Efficient COVID-19 Testing Using POMDPs

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Abstract

A robust testing program is necessary for containing the spread of COVID-19 infections before a vaccine becomes available. However, due to an acute shortage of testing kits (especially in low-resource developing countries), designing an optimal testing program/strategy is a challenging problem to solve. Prior literature on testing strategies suffers from two major limitations: (i) it does not account for the trade-off between testing of symptomatic and asymptomatic individuals, and (ii) it primarily focuses on static testing strategies, which leads to significant shortcomings in the testing program's effectiveness. In this paper, we introduced a scalable Monte Carlo tree search based algorithm named DOCTOR, and use it to generate the optimal testing strategies for the COVID-19. In our experiment, DOCTOR's strategies result in $\sim$40% fewer COVID-19 infections (over one month) as compared to state-of-the-art static baselines. Our work complements the growing body of research on COVID-19, and serves as a proof-of-concept that illustrates the benefit of having an AI-driven adaptive testing strategy for COVID-19.

1 Introduction

COVID-19 (or coronavirus) is an urgent public health crisis - within nine months, COVID-19 has infected more than 35 million people, and has resulted in $\sim$1 million deaths worldwide [World Health Organization2020]. In fact, it has been declared as a global pandemic by the World Health Organization (WHO) [Cucinotta and Vanelli2020]. Unfortunately, despite the enforcement of stringent preventive measures, the spread of COVID-19 still does not appear to be slowing down.

As studied in [Winter and Hegde2020, Salathé *et al.*, Binnicker2020], a robust COVID-19 testing program is necessary for containing the spread of infections, as it can: (i) help identify and quarantine infected patients, which can break the chain of COVID-19 transmissions and reduce the total number of infections; and at a higher level, (ii) aggregate results from COVID-19 testing programs can help epidemiologists and policy makers in determining where communities/states/countries are on the epidemic curve, which enables them to take more well-informed decisions about the removal of current stay-at-home orders [Wikipedia2020a]. However, designing the optimal testing program for COVID-19 is a challenging problem because of three major reasons. First, in addition to testing individuals with symptoms who show up at the hospital (i.e., symptomatic testing), the CDC also recommends testing individuals without symptoms in the public (i.e., asymptomatic testing) in order to detect COVID-19 early and stop transmission quickly [Centers for Disease Control and Prevention2020b]. Second, policy makers (especially in developing countries) are constrained in the number of tests (both symptomatic and asymptomatic) that they can conduct on a daily basis, and thus, they need to strategically allocate their limited number of tests among symptomatic and asymptomatic patients. Finally, an optimal testing strategy needs to be adaptive, as the number of symptomatic/asymptomatic tests per day should be increased/decreased adaptively depending on the number of positively diagnosed people in previous days of testing. Therefore, policy makers need to intelligently allocate their limited resources (i.e., limited number of COVID-19 testing kits) over a prolonged period of time in order to minimize the total (cumulative) number of COVID-19 infections.

However, to this date, while almost every country has a COVID-19 testing strategy in place, these strategies are mostly static (i.e., non-adaptive), potentially causing significant shortcomings in their effectiveness in containing COVID-19 (we validate this in our experimental analysis). In this paper, we overcome this limitation via three novel contributions. First, we propose the DOCTOR (**D**esign of **O**ptimal **C**OVID-19 **T**esting **Or**acle) model, which casts the COVID-19 testing problem as a Partially Observable Markov Decision Process (POMDP). Second, we solve DOCTOR's POMDP model using a Monte Carlo tree search based algorithm [Silver and Veness2010]. Our POMDP based algorithm has three key novelties: (i) it models the spread of the COVID-19 virus via SEIR model dynamics [Aron and Schwartz1984]; (ii) it optimally trades off between the amount of resources (i.e., testing kits) that should be invested in symptomatic versus asymptomatic testing to find the optimal testing strategy; and (iii) our POMDP model adaptively

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updates its future long term policy based on aggregate testing results (i.e., how many symptomatic and asymptomatic tests came out positive, etc.) from previous rounds. Finally, and most importantly, we also provide a rigorous experimental analysis of DOCTOR's testing strategy against static testing programs to illustrate the effectiveness of our approach. Our experiments reveal that DOCTOR's testing strategy was able to outperform state-of-the-art baselines by achieving $\sim$40% fewer COVID-19 infections, when applied to city of Santiago, Panama. The result illustrates the benefit of having an adaptive strategy.

