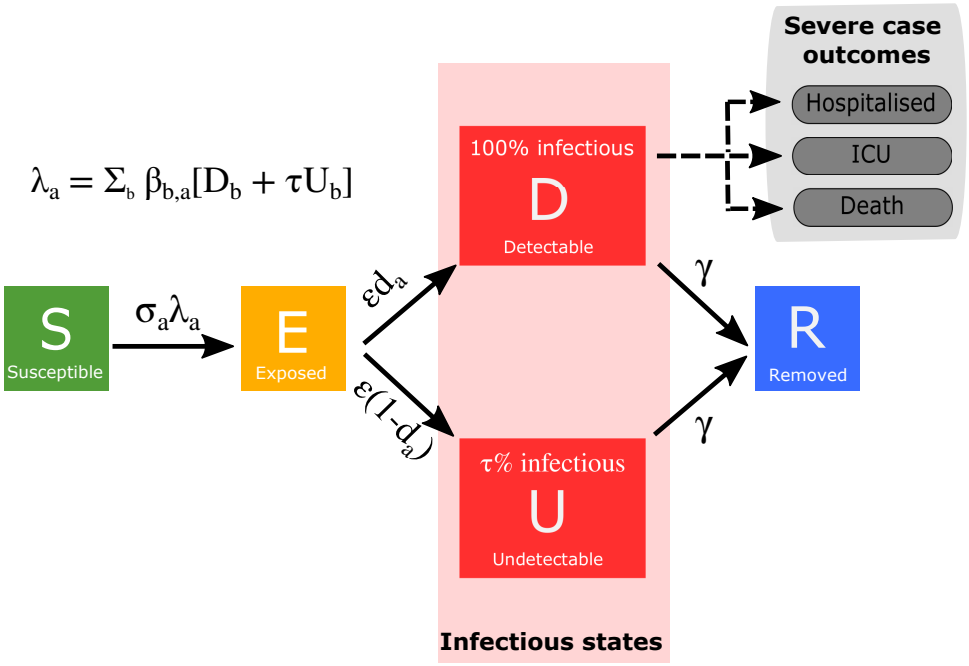
Supplementary Material
Precautionary breaks: planned, limited duration circuit breaks to control the prevalence of COVID-19.

Here we present the basic model formulation that underpins the age-structured predictions of COVID-19 dynamics in the UK, and how the parameters of this model have been inferred from the available data. Much of the background to the model formulation is covered in more detail in [1], while the parameter estimation is described in [2].

1 Model description



We first show the underlying system of equations that account for the transmission dynamics, including symptomatic and asymptomatic transmission, household saturation of transmission and household quarantining. The population is stratified into multiple compartments: individuals may be susceptible (S), exposed (E), infectious with symptoms (I), or infectious and either asymptomatic or with very mild symptoms (A). Asymptomatic infections are assumed to transmit infection at a reduced rate given by τ. To some extent, the separation into symptomatic (D) and asymptomatic (U) within the model is somewhat artificial as there are a wide spectrum of symptom severity that can be experienced.

We let superscripts denote the first infection in a household (F), a subsequent infection from a symptomatic household member (SI) and a subsequent infection from an asymptomatic household member

(SA). A fraction (H) of the first detected cases (necessarily symptomatic) in a household are quarantined (QF), as are all their subsequent household infections (QS) - we ignore the impact of household quarantining on the susceptible population as the number in quarantine is assumed small compared with the rest of the population. The recovered class is not explicitly modelled, although it may become important once we have a better understanding of the duration of immunity. Natural demography and disease-induced mortality are also ignored in the formulation of the epidemiological dynamics.

