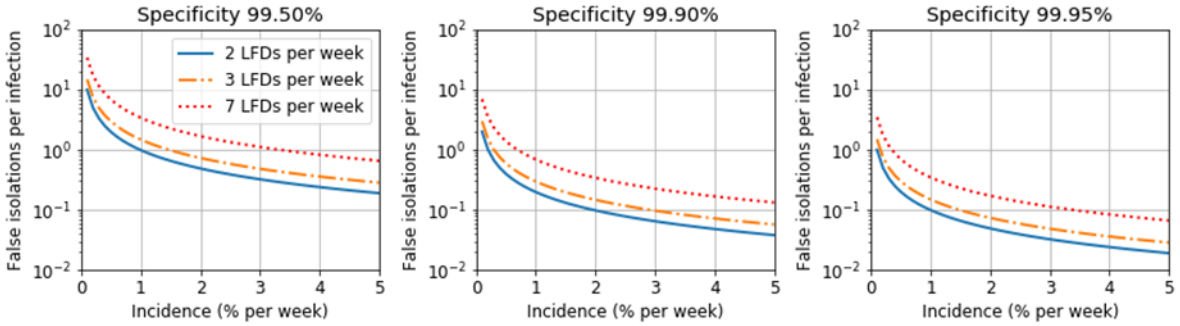

Figure 5: Plots of false positive isolations per new infection in a given week for the different test specificities and testing frequencies. (Assuming PCR has specificity 100%)

Supplementary Figures

Figure S1: Comparison of population-level average sensitivity of LFD and PCR tests in model 1 vs. model 2

Figure S1 compares the test-positive probabilities in the two models. In model 1, the population average is used to represent all people, in model 1 each person has a different viral load trajectory and test positive probability, so figure S1 shows the mean probability of a positive test performed on a large sample each day since infection. Note that model 2 predicts a marginally higher PCR positive probability, but lower LFD sensitivity.

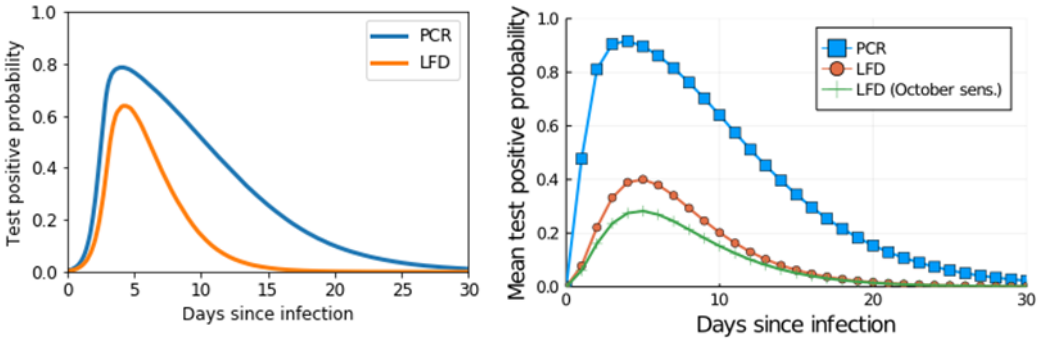

Figure S1: Left – Test positive probability used for PCR and LFD tests in model sourced from [5]. Right – Population mean test positive probability from 100,000 samples of model 2. The green curve indicates the reduced sensitivity measures observed in high-risk settings in October.

Figure S2: Model 2 average infectiousness and effect of testing

Regular testing removes infectious people from the workplace reducing their infectious potential. Figure S2 shows a visualisation of the average effect of different interventions over the course of an infection.

