Optimal Testing and Containment Strategies for Universities in Mexico amid COVID-19

Abstract

This work sets out a testing and containment framework developed for reopening universities in Mexico following the lockdown due to COVID-19. We treat diagnostic testing as a resource allocation problem and develop a testing allocation mechanism and practical web application to assist educational institutions in making the most of limited testing resources. In addition to the technical results and tools, we also provide a reflection on our current experience of running a pilot of our framework within a leading Mexican university, as well as on our broader experience bridging research with academic policy in the Mexican context.

1 Introduction

Schools and universities around the globe have suffered extended closures due to regional and national lockdown measures following the COVID-19 pandemic. Due to the severe impact of these closures on education, mental health and social divides, it has been strongly recommended that educational institutions reopen as quickly and safely as possible to ensure that future generations are not held back further [20,22]. At the same time, it has become clear that comprehensive testing strategies, including asymptomatic screening, are essential to combat the spread of the virus [5,13].

As educational institutions around the world prepare to reintroduce in-person teaching, it is imperative that they do so safely, with the help of judicious testing and containment strategies [21]. This is particularly challenging in low- and middle-income countries (LMICs) with severe constraints on testing resources. We present a testing and containment framework aimed at helping educational institutions in LMICs make the most of extremely scarce testing resources, and also provide an online allocation software to guide decision-making. Our methods, which are currently being piloted at a leading Mexican university, make use of the heterogeneity of university populations as well as pooled qPCR tests in order to balance two competing objectives: minimising potential viral spread (and subsequent critical cases), as well as minimising the number of healthy individuals who unnecessarily self-isolate under a given containment protocol.

We consider the setting in which the population is divided into categories based on characteristics which include individuals' potential exposure to the virus (based on their occupation in the institution), their geographical location, and/or the potential of an infection becoming critical. The categorisation also accounts for an individual's cost of isolation. The testing strategies we propose divide a given budget of tests among the population categories. Our mechanism utilises *group testing*, where a set of individuals (say, 10) are tested using a single pooled test. A positive test result indicates that at least one individual in the pool is infected, whereas a negative indicates that all individuals tested are healthy. As a function of the test results, we propose simple containment mechanisms and subsequently measure the performance of different test allocations according to 'health' and 'quarantine' objectives (introduced in Section 3.1).

Outline. A brief overview of the relevant literature is given below. In Section 2, we introduce our testing and containment mechanism, and outline the contagion model we developed to capture viral spread within heterogeneous university populations. Section 3 describes the family of testing and containment protocols we consider, as well as formal expressions for the multiple objectives we optimise for via Pareto front computation. We provide details on our current pilot in Section 4, with an emphasis on three main deliverables from

our software: extrapolating relevant model parameters from university data, computing the Pareto front of testing allocations, and providing a user-friendly interface for navigating and choosing testing allocations along the Pareto front. Section 5 provides further simulation evidence that our testing allocations provide long-term results over sustained periods of infection within a population. Section 6 provides a reflection regarding our experience bridging research and practice in the Mexican context. Finally, Section 7 elaborates on next steps for our pilot.

Related Work. The use of testing resources to mitigate the spread of an infectious pathogen has been intensely debated during the current pandemic [7, 16]. The idea of combining several samples into a single group test in order to reduce the numbers of tests required has previously been studied in a substantial body of literature in Computational Learning Theory [6, 8–10, 26]. Group testing has been applied against HIV and other diseases [18, 25]; in the current pandemic, it has been verified experimentally with SARS-CoV2 samples [23, 27]. A growing body of work has investigated the use of group testing as a possible way towards testing large parts of the population [1, 2, 4, 11, 12, 19]. Work in the testing literature has largely focused on minimising the number of tests required to test a population exhaustively. Turning the problem on its head, we instead consider the problem of identifying a mechanism that maximises the benefit of a fixed (and scarce) weekly testing budget.

2 Our Model for Testing and Containment

We consider a heterogeneous population of n individuals partitioned into k disjoint categories $C_1, \ldots, C_k$ of sizes $n_1, \ldots, n_k$. The partitioning is chosen to capture the heterogeneity of the population, with 'similar' individuals being placed in the same category. On a school and university campus, one might partition the population into school students, undergraduates, postgraduates, academic teaching staff, and administrators.

Throughout, we assume that the educational institution in question has a limited budget of T tests per time period that it wants to use optimally.[1] We treat the decision of how to maximise the use of limited testing resources to the population categories as a resource allocation problem that balances two objectives: reducing the virus spread and minimising the impact of quarantining on the population. In order to achieve this, we define the following testing and containment protocols, for which we can subsequently quantify these two objectives. Our protocols approach this problem via the use of *pooled* or *group* tests.