Model equations

The full equations are given by

$$
\begin{aligned}
\frac{dS_a}{dt} &= -\left(\lambda_a^F + \lambda_a^{SI} + \lambda_a^{SA} + \lambda_a^Q\right)\frac{S_a}{N_a}, \\
\frac{dE_{1,a}^F}{dt} &= \lambda_a^F \frac{S_a}{N_a} - M\varepsilon E_{1,a}^F, \\
\frac{dE_{1,a}^{SI}}{dt} &= \lambda^{SI} \frac{S_a}{N_a} - M\varepsilon E_{1,a}^{SI}, \\
\frac{dE_{1,a}^{SA}}{dt} &= \lambda^{SA} \frac{S_a}{N_a} - M\varepsilon E_{1,a}^{SA}, \\
\frac{dE_{1,a}^{Q}}{dt} &= \lambda^{Q} S - M\varepsilon E_{1,a}^{Q}, \\
\frac{dE_{m,a}^{X}}{dt} &= M\varepsilon E_{m-1,a}^X - M\varepsilon E_{m,a} \qquad X \in \{F, SI, SA, Q\} \\
\frac{dI_a^F}{dt} &= d_a(1-H)M\varepsilon E_{M,a}^F - \gamma I_a^F, \\
\frac{dI_a^{SI}}{dt} &= d_a M\varepsilon E_{M,a}^{SI} - \gamma I_a^{SI}, \\
\frac{dI_a^{SA}}{dt} &= d_a(1-H)M\varepsilon E_{M,a}^{SA} - \gamma I_a^{SA}, \\
\frac{dI_a^{QF}}{dt} &= d_a H M\varepsilon E_{M,a}^F - \gamma I_a^{QF}, \\
\frac{dI_a^{QS}}{dt} &= d_a H M\varepsilon E_{M,a}^{SA} + d_a\varepsilon E_a^Q - \gamma I_a^{QS}, \\
\frac{dA_a^F}{dt} &= (1-d_a)M\varepsilon E_{M,a}^F - \gamma A_a^F, \\
\frac{dA_a^S}{dt} &= (1-d_a)M\varepsilon (E_{M,a}^{SI} + E_{M,a}^{SA}) - \gamma A_a^S, \\
\frac{dA_a^Q}{dt} &= (1-d_a)M\varepsilon E_{M,a}^{Q} - \gamma A_a^Q,
\end{aligned}
$$

Here we have included M latent classes. The rate of progression from each latent class was ϵM, with the length of the total latent period (ϵ^{-1}) equivalent to the mean of an Erlang distribution with shape parameter M and rate parameter ϵM. Throughout we have taken $M = 3$. The infectious period, γ^{-1}, matched the mean of an exponential distribution with rate parameter γ.

The forces of infection which govern the non-linear transmission of infection obey:

$$\begin{aligned}
\lambda_a^F &= \sigma_a \sum_b \left(I_b^F + I_b^{SI} + I_b^{SA} + \tau(A_b^F + A_b^S)\right) \beta_{ba}^N, \\
\lambda_a^{SI} &= \sigma_a \sum_b I_b^F \beta_{ba}^H, \\
\lambda_a^{SA} &= \sigma_a \tau \sum_b A_a^F \beta_{ba}^H, \\
\lambda_a^Q &= \sigma_a \sum_b D_b^{QF} \beta_{ba}^H,
\end{aligned}$$

where β^H represents household transmission and $\beta^N = \beta^S + \beta^W + \beta^O$ represents all other transmission locations, comprising school-based transmission (β^S), work-place transmission (β^W) and transmission in all other locations (β^O). These matrices are taken from Prem et al [3] to allow easily translation to other geographic settings, although other sources such as POLYMOD [4] could be used.

Two key parameters, together with the transmission matrix, govern the age-structured dynamics: σ_a corresponds to the age-dependent susceptibility of individuals to infection; d_a the age-dependent probability of displaying symptoms (and hence potentially progressing to more severe disease). Taken together σ_a and d_a define the early age-distribution of identified symptomatic cases; as such we can match the dominant eigenvalue at invasion to the recorded age-distribution. However, this does not uniquely determine σ_a and d_a as either could be used to achieve the required distribution. We therefore introduce a parameter α which scales between the situation where the age-distribution is generated entirely through the probability of displaying symptoms ($\alpha = 0$, σ_a is constant) and when it is generated through differential susceptibility ($\alpha = 1$, d_a is constant). (In particular, we require $\sigma_a d_a$ to be an age-dependent value, say Q_a, and hence define $d_a \propto Q^{1-\alpha}$ and $\sigma \propto Q^{\alpha}$.)

We define τ as the reduced transmission from asymptomatic infections compared to symptomatic infections; given the probability of displaying symptoms is less in the younger age groups, this parameter also shapes the role of younger ages in onward transmission.

1.1 Amendments to within-household transmission

We require our model to capture both individual level quarantining of infected individuals and isolation of households containing identified cases. In a standard ODE framework this level of household structure is only achievable at large computational expense [5, 6], so instead we make a relatively parsimonious approximation to achieve a comparable effect.

We assume that all within household transmission originates from the first infected individual within the household (denoted with a superscript F, or QF if they become quarantined). This allows us to assume that secondary infections within a household in isolation (denoted with a superscript QS or Q) play no further role any of the transmission dynamics. As a consequence, high levels of household isolation can drive the epidemic extinct, even if within household transmission is high – an effect not achievable with the standard SEIR-type modelling approach. This improved methodology also helps to capture to some degree household depletion of susceptibles (or saturation of infection), as secondary infections in the household are incapable of generating additional household infections. A more thorough investigation of this extension to the basic model is reviewed in the Supplementary Material of [1].

