Analysis of mitigation of Covid-19 outbreaks in workplaces and schools by hybrid telecommuting

Simon Mauras, Vincent Cohen-Addad, Guillaume Duboc,
Max Duprè la Tour, Paolo Frasca, Claire Mathieu,
Lulla Opatowski, Laurent Viennot

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Abstract

The Covid-19 outbreak has led countries to implement unprecedented measures to limit virus spread within the population, impacting in particular the organization of workplaces, universities, schools. Yet, the power and limitations of such strategies remain unquantified. Here, we develop a simulation study to analyze Covid-19 transmission on three real-life contact networks from a workplace, a primary school and a high school in France, gathered by SocioPatterns, and assess the impact of organization strategies. Investigated strategies include rotations, which consist in partitioning the individuals into two groups, with a presence switch between groups on a weekly or daily frequency; and On-Off, which consist in keeping everybody together but alternating presence and telecommuting periods. Assuming baseline non pharmaceutical interventions and reactive isolation of symptomatic cases, all strategies where assessed based on a selection of criteria (outbreak probability, outbreak size, and delay before outbreak) and for reproduction numbers ranging 0.5-2. Our results are clear: whatever the network used, the ranking of the strategies based on their ability to mitigate epidemic propagation in the network from a first index case is always the same, namely, from best to worst: Rotation week-by-week, Rotation day-by-day, On-Off week-by-week, and On-Off day-by-day. The advantage of a weekly alternation over a daily alternation, despite significant, is very slight: for the attack rate when there is an outbreak in a high school for example, the numbers for On-Off are 16.8 vs. 18.4 (out of 327 individuals), a 9% improvement. Our results suggest that when the effective reproduction number $R$ within the network is less than

* S. Mauras is with IRIF, Paris. V. Cohen-Addad is with Google Research, Brand- schenleistrasse 110, 8002 Zurich, Switzerland. P. Frasca is with Univ. Grenoble Alpes, CNRS, Inria, Grenoble INP, Gipsa-lab, F-38000 Grenoble, France. C. Mathieu is with CNRS, IRIF, Paris. L. Opatowski is with Université Paris-Saclay, UVSQ, Univ. Paris-Sud, Inserm, CESP, Anti-infective evasion and pharmacoepidemiology team, Montigny-Le-Bretonneux, France, and with Institut Pasteur, Epidemiology and Modelling of Antibiotic Evasion unit, Paris, France. L. Viennot is with INRIA, IRIF, Paris.

NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.
1.34, therefore assuming concurrent implementation of social distancing and other non pharmaceutical interventions, all four strategies efficiently control the outbreak by decreasing effective $R$ to less than 1; the choice between them should therefore be guided by considerations of practical feasibility.

1 Introduction

While the world awaits a vaccine or an effective cure, the Covid-19 pandemic must be contained by the deployment of suitable Non-Pharmaceutical Interventions (NPIs), so as not to overwhelm the healthcare systems. So far, besides mask wearing and hygiene, governments had largely resorted to generalized lockdown orders, which have severe adverse effects on economy and society, as well as to milder restrictions such as partial school closures, curfews, and restrictions to leisure activities such as gyms and restaurants. Such NPIs and organizational adaptations have to balance the competing goals of limiting contagion and maintaining an adequate level of social and economic activity. Assessing the performance of containment and mitigation strategies with respect to the propagation of the epidemic is therefore critical to making the right policy choices and has attracted an immense research effort from all disciplines, from medical science to economics, engineering, and social, computer and statistical sciences [19, 24, 10, 6, 8, 14].

Within this broad policy and research question, our work concentrates on the role of telecommuting and how to effectively include telecommuting in the schedules of schools, workplaces or other organizations. Our purpose is to assess and compare several telecommuting strategies in workplaces and schools. This comparison is obtained from a fine-grained simulation study on actual contact networks for populations of few hundreds individuals in these environments.

Coming up with a precise assessment of the effects on the epidemic of these strategies indeed requires a precise understanding of the spreading of contagion in different environments [32, 30]. To achieve this, two main ingredients are needed: (1) fine-grained information about contacts between individuals in different environments; and (2) the specific behavior of SARS-CoV2 transmission. The latter information includes the probability of contamination by individuals in different conditions, such as asymptomatic or symptomatic, as well as the possible presence of “super-spreaders” [23]. Equipped with this information, one can then simulate the behavior of the coronavirus epidemic in the different work environments and evaluate the effectiveness of various strategies.