Group Testing. In what follows, we assume that we have access to group testing (also known as pooled testing) for COVID-19. In a group test of size $g \in \mathbb{N}$, samples from g individuals are pooled into one sample and subjected to a single qPCR test. A positive result on the pooled test implies that at least one of the g individuals is infected, and a negative result implies that all are healthy. We let $G \in \mathbb{N}$ denote the upper bound on feasible group sizes, which is dictated by biological and laboratory constraints. Our partner laboratories in Mexico have validated the group testing methodology of Sanghani et al. [24], which permits testing with groups up to size 10.

Testing Strategies. Recall that T is the number of tests available to the educational institution per time period. We consider a space of testing protocols parameterised by a pair of vectors $(\boldsymbol{t}, \boldsymbol{g})$, where $\boldsymbol{t} \in \mathbb{N}^k$ and $\boldsymbol{g} \in \{1, \ldots, G\}^k$. A *testing strategy* $(\boldsymbol{t}, \boldsymbol{g})$ specifies the number of tests allocated to each population category, and their group sizes: t_i tests are allocated to disjoint groups of size g_i from category C_i uniformly at random.[2] Note that this implies the constraints $g_i \leq G$ and $t_i g_i \leq n_i$, for every category C_i. We also impose the budget constraint $\sum t_i = T$ on any testing strategy, as we wish to maximise the use of the given testing budget. We say that a testing strategy $(\boldsymbol{t}, \boldsymbol{g})$ is feasible if it satisfies these constraints.

[1] In our pilot study, the university has sufficiently many tests to test approximately $1-6\%$ of a campus population individually every week.

[2] Note that $g_i = 1$ for some category C_i implies that the testing strategy performs individual tests for category C_i.

Containment Protocol. We propose a conceptually simple containment protocol: whenever a group test is negative, everyone in the group continues to function normally. If the test is positive, everyone in the group is told to self-isolate for a given period of time. In our pilot study, individuals are quarantined for 14 days. Note that this reduces the number of tests required to test a large number of individuals, and thus has the potential of catching more infectious people. On the other hand, it might lead to healthy individuals self-isolating unnecessarily. In section 3, we describe how testing strategies can choose a desired trade-off between these conflicting objectives for each category, by selecting appropriate group sizes at which to test individuals in each category.

Contagion Model. For each category, we define parameters that govern contagion in the population. Fix any category C_i. We assume that all individuals in category C_i are independently infected with probability $p_i \in [0, 1]$ (and healthy with probability $q_i = 1 - p_i$). Each newly infected individual in C_i has probability v_i of developing a "critical" infection. Here the scope of 'criticality' is defined by the university; it might, for instance, denote all cases leading to hospitalisation or death, or it may encompass all symptomatic infections.

After performing a given testing strategy $(\boldsymbol{t}, \boldsymbol{g})$, it is possible that some infected individuals are not self-isolating, as they have not been subjected to a group tests. In order to quantify the performance of different testing and containment protocols, our model assumes a single step of contagion, whereby each infected individual who is not self-isolating may infect others. Each individual in C_i is assumed to be in contact with $d_{ij} \in \{0, \ldots, n_j\}$ individuals from C_j. Moreover, each susceptible (healthy) individual in category C_i is infected by an infectious neighbour in C_j with transmission probability $\pi_{ij} \in [0, 1]$. The parameters $d_{i,j}$ and $\pi_{i,j}$ can be interpreted as connectivity or 'exposure parameters' between categories C_i and C_j. We note that $d_{i,j}$ and $\pi_{i,j}$ need not be symmetric.

3 COVID Testing Allocation as an Optimisation Problem

We can now formally define the optimisation problem underlying our choice of optimal testing strategies to contain viral infections while minimising the disruption on education at the institution. Recall that our goal is to balance the two objectives of reducing 'critical cases' while minimising the number of unnecessarily self-isolating individuals.

3.1 Our Objectives

For a given feasible testing strategy $(\boldsymbol{t}, \boldsymbol{g})$, we define our *health objective* $O_H(\boldsymbol{t}, \boldsymbol{g})$ as the expected number of critical cases that are prevented in our single-step contagion model when compared to no testing. For each category C_i, we also define the *category quarantine objective* $O_{Q,i}(\boldsymbol{t}, \boldsymbol{g})$, which denotes the expected number of unnecessarily self-isolating individuals in category C_i under $(\boldsymbol{t}, \boldsymbol{g})$. Notice that by maximising $O_{Q,i}$, a mechanism prioritises minimising unnecessary quarantining of individuals in the i-th category.