1.2 Capturing social distancing

Age-structured contact matrices for the United Kingdom were obtained from Prem et al. [3] and used to provide information on normal levels household transmission (β^H_{ab}, with the subscript ab corresponding to transmission from age group a against age group b), school-based transmission (β^S_{ab}), work-place transmission (β^W_{ab}) and transmission in all other locations (β^O_{ab}).

We assume that any instigated non-pharmaceutical interventions (patterns of social-distancing or lockdown measures) leads to a reduction in the work, school and other matrices while increasing the strength of household contacts. Any given level of non-pharmaceutical interventions (NPIs), captured by the parameter ϕ between zero and one, therefore scales the scales the four transmission matrices between their normal values (when $\phi = 0$) and their value under the most severe lockdown ($\phi = 1$).

This level of NPIs, is inferred as a slowly varying parameter in the MCMC processes on a weekly basis. In turn the weekly value of ϕ allows us to calculate the growth rate r by an eigenvalue approach.

2 Parameter Inference

As with any model of this complexity, there are multiple parameters that determine the dynamics. Some of these are global parameters and apply for all geographical regions, with others used to capture the regional dynamics. Some of these parameters are matched to the early outbreak data (including the resultant age-distribution of infection), however the majority are inferred by an MCMC process (Table 1).

We would highlight that the parameters of α and τ are key in determining age-structured behaviour and are therefore essential in quantifying the role of school children in transmission [7]. We argue that a low τ and a low α are the only combination that are consistent with the growing body of data suggesting that levels of seroprevalence show only moderate variation across age-ranges [8], yet children do not appear to play a major role in transmission [9, 10] - as evidenced by the relatively low numbers of school-based outbreaks.

Throughout the current epidemic, there has been noticeable heterogeneity between the different regions of England and between the devolved nations. In particular, London is observed to have a large proportion of early cases and a relatively steeper decline in the subsequent lock-down than the other regions and the devolved nations. In our model this heterogeneity is captured through three regional parameters (D^R_S, H^R_S and I^R_S) which act on the heterogeneous population pyramid of each region to generate key observables.

Table 1: Key model parameters and their source

Parameter	Description	Source
β	Age-dependent transmission, split into household, school, work and other	Matrices from Prem *et al.* [3]
γ	Recovery rate, changes with τ, the relative level of transmission from undetected asymptomatics compared to detected symptomatics	Fitted from early age-stratified UK case data to match growth rate and R_0
d_a	Age-dependent probability of displaying symptoms (and hence being detected), changes with α and τ	Fitted from early age-stratified UK case data to capture the age profile of infection.
σ_a	Age-dependent susceptibility, changes with α and τ	Fitted from early age-stratified UK case data to capture the age profile of infection.
H^R	Household quarantine proportion $= 0.8\phi_R$	Can be varied according to scenario
N_a^R	Population size of a given age within each region	ONS
ε	Rate of progression to infectious disease ($1/\varepsilon$ is the duration in the exposed class). $\varepsilon \sim 0.2$	MCMC
α	Scales the degree to which age-structured heterogeneity is due to age-dependent probability of symptoms ($\alpha = 0$) or age-dependent susceptibility ($\alpha = 1$)	MCMC
τ	Relative level of transmission from asymptomatic compared to symptomatic infection	MCMC
ϕ^R	Regional relative strength of the lockdown restrictions; scales the transmission matrices. Can also be varied according to scenario.	MCMC
σ^R	Regional modifier of susceptibility to account for differences in level of social mixing	MCMC
E_0^R	Initial regional level of infection, rescaled from early age-distribution of cases	MCMC
S_T	Sensitivity of the serological test	MCMC
S_D	Rate of decay of seropositivity associated with the serological test	MCMC
D_S^R	Regional scaling for the mortality probability $P_a(\text{Death}\|\text{Hospitalised})$)	MCMC
H_S^R	Regional scaling for the hospitalisation probability $P_a(\text{Hospitalised}\|\text{Symptomatic})$)	MCMC
I_S^R	Regional scaling for the ICU probability $P_a(\text{ICU}\|\text{Symptomatics})$)	MCMC

2.1 Public Health Measurable Quantities

The main model equations focus on the epidemiological dynamics, allowing us to compute the number of symptomatic and asymptomatic infectious individuals over time. However, these quantities are not directly measured - and even the number of confirmed cases (the closest measure to symptomatic infections) is highly biased by the testing protocols at any given point in time. It is therefore necessary to convert infection estimates into quantities of interest that can be compared to data. We considered seven such quantities which we calculated from the number of new symptomatic infections on a given day I_a^d.