Most previous work on computational simulation of epidemics has focused on synthetically generated populations, sometimes at very large scale (e.g. a whole country [7]), possibly because of the limited availability of detailed data about human contacts in the relevant environments. Here instead, we build our simulations on (publicly available) empirical data collected in schools and workplaces [18]. Simulation on small-scale actual networks allows to visualize the detailed evolution of the epidemics in these environments (see Figure 3).
and, leveraging this understanding, yields explicit recommendations about the effectiveness of the strategies.

Figure 1: Contact graphs. (a-c) Three contact networks on their busiest day: (a) on day 2, primary school with 242 students, (b) on day 1, workplace with 217 workers, (c) on day 2, high school with 327 students. Node colors correspond to known groups (classes or department). We see that the majority of contacts happen within the same groups. (d) A synthetic random graph with 9 groups selected randomly. For better visualization, in the four graphs only edges representing at least 3 contacts are drawn.

2 Results

Using detailed data describing between-individual interaction proximity in primary school, high school or in a workplace, we aim at measuring how the virus spreads within these specific settings and assess which kind of hybrid telecommuting is the most likely to prevent its dissemination.

We explored three contact networks representing close contacts in a primary school, a high school, and a workplace in France (Figure 1) over 2 to 10 days. We develop a model (Figure 2) for SARS-CoV2 transmission over a contact networks, that captures the virus clinical and transmissibility characteristics, including super-spreading events, a significant proportion of asymptomatic individuals, etc. In order to characterize SARS-CoV2 transmission level in simulations, we defined different metrics: the probability that an outbreak occurs, the delay until an outbreak starts, and the expected total number of infected patients in case of outbreak. As expected, the simulation of virus importation through
Figure 2: The infection model for SARS-CoV-2. The incubation (Exposed, green) lasts on average 3.7 days and is followed by an infectious period (Infectious, orange) of mean 9.5 days. For symptomatic patients, symptoms appear 1.5 days after the beginning of infectiousness on average, and we assume that those patients self-isolate after one day of symptoms. Asymptomatic individuals do not isolate.

an index case in the network with no measure implemented leads to a high probability of outbreak (27%, in the baseline case for a high school) and a large number absolute of contagions in that case (38 students on average, in a school of size 327), no matter the studied network.

Five containment strategies were implemented and assessed here. Two "On-Off" strategies which consist in allowing the whole group of individuals (pupils / workers) at the premises (1) every other day, or (2) every other week. We also consider two "rotation" strategies which consists in allowing half the individuals on (1) odd days, while the other half is allowed on even days, or (2) odd weeks, while the other is allowed on even weeks. Finally, we additionally consider the case of full-time telecommuting as a benchmark. In all these scenarios, we allow the individuals to maintain a small fraction of their original interactions even while telecommuting (thereby modeling the case of imperfect compliance by the individuals).

Our results are clear: no matter which contact network they are tested on, no matter the underlying comparison metric (probability of outbreak, the length of time until outbreak, or the expected total number of infected patients when there is an outbreak), the rankings of the four strategies are consistent (see Figure 3): the rotation strategies significantly dominate the On-Off strategies which in turn significantly dominate the absence of any policy. As expected, the full-time telecommuting (with persistent contacts only) dominates all strategies.

To provide a precise explanation of these findings, we analyse the impact of strategies on the effective reproductive number in the different graphs. If the effective reproductive number is $R_0$ in the absence of strategy (induced by a certain choice of model parameters), what is the actual effective reproductive number $R_{\text{effective}}$ (for the same choice of parameters) if some strategy is in place? The answer is given in the of Fig. 4. In this figure and in the rest of this section, we present the results for the contact graph of a high school only (the "middle" case between primary school and workplace, in structural terms). The results for a primary school and for a workplace are qualitatively the same, and can be found in the SI.