The health objective O_H is optimised by minimising the number of individuals who are not tested, whereas the containment objectives $O_{Q,i}$ are minimised by reducing the number of healthy individuals that are quarantined unnecessarily as a result of a positive group test. Note that our objectives are conflicting: larger group sizes increase the reach of testing and lead to fewer untested but infected individuals, while smaller group sizes reduce the number of healthy individuals who are quarantined unnecessarily. To begin with, we define the unnecessary quarantine objective.

Minimising Unnecessary Quarantine. Although it is desirable for our testing strategies to maximise O_H, doing so comes at the cost of increasing the number of individuals who are told to unnecessarily quarantine. To account for this, recall that the *category quarantine objective* $O_{Q,i}$ gives the expected number of unnecessary quarantines in category C_i for each testing strategy. Each individual is independently healthy with probability $q_i = 1 - p_i$. This means that for a single group test of size g_i, the probability that the test is positive is given by $1 - q_i^{g_i}$, and the expected number of healthy individuals in a group of size g_i conditioned on a positive test is $g_i - \frac{g_i p_i}{1 - q_i^{g_i}}$. With this in hand, we can compute the expected number of

healthy individuals that are under unnecessary quarantine after a single group test as follows: $g_i(q_i - q_i^{g_i})$. Finally, since we have t_i of such group tests allocated randomly to C_i, we obtain the complete expression for the i-th quarantine objective:

$$O_{Q,i}(\boldsymbol{t}, \boldsymbol{g}) = t_i g_i (q_i - q_i^{g_i})$$

Preventing Critical Cases. To completely specify our health objective O_H, we define the following auxiliary variables:

- $u_i = \frac{n_i - t_i g_i}{n_i}$. This is the probability that a given individual in C_i is not tested.
- $z_i = u_i q_i + (1 - u_i) q_i^{g_i}$. This is the probability that an individual in C_i is both not under quarantine and healthy before the contagion step of our model.
- $\alpha_{i,j} = (p_j u_j (1 - \pi_{i,j}) + (1 - p_j u_j))^{d_{i,j}}$. This is the expected probability that an individual from C_i who is healthy and not under quarantine becomes infected from untested and infected individuals in C_j.
- $f_H(\boldsymbol{t}, \boldsymbol{g}) = \sum_i n_i v_i z_i \left(1 - \prod_j \alpha_{i,j}\right)$. This represents the expected number of critical cases that occur in the contagion step of our model.

$$O_H(\boldsymbol{t}, \boldsymbol{g}) = f_H(\boldsymbol{0}, \boldsymbol{0}) - f_H(\boldsymbol{t}, \boldsymbol{g})$$

To provide some intuition for this model, let us focus on a given individual in C_i. If they are in a positive test, they quarantine and are hence not susceptible for contagion. If they are healthy and not under quarantine (which happens with probability z_i), they may then be infected by untested, infected individuals from any C_j. An individual in C_j is untested with probability u_j, and the overall probability that an infection from C_j is received from $d_{i,j}$ interactions from individuals in C_j is given by $\alpha_{i,j}$. As we are interested in the number of critical contagion infections we prevent, we measure the performance of $(\boldsymbol{t}, \boldsymbol{g})$ relative to a testing strategy where no tests are used (given by $f_H(\boldsymbol{0}, \boldsymbol{0})$). We refer to Appendix A for a details on the construction of O_H.

3.2 Solutions on the Pareto Frontier

As mentioned in the previous sections, our objectives compete with each other and it follows that there no testing strategy that dominates all other strategies in all objectives. On the other hand, it is possible to rule out strategies that perform worse than other potential feasible strategies. The remaining solutions line on the Pareto frontier, which is a natural solution concept in multi-objective optimisation. Defined below, the Pareto frontier, provides a set of mechanisms that maximally exemplify the trade-offs incurred in all objectives.

Definition 1 (Pareto Dominance)**.** *Suppose that* $(\boldsymbol{t}, \boldsymbol{g})$ *and* $(\boldsymbol{t}', \boldsymbol{g}')$ *are two distinct testing strategies. We say that* $(\boldsymbol{t}, \boldsymbol{g})$ Pareto-dominates $(\boldsymbol{t}', \boldsymbol{g}')$ *if, and only if, the following hold:*

$$O_H(\boldsymbol{t}, \boldsymbol{g}) \geq O_H(\boldsymbol{t}', \boldsymbol{g}') \text{ and } O_{Q,i}(\boldsymbol{t}, \boldsymbol{g}) \leq O_{Q,i}(\boldsymbol{t}', \boldsymbol{g}') \ \forall i \in [k]$$

with one of the inequalities being strict. We denote this relation by $(\boldsymbol{t}, \boldsymbol{g}) \succ_P (\boldsymbol{t}', \boldsymbol{g}')$.