1. **Hospital Admissions:** An age-dependent fraction of symptomatic individuals are assumed to need hospital treatment, with a distributed lag between infection and hospitalisation.
2. **ICU Admissions:** Similarly, an age-dependent fraction of symptomatic individuals are assumed to need treatment in an Intensive Care Unit. This is not a quantity that is generally reported, and therefore we cannot match our model predictions to this data source.
3. **Hospital Beds Occupied:** By convolving hospital admissions with the distributions of lengths of stay, we can estimate the number of hospital beds occupied.
4. **ICU Beds Occupied:** A similar process generates the number of occupied ICU beds.
5. **Number of Deaths:** Mortality is assumed to occur to a fraction of hospitalised individuals, with the probability of mortality dependent upon age, and occurring after a distributed lag.
6. **Proportion testing seropositive:** Seropositivity is a function of time since the onset of symptoms; we therefore define an increasing sigmoidal function followed by slow exponential decay which determines the probability that someone who first displayed symptoms q days ago would generate a positive serology test from a blood sample. The shape of this sigmoidal function is matched to data from PHE, while the peak sensitivity of the test (S_T) and the decay of seropositivity (S_D) are free parameters determined by the MCMC. We match our age-dependent prediction against antibody seroprevalence from weekly blood donor samples from different regions of England (approximately 1000 samples per region) [11].
7. **Proportion of Pillar 2 positives:** Given that the raw number of detected cases in any region is substantially influenced by the number of tests conducted, we consider the proportion of pillar 2 tests that are positive as a less biased figure. We assume that those symptomatically infected with COVID-19 compete with individuals suffering symptoms for other infections for the available testing capacity. This leads to proportion of pillar 2 tests that are positive being a saturating function of the number of symptomatic infections, with a single scaling parameter.

We compared these model predictions to the data by assuming that the true numbers are drawn from a negative binomial distribution with the model value as the mean, while the true proportions (seropositives and Pillar 2 positives) are from a beta-binomial.

References

[1] Keeling MJ, Hill E, Gorsich E, Penman B, Guyver-Fletcher G, *et al.* Predictions of COVID-19 dynamics in the UK: short-term forecasting and analysis of potential exit strategies. *PLoS Comp. Biol.* **17**(1):e1008619 (2021). doi:10.1371/journal.pcbi.1008619.

[2] Keeling MJ, Dyson L, Guyver-Fletcher G, Holmes A, Semple MG, *et al.* Fitting to the UK COVID-19 outbreak, short-term forecasts and estimating the reproductive number. *medRxiv* page 2020.08.04.20163782 (2020). doi:10.1101/2020.08.04.20163782.

[3] Prem K, Cook AR, Jit M. Projecting social contact matrices in 152 countries using contact surveys and demographic data. *PLOS Comput. Biol.* **13**(9):e1005697 (2017). doi:10.1371/journal.pcbi.1005697.

[4] Mossong J, Hens N, Jit M, Beutels P, Auranen K, *et al.* Social Contacts and Mixing Patterns Relevant to the Spread of Infectious Diseases. *PLoS Med.* **5**(3):e74 (2008). doi:10.1371/journal.pmed.0050074.

[5] House T, Keeling MJ. Deterministic epidemic models with explicit household structure. *Mathematical biosciences* **213**(1):29–39 (2008).

[6] Hilton J, Keeling MJ. Incorporating household structure and demography into models of endemic disease. *Journal of the Royal Society Interface* **16**(157):20190317 (2019).

[7] Keeling MJ, Tildesley MJ, Atkins BD, Penman B, Southall E, *et al.* The impact of school reopening on the spread of COVID-19 in England. *Philos. Trans. R. Soc. B Biol. Sci.* **376**(1829):20200261 (2021). doi:10.1098/rstb.2020.0261.

[8] Pollán M, Pérez-Gómez B, Pastor-Barriuso R, Oteo J, Hernán MA, *et al.* Prevalence of sars-cov-2 in spain (ene-covid): a nationwide, population-based seroepidemiological study. *The Lancet* **396**(10250):535–544 (2020).

[9] Fontanet A, Tondeur L, Madec Y, Grant R, Besombes C, *et al.* Cluster of COVID-19 in northern France: A retrospective closed cohort study. *medRxiv* page 2020.04.18.20071134 (2020). doi:10.1101/2020.04.18.20071134.

[10] Heavey L, Casey G, Kelly C, Kelly D, McDarby G. No evidence of secondary transmission of COVID-19 from children attending school in Ireland, 2020. *Eurosurveillance* **25**(21):2000903 (2020). doi:10.2807/1560-7917.ES.2020.25.21.2000903.

[11] Public Health England. National covid-19 surveillance reports (2020). URL https://www.gov.uk/government/publications/national-covid-19-surveillance-reports. [Online] (Accessed: 29 September 2020).