We first observe that if $R_0$ is lower than 1, then as expected the epidemics...
Figure 3: Comparison of the effects on SARS-Cov2 outbreak of containment strategies implemented in the contact graph of a high school when $R_0 = 1.25$. The three panels respectively correspond to three relevant metrics: (top) the probability that at least 5 people are infected besides patient 0 (which we define as ‘Outbreak’ event); (middle) the average number of days until 5 people are infected besides patient 0; (bottom) the average total number of people infected when there is an outbreak. The ranking of the strategies by effectiveness is the same irrespective of the metric. In order from worst to best: None (no strategy), daily On-Off, weekly On-Off, daily Rotation, weekly Rotation, Full telecommuting. Observe that weekly and daily alternations are very similar in terms of the probability of outbreak and of duration until outbreak, because those measures depend on the beginning of the epidemic only; but the total number of infected people presented on the bottom panel shows that in the long run weekly alternation is a little bit better than daily alternation, both for On-Off (16.8 vs 18.4) and for Rotation (13.0 vs. 13.4).
Figure 4: Impact of the strategies for the high school contact graph. The x-coordinate gives the value of the baseline reproduction number $R_0$ (mean number of persons infected by index case). For each strategy the y-coordinate gives the mean value of the effective reproduction number as a result of using the strategy. Thus, for our baseline value $R_0 = 1.25$ (dotted vertical line), doing nothing leads to $R_e = 1.25 > 1$, whereas, as long as $R_0 < 1.34$, all strategies lead to $R_e < 1$. For each curve, the shaded areas correspond to 95% confidence intervals on the estimate of $R_0$ (as a function of $p$: horizontal error bar) and on the estimate of $R_e$, as a function of $p$ and of the strategy: vertical error bar.
Table 1: Contact graphs characteristics. The three studied Sociopatterns contact networks and the synthetic random graph are detailed in the table. Averaging over the days on which the data was gathered, the high school, in which data was gathered over 5 school days, comprised 327 individuals (students and teachers), each of which was in contact with 35 persons on average, and the student had 230 20-second contacts per day on average. The primary school has the highest number of contacts per person in a day, followed by the high school, and finally by the workplace.

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3 Materials and Methods

Key elements in constructing our simulations are the choice of the contact networks and the definition of the disease transmission model, which we describe below.

Contact networks. We use traces for three different places, that are available from the SocioPatterns project (http://www.sociopatterns.org). The project collected longitudinal data on physical proximity and face-to-face contacts between individuals in several real-world environments.

1. A primary school (see [16, 29]) where 242 persons participated in 2009 over 2 days (coverage of 96% among children and 100% among teachers).

2. A workplace Institut de Veille Sanitaire (see [18]) where 232 employees participated in 2015 over two weeks (10 working days, coverage around 70% of the employees according to a previous deployment [17]).
3. A high school (see [13]) where 329 individuals (students) participated in 2013 over 5 days (coverage of 86% of the students in the 9 participating classes).

For each day on which data was gathered we extract a graph aggregating the data for that day: a node corresponds to an individual, an edge corresponds to a face to face contact within 1.5 meters within a 20 seconds time interval (interactions were measured using active radio-frequency identification devices (RFID)), and the weight of the edge is the number of such short contacts during the day.

For comparison, we also generate a synthetic random graph, calibrated so that its main parameters (total number of nodes, of edges, and of contacts) match those of the high school contact network: more precisely, each edge is generated by selecting uniformly at random two nodes with one associated contact (rejecting loops and already generated pairs) and each of the remaining contacts is associated to an edge selected uniformly at random among the previously generated edges. Table 1 lists the main parameters of the graphs obtained by averaging over all days on which data was gathered.

Figure 1 displays the three contact graphs on their busiest day, together with the synthetic random graph obtained. The node colors correspond to groups (classes or work departments) for the real-world contact graphs, and are chosen uniformly at random among 9 colors for the synthetic random graph.