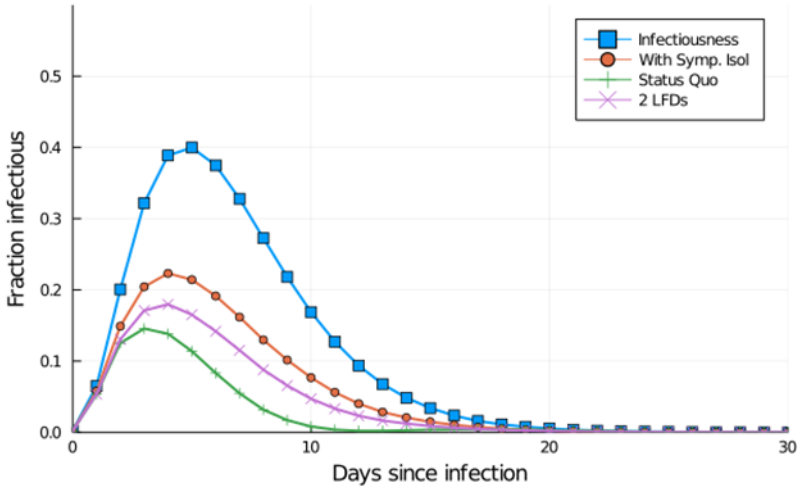

Figure S2: Fraction of people in model 2 who are infectious and not isolating on each day since infection. The blue line is the baseline infectiousness. Orange shows the case when symptomatics self-isolate. The green line shows the extra effect of 2 the status quo testing arrangement. The purple line shows the effect of removing the weekly PCR. The interventions shown assume 70% adherence to LFD testing and LFD sensitivity based on all 2021.

Figure S3: Model 2 test sensitivity and delays

Figure S3 gives a visualisation of some of the data used in model 2 based on the results in [9].

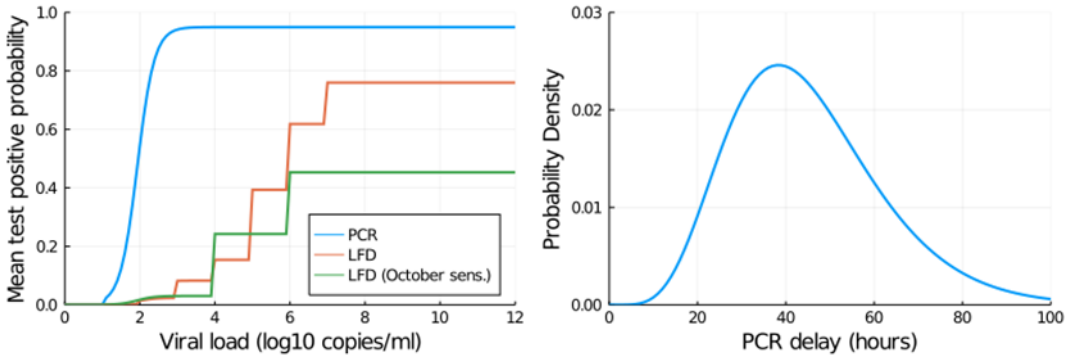

Figure S3: Left: Test sensitivity vs. viral load relationships used to model testing in model 2. Right: The distribution of PCR test delays used in model 2 (from time of test to receipt of result).

Figure S4: Model 2 sensitivity to baseline PCR sensitivity

One reason for the discrepancy between models is the difference in maximum sensitivity of PCR tests. In model 2 we assume that this is 95%, although there is a lack of reliable data on the sensitivity of PCR self-swabs due to the lack of a benchmark. Data from a study in healthcare workers suggest the PCR false negative rate (FNR) is actually ~20% [3, 5]. Therefore, we consider three scenarios in figure S4, corresponding to an FNR of 0%, 5% and 20%.

Note that, in model 2, the sensitivity of LFDs is defined relative to PCR, so a reduction in PCR sensitivity also reduces LFD sensitivity, hence the effect on all intervention scenarios is similar.