Our main approach consists of precisely finding the family of feasible testing strategies that are not Pareto-dominated.

Definition 2 (Pareto Frontier)**.** *The Pareto frontier* S_P *consists of the set of testing strategies that are not Pareto-dominated by any other testing strategy.*

Our Approach. We compute the Pareto frontier S_P for the class of testing mechanisms described above. Notice that no two mechanisms of equal $\boldsymbol{g}$ values Pareto dominate each other as increasing the number of tests used in C_i increases O_H but also increases $O_{Q,i}$. As such, we need only consider pairwise comparisons between mechanisms with different $\boldsymbol{g}$ values. With S_P in hand, our web application provides policy makers a principled and intuitive way to choose testing mechanisms from S_P that fit their institutional needs.

4 Details of the Pilot Study

A pilot of our methodology is currently underway at several campuses of a leading Mexican university. These were chosen for two reasons: they are in close proximity to university testing facilities with the capacity to carry out group tests, and they are located in states in which have recently exited lockdown. Therefore, students are able to return to a "hybrid" teaching format, in which a subset of students are allowed to return to in-person classes, and the university provides preemptive monitoring of infections via a limited testing budget per campus.

In line with our model from Section 2, our partners have partitioned the population of each campus into 4 categories: faculty (teaching and research), administrative assistance, middle/high school students[3], and undergraduate/graduate students. Over the course of the next month, health administrators from the university will be using our software to guide their decision-making in terms of how to allocate limited COVID-19 tests per campus. Our software pipeline completes three key tasks:

1. Extrapolating key model parameters from university data
2. Computing the Pareto front of testing allocations given model parameters
3. Providing a user-friendly tool for navigating multiple solutions along the Pareto front of allocations

Our software will be made freely available under an open source licence on GitHub.[4]

4.1 Model Parameter Estimation

We estimate the parameters for the model using data provided by our university partners from Mexico pertaining to course records, attendance records for these courses, and information regarding the buildings visited by the individuals in the population. More specifically, our partnering university in Mexico currently maintains internal anonymised databases with the following information:

- Per individual information regarding membership in the aforementioned categories.
- Information on taught courses (instructors, student attendance, classroom size/ventilation, classroom location).
- COVID-19 test results
- Residual water test results.[5]

We use this information to directly estimate the connectivity parameters $d_{i,j}$ of each of the 5 categories specified. To do so we look at each student from category C_i and count the number of classroom interactions they have with individuals of category C_j (we count repeat interactions as well). We take the average over all individuals in C_i to produce d_{ij}. Notice that d_{ij} is no longer integral, but this is not an issue when computing the O_H as per the formula in Section 3.1. This process is repeated for all $i, j \in [k]$ (where we allow $i = j$).

[3] Our partner institution also teaches middle and high school students at various campuses

[4] A link to the current GitHub repository has been omitted due to the double-blind reviewing process.

[5] Residual water results can alert administration of the presence of COVID-19 at the building level of a given campus (NEED CITATION)

In order to estimate transmission probabilities, we implement methodology from Buonanno et al. [3], alongside key input from epidemiological experts from our partner university. More specifically, the epidemiologists provide us with reasonable estimates to key parameters to the model of Buonanno et al. (such as room ventilation rates and individual inhalation/exhalation rates), which are informed by the data contained within the databases mentioned above, since they contain information on classroom density. For a given $i, j \in [k]$, we let π_{ij} be the average transmission probability from individuals of C_j to individuals of C_i as per our contagion model.

Baseline probabilities of infection p_i are estimated using results of the previous COVID-19 test results and additional residual waste water tests. Finally, although the vulnerability rate v_i of a category will eventually be provided to us by epidemiological experts from our partner university, we are currently running our optimisation with $v_i = 1$ for the pilot, so that O_H represents the total number of infections prevented.

4.2 Computing the Pareto Frontier

Our algorithm follows a greedy approach for the computation of S_P. Once the parameters are loaded into the model, we first compute the number of critical cases as if no testing was applied ($O_H(\mathbf{0}, \mathbf{0})$ under the context of Section 3.1). With this in hand, we iterate over all possible $(\boldsymbol{t}, \boldsymbol{g})$ testing and containment allocations, under the budget and group constraints, and evaluate the health O_H and each of the quarantine objectives $O_{Q,i}$. Upon every iteration the solutions which aren't Pareto-dominant are ruled out. Notice that, once an allocation is dominated and discarded, transitivity ensures that the assignment doesn't lie in the Pareto frontier.