COVID-19 is the greatest public health crisis that the world has experienced in the last century. Tackling it requires the collective will of experts from a variety of disciplines. While a lot of efforts have been made by AI researchers in developing agent-based models for simulating the transmission of COVID-19 [Wilder *et al.*2020, Yang *et al.*2020, Hu *et al.*2020], we believe that AI's enormous potential can (and should) be leveraged to design decision support systems (e.g., in the allocation of limited healthcare resources such as testing kits) which can assist epidemiologists and policy makers in their fight against this pandemic. Our work represents the first step in developing such a decision support system, and should serve as a proof-of-concept that illustrates the benefit of having an AI-driven adaptive testing strategy.

2 The COVID-19 Testing Setup

SEIR Transmission Model. The SEIR model is a popular epidemiological model for simulating the progression of an epidemic through a population of individuals, and it has been used to successfully simulate the outbreak of many infectious diseases, e.g., Ebola [Lekone and Finkenstädt2006], COVID-19 [Karunditu *et al.*2019, Pandey *et al.*2020], etc. In the standard SEIR model, a population of N individuals is split into four compartments: (i) Susceptible (**S**), i.e., individuals who have never been infected or exposed to the COVID-19 virus; (ii) Exposed (**E**), i.e., individuals who have been exposed to the virus, but are not infectious yet; (iii) Infectious (**I**), i.e., individuals who have been infected and can spread infection to other individuals; and (iv) Recovered (**R**), i.e., individuals who have recovered or died from the virus. Each of the four compartments represent a distinct phase in the progression of infectious diseases.

Further, to capture the most essential characteristics of COVID-19 transmission, we made two major adaptations to the standard SEIR model: (i) similar to He et al. [He *et al.*2020], the $\mathbf{I}$ class is split into $\mathbf{I_1}$ and $\mathbf{I_2}$, which represents asymptomatic and symptomatic infected patients, respectively; (ii) we introduce a new compartment class named Hospitalization/Quarantine (**H/Q**), which represents individuals who are either hospitalized or are observing strict quarantine orders. Our two adaptations are necessary for modeling COVID-19 as (i) there is a high asymptomatic rate of COVID-19 infections [Centers for Disease Control and Prevention2020a, Carl Heneghan2020, Nishiura *et al.*2020], which can not be distinguished by the single $\mathbf{I}$ class in the standard SEIR model; and (ii) introducing the **H/Q** compartment enables us to model infected individuals who do not spread infection to anybody else (either because they are hospitalized or they observe strict stay-at-home quarantine orders).

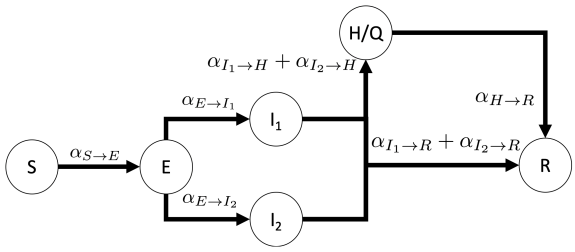


Figure 1: Flow Dynamics of our SEIR Model

Our SEIR model dynamics proceed in a series of discrete time steps. Let there be a population of N individuals that undergo SEIR model transmission dynamics. Let T denote the number of time steps for which the SEIR model dynamics are allowed to run. Each individual $n \in \{1, N\}$ belongs to exactly one compartment at time $t = 0$. At each time $t \in \{1, T\}$, individuals in each compartment 'flow' to the next adjacent compartment at pre-determined rates. The flow dynamics of our model are explained in Figure 1. In particular, individuals in **S** move to **E** at a rate $\alpha_{S \to E}$, individuals in **E** move to $\mathbf{I_1}$ and $\mathbf{I_2}$ at rates $\alpha_{E \to I_1}$ and $\alpha_{E \to I_2}$, respectively. Similarly, individuals in $\mathbf{I_1}$ and $\mathbf{I_2}$ move to **R** at rates $\alpha_{I_1 \to R}$ and $\alpha_{I_2 \to R}$. Also, individuals in **H/Q** move to **R** at a rate $\alpha_{H/Q \to R}$. Finally, individuals in **R** do not take further part in transmission dynamics (i.e., we assume infected individuals upon recovery cannot be re-infected).