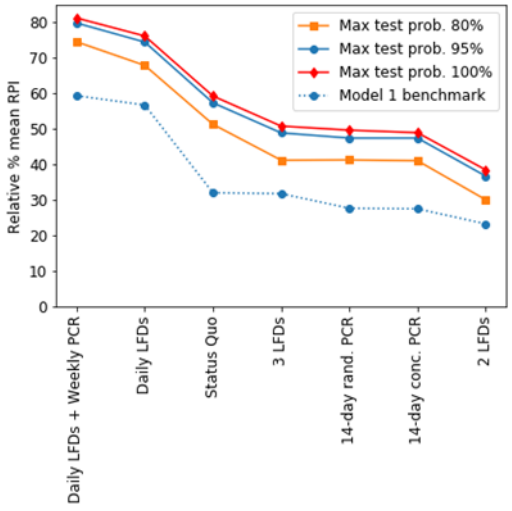

Figure S4: The relative reduction in total infectious days in model 2 assuming different values for the maximum PCR sensitivity (as labelled). The dotted line shows the comparison to the prediction of model 1. In all cases we assume 70% adherence and model 2 test sensitivity is from all 2021 data. The corresponding predictions from model 1 (from figure 3) are replotted for comparison.

Figure S5: Sensitivity to confirmatory PCR sensitivity alone

The effect of false negatives from confirmatory PCRs is close to negligible in the above models, due to the high sensitivity assumed (95% in model 1, viral load dependent in model 2 but in most cases ~95%) and because subsequent tests are likely to catch false negatives. We test the effect of the FNR on confirmatory PCR in figure S5. Note that in this case, we assume for model 2 that the FNR for confirmatory PCRs is fixed, and not dependent on viral load (and all other parameters remain unchanged). Interestingly, we see that it has very little effect on the impact, one reason for this is because the majority of the impact is from the first two days of isolation (while waiting for the confirmatory PCR result). This may be sensitive to changes in model assumptions about the infectious period – however both model 1 and model 2 agree on this point.

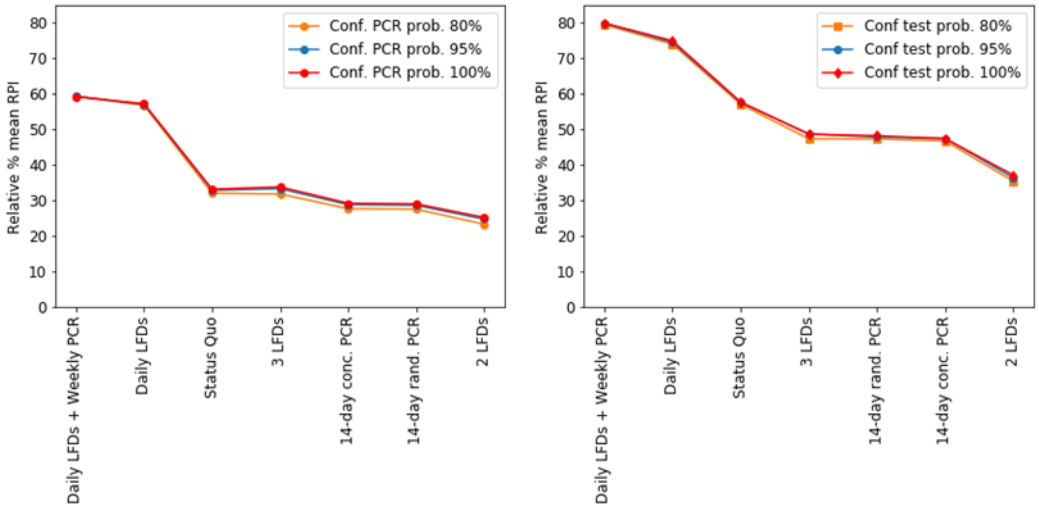

Figure S5: The same results as the bottom panel of figure 3, but varying the sensitivity of confirmatory PCRs only. Left: Model 1. Right: Model 2 with test sensitivity from all 2021 data. In all cases we assume 70% adherence.

