

COVID-19 and heterogeneous transmission rates model

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SEIR model with subgroups and behaviour change

Uppercase letters (S , E etc.) denote proportions of individuals in the population in a given state (susceptible, exposed etc.) at time t . Index i indicates different groups in the model; these can index over e.g. age groups, professions or any other groups with differential transmission rates (within or across groups). This is outlined later in the text. With exception of λ we assume that all parameters (p and the ones assigned Greek letters) are constant over time.

The derivatives over time are as follows:

$$dS_i = -\lambda_i(t)S_i + \phi_i R_i \quad (1)$$

$$dE_i = \lambda_i(t)S_i - \gamma_{1,i}E_i \quad (2)$$

$$dAs_i = \gamma_{1,i}E_i p_{a,i} - \gamma_{2,i}As_i$$

$$dI_i = \gamma_{1,i}E_i(1 - p_{a,i}) - \gamma_{2,i}I_{1,i}$$

$$dD_i = \gamma_{2,i}I_i p_{d,i}$$

$$dR_i = \gamma_{2,i}I_i(1 - p_{d,i}) + \gamma_{2,i}As_i - \phi_i R_i$$

The time-dependent $\lambda(t)$ is a function of number of infections, number of contacts, reduction in contacts $cr(t)$, and the risk of transmission during each contact q .

$$cr(t) = \dots TBD \quad (3)$$

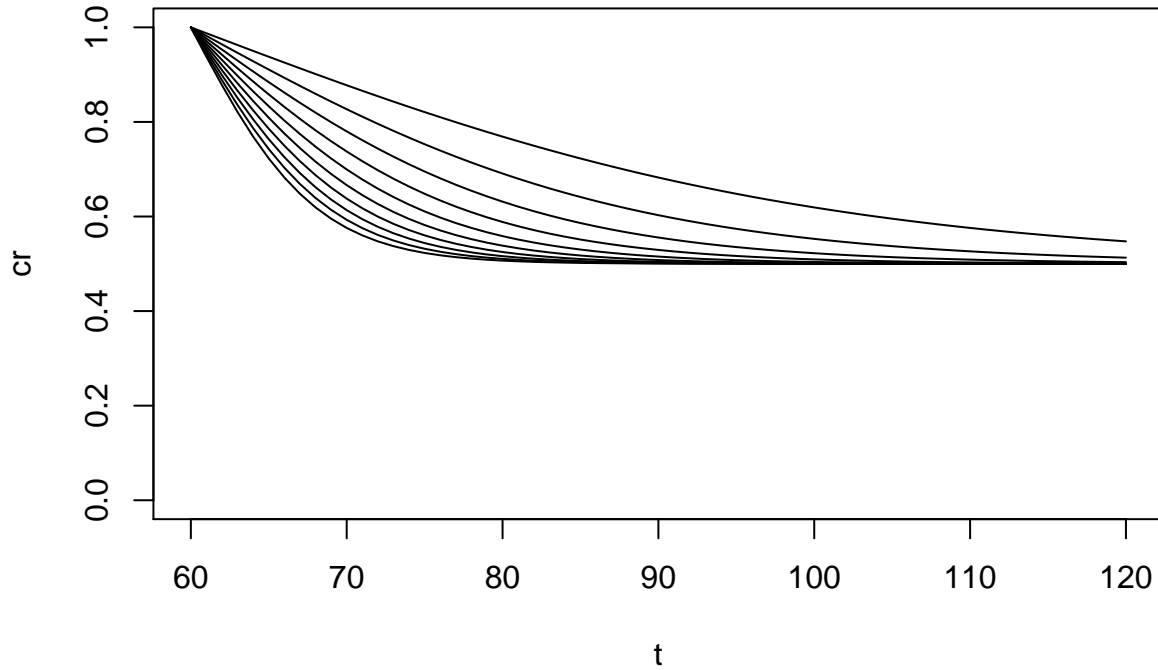
$$\lambda_i(t) = \sum_{j=1, \dots, N} c(i, j) \cdot (I_j + As_j) \cdot q \cdot cr(t) \quad (4)$$

$$(5)$$

The model assumes homogeneous mixing within each group (at the contact rate $c(i, i)$ specific to each group) and differential rates of contact across groups ($c(i, j)$ for $i \neq j$).

(TBD - for now just a concept) Contact rate reduction over time is implemented as a logistic function scaling contacts from the initial value of 1 to the final value of f at some rate k , that is $cr(t) = f + \frac{2f}{1 + \exp(k(t - t^*))}$ for $t > t^*$; t^* can be related to introduction of social distancing policies or behaviour adjustment.

logistic contacts reduction with $t^* = 60$, k from .05 to .25, $f = .5$



Model parameters

Model parameters are as follows:

Name	Value	Reference
N_c	1	See below
$c_{i,j}$	See below	See below
R_0	2.5	See below
γ_1	0.1961	Verity et al. (2020) (5.1 days)
γ_2	0.1538	Verity et al. (2020) (6.5 days)
p_a	0.43	Oran and Topol (2020)
p_d	0.0066	Verity et al. (2020) (Chinese data)
δ	0	Assumption, scenario dependent
κ	0	Assumption, scenario dependent
ϕ	0	Assumption, scenario dependent

Where a single value is given for a group-specific variable, that indicates the default value is constant across all groups.

