**MODEL SUMMARY – ENHANCED SHIELDING**

**Model Equations**

Eqn1.1

1. **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) - DESCRIPTION WHO DOES THIS INCLUDE
* Shielders Population (NS) - DESCRIPTION WHO DOES THIS INCLUDE
* Remainders Population (NR) - DESCRIPTION WHO DOES THIS INCLUDE

For illustrative purposes, a population structure of 20% vulnerable, 20% shielders and 60% remainders was used as a baseline scenario **(Table 1)**. A total infectious fraction of 0.0001 (split according the population structure) 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)**.

**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 | Removed fraction of the population who are vulnerable | 0 |
| RS | Removed fraction of the population who are shielders | 0 |
| RR | Removed fraction of the remainder population | 0 |

**Table 2** – Parameter Descriptions and Values

|  |  |  |
| --- | --- | --- |
| Parameters | Description | Value |
| R0 | Baseline basic reproduction number (to calculate γ) | 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 |

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 (**MENTION REASON AND R0 BALANCING HERE**). However, these three sub-groups are functionally identical and were only used to improve transparency in the modelling process, with the model output being aggregating into a unified “remainder” population.

**Table 3** – Generic WAIFW matrix used for the model

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| 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** |

To model the effect of an enhanced shielding strategy on COVID-19 transmission, four intervention “phases” were considered. These phases describe alterations to 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 disease control measures.

In the context of the enhanced shielding strategy, the intervention phases were assumed impact the βx values differently (through reductions in R0), to reflect the loosening or tightening of social distancing measures throughout the progression of the outbreak (**Table 4**).

* Explanation of “ramping” in phase 3

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phases | Description of Intervention Phase | Duration | β1 | β2 | β3 | β4 |
| Phase 1 | WHAT DOES THIS REPRESENT? | Up till I(t) = 0.0277 | Baseline (the same value) | | | |
| Phase 2 | WHAT DOES THIS REPRESENT? | 6 Weeks | ↓↓\* | ↓ | ↓ | ↓↓ |
| Phase 3  Phase 4 | WHAT DOES THIS REPRESENT? | 12 Weeks | Linear Change to Phase 4 | | | |
| WHAT DOES THIS REPRESENT? | Until End of Model | ↓ | ↑ | ↑↑ | ↓ |

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

* Description of baseline trigger dates, R0 values etc.

1. **Description of Sensitivity Analysis**

To explore the sensitivity of the model to variation in the enhanced shielding strategy and to uncertainty in model parameters, several sensitivity analyses were conducted. These aimed to explore:

* Variation in Phase 1 R0
* Variation in Phase 2 R0
* Variation in trigger date
* Variation in Ramping up/down periods
* Bram’s optimisation

Due to the uncertainty surrounding many model parameters and th

1. **Description of FAST Analysis**

We determine which model parameters have most influence on the outcome values (height of second peak Iv, whether the second peak if 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.

Refs:

* Saltelli A, Tarantola S, Chan KPS. 1999A quantitative model-independent method for global sensitivity analysis of model output. Technometrics 41, 39–56. (doi:10.2307/1270993)
* Makowski D, Naud C, Jeuffroy M-H, Barbottin A, Monod H. 2006Global sensitivity analysis for calculating the contribution of genetic parameters to the variance of crop model prediction. Reliability Eng. Syst. Safety 91, 1142–1147. (doi:10.1016/j.ress.2005.11.015)
* Neumann MB, Gujer W, von Gunten U. 2009Global sensitivity analysis for model-based prediction of oxidative micropollutant transformation during drinking water treatment. Water Res. 43, 997–1004. (doi:10.1016/j.watres.2008.11.049)
* R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL:https://www.R-project.org/.

1. **Software used**