**SARS-Cov2 transmission model.** We model the introduction of the virus in a network by randomly sampling an index case uniformly among the nodes to determine the patient initially infected. We assume a natural history derivating from the classical SEIR transmission model (see Figure 2): initially individuals are susceptible (S); once contaminated, having been exposed (E), they go through an incubation period, after which they become infectious (I) after which they are assumed to recover (R) and develop immunity. An individual may be symptomatic or asymptomatic. In the former case, before developing symptoms she goes through a pre-symptomatic phase that is already infectious. We assume that transmission between an infectious and a susceptible individual happens through proximity contacts as the ones recorded in the contact network. To every 20-second contact is associated an independent small risk of transmission, so that the transmission risk increases with the duration of contact. The time step of the simulation is one day, which is consistent with the time scale of the SEIR model: if the risk for one contact equals \( p \) and if an infectious person is in contact with a susceptible person for 15 minutes during the day, then the probability of transmission during that day equals \( 1 - (1 - p)^{45} \), which for \( p = 0.001 \) approximates 4.4%. The rate of instantaneous transmission from infectious to susceptible individuals is calibrated so that, without mitigation strategies, the expected number \( R \) of individuals infected by the first case equals 1.25. See the trees of Figure 5 for examples of transmission scenarios over time, featured as tree structures where each node points to the nodes it has infected.
Figure 5: Epidemic propagation in the contact graph of a highschool, under different strategies: each panel corresponds to an example simulation for a given strategy; strategies are sorted as by effectiveness (according to our three metrics), from none (business as usual) to full telecommuting. In each panel, the horizontal axis corresponds to time (in days), and each white or gray column corresponds to one week. The vertical axis shows the prevalence (percentage of infectious persons in the workplace): its evolution is represented by the grey curves in the background. For each strategy, the epidemic propagation over the contact graph is shown as a tree, where each node represents an infected person and points to the persons it infects. Nodes corresponding to symptomatic (resp. asymptomatic) persons are circled in blue (resp. red). Similarly a blue (resp. red) arrow corresponds to a contamination by a symptomatic (resp. an asymptomatic) person. The thickness of arrows indicates the super-spreading factor. The node color corresponds to the group of the person (class in the case of schools). All the propagation trees are generated using the same realizations of the probabilistic events, so that the differences between the trees are not artifacts of their randomness, but solely depend on the different strategies in place.
The model parameters are summarized in Table 2. The duration of the incubation period follows a Gamma distribution with mean 5.2 days and shape 5 [22, 12]. The pre-symptomatic period has length 1 day with probability 50% and 2 days with probability 50%, consistent with published studies [9] (Table S1 p.20). The remaining duration of infectiousness follows a gamma distribution with mean 8 [8] and shape 10. The fraction of asymptomatic individuals equals 40%, within the range of [26, 25]. Symptomatic individuals are assumed to self-isolate after one day of symptoms and therefore do not cause further contaminations; on the other hand, asymptomatic individuals stay in the system and potentially transmit the virus throughout their infectious period.

In the SEIR model we do not include a finer modeling of the progress of the disease, such as hospitalization or death, nor the possibility that immunity is lost after some time. The reason is that, contrary to much recent work like [19, 8] that focused on nation-wide interventions on a time scale up to months, we are interested in modeling the early stages of an epidemic outbreak in a relatively small organization, rather than its long-term evolution at the nation scale.

Persistent contacts. All simulations are initialized with an index case assumed to have been contaminated by the outside world. We focus on contamination of people in the contact graph. Since our proposed strategies act on the school or work social networks and aims at limiting transmission clusters occurring in these specific locations, we do not model contagion of/from people who are not in the contact network. This choice is consistent with studies with similar focus [10].

Nevertheless, contacts with friends or colleagues who belong to the social network may also happen outside the direct school/work environment. To model such interactions, we assume that there exists an external graph $G_{ext}$ of persistent contacts, which is obtained from the contact network by applying a dampening factor of 25% to all contacts. This quantity stems from imagining a scenario in which someone working from home would invite colleagues or fellow students to come and interact for roughly two hours during the day instead of eight hours (hence the 25%); and the persons invited would be selected from among their usual school/work contacts.

Superspreaders. In the Covid-19 epidemic, the number of persons contaminated by an infectious person has a large variance [23, 4, 11, 1, 27, 3]: many people contaminate nobody, but a small fraction of the people (termed ‘superspreaders’) are responsible for many contaminations. Such superspreading events may be due to several factors including a higher viral load or infectiousness of the superspreader, a particularly high number of contacts, and whether those contacts occur in a confined space with poor ventilation [21].

Here, we model superspreading as follows: for each day and for each contagious person, a random superspreading factor $p_{super}$ is chosen independently, where $E[p_{super}] = 1$. Then, on that day, for each short contact with a susceptible person, there is contamination with probability $p_0p_{super}$ if the infectious person
is symptomatic and $p_0p_{super}/2$ if the infectious person is asymptomatic, where $p_0$ is a parameter of the model.