Figure S6: Model 2 sensitivity to viral load parameters

The results of model 2 are dependent on the non-representative sample of viral load trajectories in the data from [7]. However, figure S6 compares these to an alternative model derived from the data in [6], the full details of which will be published elsewhere. The key model parameters are contained in table S1, and a comparison of the trajectories for the two models is given in figure S7. We see that the model makes remarkably similar predictions for the relative effect, suggesting that it is the testing patterns and sensitivity that dominate the results in figure 3, not the specifics of the viral load model. We do see a slight difference as the narrower infectious window predicted by the alternative parameterisation results in more frequent testing being marginally more effective, and less frequent testing marginally less effective.

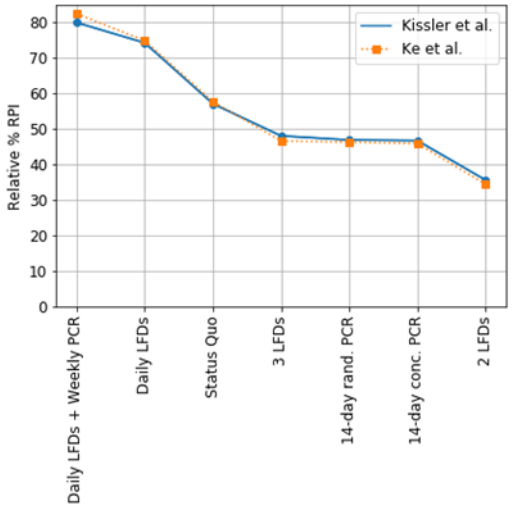

Figure S6: Plot of model 2 results for reduction in total infectious days (70% adherence, 2021 LFD sensitivity) vs. alternative model parameterisation based on the data in [6] (labelled Ke et al.).

Figure S7: Comparison of Model 2 with alternative parameterisation

The viral load trajectories and infectivity profiles predicted by the alternative parameterisation of model 2 are substantially different, as shown in figure S7. The alternative parameterisation has less heterogeneity in viral load dynamics, but includes heterogeneity in peak infectiousness.