Our goal in the COVID-19 testing problem is to minimize the cumulative number of individuals that are infected by COVID-19 (i.e., individuals in $\mathbf{I_1}$ and $\mathbf{I_2}$) across T time-steps of transmission. In order to achieve this goal, we need to formulate a sequential testing policy (formally defined below) that optimally allocates available testing kits to test symptomatic and asymptomatic individuals. We now elaborate on this distinction between conducting tests for symptomatic and asymptomatic individuals.

Symptomatic VS Asymptomatic Testing. As part of the optimal testing policy, we assume that the policy maker is allowed to use his/her available COVID-19 testing kits to conduct two different kinds of tests: (i) Targeted Symptomatic Testing; and (ii) Random Asymptomatic Testing.

Targeted Symptomatic Testing (symptomatic testing, in short) focuses only on the people who exhibit COVID-19 symptoms and seek care at hospitals. The testing kits that are allocated for symptomatic testing would be distributed (in advance) across different hospitals. Only patients that show up at hospitals with COVID-19 like symptoms will be tested using these symptomatic testing kits. In our SEIR model, individuals in $\mathbf{I_2}$ can get tested using symptomatic testing kits (as all individuals in $\mathbf{I_2}$ are symptom-showing COVID-19 patients). In addition, we assume that a fraction of individuals in other compartments can suffer from Influenza Like Illnesses (ILI), and hence these ILI patients also show up at hospitals with COVID-19 like symptoms (we set this ILI fraction to 0.24 in our experiments, based on prior results [Silverman *et*

*al.*2020]). Thus, in our SEIR model, these ILI patients can also be tested with symptomatic testing kits.

Unfortunately, symptomatic testing is not sufficient by itself, as (i) a large proportion of COVID-19 patients are asymptomatic (i.e., do not exhibit any symptoms), and hence they may never go to hospitals to get treated [Centers for Disease Control and Prevention2020a, Carl Heneghan2020, Nishiura *et al.*2020]. However, such asymptomatic patients can still spread the virus very rapidly among other individuals [Bai *et al.*2020, Yu and Yang2020]. (ii) Further, due to this large population of asymptomatic virus carriers, it is very difficult for epidemiologists and policy makers to understand where they are on the epidemic curve solely on the basis of symptomatic testing. In order to address this issue, we also consider Random Asymptomatic Testing as an option available to the policy maker. In our SEIR model, Random Asymptomatic Testing (asymptomatic testing, in short) focuses on all the individuals in $\mathbf{S}$, $\mathbf{E}$, $\mathbf{I_1}$, $\mathbf{I_2}$ and $\mathbf{R}$, and randomly samples m individuals uniformly from these compartments to conduct COVID-19 tests on them (if the testing policy allocates m testing kits for asymptomatic testing).

Note that the positive COVID-19 diagnosis rate per test is much higher for symptomatic tests as compared to asymptomatic tests. Thus, while asymptomatic tests are essential to tackle infectious individuals in $\mathbf{I_1}$, they are not as efficient as symptomatic tests in discovering COVID-19 patients. To increase the efficiency of asymptomatic tests, we also incorporate group testing for asymptomatic tests in our optimal testing problem [Sunjaya and Sunjaya2020, Yelin *et al.*2020].

3 DOCTOR POMDP

We cast the optimal testing problem as a POMDP because of three reasons. First, we have partial observability of the sizes of the $\mathbf{S}$, $\mathbf{E}$, $\mathbf{I_1}$ and $\mathbf{R}$ compartments in the optimal testing problem (similar to POMDPs). Second, similar to sequential POMDP actions, we are allowed to make D sequential changes to the testing policy (one change per each of the D decision points). Finally, POMDP solvers have recently shown great promise in generating near-optimal policies efficiently [Yadav *et al.*2016b, Yadav *et al.*2016a, Yadav *et al.*2017, Ghandali *et al.*2020]. We now explain how we map the optimal testing problem into a POMDP.

