Supplementary Material - Modelling Description:

Models were written in Python 3.7 and are intentionally simple in order to facilitate communication. They should not be regarded as numerically accurate predictions of a local outbreak. Nevertheless, we used epidemiological parameters derived from the best available estimates at the time of model production.

The underlying network:
Both Wave 1 and Wave 2 models are network models of disease in which a set of individuals are joined by undirected edges, to give an overall network (or graph) of connections. When individuals u and v are joined by a connection, we say that u and v are *adjacent*. To produce our base network, we generated household groups (in Wave 1 of size 2, 3 or 4 individuals, in Wave 2 of size 2 or 3 individuals, all sizes equally likely) with exactly one simulated child in each household. All individuals within a household are all pairwise adjacent in both Wave 1 and Wave 2. When simulating CCCs we use a uniform size of three households in a CCC, and every child within a household in a CCC is adjacent to all individuals in all households in that CCC. Adults within a CCC are not directly linked to each other (unless by some other type of simulated connected, e.g. a random interaction). In Wave 1 we also simulated either full school return, in which case we added connections between all pairs of children or part-time school return in which case we divided the children into two groups, and added all connections between children within one group. In Wave 2 removed the school scenario, and instead included a grandparent-childcare scenario in which each household is allocate a grandparent, and the grandparent has connections to every member if their associated household (effectively joining that household). In both Wave 1 and Wave 2, we incorporated extra contacts or mixing, with connections added uniformly. These extra contacts were between any pair or people in Wave 1, or within either the group of children or the group of adults in Wave 2. In Wave 1, we included a slider to allow a user to select the number of random extra contacts to add, in Wave 2 we set this at a fixed level, with each possible contact having a uniform 10% probability. In all cases the network is static within a single simulation, and there is no modelling of behaviour change over time.

The disease model:
In both Wave 1 and Wave 2, the disease model is essentially a compartmental-style network model of disease in which a node can have any of several disease states. In Wave 1, we included only the states S for individuals who are susceptible to the disease, and I for individuals who are infectious. Note in particular that in Wave 1 there was no recovery nor latent period. In Wave 2, we also included a state R for recovered individuals who were assumed to be immune and a state E for those who have been exposed to the disease but are not yet infectious. Neither wave includes additional states that would be required in a fully realistic model such as: severely ill people, dead people, pre-symptomatic people, etc. In the standard language of compartmental disease models, Wave 1 is an SI model, and Wave 2 a $SEIR$ model. Time proceeds in discrete time-steps, and at each time step every currently-infectious person has a 5% chance of infecting each person connected to them in the network (we do not distinguish between different kinds of contacts). In Wave 2, we decreased the infectiousness of children to be 70% that of adults to reflect emerging evidence that children may be less infectious than adults. If a susceptible individual had multiple infectious contacts at a time step, they have multiple independent chances of being infected by those different contacts. Progression from E to I and I to R are modelled using a simple rate; that is, we use a fixed probability at each time step that an individual who is in E will become infectious and move to I, and a fixed probability at each time step that an individual who is in I will recover and move to R. There is emerging evidence that these rates are impacted by age, but for simplicity here we have used a fixed rate for all individuals. We chose these rates to simulate roughly realistic latent and infectious periods - estimates for these are changing as the pandemic proceeds and evidence emerges, and we favoured simple round numbers over precise estimates that might have implied more model precision than is appropriate. We used a latent period of 2 days, and an infectious period of 12 days, giving a rate from E to I of $1/2$, and a rate from I to R of $1/12$. We seeded all simulations with a single infectious child.

Again, note that there is no modelling of testing, isolation, or behaviour change due to symptoms.

Code used in Wave 2 is available for perusal at:
https://colab.research.google.com/drive/1n3fEV3Ygc62GLJ90cHeEnaus-fhJycU0?usp=sharing Upon publication of the associated manuscript, we plan a more permanent repository for this code.

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