In order to ameliorate run-time computation, by not going through every feasible solution at the actual implementation, a bucketing scheme was applied and the group tests sizes were fixed. For each of the objectives, O_H and every $O_{Q,i}$, a bucket size is fixed. Each bucket size determines the factor for which we allow the objectives values to be multiples of. This way, the objective values that are near each other (by a factor of the bucket size) are aggregated together. The group sizes are fixed and iterated by 1, 3, 5, and 10. To enable the user the ability to obtain the desired number of solutions through a binary search over the bucket sizes. The technical details of the implementation are given in Appendix B.

4.3 Web Application

We have developed a web application that assists university administrators explore the Pareto frontier to identify testing strategies that match their priorities. A demo is available at demo.testandcontain.com. On the basis of data provided by the educational institution, all Pareto-dominant testing strategies are computed as described in Section 3 and made available to view through the web application. For each strategy $(\boldsymbol{t}, \boldsymbol{g})$, the application displays how well it does on each of the health and containment objectives. In order to identify desirable strategies, administrators can set thresholds on the expected number of people in each category unnecessarily self-isolating and the number of critical new cases, allowing them to find the desired balance between the different objectives. In general, there will be more than one strategy that satisfies the thresholds. The app shows the number of strategies, as well as their containment and health outcomes, and allows the user to iterate through and compare multiple solutions.

4.4 Preliminary Results

For a campus setting similar to one of our partnering university in Mexico, we implemented our algorithm without bucketing in order to see how many testing and containment allocations did the algorithm discarded. This particular campus has a population of 965 people, comprised by three categories: students, professors, and cafeteria workers. The rest of the parameters were slightly modified from what was initially provided for privacy reasons. With this particular configuration we were able to rule out 78% of allocations, with the Pareto frontier containing the other 22%.

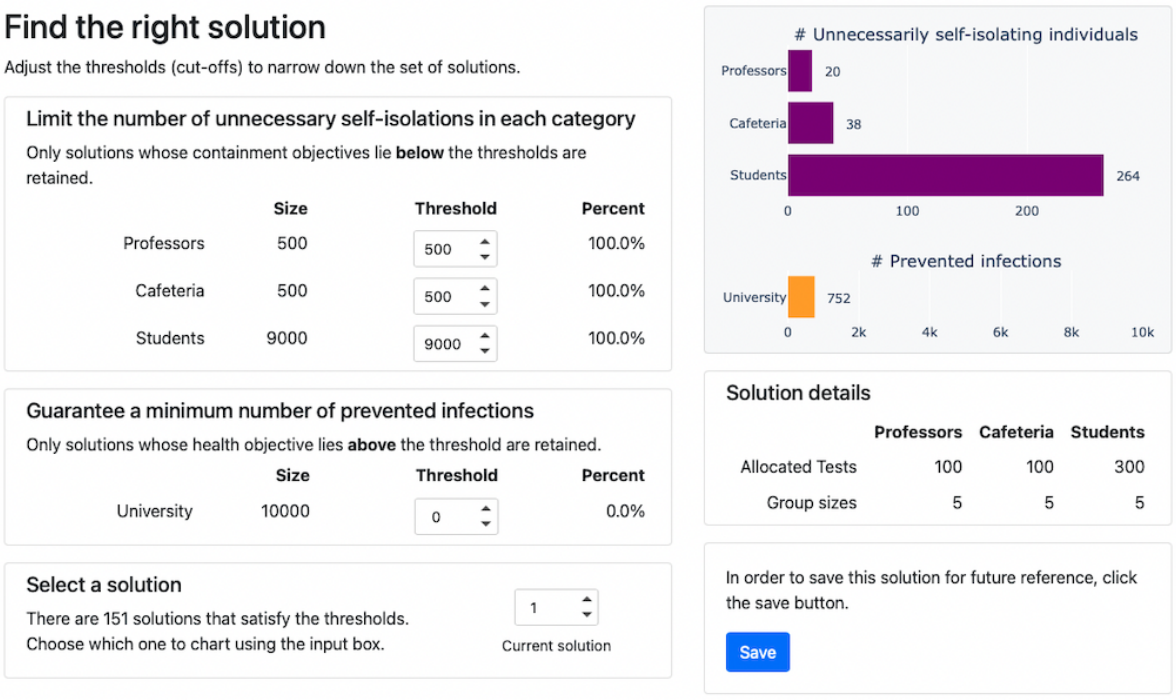

Figure 1: The Test and Contain web application.