States. A POMDP state in our problem is a tuple $s = \mathbf{S}, \mathbf{E}, \mathbf{I_1}, \mathbf{I_2}, \mathbf{H/Q}, \mathbf{R}$, where variables $\mathbf{S}$, $\mathbf{E}$, $\mathbf{I_1}$, $\mathbf{I_2}$, $\mathbf{H/Q}$ and $\mathbf{R}$ denote the number of individuals present inside the corresponding compartments of the SEIR model. For a POMDP state to be valid, we require $\mathbf{S} + \mathbf{E} + \mathbf{I_1} + \mathbf{I_2} + \mathbf{H} + \mathbf{R} = N$. Our POMDP has $\binom{N+5}{5}$ states.

Actions. At each decision point $d \in \{1, D\}$, the policy maker has a total of U_{cap} COVID-19 testing kits that need to be allocated for testing individuals. An action inside our POMDP is a tuple $a = b_1, b_2$, s.t. $b_1 \geq 0$, $b_2 \geq 0$ and $b_1 + b_2 = U_{cap}$. Intuitively, b_1 and b_2 represent the number of testing kits that have been allocated for testing symptomatic and asymptomatic individuals, respectively. Our POMDP has $U_{cap} + 1$ different actions.

Observations. Upon taking a POMDP action, we assume that the policy maker can "observe" the COVID-19 test results (positive or negative) of all individuals who were tested as part of the POMDP action. Formally, upon taking action B_d at decision point d, the POMDP observation is denoted as a binary vector (of length U_{cap}) $\mathbf{\Theta} = \theta_1, \theta_2, \ldots, \theta_{U_{cap}}$. The variable $\theta_i = 1, \forall i \in \{1, U_{cap}\}$ represents whether the i^{th} individual (who was tested in POMDP action B_d) was diagnosed with COVID-19 ($\theta_i = 1$) or not ($\theta_i = 0$). Our POMDP has $\mathcal{O}(2^{U_{cap}})$ observations.

Rewards. The cost $R(s, a, s')$ of taking action a in state s to reach state s' is the number of active infected individuals in state s'. Over D decision points, DOCTOR's cost function serves as a proxy for minimizing the cumulative number of COVID-19 infections.

Transition & Observation Probabilities. Computation of exact transition and observation probability matrices ($T(s'|s, a)$ and $O(o|a, s')$, respectively) is infeasible in our POMDP because these matrices are prohibitively large (due to large sized state, action and observation spaces). Therefore, we follow the paradigm of large-scale online POMDP solvers [Silver and Veness2010, Eck and Soh2015] by using a generative model $\Lambda(s, a) \sim (s', o, r)$ of the transition and observation probabilities. This generative model allows us to generate on-the-fly samples from the exact distributions $T(s'|s, a)$ and $\Omega(o|a, s')$ at low computational costs. Given an initial state s and an action a, our generative model Λ simulates the random process of SEIR model dynamics (as explained in Figure 1) to generate a random new state s', an observation o and the obtained reward r. Simulation is done by "*playing*" out our SEIR model to generate sample s'. The observation sample o is then determined from s' and a. Finally, the reward sample r depends on the number of active infected COVID-19 patients in s' (as defined above). This simple design of the generative model allows significant scale and speed up.

Initial Belief State. In our experiments, we initialize the belief state to be as close as possible to the real-world. In particular, the initial belief state is uniformly distributed over all POMDP states s in which $\mathbf{I}$ is set to the current number of COVID-19 infections in the population of interest. Then $\mathbf{I_1}$ and $\mathbf{I_2}$ are split from $\mathbf{I}$ based on COVID-19 asymptomatic rate ϕ (we experiment with different ϕ values). For example, if we instantiate a SEIR model for Santiago, the initial belief state contains all states in which $\mathbf{I}$ is equal to current number of active cases in Santiago. And if we assume the $\phi = 0.7$, then $|\mathbf{I_1}| = 0.7\,|\mathbf{I}|$, and $|\mathbf{I_2}| = 0.3\,|\mathbf{I}|$.

