**MODEL SUMMARY – ENHANCED SHIELDING**

**Description of Model Structure**

A frequency-dependent SIRS-type model was used to explore the effect of enhanced shielding with three sub-populations being modelled:

* Vulnerable Population (NV) - Those who have risk factors that place them at elevated risk of developing severe disease if infected with COVID-19 and so would remain shielded whilst the rest of the population is gradually released from lockdown.
* Shielders Population (NS) - Those who have contact with the vulnerable population and include carers, certain care workers and healthcare workers. It is expected that they would also continue some shielding whilst the rest of the population is released from lockdown.
* Remainders Population (NR) - The majority of the population – those that are not vulnerable or shielders.

For the baseline scenario, a population structure of 20% vulnerable, 20% shielders and 60% remainders was used **(Table 1)**. A total infectious fraction of 0.0001 (split equally across the population) was used as the initial conditions to seed infection. Model parameters were chosen to best describe the transmission dynamics of COVID-19 in the UK using current assumptions (as of publication) regarding the values of key epidemiological parameters **(Table 2)**.

The SIRS model assumes that the number of new infections in a sub-population is a function of the fraction of the sub-population that is susceptible (SX), the fraction of the sub-population that is infectious (IX) and the rate of infectious transmission between the two sub-populations (βX). Infectious individuals subsequently recover at a rate γ that equates to an 8.6 day infectious period. Recovered individuals are assumed to lose immunity and return to being susceptible over 365 days (**Eqn 1.1**).

**Table 1** – SIRS Model Compartments and Initial Conditions

|  |  |  |
| --- | --- | --- |
| Compartment | Description | Initial Conditions |
| SV | Susceptible fraction of the population who are vulnerable | 0.2 – 0.00002 |
| SS | Susceptible fraction of the population who are shielders | 0.2 – 0.00002 |
| SR | Susceptible fraction of the remainder population | 0.6 – 0.00006 |
| IV | Infectious fraction of the population who are vulnerable | 0.00002 |
| IS | Infectious fraction of the population who are shielders | 0.00002 |
| IR | Infectious fraction of the remainder population | 0.00006 |
| RV | Recovered fraction of the population who are vulnerable | 0 |
| RS | Recovered fraction of the population who are shielders | 0 |
| RR | Recovered fraction of the remainder population | 0 |

**Table 2** – Parameter Descriptions and Values

|  |  |  |
| --- | --- | --- |
| Parameters | Description | Value |
| R0 | Baseline basic reproduction number | 2.8 |
| T2 | Doubling time | 3.3 days |
| βx | Per capita rate of infectious transmission | Varies (see Table 3) |
| γ | Per capita rate of recovery | 0.1167 day-1 |
| ζ | Per capita rate of immunity loss | 0.0027 day-1 |

Eqn1.1

**WAIFW Matrix and Modelling Transmission**

A “who acquires infection from whom” (WAIFW) matrix was created to describe infectious transmission between the three sub-populations (**Table 3**). The remainder population was split into three subgroups to explicitly model differences in contact/transmission between the subgroups.

Remainder sub-populations were split in three sub-groups to give greater flexibility in the frequency dependent framework, enabling variation to be modelled in the transmission rates between different subpopulations, whilst, critically, maintaining a globally balanced R0. However, these three sub-groups are qualitatively identical and the sub-groups are being aggregating into a unified “remainder” population for the model output.

Four values of β were used to parameterise the model: β1 describes transmission within and between the vulnerable and shielder subpopulations, β2 describes transmission between shielders and the remainder subpopulations, β3 describes transmission within the remainder subpopulations and β4 transmission between remainder and vulnerable subpopulations (Table 3).

**Table 3** – Generic WAIFW matrix used for the model and the transmission parameters β, which defines transmission between subpopulations

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| To/From | | Vulnerable | Shielders | Remainders | | |
| **Remainders 1** | **Remainders 2** | **Remainders 3** |
| Vulnerable | | **β1** | **β1** | **β4** | **β4** | **β4** |
| Shielders | | **β1** | **β1** | **β2** | **β2** | **β2** |
| Remainders | **Remainders 1** | **β4** | **β2** | **β3** | **β3** | **β3** |
| **Remainders 2** | **β4** | **β2** | **β3** | **β3** | **β3** |
| **Remainders 3** | **β4** | **β2** | **β3** | **β3** | **β3** |

**Modelling Enhanced Shielding**

To model the effect of an enhanced shielding strategy on COVID-19 transmission, four intervention “phases” were considered. These phases describe social distancing measures which aim to control a simulated COVID-19 epidemic. Interventions were modelled as alterations in the R0 values (translated into β values), representing changes in infectious pressure resulting from these control measures.

