Contact matrices estimated from the CoMix social contact survey
Additional report provided during survey week 56

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Data up to 29th March 2021

Summary

- We present contact matrices for nine key periods of the epidemic for England.
- We present R_c, which represents R_0 under the various control measures.
- We estimate R_c was lowest during the first and third lockdown and during the christmas break
- We estimate R_c was highest during September and October, when schools had returned
- We present estimates of R_c based on CoMix contact matrices for the old and new (B.1.1.7) variants and combined estimates based on SGTF data.
- Estimates suggest that Lockdown 3 would not have been sufficient to suppress transmission without acquired immunity in the population.

Main

We present contact matrices for nine key periods in the epidemic in England and to the associated change in the dominant eigenvalue relative to Lockdown 1 (Figure 1) [1]. All periods of the epidemic had higher dominant eigenvalues than Lockdown 1. The period with the highest dominant eigenvalue was the period after the summer break when schools reopened (4th Sept - 26th October 2020), where the dominant eigenvalue was over twice as high as lockdown 1. This period was also the most sensitive to assumptions about age-dependent susceptibility and infectiousness. In contrast, the christmas period and Lockdown 3, which had very similar dominant eigenvalues to Lockdown 1.

We summarise the change in potential for transmission by estimating the basic reproduction number (under control measure) over rolling two weekly periods for both older variants and B.1.1.7. We present R_c which represents R_0 under control measures. We used a baseline value of R_0 for COVID-19 as 2.6 with a standard deviation of 0.56 and applied a scale factor of 1.5 giving an R_0 of 3.9 for the B.1.1.7 variant, see methods for further details.

For older variants we estimate R_c to be below 1.0 during Lockdown periods and remained below 1.0 for a period over the summer immediately after lockdown 1 was relaxed. However we estimate R_c to have been above 1.0 during all other periods. In contrast, our estimates suggest that for B.1.1.7 R_c was likely to have been above 1.0 even in periods of lockdown, suggesting that this variant would have been difficult to control with the same measures in the absence of some acquired immunity in the population (note that R_c is calculated in the absence of immunity).

