Uncertainty quantification and sensitivity analysis of COVID-19 exit strategies in an individual-based transmission model

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### S1 Table

**Overview of parameter values used in the analysis.** Overview of the values of the parameters in the SEIR model. In the last column we indicate the respective parameter in the computational model (or which computational parameter is affected).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Value(s)</th>
<th>Computational model parameter</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\nu_E$</td>
<td>average incubation time</td>
<td>4.6 days</td>
<td>exposed_time</td>
</tr>
<tr>
<td>$\alpha_E$</td>
<td>shape of Weibull distribution for incubation time</td>
<td>20 (considered as uncertain in parts of the analysis)</td>
<td>shape_exposed_time</td>
</tr>
<tr>
<td>$\nu_I$</td>
<td>average duration of infectiousness</td>
<td>5 days (considered as uncertain in parts of the analysis)</td>
<td>avg_duration_infectiousness</td>
</tr>
<tr>
<td>$\alpha_I$</td>
<td>shape of the Weibull distribution for duration of infectiousness</td>
<td>1</td>
<td>infected_time</td>
</tr>
<tr>
<td>$N$</td>
<td>total population size</td>
<td>$10^6$</td>
<td>n_agent</td>
</tr>
<tr>
<td>$K$</td>
<td>number of superclusters</td>
<td>20</td>
<td>n_supercluster</td>
</tr>
<tr>
<td>$J$</td>
<td>number of cluster per supercluster</td>
<td>1000</td>
<td>n_cluster</td>
</tr>
<tr>
<td>$\sigma$</td>
<td>standard deviation of cluster-level sampling weights for the multinomial distribution of clusters population sized</td>
<td>0.95</td>
<td>cluster_size_sd</td>
</tr>
<tr>
<td>$\beta$</td>
<td>overall contact rate</td>
<td>0.5 (considered as uncertain in parts of the analysis)</td>
<td>contact_rate</td>
</tr>
<tr>
<td>$\alpha$</td>
<td>shape and rate of $\Gamma$ distribution for variations in individual relative contact rates (relative to $\beta$)</td>
<td>3.4</td>
<td>contact_shape</td>
</tr>
<tr>
<td>$\vartheta$</td>
<td>level of assortative mixing</td>
<td>0.26</td>
<td>contact_assort</td>
</tr>
<tr>
<td>$\theta_{SC}$, $\theta$</td>
<td>weights for transmission coming from superclusters and the general population, respectively; the derived weight for transmission coming within cluster is $1 - \theta_{SC} - \theta$</td>
<td>0.05, 0.05</td>
<td>population_mixing, supercluster_mixing</td>
</tr>
<tr>
<td>Parameter</td>
<td>Description</td>
<td>Value or Expression</td>
<td></td>
</tr>
<tr>
<td>-----------</td>
<td>-------------</td>
<td>---------------------</td>
<td></td>
</tr>
<tr>
<td>$\mu$</td>
<td>relative level to which transmission is reduced on average in supercluster $k$</td>
<td>(considered as uncertain in parts of the analysis)</td>
<td></td>
</tr>
<tr>
<td>$\tau$</td>
<td>size of the Beta distribution for inter-individual variation in the effect of contact-related interventions</td>
<td>$\infty$ (i.e. no variation) (considered as uncertain in parts of the analysis)</td>
<td></td>
</tr>
<tr>
<td>$\varphi$</td>
<td>multiplier for the contribution and exposure of a supercluster to population-level transmission in case of isolation</td>
<td>0.5 in case of isolation of the supercluster as part of the phased opening strategy, 1 otherwise</td>
<td></td>
</tr>
<tr>
<td></td>
<td>total running time in days</td>
<td>550</td>
<td></td>
</tr>
<tr>
<td></td>
<td>standard deviation of the softmax-transformed cluster-level sampling weights for the multinomial distribution of the expected number of clusters per supercluster</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>external force of infection assumed to be continuously present over time</td>
<td>$50/(365 \cdot n_{agent})$ for FC and CT; 0 for IL and PO</td>
<td></td>
</tr>
<tr>
<td></td>
<td>initial number of infected cases</td>
<td>50</td>
<td></td>
</tr>
<tr>
<td></td>
<td>scalar value for cumulative incidence of cases after which interventions are started</td>
<td>9500</td>
<td></td>
</tr>
</tbody>
</table>