At last, in this paper, we solve the DOCTOR POMDP model using POMCP [Silver and Veness2010], a well-known online POMDP solver that relies on Monte Carlo tree search to find near-optimal online policies.

4 Experimental Results

We evaluate DOCTOR's effectiveness in controlling the spread of COVID-19 by applying its testing strategy (in simulation) to the city of Santiago, Panama (a country with the world's highest COVID-19 infections per capita [Armstrong2020]). Our experiments are run on a 2.8 GHz Intel Xeon processor with 256 GB RAM. All experimental results are averaged over 100 runs and are statistically significant un-

der bootstrap-t ($p = 0.05$). In these experiments, we use a default value of $N = 89,000$ (which is Santiago's population [Wikipedia2020b]), $D = 30$ and $T = 30$. Based on findings in [Sunjaya and Sunjaya2020, Yelin *et al.*2020], COVID-19 test sensitivity and specificity values are set to 0.90 and 0.99, respectively. Also, we set a default budget constraint of $U_{cap} = 500$ testing kits per decision point in our experiments (unless specified otherwise). The POMCP-based DOCTOR model is run with 2^{10} Monte-Carlo simulations at each decision point. Further, in all our experiments, we use results from [Foundation2020] to instantiate our SEIR model with the following values of flow rates: $\alpha_{E\to I_1} = \frac{7}{50}$, $\alpha_{E\to I_2} = \frac{3}{50}$, $\alpha_{I_1\to R} = \frac{1}{14}$, $\alpha_{I_2\to R} = \frac{1}{14}$, and $\alpha_{H/Q\to R} = \frac{1}{14}$. In particular, the value of $\alpha_{S\to E}$ is dependent on the basic reproduction number of COVID-19 (R_0) and the number of individuals in $\mathbf{I}$, which is denoted as $\alpha_{S\to E} = \frac{\beta\cdot\mathbf{S}\cdot\mathbf{I}}{N}$, $\beta = \frac{R_0\cdot\alpha_{I_1\to R}\cdot\alpha_{I_2\to R}}{2}$, where β represents the COVID-19 transmission rate. Based on [Liu *et al.*2020, Zhang *et al.*2020], we assume $R_0 = 2.0$.

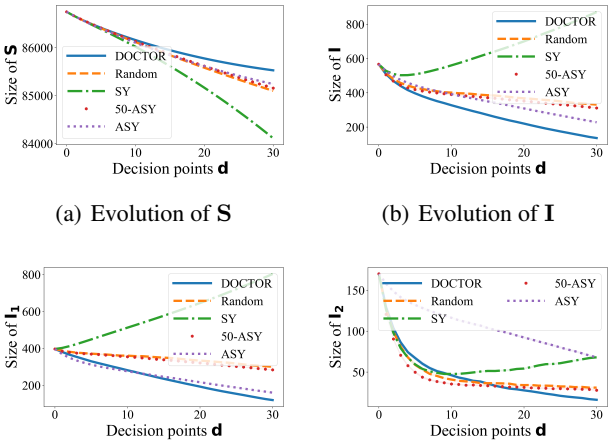
Baselines. We compare DOCTOR against four different baseline testing strategies. We use (i) 100% symptomatic testing (SY in the figures), i.e., allocate all available testing kits to symptomatic individuals at each decision point. We use SY as a baseline as this has been the primary testing strategy used by Panama's government until now, e.g., Panama had not tested asymptomatic individuals until 4^{th} September, 2020 [PanaTimes2020]. Using this baseline allows us to compare DOCTOR with a real-world government's effort (in simulation). Next, we use (ii) 100% asymptomatic testing (ASY), i.e., allocate all available testing kits to asymptomatic individuals; (iii) 50% symptomatic and 50% asymptomatic testing (50-ASY), i.e., equally divide testing kits among symptomatic and asymptomatic individuals; and finally (iv) a uniform random testing policy (Random), i.e., select a random testing action B_d at every decision point $d \in D$.