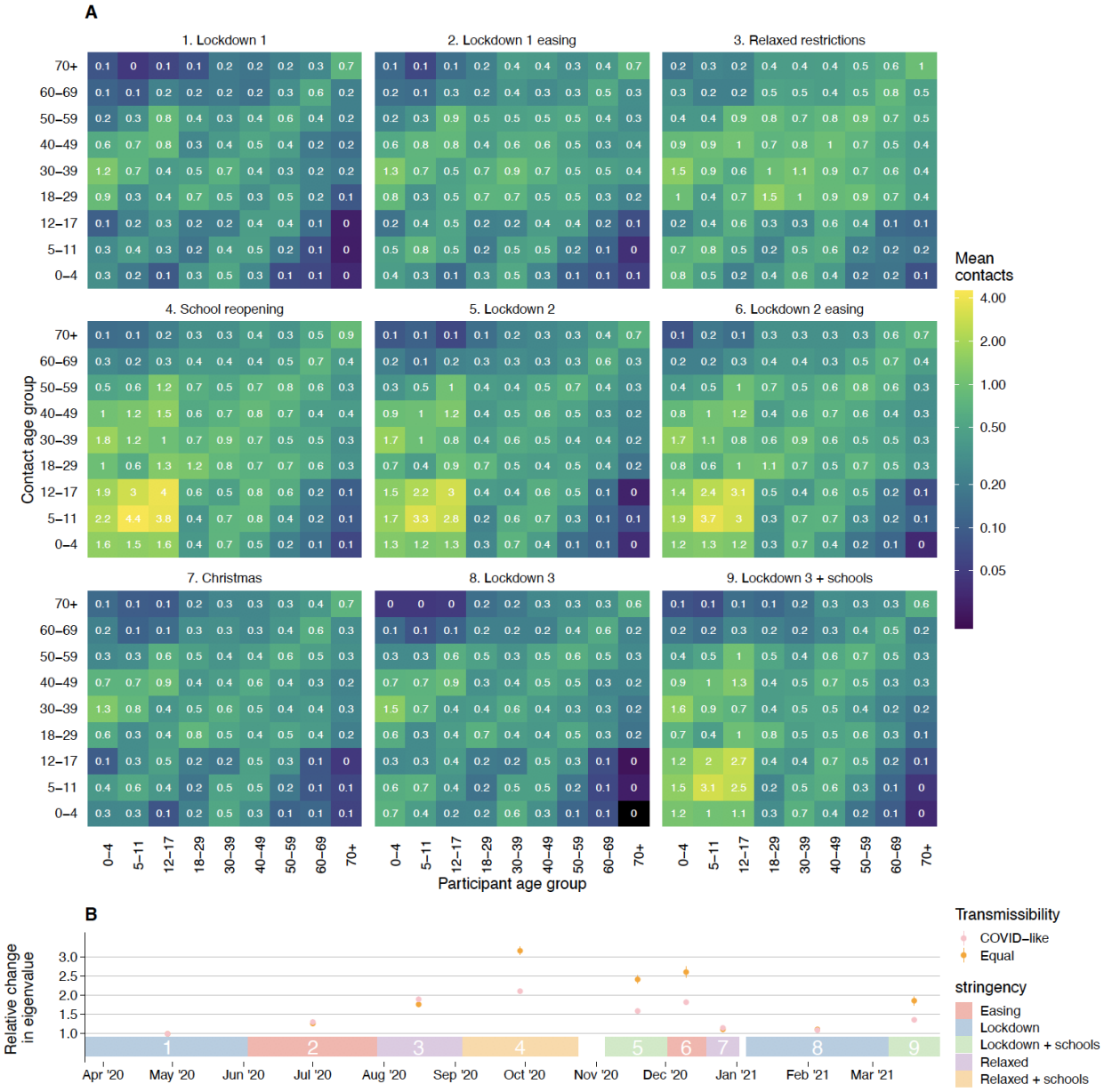

Figure 1. Contact matrices and their dominant eigenvalues for England in each period considered. *A) Contact matrices for England in periods 1 - 9 (1. Lockdown 1, 2. Lockdown 1 easing, 3. Relaxed restrictions, 4. School reopening, 5. Lockdown 2, 6. Lockdown 2 easing, 7. Christmas, 8. Lockdown 3, 9. Lockdown 3 with schools open), B) Points show relative change in R_c (compared to Lockdown 1) based on the dominant eigenvalues of effective contact matrices calculated for periods 1 - 9, with equal transmissibility in all age groups and age-stratified transmissibility based on Davies et. al. for SARS-CoV-2. coloured blocks show durations of each period as annotated. (available here: https://doi.org/10.5281/zenodo.4677018)*

Table 1. Change in dominant eigenvalue relative to Lockdown 1

Date	*Period*	*Increase in R_c **Equal** Transmissibility*	*Increase in R_c **COVID Like** Transmissibility*
24 Mar 2020 - 03 Jun 2020	*1. Lockdown 1*	*1 (1 - 1)*	*1 (1 - 1)*
03 Jun 2020 - 29 Jul 2020	*2. Lockdown 1 easing*	*1.26 (1.21 - 1.31)*	*1.3 (1.24 - 1.37)*
29 Jul 2020 - 04 Sep 2020	*3. Relaxed restrictions*	*1.76 (1.71 - 1.81)*	*1.9 (1.83 - 1.96)*
04 Sep 2020 - 24 Oct 2020	*4. School reopening*	*3.17 (3.06 - 3.27)*	*2.12 (2.05 - 2.18)*
05 Nov 2020 - 02 Dec 2020	*5. Lockdown 2*	*2.42 (2.31 - 2.53)*	*1.6 (1.54 - 1.66)*
02 Dec 2020 - 19 Dec 2020	*6. Lockdown 2 easing*	*2.61 (2.48 - 2.76)*	*1.82 (1.75 - 1.89)*
19 Dec 2020 - 02 Jan 2021	*7. Christmas*	*1.1 (1.06 - 1.14)*	*1.14 (1.1 - 1.19)*
05 Jan 2021 - 08 Mar 2021	*8. Lockdown 3*	*1.1 (1.07 - 1.13)*	*1.08 (1.04 - 1.11)*
08 Mar 2021 - 30 Mar 2021	*9. Lockdown 3 + schools*	*1.85 (1.74 - 1.97)*	*1.35 (1.29 - 1.42)*