5 Simulations

We developed a network-based susceptible-infected-recovered-quarantined (SIRQ) model on a simulated university population consisting of 9,000 students, 500 professors, and 500 cafeteria workers. Professors and cafeteria workers were assumed to have a much higher degree of connection than students. Using the definition of the exposure parameter $d_{i,j}$ from section 2 and the method for estimating it from section 4.1, we obtained

$$d_{i,j} = \begin{pmatrix} 4.92 & 1.34 & 1.27 \\ 24.28 & 1.44 & 1.26 \\ 23.0 & 1.26 & 1.44 \end{pmatrix}, \tag{1}$$

with $i = 1$ assigned to students, $i = 2$ to cafeteria workers, and $i = 3$ to professors. A simple example of how $d_{i,j}$ can be used is the following: on average, a professor is exposed to 23 students ($d_{3,1}$) whereas a student is only exposed to 1.27 professors ($d_{1,3}$). In the infection model we developed, at each time step an infected node recovers with probability $\gamma = 0.0427$ and, unless it is quarantined, infects one or more of its susceptible neighbouring nodes, each with probability $\beta = 0.01$. These parameters were chosen such that average number of secondary infections is $R_0 \sim 3$ on the simulated network [17]. It has been shown that the testing and containment strategy we developed performs better than a random allocation of tests [14,15]. In these simulations, we show two different solutions on the Pareto frontier. We select allocation profiles with different values of the quarantine objectives $O_{Q,i}$. In allocation profile (A), we prioritise minimising professor quarantine over cafeteria workers and students. In allocation profile (B), we prioritise both professors and cafeteria workers equally. The results of are shown in Figure 2. As expected, the different allocation profiles lead to different numbers of professors and cafeteria workers being in quarantine at any one point in time. This simple example shows the flexibility offered by our approach to find solutions that can be tailored according to the priorities of each educational institution.

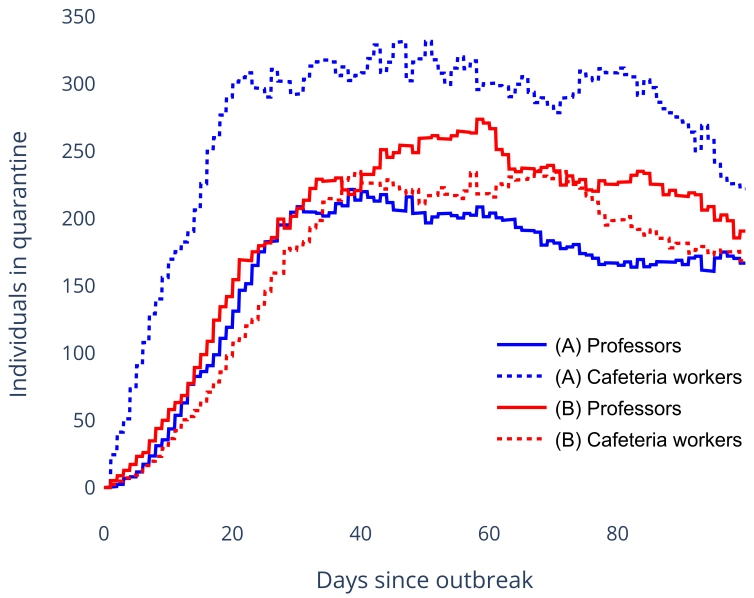

Figure 2: Number of quarantined professors (solid lines) and cafeteria workers (dotted lines) for two different allocation profiles (A) and (B). (A) prioritises minimising professor quarantine over cafeteria workers, and in (B) both have equal priority.

6 Reflections on Bridging Research and Practice

In this section we would like to point out some learnings from our experience

- The importance of local research councils
- Conversation that needs to happen between health administrator taking decisions and the team, since they are the ones that have to implement the tool anyways, and although you might have an incredibly interesting solution concept, if it's too complicated it's worthless in practice
- The importance of having someone on the team with a local connection, and Spanish (Though not necessary, it helps)
- Potentially this is a good place to talk about privacy issues and how they were dealt with (as this is one of the bullet points from the EAAMO CfP)
- Potentially can talk about issues navigating political space?

7 Future Work

The optimisation-based approach presented here allocates limited COVID-19 tests within an educational institution. We note that our approach can be applied in any context in which a heterogeneous population can be meaningfully partitioned into categories. Furthermore, the web application created in collaboration with our collaborators in Mexico allows university administrators to intuitively visualise the trade-offs between different Pareto-dominant testing strategies, facilitating their decision-making process. As we are implementing our methodology with partner institutions in Mexico, we hope that these techniques can be of greater social good in geographies where testing resources are limited.