**Calibration of the contamination probability.** The contamination parameter $p_0$ is calibrated so that the baseline reproduction number $R_0$, defined as the average number of persons infected by the index case, equals 1.25, a value chosen to implicitly take into account implementation of barrier measures including social distancing, mask usage or hand washing. The idea of inferring $p_0$ from the model is inspired by [31]. We find that $p_0 = 0.001$ in the primary school contact graph, $p_0 = 0.003$ in the high school contact graph, and $p_0 = 0.008$ in the workplace contact graph. Several values of $R_0$ were investigated, ranging from 0.5 to 2, corresponding (for high schools) to $p$ ranging from 0.0012 to 0.0084.

**Strategies.** Several non-pharmaceutical strategies were used or recommended across the world depending on activity type (school, workplace, university) or country. Here we concentrate on strategies at the level of the work/school environment which focuses on presence-sheet organization and promotion of hybrid telecommuting with partial use or partial closure of school or work environments. First, we consider on-off strategies, in which alternatively, either 100% of employees or students do face-to-face work, or 100% do telecommuting (distance learning). Such a strategy has, for example, been recommended as a way to exit the lockdown by alternating 4 days on and 10 days off [20]. (Venezuela had a temporary exit strategy in which businesses were allowed to reopen on a week-on-week-off basis[1].) Second, we consider rotation strategies, in which 50% of employees or students do face-to-face while the other 50% do distance learning, periodically switching between the two groups. (Organizing work with rotating shifts was one of the actions recommended by the CDC[2].) We implement both types of strategies with different alternations: daily alternation (even day, odd day, not counting weekends) and weekly alternation (even week, odd week). Finally, we consider a full telecommuting strategy. This results in five strategies, which we compare in their ability to reduce the likelihood and intensity of epidemic outbreaks.

**Evaluation criteria.** More precisely, strategies are evaluated based on three criteria: the probability of epidemic outbreak occurs, defined as the percentage of simulations for which at least 5 persons were infected besides the index case; the velocity of outbreak (number of days until five persons are infected, given there is an outbreak); and the cumulative number of infections until extinction of the epidemics, given there is an outbreak.

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1As reported in [https://venezuelanalysis.com/news/14924](https://venezuelanalysis.com/news/14924)
2See [https://www.cdc.gov/coronavirus/2019-ncov/downloads/php/CDC-Activities-initiatives-for-COVID-19-Response.pdf](https://www.cdc.gov/coronavirus/2019-ncov/downloads/php/CDC-Activities-initiatives-for-COVID-19-Response.pdf)
4 Discussion

Summary. By simulating SARS-CoV2 transmission over a diversity of contact networks, we show how (hybrid) telecommuting reduces the virus transmission in schools and workplaces. We focused on three types of strategies: On-Off, Rotation, and Full telecommuting. Our results highlight that, whatever the contact network, these measures significantly reduce the risk of outbreak, lengthen the time until the outbreak occurs, and reduce the attack rate. This conclusion holds even though we assume some persistent contacts between individuals and a fraction of their workplace contacts, when they are not at the work location (for example, colleagues meeting outside work). The rankings of the strategies are consistent (Figure 3): Full telecommuting (with persistent contacts only) significantly dominates the Rotation strategies which significantly dominate the On-Off strategies which in turn significantly dominate the absence of any policy.

These results can be intuitively explained. To differentiate between the types of strategies, observe that Rotation strategies induce fewer contacts overall than On-Off strategies, because they involve the presence of smaller groups and thus (we could say that the number of contacts of an individual grows at least proportionally with the number of colleagues that are present at the same time). To make this insight more precise, observe that the curves of Figure 4 plotting $R_e$ as a function of $R_0$ are almost linear. Indeed, a back-of-the-envelope calculation suggests that the strategies reduce the average number of contacts, for each individual over a 2-week period, by the following ratios: On-off 63%; Rotation 44%; Full Telecommuting 26%. These ratios do not suffice to determine the ranking, because of nonlinear effects: a person with 500 contacts with 500 different people will infect more people on average (namely, $500p$ if the probability of transmission for one contact is $p$) than another person, also with 500 contacts, but all with the same person (namely, $1 - (1 - p)^{500} < 500p$). Non-linearity is a reason to recommend a reduction in degree, i.e., concentrating one’s contacts over a small number of individuals: if one only has 3 neighbors, then, even if there are many contacts with them, at most 3 persons will be infected. This argument is even more relevant to cope with potential superspreaders, whose presence is also a source of nonlinearity. Note that the advantage of rotation strategies has also been argued in papers like [10, 2] based on mathematical arguments that use deterministic compartmental models.