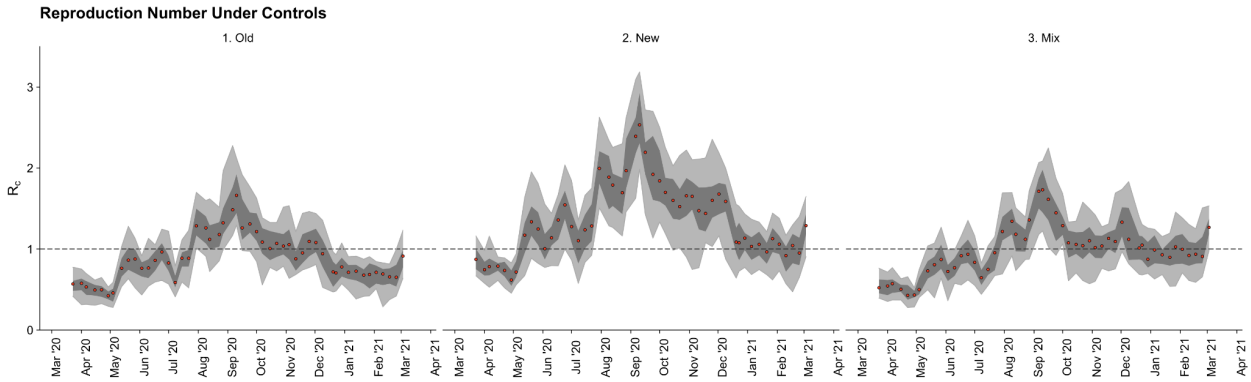

Figure 2. Reproduction number under controls (R_c) estimated from CoMix contact data over the first 12 months of the SARS-CoV-2 Epidemic in England. *Panels show (left to right) R_c based on estimates from April 2020, R_c based on assumed 50% increased transmissibility of B.1.1.7 and R_c based on a mix of variants based on proportion of cases with SGTF. Points show mean R_c value, dark and light ribbons show 75% and 90% bootstrapped CI.*

Methods

CoMix is a behavioural survey, launched on 24th of March 2020. The sample is broadly representative of the UK adult population. Participant's are invited to respond to the survey once every two weeks. We collect weekly data by running two alternating panels. Parents complete the survey on behalf of children (17 years old or younger). Participants record direct, face-to-face contacts made on the previous day, specifying certain characteristics for each contact including the age and sex of the contact, whether contact was physical (skin-to-skin contact), and where contact occurred (e.g. at home, work, while undertaking leisure activities, etc). Further details have been published elsewhere [2]. The contact survey is based on the POLYMOD contact survey [3].

We constructed age-stratified contact matrices for nine age-groups (0-4, 5-11, 12-17, 18-29, 30-39, 40-49, 50-59, 60-69, and 70+). For children participants and contacts, we did not have exact ages and therefore sampled from the reported age-group uniformly. We fitted a truncated negative binomial model to calculate the mean contacts between each participant and contact age-groups. To find the population normalised symmetrical contact matrix, we multiplied the columns of the matrix by the mean-normalised proportion of the UK population in each age-group. For rounds one to six and 17 to 19, where no child participants were surveyed, we used contacts reported by children in rounds seven and eight to construct a full contact matrix. To account and correct for variation in contact patterns at weekends, we calculated rates of contact between age groups for weekends and weekdays separately and combined them by taking the weighted mean for each combination of age-groups . We applied a truncation of 50 contacts per participant per contact age group.

We constructed CoMix matrices for nine key periods during the UK epidemic (Figure 1)

Table 2. dates of key periods of the COVID-19 epidemic in England

Date	**Period**
23rd March - 3rd June 2020	1. Lockdown 1
4th June - 29th July 2020	2. Lockdown 1 easing
30th July - 3rd Sep 2020	3. Reduce restrictions
4th Sept - 26th October 2020	4. Schools open
5th November - 2nd December 2020	5. Lockdown 2
3rd December - 19th December 2020	6. Lockdown 2 easing
20 December 2020 - 2nd January 2021	7. Christmas
5th January - 8th March 2021	8. Lockdown 3
8th March - 29th March 2021	9. Lockdown 3 with schools open

For each period we calculated the dominant eigenvalue of the infectiousness and susceptibility corrected contact matrix ($\mathbf{C}_{SI}$) calculated from the measured contact matrix described above $\mathbf{C}_t$ and assumed relative susceptibility and infectiousness vectors **s** and **i**:

$$\mathbf{C}_{SI} = \mathbf{C}_t \circ (\mathbf{i} \otimes \mathbf{s})$$

We used two scenarios of infectiousness and susceptibility:

1. Equal infectiousness and susceptibility.
2. Susceptibility and infectiousness profiles estimated in Davies et al. [4] (Table 3), in line with the approach we have applied in previous reports. [5]

Table 3 Susceptibility and infectiousness profiles taken from Davies et.al.[4]

	Susceptibility	Infectiousness	Clinical Fraction
0-4	0.4	0.645	0.29
5-10	0.4	0.645	0.29
11-17	0.4	0.605	0.21
18-29	0.79	0.635	0.27
30-39	0.86	0.665	0.33
40-49	0.8	0.7	0.4
50-59	0.82	0.745	0.49
60-69	0.88	0.815	0.63
70+	0.74	0.845	0.69

Using the same approach, we constructed an age-stratified contact matrix for POLYMOD with the same age bands. Since contacts in polymod are right censored at 29, we corrected for this by fitting a truncated negative binomial distribution. For all participants with 29 recorded contacts, we increased the number of contacts according to the fitted distribution with a left censor at 28, and assigned age-groups proportionally to the contacts the participant reported.

By constructing two-weekly rolling contact matrices $\mathbf{C}_{SI}$ with age-dependent infectiousness and susceptibility as per Davies et al., we calculated the basic reproduction number (R_c):

$$R_c = r \; Eig\,(\mathbf{C}_{SI})$$

Where *r* is scales the dominant eigenvalue to R_c, which we approximated under three conditions:

1. Assuming approximate transmissibility of initial variants of SARS-CoV-2 (prior to the emergence of B.1.1.7). For this we set the scale factor as the ratio of an estimate of R_c under 'normal contact patterns' sampled from a normal distribution with mean of 2.6 and standard deviation of 0.56 and the dominant eigenvalue the POLYMOD contact matrix.
2. Assuming approximate transmissibility of B.1.1.7, for which we applied an additional factor of 1.5 on condition 1.
3. A mix of 1 and 2, where the mix of variants was assumed to follow the ratio of S-gene drop out from PCR tests in England (SGTF) (Figure 3). We used data from … between October 2020 and February 2021. The mix of variants prior to and after this period were assumed to be 0% and 100% B.1.1.7 respectively.

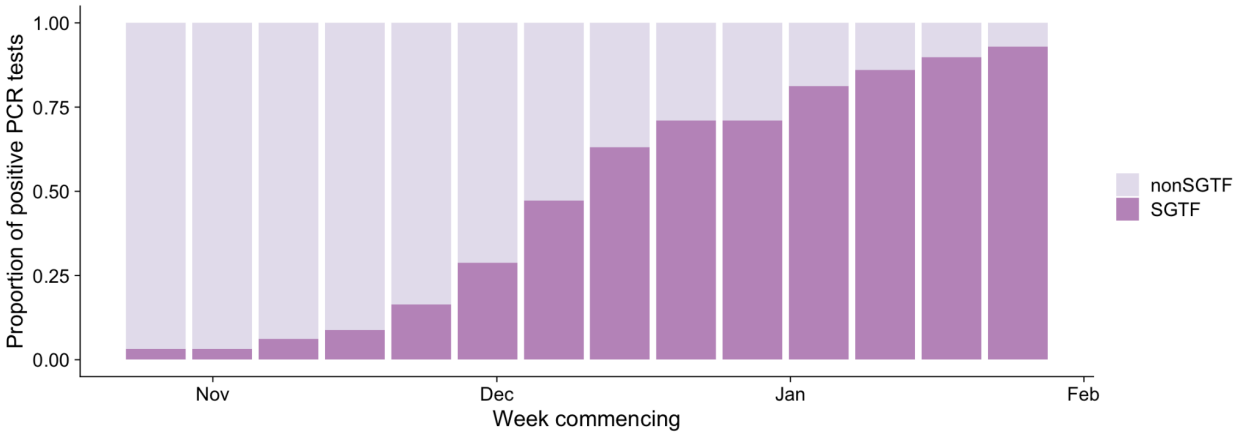

Figure 3. Increase in SGTF tests between October 2020 and February 2021. *Bars show the weekly proportion of positive PCR tests that failed to show s-gene response (SGTF), indicative of the infection being of the B.1.1.7 variant of SARS-CoV-2.*

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