- Assess the performance of the pilot (which includes cases caught, but also perceptions of the algorithm)

- Extend pilot to other campuses
- Reaching out to state government after pilot?
- Exiting out of lockdown (Bayesian analysis of group tests, finding the healthy)
- Reinforcement learning

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A Modelling the Health Objective

Recall that $O_H(\boldsymbol{t}, \boldsymbol{g})$ denotes the expected number of critical cases that are prevented in our single-step contagion model under testing strategy $(\boldsymbol{t}, \boldsymbol{g})$. In order to state the expected number of critical cases that occur for a given testing strategy, we first determine the probability that an individual who is healthy and not self-isolating is infected by one of its neighbours in the population graph.

Suppose w is an individual from C_i who is healthy and not self-isolating following testing (but prior to the contagion step). We first study the probability that w is infected by someone from category C_j, where $1 \leq j \leq k$. As t_j groups of size g_j are chosen for testing uniformly at random from C_j, $n_j - t_j g_j$ individuals in C_j remain untested. It follows that the number of untested contacts of w in C_j can be modelled as a random variable $\boldsymbol{u} \sim \mathsf{Bin}\left(d_{ij}, \frac{n_j - t_j g_j}{n_j}\right)$. Moreover, each untested contact has an i.i.d. probability p_j of being infected. We let $\boldsymbol{\ell}_j \sim \mathsf{Bin}(\boldsymbol{u}, p_j)$ denote the number of infected contacts of w in C_j. Putting these together, we get that $\boldsymbol{\ell}_j \sim \mathsf{Bin}\left(d_{ij}, \frac{p_j(n_j - t_j g_j)}{n_j}\right)$.

This allows us to determine the probability that w is not infected by any of its $\boldsymbol{\ell}_j$ infected contacts in C_j. Since an infected individual fails to infect a healthy contact with probability $1-\pi_{ij}$, the probability that w is not infected by any of their contacts in C_j is given by $(1-\pi_{ij})^{\boldsymbol{\ell}_j}$. In order for w to remain healthy in our one-step contagion model, it must avoid infections from contacts across all categories. Thus, the overall probability of remaining healthy is $\prod_{j=1}^{k}(1-\pi_{ij})^{\boldsymbol{\ell}_j}$ and it follows that w is infected with probability $1-\prod_{j=1}^{k}(1-\pi_{ij})^{\boldsymbol{\ell}_j}$.

We now analyse the number of critical cases that occur following our testing and containment mechanism under testing strategy $(\boldsymbol{t},\boldsymbol{g})$. This number can be compared to the outcome when no tests are applied (which can be understood as testing strategy $(\mathbf{0},\mathbf{0})$) to obtain the number of critical cases prevented by strategy $(\boldsymbol{t},\boldsymbol{g})$.

Let z_i denote the probability that an individual w from C_i is healthy and not self-isolating following testing (but prior to the contagion step). Note that this can only happen if w is either not part of any group tests, or they are tested and the outcome is negative. These disjoint events happen with probability $\frac{n_i-t_ig_i}{n_i}q_i$ and $\frac{t_ig_i}{n_i}q_i^{g_i}$, respectively. (Recall that $q_i=1-p_i$.). It follows that $z_i=\frac{n_i-t_ig_i}{n_i}q_i+\frac{t_ig_i}{n_i}q_i^{g_i}$.

Next recall that a healthy individual w is infected by any of its contacts in the contagion step with probability $1-\prod_{j=1}^{k}(1-\pi_{ij})^{\boldsymbol{\ell}_j}$, where we once more let $\boldsymbol{\ell}_j\sim\mathsf{Bin}\left(d_{ij},\frac{p_j(n_j-t_jg_j)}{n_j}\right)$ denote the number of infected contacts of w in category C_j. Moreover, if w becomes infected in the contagion step, they have a v_i probability of becoming critical. This in turn means that the probability that an individual in C_i is initially healthy and then develops a critical infection from contagion is $v_iz_i\left(1-\prod_{j=1}^{k}(1-\pi_{ij})^{\boldsymbol{\ell}_j}\right)$. Hence the total number of critical infections from contagion is given by the random variable

$$\sum_{i=1}^{k}n_iv_iz_i\left(1-\prod_{j=1}^{k}(1-\pi_{ij})^{\boldsymbol{\ell}_j}\right).$$