To differentiate between weekly and daily alternations, observe that a weekly alternation is naturally in phase with the natural duration of the incubation period and inter-generation time of the disease, therefore effectively breaking the contact chains. Consistently, Figure 3 (as well as Figures 8 and 9) show that weekly alternations are better than daily alternations. Indeed, an infected person becomes contagious after 3.7 days on average, and, if he is infected during his five days of in-person work/school, he is therefore likely to be telecommuting during its period of contagiousness. This intuition has already been discussed since [10] and has been elaborated through various mathematical and simulation arguments [2, 14]. The effect is not very visible for short-term events such as
the probability of an outbreak (Figure 4) but is enough to reduce the attack rate somewhat, since the latter accumulates over a longer time.

An illustration of the simulation of the strategies can be viewed on Figure 5. The propagation trees we observe (see also Figures 14, 15, 16) are likely to occur in reality when an index case is infected inside a working place or school. We observe that transmissions often occur between nodes of the same color, i.e. inside groups (classes in school and departments at work), reflecting the higher density of contacts within groups (see Figure 1). We also observe that a large fraction of the transmissions are due to asymptomatic cases. This is expected as asymptomatic individuals do not isolate. The superspreaders are easy to identify and account for many transmissions as well. In Figure 5, a superspreader effect in week 2 seem to be the origin of a large propagation. We can visualize how the various strategies help mitigate that effect.

Implementation and choice in practice Of course, the choice of strategies also crucially depends on other criteria: feasibility in practice, ease of implementation, etc. For example, even though hybrid teaching has been used in many universities in France since the beginning of the epidemic, it may be more convenient for an instructor to teach on and off to the full group either online, or onsite. On the other hand, in sectors like manufacturing a minimum of workers on site may be essential to maintain production, and then rotation will be the most appealing strategy. We note that the main ingredient differentiating Rotation from On-Off is the breaking of the groups (except for the persistent contacts described above). A strategy in a school that would, for example, bring in all 9th and 11th graders on even weeks and all 10th and 12th graders on odd weeks would resemble On-Off more than Rotation, because it would not break the groups of students who are in contact. To summarize: (1) when $R_0$ is moderately high, all types of hybrid telecommuting strategies reduce it to less than 1, and the choice between them should primarily be done on the basis of practical considerations. (2) To help prevent dissemination of the disease, it is preferable to alternate over longer periods (weekly rather than daily), but the difference is so slight that practical, psychological, and other considerations should determine the alternation time.

Validity of the model and robustness of the results. Because a lot of uncertainty exists regarding SARS-CoV2 epidemiology and natural history, we estimated from our simulations some of the outbreak key characteristics to assess their realism.

Are our values for the baseline probability of transmission comparable to the literature? There is a known estimate of $p = 0.003$ for the transmission of influenza from an infectious to a susceptible individual in 20 seconds of contact [28], so this is of the same order of magnitude as the values $p =$

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3In hybrid teaching, teachers have to manage distance-teaching for half of a group and onsite-teaching for the other half.
Is the dispersion of supercluster events in our model distributed like in the literature? It has been suggested that about 80% of transmission events are caused by about 10% of the total cases (see [11] for example). We do not quite reach that level of dispersion, but in our baseline model for high schools, we see that there is already much dispersion: 20% of the choices for the index case lead to 68% of the infections at the next generation.

Is the generation time of our model consistent with the literature? The generation time is the average number of days until the persons infected by the index case are infected. In our baseline model, we have a generation time of 7.5 days. This is a weighted average of two types of events: contagions by asymptomatic persons, whose average equals 9.5 days, and contagions by symptomatic persons, whose average equals 5.5 days, which is consistent with an estimate of 5.2 for the Singapore cluster [15] (and a little higher than for the Tianjin cluster).

Are our results for $R_e$ (Figure 4) comparable to [20]? In our model, if we set $R_0 \sim 1.15$, making people go to work 7 days a week yields $R_W = 1.48$; we then obtain that for full telecommuting $R_L = R_e \sim 0.53$, and simulating the “4 days on, 10 days off” On-Off strategy from [20] yields $R_e \sim 0.82$. Thus, this is consistent with the findings from [20]: for $R_W = 1.5$ and $R_L = 0.6$ they find that $R_e = 0.86$. We also note that from the above calculation, our baseline intensity set at 25% for persistent contacts happens to yield a ratio $R_W/R_L$ that is almost the same as in [20], further confirming our choice of 25%.