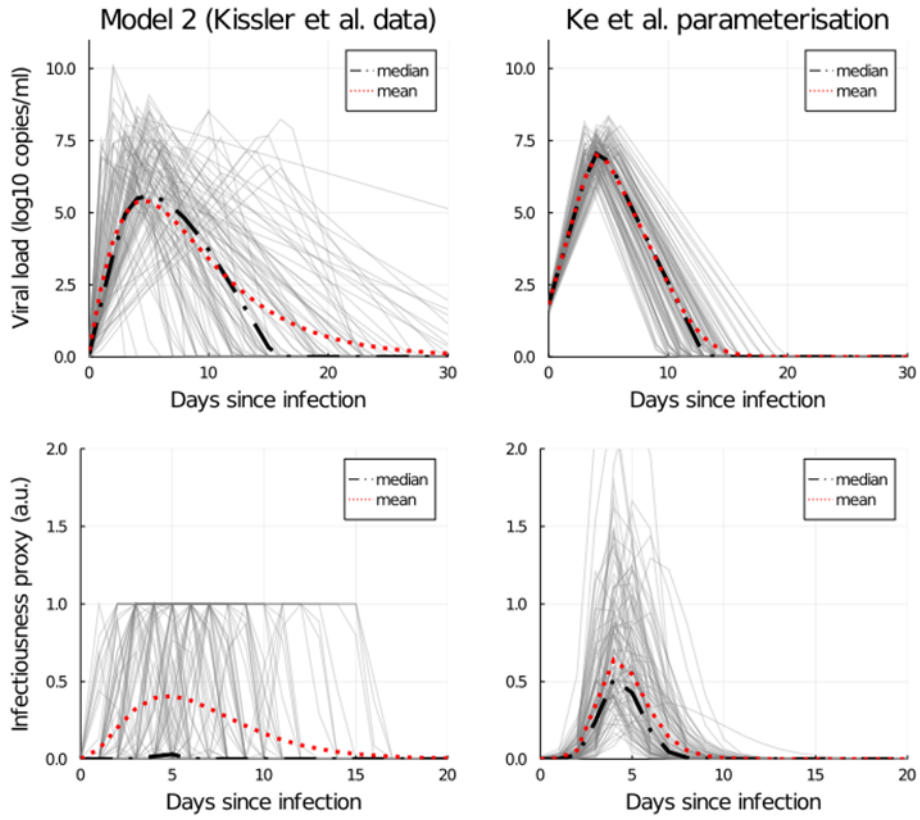

Figure S7: Top: Comparison of viral load trajectories generated by model 2 (left) and the alternative parameterisation (right). Note viral loads less than 0 log10 copies/ml are set a value of 0 in the plot for visibility. Bottom: Comparison of the infectiousness proxy used in the corresponding models. In all

plots the grey lines show 100 random samples, while the red and black dotted lines show the mean and median trajectories respectively.

Table S1: Alternative parameterisation of model 2

We fitted a piecewise exponential model to peaks of the individual viral load curves derived in [6]. This is because the dynamic model presented in that paper leads to an unrealistic second peak of viral load at late times. The viral load (in copies/ml) in this model is given by

$$C(t) = C_p \begin{cases} \exp\left[-\left(t_p - t\right)/\tau_r\right] \\ \exp\left[-\left(t - t_p\right)/\tau_d\right] \end{cases},$$

where t is time measured in days, τ_r is the inverse growth rate, τ_d is the inverse decay rate, t_p is the peak viral load time, and C_p is the peak viral load in copies/ml. We found that some of the parameters of the model were correlated, so we fitted a multivariate lognormal distribution to the values of C_p, τ_r, τ_d, and t_p for all individuals.

We also used the model of infectiousness as a function of viral load given in [6]

$$J(C) = \frac{J_p C^h}{C^h + K_m^h}$$

We found there was no significant correlation between the parameters of J and the peak viral load, and so these are assumed independent of the parameters of the viral load model. K_m is a fixed parameter and we fitted a multivariate lognormal to the distribution of the random variables J_p and h. Note that the infectivity is in arbitrary units so to make this comparable to model 2 we normalise J_p to have mean 1.

Model parameters	**Interpretation**	**Value**
$\boldsymbol{\mu}_{VL}$	Vector of means of $\log(C_p)$, $\log(\tau_r)$, $\log(\tau_d)$, and $\log(t_p)$ respectively.	[17.55, 1.39, -1.20, -0.67]
$\boldsymbol{\Sigma}_{VL}$	Covariance matrix of $\log(C_p)$, $\log(\tau_r)$, $\log(\tau_d)$, and $\log(t_p)$.	$\begin{matrix} 0.909 & 0.044 & -0.011 & 0.081 \\ 0.044 & 0.033 & 0.029 & 0.005 \\ -0.011 & 0.029 & 0.029 & 0.0004 \\ 0.081 & 0.005 & 0.0004 & 0.027 \end{matrix}$
$\boldsymbol{\mu}_J$	Vector of means of $\log(J_p)$, $\log(h)$.	[-0.169, -0.108]
$\boldsymbol{\Sigma}_J$	Covariance matrix of $\log(J_p)$, $\log(h)$.	$\begin{bmatrix} 0.3387 & 0.0265 \\ 0.0265 & 0.1270 \end{bmatrix}$
K_m	Fixed infectivity scale parameter	4.0×10^6 copies/ml

Table S1: Parameters of the multivariate distributions used in the alternative parameterisation of model 2. These distributions are sampled from to generate models of individual viral load and infectivity trajectories.