A note on calculation and interpretation of R_0 when modelling many groups

R_0 is the average number of secondary infections produced by an individual in a fully susceptible population. In a model with homogeneous mixing R_0 depends on two parameters only, risk of infection (average number of contacts per person times risk of transmission per each contact) and the length of infection. For compartmental models (with a matrix c spanning multiple groups) the calculation must take into account different levels of mixing within groups and rates of contact across groups. Diekmann, Heesterbeek, and Roberts (2010) provide a canonical method for deriving R_0 when modelling many subpopulations. The method is based on calculation of the dominant eigenvalue in the *next generation matrix* for compartments, essentially an “ R_0 matrix”.

Note an important (albeit purely theoretical) implication of using the *dominant* eigenvalue: if there is no transmission across groups, R_0 is by definition the highest of “in-group” R_0 ’s. That is why R_0 has to be interpreted carefully, as a mean behaviour across groups, and ultimately it might not be a useful statistic for modelling heterogeneous behaviour. For models with realistic transmission structures this should not be a problem.

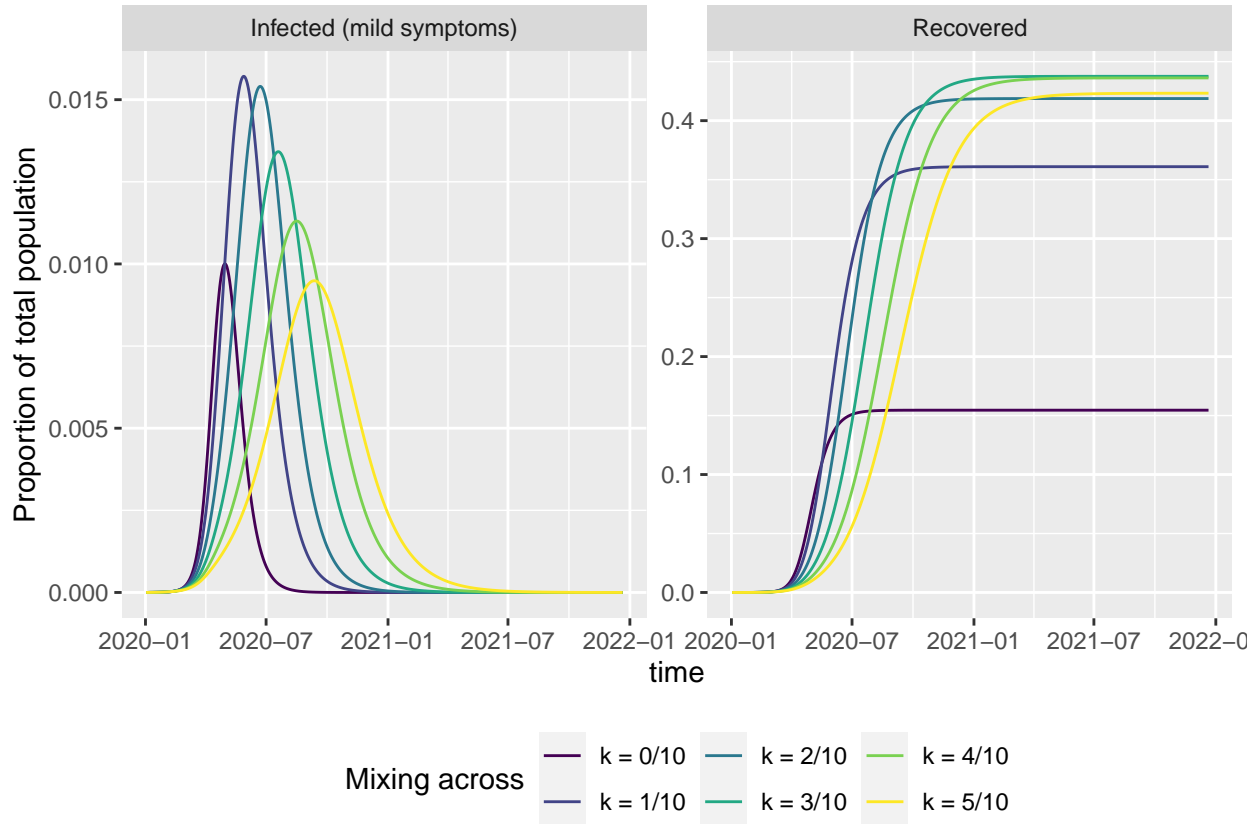
Simulations of heterogeneous contact rates

Need to double check the model, some values are not realistic.