Is the baseline value $R_0 = 1.25$ of our model realistic? This corresponds to estimates in France at the date of October 15, 2020. This is much lower than the estimates from a few months earlier because of non pharmaceutical interventions such as frequent hand hygiene, generalization of masks and increase of distances between individuals.

Sensitivity with respect to $R_0$ were carried out investigating a range of values between 0 and 2.5. Higher $R_0$ values led to higher risks of outbreaks and bigger outbreak sizes (reaching 142 for $R_0 = 2$), but the investigated strategies always reduced the global risk compared with "no strategy". As observed on Figure 4, we show that for $R_0 < 1.34$, all investigated strategies work at reducing $R$ to below 1.

In addition, a series of sensitivity analyses were run to assess to which extent our results are sensitive to these assumptions.

For simplicity, in the main text we only presented our results for the high school contact graph: the corresponding results for the other graphs are presented in Figures 6, 7 and 8. Sensitivity analyses were carried out to assess the robustness of our results with respect to models assumptions and parameter values: they are presented in Figures 9 through 13 and commented in the accompanying captions.

\[^4\] The weekly report of Santé Publique France at that date estimated for the effective reproduction number to be 1.35 or 1.20 or 1.13, depending on which type of data the estimate was based on.
Our sensitivity analysis shows that although the evolution of the epidemic varies greatly with those parameters, the variations are smooth and the ranking of the strategies is always respected. We observe that the duration of the epidemic until outbreak is the least sensitive measure. The most sensitive measure is the total number of infected people when there is an outbreak. This quantity becomes much larger when the contact graph is replaced by a (calibrated) homogeneous graph (Figure 6); when the graph of persistent contacts is replaced by a (calibrated) complete graph (Figure 11); when \( R_0 \) increases (Figure 8); and when the shape parameter of the transmission probability distribution increases, due to superspreaders.

Limitations of our study Because we aim at modelling transmission using rather simple assumptions, the results presented here should be interpreted in the light of the following assumptions. First, we explored empirical contact graphs that were built from publicly available data collection in just three schools and workplaces. Even though that is too small to be representative of all schools and workplaces, we believe that the key characteristics of those networks (such as their community structure and their degree distribution) are typical of the social groups under study. In addition, despite the significant differences between the three empirical graphs, our results are consistent across all of them, suggesting their broad relevance. Furthermore, our qualitative conclusions also extend to synthetic random graphs as described in Materials and Methods. However, the random graph produces results that are quantitatively rather different from the original graph that has been used to tune its parameters (see Figure 6): this difference cautions against deriving quantitative predictions from random models.

Second, the three investigated graphs themselves are small. However, much of our study is focused on the emergence of an outbreak from a single index case, and for that, whether the graph has 100 or 100000 nodes is not important. Third, we only consider virus transmission within the contact network from a single initial index case, neglecting transmissions potentially occurring through other external contacts, which could for instance include family members or external friends. At high community circulation level of the virus, individuals are also exposed to the virus from other sources than the school or work place, this chance being potentially increased over telecommuting periods. Because our objective was not to provide prediction about the expected prevalence in schools or workplaces but rather to evaluate the network-associated virus dissemination risk, we focused on the quantification of this risk following a unique introduction of the virus by a network member. Acquisition from the community was therefore only considered for the index case. Nevertheless, to more realistically mimic contact patterns in a situation where a full lockdown is not implemented, we allowed for the telecommuting individuals to maintain a proportion of their contacts with colleagues or friends. This could depict a situation where compliance with telecommuting orders is low. In a case of a strict lockdown, during which individuals have also restricted contacts over their telecommuting periods,
they are not able to visit colleagues or school friends, so there are no persistent contacts, and the situation depicted here overestimates the risk of outbreak. More precisely, consider the top left panel of Figure 11. When a strict lockdown causes removal of all persistent contacts (that situation is obtained in the simulation by multiplying the contact graph by a factor of 0%), the outbreak probability drops from 27% to 20%.

Fourth, we leave open for further work the question of incorporating the possibility that some people are more fragile than others, hence more likely to get infected when put in contact with an infectious individual.