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[12] Singanayagam, A. et al. 2021. *Community Transmission and Viral Load Kinetics of SARS-CoV-2 Delta (B.1.617.2)Variant in Vaccinated and Unvaccinated Individuals*. Technical Report #ID 3918287. Social Science Research Network.
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Annex B Age-based NPIs: Simple model insight

20/12/2021

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Summary:

- With such a high infectivity (doubling time of 2 days, R0 ~ 10), without any intervention, essentially all those who can get infected do get infected, but this strongly depends on modelling assumptions about the population immunity profile to Omicron, so we explore all-or-nothing VS leaky protection from vaccination.
- Immunity assumptions about protection from infection (no hospitalisation or severe disease in the model):
    - 0% for 0 or 1 doses
    - 30% for 2 doses
    - 70% for 3 doses (booster)
    - 28m boosters given (48% of all 12+, as of Dec 19), given to all 55+ and some of 0-54
- Two extreme scenarios for reduction in contacts are considered:
    - Only within the 55+ group, proxy for free mixing of them with family members
    - Both within the 55+ group and between 55+ and 0-54 (in both directions), proxy for taking extreme steps to reduce within-household transmission and family interaction.
- Key results:
    - Assuming all-or-nothing vaccine efficacy, about 1/3 of the population is assumed perfectly immune and all the rest gets infected; for leaky vaccine, everyone could potentially get infected, so baseline (i.e. no NPIs) final size is much larger.
    - Age-based NPIs have virtually no impact in the 0-54 group
    - Reduction only in contacts among the 55+ has no impact, unless accompanied by reductions in contacts between age groups
    - With 80% reduction in contacts both within 55+ and between 55+ and 0-54, about 1/2 of the cases in the 55+ could be averted if vaccine is all-or-nothing (but 2.5m would still get infected) and about 3/4 if vaccine is leaky (but this now means 4m, a larger absolute numbers). Absolute numbers are not expected to be precise, with all the caveats of this extremely simplistic model.
    - Intuitively, the wave is much larger in the 0-54 than in the 55+ due to a combination of higher protection in the 55+ and a lower contact rate (resulting in a slower, less peaky epidemic)

Further considerations:

- An age-based lockdown is potentially highly socially divisive, and possibly met with low adherence: those 55+ who are worried about themselves will likely reduce their contacts anyway, while the others might ignore recommendations.
- There is no evidence anything like this has been achieved in the past (e.g. care homes badly affected, cases in all ages, etc.): we now have better treatment, vaccines, etc. but also Omicron seems to be spreading even faster than wild-type.
- It is as yet unclear what the relative severity of a 55+ case (likely with booster) is, compared to a younger case, so the usefulness of limiting infections in the elderlies, though reasonable, is uncertain.
- Despite modelling these scenarios, we are personally doubtful such a policy alone would bring substantial benefits, as it relies heavily on individuals' choices on adherence (e.g. we believe 80% reduction in contacts is unrealistically high). Furthermore, a free-fall epidemic in the 0-54, less likely to have received their boosters, is likely to present significant hospital burden anyway (not quantified here).

Results:

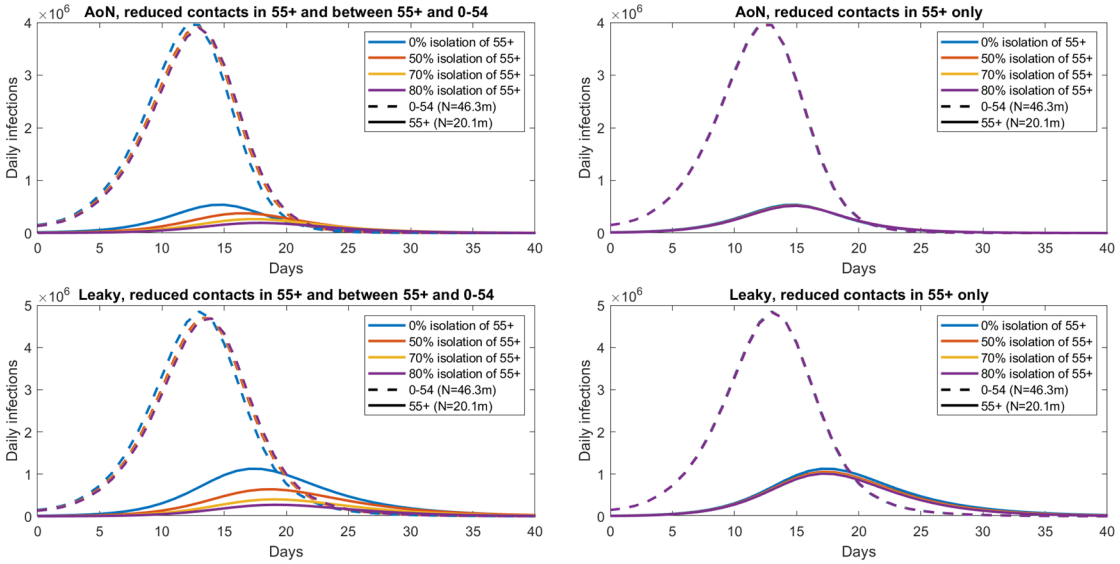

Figure 1: Epidemic dynamics in 0-54 (dashed) and 55+ (continuous lines) for 4 scenarios of reduction in contacts both within the 55+ and between 55+ and 0-54 (left), or among the 55+ only (right column), and assuming vaccine effectiveness in the population is all-or-nothing (top) or leaky (bottom row).

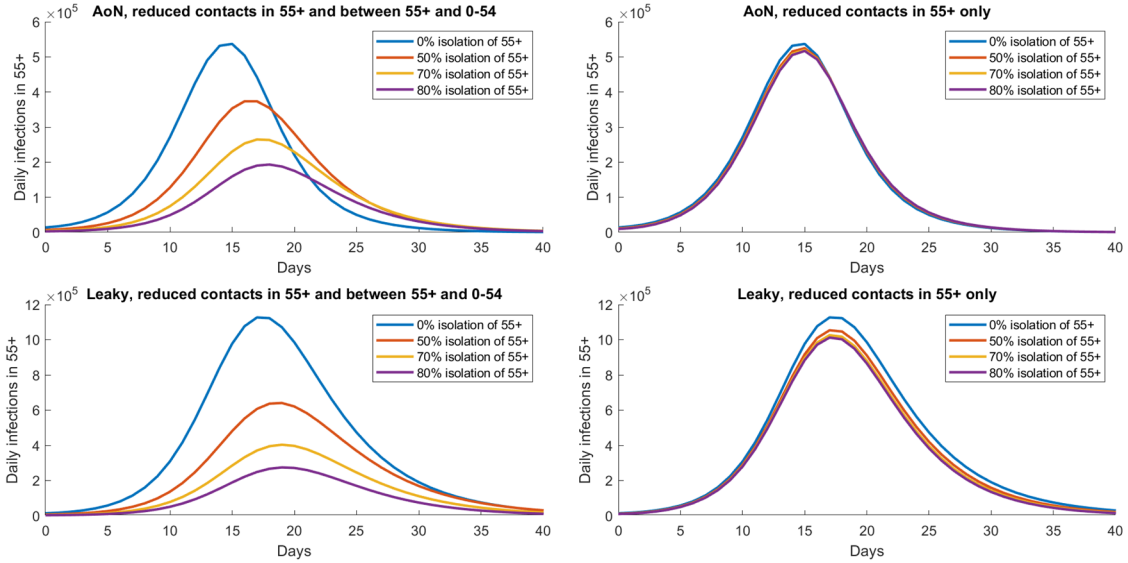

Figure 2: Zoom on the epidemics in the 55+ only from Figure 1. Note: absolute numbers are to be taken with caution, as they rely on assumptions on contact patterns and precise values of doubling times, which are uncertain.