By applying linearity of expectation and exploiting the independence of random variables $\boldsymbol{\ell}_j$ we obtain its expectation

$$\sum_{i=1}^{k}n_iv_iz_i\left(1-\prod_{j=1}^{k}\mathbb{E}\left[(1-\pi_{ij})^{\boldsymbol{\ell}_j}\right]\right). \tag{2}$$

It remains to compute $\mathbb{E}\left[(1-\pi_{ij})^{\boldsymbol{\ell}_j}\right]$. We can transform this expression into $\mathbb{E}\left[\exp(\ln(1-\pi_{ij}))\boldsymbol{\ell}_j)\right]$, and substitute $t=\ln(1-\pi_{ij})$ into the closed form expression of the moment-generating function[6] for a binomially distributed random variable to obtain

$$\mathbb{E}\left[(1-\pi_{ij})^{\boldsymbol{\ell}_j}\right]=\left(1-\frac{\pi_{ij}p_j(n_j-t_jg_j)}{n_j}\right)^{d_{ij}}.$$

Substituting this expression into (2), we see that the expected number of total critical infections from contagion under testing strategy $(\boldsymbol{t},\boldsymbol{g})$ is given by

$$f_H(\boldsymbol{t},\boldsymbol{g})=\sum_{i=1}^{k}n_iv_iz_i\left(1-\prod_{j=1}^{k}\left(1-\frac{\pi_{ij}p_j(n_j-t_jg_j)}{n_j}\right)^{d_{ij}}\right). \tag{3}$$

Note that we can determine the number of critical cases that occur without any testing by evaluating (3) with testing strategy $(\mathbf{0},\mathbf{0})$. (In this case z_i is just q_i.) Putting this together, we define our healthcare objective as follows:

$$O_H(\boldsymbol{t},\boldsymbol{g})=f_H(\mathbf{0},\mathbf{0})-f_H(\boldsymbol{t},\boldsymbol{g})$$

[6]The moment-generating function for random variable $X\sim\mathsf{Bin}(n,p)$ is given by $M_X(t)=(pe^t+1-p)^n$.

B The Bucketing Scheme

Both in our simulations and in the scenarios utilising the data provided by our university partners from Mexico, the Pareto frontier computation outputs thousands of possible solutions, $|S_P| > 1000$. As it can be a daunting task for policy makers to select appropriate solutions for their means, we've developed a bucketing scheme that enables the end user to choose as many solutions as they want the algorithm to generate. The bucketing works in the following way: for each of the objectives O_H and the $O_{Q,i}$'s we set bucket sizes for each, denoted by ρ_H for the health objective and ρ_{Q_i} for each of the quarantine objectives. For each of the objectives, we round up each to the nearest multiple of the bucket size, $\lfloor \frac{O_H(\boldsymbol{t},\boldsymbol{g})}{\rho_H} \rceil \rho_H$ and $\lfloor \frac{O_{Q,i}(\boldsymbol{t},\boldsymbol{g})}{\rho_{Q_i}} \rceil \rho_{Q_i}$. And we redefine Pareto-dominance for two distinct testing and containment mechanisms $(\boldsymbol{t}, \boldsymbol{g})$ and $(\boldsymbol{t}', \boldsymbol{g}')$ by stipulating that $(\boldsymbol{t}, \boldsymbol{g})$ *Pareto-dominates* $(\boldsymbol{t}', \boldsymbol{g}')$ if and only if the following hold:

$$\left\lfloor \frac{O_H(\boldsymbol{t}, \boldsymbol{g})}{\rho_H} \right\rceil \rho_H \geq \left\lfloor \frac{O_H(\boldsymbol{t}', \boldsymbol{g}')}{\rho_H} \right\rceil \rho_H \text{ and } \left\lfloor \frac{O_{Q,i}(\boldsymbol{t}, \boldsymbol{g})}{\rho_{Q,i}} \right\rceil \rho_{Q,i} \leq \left\lfloor \frac{O_{Q,i}(\boldsymbol{t}', \boldsymbol{g}')}{\rho_{Q,i}} \right\rceil \rho_{Q,i} \ \forall i \in [n].$$

To obtain the desired number of solutions we utilise binary search. We first calculate the ranges of the health objective ρ_H and of each quarantine objectives $\rho_{Q,i}$ without bucketing in the Pareto frontier and set the initial buckets as $\boldsymbol{\rho} = (\rho_H, \rho_{Q,1}, \ldots, \rho_{Q,k})$. We then run a binary search with $\alpha \in [0, 1]$ over $\boldsymbol{\rho}$ to find the desired number of solutions with a confidence of plus or minus 5 solutions by recomputing the Pareto frontier with the new buckets $\alpha\boldsymbol{\rho}$.