Fifth, the implementation of the proposed strategies could be in practice different from what we assume in our analysis. Throughout our simulations, Rotation is significantly better than On-Off. However, we always assume that in the rotation strategy, individuals are randomly partitioned into two groups. It is likely that, in reality, people would probably try to be in the same group as the colleagues with whom they interact the most. Such a partition would go against the advantage of Rotation over On-Off.

Finally, consider the role of asymptomatic transmissions. Considering the transmission trees on Figures 5, 14, 15, and 16, one notes that many of the transmissions occur from asymptomatic cases. Indeed, in our simulations, for the high school contact network 56% of transmissions on average come from asymptomatic individuals. Compared to symptomatic individuals, asymptomatic individuals are less infectious but do not self-isolate, so they have a reduced rate of transmission but over a longer period of time. This assumption is consistent with current recommendations in school and workplaces where individuals are asked to stay at home when they have any suspect symptoms. Imperfect compliance with isolation recommendations, if mildly symptomatic individuals maintain social contacts and potentially spread the virus, would result in an increased risk of outbreak in all settings.

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A graph of contacts between people that are at work on day $d$.

A random graph.

A sociopattern graph.

A scaled graph of contacts between people that are not both at work.

Fraction of outside contacts.

Patient initially infected.

Day of infection of $v_0$.

Probability of being symptomatic.

Transmission probability during a 20-second contact.

Asymptomatic transmission factor.

Superspreading transmission factor.

Probability of transmission.

Length exposed period.

Length presymptomatic period.

Length symptomatic period.

Number of days of symptoms before isolation.

Outbreak event that at least 5 persons are infected besides $v_0$.

The average date of infection of the persons infected by $v_0$.

The average number of persons infected by $v_0$.

| Parameter | Description | Value |
|-----------|-------------|-------|
| $d$       | Day of infection | null hypothesis |
| $v_0$     | Patient initially infected | random uniform |
| $q$       | Probability of being symptomatic | 60% |
| $p$       | Probability of transmission | $p = p_0 \cdot p_{\text{sympt}} \cdot p_{\text{super}}$ |
| $p_0$     | Asymptomatic transmission factor | 0.5 |
| $p_{\text{sympt}}$ | Symptomatic transmission factor | $\frac{1}{2}$ when asymptomatic, 1 otherwise |
| $p_{\text{super}}$ | Superspreading transmission factor | mean = 1, Gamma(shape=0.1) |
| $l_e$     | Length exposed period | mean = 3.7, Gamma(shape=5) |
| $l_{\text{sympt}}$ | Length symptomatic period | mean = 1.5, uniformly 1 or 2 days |
| $l_{\text{sympt}}$ | Length asymptomatic period | mean = 8, Gamma(shape=10) |
| $I$       | Number of days of symptoms before isolation | 1 |
| $R_0$     | Average number of person infected by $v_0$ | mean from [9] |

Table 2: The first table gives the reference values of the parameters used in our simulations, with the supporting references. The second table summarizes some notation.
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A  Our results for the other contact networks

The supplementary information has three groups of figures. In the first group, we present results analogous to the results already given in the main body of the paper for the high school contact graph, when the contact graph is a primary school, or a workplace, or a random graph calibrated to resemble the high school contact graph. In the second group, we do a systematic sensitivity analysis of all the parameters used in the model. Our observations are presented in the caption of each figure.

Color coding of measures studied  For added readability, in Figures 6, 7 and 8 just like in Figure 3, the color of the background encodes the parameter studied: probability of outbreak in blue, duration until outbreak in green, and final total number of people infected when there is an outbreak in red.

B  Details about the simulations

Finally, here are some details about the program implementing the simulation.

Rounding reals to integers while preserving the mean of the distribution  Since the process is discrete, with one discrete step equal to one day, we need times to be integers. A random variable drawn from a Gamma distribution is a real number, so we need to round it to an integer. To perform that without changing the mean of the distribution, we used randomized rounding: if $X = 5.4$ for example, then with probability 40% it is rounded to 6 and with the complementary probability 60% it is rounded to 5, thus the average rounded value equals 5.4.

Number of executions performed  To perform the simulations of the paper, we proceeded as follows: for each possible index case, for each possible day when that person gets infected (given that the On-Off and Rotation strategies have a period of 2 weeks, there are 14 possibilities for the starting day), do 10 random executions. Thus, for high schools, each quantity is obtained by averaging over $327 \times 14 \times 20 = 91560$ random executions.