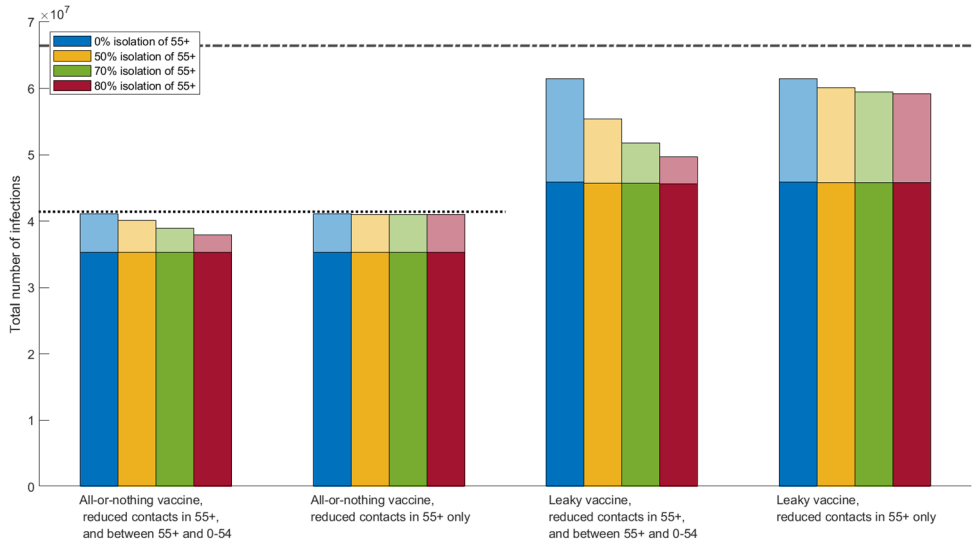

Figure 3: Final epidemic size 0-54 (bottom, full coloured part of each bar) and 55+ (whiter top of each bar) for 4 scenarios of reduction in contacts (colours) both within the 55+ and between 55+ and 0-54 (first and third group from the left), or among the 55+ only (second and fourth), and assuming vaccine effectiveness in the population is all-or-nothing (first two groups on the left) or leaky (last two groups on the right). Dash-dotted line gives total UK population, while dotted line given total susceptible population assuming all-or-nothing vaccine (left two groups only).

Methods:

- This is a simple model with 2 age groups and a 2x2 POLYMOD matrix of contacts, with a probability of transmission across a contact that is roughly calibrated to give a doubling time of 2 days.
- When vaccine is assumed to be leaky, the model is expanded to a 4x4 matrix where groups 1-3 are the 0-54 with <2, 2 and 3 doses, and group 4 gives the 55+ (all assumed boostered).
- Initial conditions are roughly calibrated so that they correspond to total cases as of 19 Dec 2021, but this has only limited impact on the dynamics and no impact on the final size bar plot.
- R0 is just “very high”, as we don’t really know what its real value might be. However, we have given the model an SEEILR structure with average sojourn times of 1.5 days in each latent classe E1 and E2, and in I (infectious pre-symptomatic), and a late infectious stage L of 3.5 days on average. This given an incubation period of around 4.5 days, and an overall infectious period of around 5 days. It might not be perfect, but anything simpler would have distorted excessively the relationship between the growth rate and R0 (e.g. in a simple SIR model, the epidemic would be much faster for the same R0, compared to here).
- With the parameters chosen for the figures, in the all-or-nothing case R0 = 9.3, and the doubling times are 2 days in 0-54 and 2.1 days in the 55+.
- Sensitivity analysis: an R0 = 6 corresponds, in this model, to a doubling time of 2.6 days in the 0-54 and 3 days in the 55+. Results are qualitatively similar, but peak incidence in 0-54 is 3m cases rather than 4m (AoN) and 3m rather than 5m (leaky).
- The generation time is assumed unchanged compared to Delta.