Consider a 2-compartmental model with 20% of population being super-spreaders (2.6 secondary infections) and the other 80% “normal” spreaders (1.1 secondary infections). We can set $q = \gamma_1$ and

$$c = \begin{pmatrix} 2.6k & 1.1(1-k) \\ 2.6(1-k) & 1.1k \end{pmatrix}$$

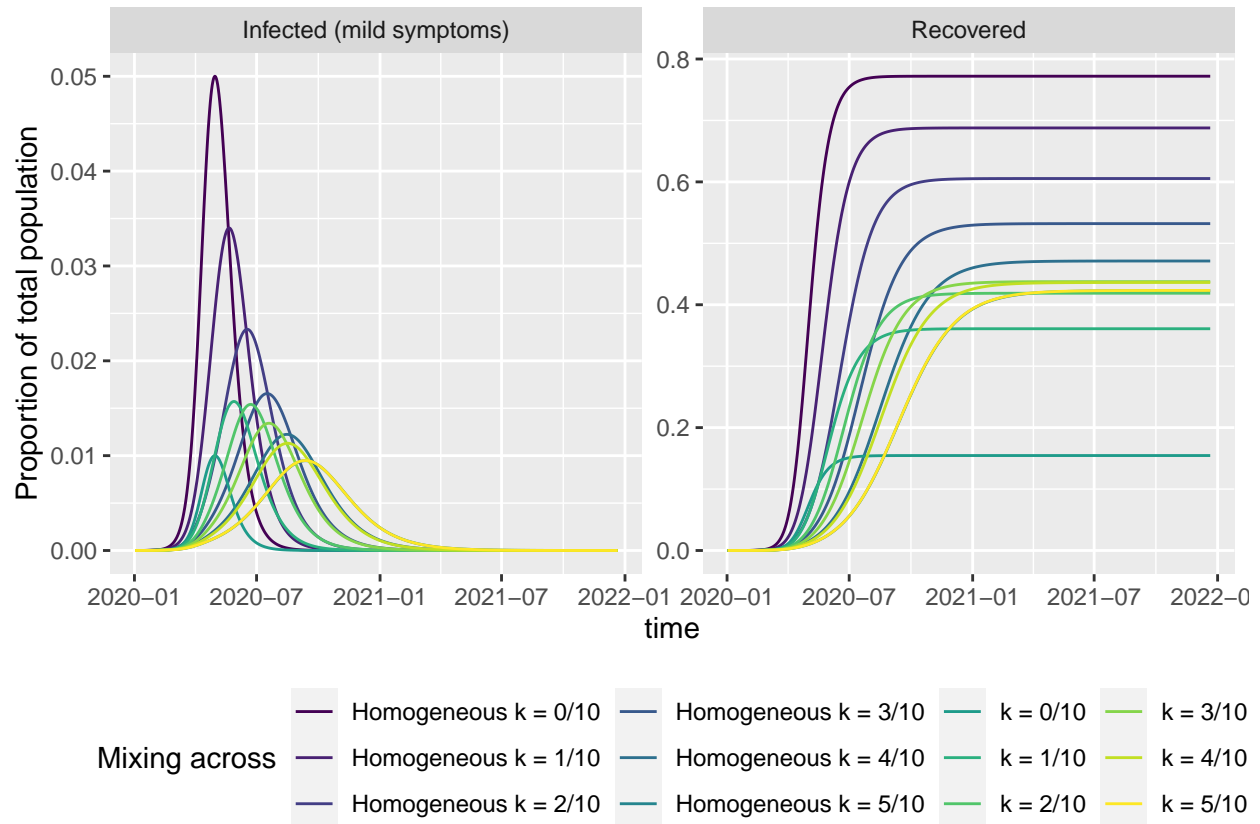
where $k \in [0, 1]$ is the degree of mixing across groups. This parameter has very strong influence on the course of the epidemic:



R_0 values are as follows:

```
## $'k = 0/10'
## [1] 2.6
##
## $'k = 1/10'
## [1] 2.360863
##
## $'k = 2/10'
## [1] 2.168767
##
## $'k = 3/10'
## [1] 2.025086
##
## $'k = 4/10'
## [1] 1.922465
##
## $'k = 5/10'
## [1] 1.85
```

To illustrate the difference with a homogeneous mixing models, we add homogeneous mixing curves *with exactly the same R_0 's* as above but no super-spreaders vs normal-spreaders division:



Need to improve the above. Also need to check the model – the differences might be overstated

References

- Diekmann, O., J. a. P. Heesterbeek, and M. G. Roberts. 2010. "The Construction of Next-Generation Matrices for Compartmental Epidemic Models." *Journal of the Royal Society, Interface* 7 (47): 873–85. <https://doi.org/10.1098/rsif.2009.0386>.
- Oran, Daniel P., and Eric J. Topol. 2020. "Prevalence of Asymptomatic SARS-CoV-2 Infection." *Annals of Internal Medicine*, June. <https://doi.org/10.7326/M20-3012>.
- Verity, Robert, Lucy C. Okell, Ilaria Dorigatti, Peter Winskill, Charles Whittaker, Natsuko Imai, Gina Cuomo-Dannenburg, et al. 2020. "Estimates of the Severity of Coronavirus Disease 2019: A Model-Based Analysis." *The Lancet Infectious Diseases* 0 (0). [https://doi.org/10.1016/S1473-3099\(20\)30243-7](https://doi.org/10.1016/S1473-3099(20)30243-7).