In the context of the enhanced shielding strategy, the intervention phases were assumed to impact the βX values differently, to reflect the loosening or tightening of social distancing measures throughout the progression of the outbreak (**Table 4**). The transition from phase 1 to phase 2 represents the hard lockdown implemented on the 24th March 2020, phase 3 represents a progressive release (for the remainder subpopulation) or tightening (for the vulnerable subpopulation) of restrictions applied over a 12 week period. Phase 4 represents the end point of the gradual transition of phase 3.

**Table 4** – Description of Phased Enhanced Shielding Strategy

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phases | Description of Intervention Phase | Duration | β1 | β2 | β3 | β4 |
| Phase 1 | Represents the “business as usual” approach that was operating pre-lockdown. | Up until R(t+7) = 0.06 | **Baseline (the same value)** | | | |
| Phase 2 | Represents the nationwide lockdown that was applied approximately equally to all subpopulations | 6 Weeks | **↓↓\*** | **↓** | **↓** | **↓↓** |
| Phase 3 | Represents a progressive change in restrictions – a progressive release of regulations to the remainder subpopulation and a progressive tightening of restrictions applied to the vulnerable subpopulation | 12 Weeks | **Linear Change to Phase 4** | | | |
| Phase 4 | Represents the long-term application of the released restrictions to the remainder subpopulation and long-term enhanced shielding of vulnerable subpopulations | Until End of simulation | **↓** | **↑** | **↑↑** | **↓** |

\*Arrows represent increases or decreases to βx relative to the previous phase, with the number of arrows representing the strength of the change.

The model simulations start on day 0 and we implement lockdown on a selected “trigger day" which corresponds to where the proportion of total recovered individuals is 0.06 seven days after the trigger day. The R0 values that are modelled in the baseline scenario are shown in Table 5.

**Table 5** – R0 values for the different phases

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phases | Duration | β1 | β2 | β3 | β4 |
| Phase 1 | Up till R(t+7) = 0.06 | 1.7 | 1.7 | 1.7 | 1.7 |
| Phase 2 | 6 Weeks | 0.8 | 0.9 | 0.9 | 0.8 |
| Phase 3  Phase 4 | 12 Weeks (Gradual transition to…) | 0.4 | 1.85 | 2.25 | 0.4 |
| Until End of Model | 0.4 | 1.85 | 2.25 | 0.4 |

**Sensitivity Analysis**

To test the susceptibility of the core results to key parameters and uncertainty in the model formulation, several sensitivity analyses were conducted. These explored:

1. Varying phase 1 R0 values from the baseline value of 1.7 (1.4 – 2.0)
2. Varying phase 2 R0 values from the baseline value of 0.8/0.9 (0.6/0.7 – 1.0/1.1)
3. Varying the trigger day from day 71 (R(t+7) = 0.06) to day 46 and 96.
4. Varying the duration of the phase 3 ramp-down (β1 & β3) and ramp-up (β1 & β3) from baseline of 12 weeks (6 – 18 weeks)
5. Assessing the sensitivity of the main model output to individual beta values in the WAIFW matrix

**Description of FAST Analysis**

We determine which model parameters have most influence on the outcome values (height of second peak fraction of the vulnerable population that are infectious (Iv) , whether the second peak of Iv is higher than the first peak and the cumulative fraction of Iv one year after the start of lockdown) by computing the total sensitivity index *D*Ti using the extension of Fourier amplitude sensitivity test (FAST) as described in Saltelli *et al.* [ref Saltelli].

The extended FAST method is a variance-based, global sensitivity analysis technique that has been largely used for studying complex agricultural, ecological and chemical systems (see [ref Makowski, ref Neumann] for examples). Independently of any assumption about the model structure (such as linearity, monotonicity and additivity of the relationship between input factors and model output), the extended FAST method quantifies the sensitivity of the model output with respect to variations in each input parameter by means of spectral analysis.

It provides measures of the amount of variance of the prevalence that arise from variations of a given parameter in what is called a total sensitivity index, *D*Ti. It therefore captures the overall effect of parameter variations on the chosen outcome values (i.e. including first- and higher-order interactions between model parameters). For example, a value of *D*Ti = 0.10 indicates that 10% of the total observed variation of the prevalence is explained by the parameter under consideration. The sensitivity analysis was carried out using R [ref R (version 3.6.3)]. For the sensitivity analysis, we used a parameter range of -25% to +25% of the baseline value for all parameters under investigation.

**Software used**

SIRS model implemented in R and C++ independently (code available at <https://github.com/bvbunnik/COVID-19-enhanced-shielding.git>). Package “desolve” was used in R to implement model structure and analysis. Package “ggplot2” was used for all output plotting.

**References**

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