4.1 DOCTOR's performance in Panama

First, we evaluate the performance of DOCTOR's testing policy against all other baselines, when applied to the city of Santiago, the 5^{th} largest city in Panama. Since city-level COVID-19 case information is not available for Panamanian cities, we initialize Santiago's SEIR model using Panama's country-level COVID-19 case information. In particular, we set the initial SEIR compartment proportions to $\mathbf{S} = 97.47\%, \mathbf{E} = 0.27\%, \mathbf{I_1} = 0.45\%, \mathbf{I_2} = 0.19\%, \mathbf{R} = 1.62\%, \mathbf{H/Q} = 0\%$, which matches the COVID-19 infection numbers in Panama on 2^{nd} September, 2020. Note that $\mathbf{H/Q}$ is set to zero because we only count $\mathbf{H/Q}$ from the beginning of the testing period. Next, DOCTOR and the other baselines were used to solve an optimal testing problem (defined according to this instantiated SEIR model and the other parameter values described above).

Figure 2 compares the result of *executing* DOCTOR's testing policy against baselines by tracking the evolution of the underlying SEIR model over $D = 30$ decision points. Figures 2(a), 2(b), 2(c) and 2(d) show the progression in the sizes of $\mathbf{S}$, $\mathbf{I}$, $\mathbf{I_1}$ and $\mathbf{I_2}$ compartments of the SEIR model (respectively) over $D = 30$ decision points. The X-axis in these figures represents the different decision points, and the Y-axis shows the size of the different compartments. For example, DOCTOR's testing strategy achieved a size of $|\mathbf{S}| = 85,528$, $|\mathbf{I}| = 136$, $|\mathbf{I_1}| = 120$ and $|\mathbf{I_2}| = 16$ after the 30^{th} decision point.

Figure 2(b) shows that DOCTOR significantly outperforms all baselines - its testing strategies result in $\sim 40\%$ fewer COVID-19 infections by the 30^{th} decision point (as compared to ASY, the next best performing baseline). Further, this figure shows that SY performs very poorly - it performs $\sim 60\%$ worse than Random and ASY-50, and it leads to a $\sim 550\%$ increase in COVID-19 infections over DOCTOR. This establishes the superior performance of DOCTOR over SY (and other baselines), which illustrates the potential benefits of using DOCTOR's adaptive strategy in Panama.



(a) Evolution of $\mathbf{S}$ (b) Evolution of $\mathbf{I}$

(c) Evolution of $\mathbf{I_1}$ (d) Evolution of $\mathbf{I_2}$

Figure 2: Evaluating DOCTOR's performance in Panama

Figures 2(c) and 2(d) provide a preliminary insight into how DOCTOR achieves significant reductions in the number of COVID-19 infections. Specifically, these figures show why baseline testing strategies fail: (i) ASY performs only $\sim 30\%$ worse than DOCTOR in minimizing asymptomatic infections $|\mathbf{I_1}|$, but performs $\sim 300\%$ worse than DOCTOR in minimizing symptomatic infections $|\mathbf{I_2}|$ (since ASY only tests asymptomatic individuals). (ii) On the other hand, SY performs $\sim 300\%$ worse than DOCTOR in minimizing $|\mathbf{I_2}|$, and performs $\sim 550\%$ worse than DOCTOR in minimizing $|\mathbf{I_1}|$ (since SY only focuses on symptomatic individuals). (iii) ASY-50's behavior is not as extreme as SY (in Figure 2(c)) or ASY (in Figure 2(d)), yet it performs worse than DOCTOR due to its lack of adaptivity. (iv) DOCTOR is the only strategy which intelligently minimizes both $|\mathbf{I_1}|$ and $|\mathbf{I_2}|$ by adaptively changing the allocation of testing kits according to the stage of the epidemic. (v) Further, DOCTOR's testing strategy results in the largest $|\mathbf{S}|$ at the end of the 30^{th} decision point (Figure 2(a)), which illustrates DOCTOR's (relative) success in preventing susceptible individuals in $\mathbf{S}$ from getting infected. These figures show that at least in simulation, DOCTOR was highly effective in controlling the number of COVID-19 infections in Santiago.

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