COVID-19 Mathematical Modeling for Cornell's Fall Semester

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Executive Summary:

- Initial modeling results suggest that a combination of contact tracing, asymptomatic surveillance, and low initial prevalence (supported through testing students prior to, and upon, returning to campus) can achieve meaningful control over outbreaks on Cornell's Ithaca campus in the fall semester if asymptomatic surveillance is sufficiently frequent and if we have sufficient quarantine capacity. This would dovetail with a complementary effort at Cornell to reduce transmissions through housing policy, class organization, and regulations on social gatherings.

- We use our model to predict outcomes for a full return of students, faculty and staff in the fall semester over a 16 week time period, with cases imported from returning students and from Tompkins county, counterbalanced by aggressive asymptomatic surveillance where every member of the campus community is tested every 5 days. The course of the epidemic is random and we directly model that randomness. Accordingly, our model produces a range of potential futures. In the median random potential future, under our nominal set of parameters, 3.6% of the campus population (1254 people) become infected, and 0.047% of the campus population (16 people) require hospitalization. The 90% quantile rises to 4.02% infected and 0.051% requiring hospitalization. Of the 1254 infections in the median outcome, 570 are due to direct outside infections and ensuing additional infections prior to isolation, while 31 (0.09% of the campus population) are infected before arrival to campus but missed in the test-on-return protocol. There are an additional set of people infected before arrival, found through test-on-return, and isolated in Ithaca (22 people) or at home prior to travel (180 people).

- Outside infections from Tompkins County are predicted to be a significant source of cases. Testing every 5 days is sufficient to keep these imported cases from growing into large epidemics, but even low prevalence (e.g., 0.1%) creates a steady stream of imported cases, each of which then creates 2-3 more cases on campus before we catch the cluster. Over the course of a semester, outside infection can dominate returning students as a disease source. Measures that would reduce outside prevalence, especially among those that interact most closely with the Cornell community, are likely to also improve on-campus health outcomes and reduce

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quarantine needs. This includes using results from on-campus surveillance to identify transmission vectors, reducing transmission of virus from Cornell to the broader community, and expanding access to testing. Measures reducing contact between the Cornell community and those outside would have similar benefits.

- Peak Quarantine Capacity: Our preliminary nominal analysis suggests that the number of people that would need to be quarantined or isolated in the peak period following move-in is 700. This estimate includes members of the Cornell community who could self isolate, so should be taken as an over-estimate of the needed quarantine capacity. It is highly sensitive to assumptions. Due to the uncertainty this creates, we recommend planning for a peak capacity greater than 700.

- Sustained Quarantine Capacity: Outside infections create a sustained need for quarantine and isolation capacity. While lower than peak capacity requirements, these may be significant, with hundreds of people quarantined or isolated at any given time. Since the greatest sustained source of infection will be interaction with the outside community, the quarantined population is likely to contain a larger fraction of faculty, staff, and students living off campus than the peak load following move-in. Work is ongoing to quantify these needs.

- To provide context, we also model what would happen if we did **not** open Cornell for a residential fall semester and did full virtual instruction instead. Our nominal parameters assume that 9000 students would remain in Ithaca but outside the control of the University in off-campus apartments without asymptomatic surveillance, and that a population of 15000 faculty, staff, and graduate students would remain on campus *with* asymptomatic surveillance. The median number of infections over a 16-week period in the no-reopen scenario is ~ 7200, which is significantly larger than the ~ 1200 that occur under the nominal fall-reopen parameters. This is because the loss of asymptomatic screening allows cases to grow significantly in the unmonitored student population. It is also because infections from outside Cornell, a large driver of cases in the residential-campus scenario, continue to drive cases.

- Our analysis of virtual instruction assumes that (1) virtual instruction allows asymptomatic screening only for those faculty, staff and graduate students who are assumed to continue to work/study on campus, with students living locally but taking classes remotely not included; (2) social distancing interventions are effective enough for virtual instruction students in Ithaca that contacts and transmission are comparable to residential instruction; and (3) gateway testing can be implemented for those returning to Ithaca for virtual instruction. Also note (4) our nominal scenario for residential instruction assumes full compliance with testing, quarantine and isolation. Assumptions (2) and (3) are likely overly optimistic for virtual instruction while assumption (4) may be overly optimistic for residential instruction. Other assumptions would create different predictions. Work continues to understand sensitivity to parameter choice but early results suggest the conclusion that residential instruction has better health outcomes than virtual instruction is robust to assumptions.

- In all of our modeling results, modifying modeling parameters by only a modest amount from nominal values can result in substantially different numbers of infections and hospitalizations. Some parameter combinations, that we consider to be not implausible, can yield extremely serious consequences if interventions do not adjust to meet the challenge. Such outcomes point to the need to design a robust early-warning system. Regular asymptomatic testing as evaluated here can supply this early warning.

- Moreover, such scenarios suggest that the best course of action may be one that can *adapt* to facts on the ground, e.g., by adjusting asymptomatic screening frequency based on observed prevalence, or by beginning with stronger protections for vulnerable populations that can be relaxed if the risk level permits.

- In addition to uncertainty about parameters, our model cannot fully capture the intricacies of the real world. For example, it is difficult to accurately capture the interactions between the Cornell and non-Cornell communities. We developed a second model of outside infections that would appear equally reasonable to the one we present here, but whose number of outside infections imported is a factor of 3 smaller when passed the same raw parameters. A full list of model limitations is given in the report.

- Under a range of plausible parameter settings, regular asymptomatic testing is essential to keeping the epidemic under control; without it we see a significant increase in infections and hospitalizations. We envision that this asymptomatic testing would be enabled by the capacity at Cornell's Animal Health Diagnostic Center, with costs controlled through group testing. Work continues with collaborators in the College of Veterinary Medicine to validate group testing protocols and obtain regulatory approval. While substantial cost savings may be possible with large pool sizes (20 or more), we focus our analysis on a more conservative method using pools of size 5 in which we are more confident that a false negative rate of 10%, which is comparable to that of individual testing, can be achieved. (This false negative rate does not include a post-exposure low viral load period during which we assume PCR cannot detect infection).

- A small number of cases originating from Cornell students or employees could multiply in the broader community given that aggressive asymptomatic screening is not available to the general public, especially as social distancing measures are lifted. The cases thus created could then return to re-infect the Cornell community. This proliferation of cases in the broader community is not captured by our model.

- Modeling suggests other opportunities for reducing infections and hospitalizations: increasing the number of infectious cases identified with each contact trace by encouraging students to take phone calls from health department contact tracers; controlling the number of contacts per day and transmission probability per contact through housing policy, classroom design, and regulations on social gatherings; leveraging on-campus surveillance to alert Tompkins County to vectors infecting individuals on campus (e.g., Ithaca City Schools, a business in Collegetown); and perhaps even expanding test access beyond the Cornell community to help reduce prevalence in Ithaca and thus reduce outside infections.

- There are also unmodeled opportunities to reduce infection. Of interest is directed asymptomatic surveillance, e.g., follow-up testing on a dorm floor if a resident living on that floor is identified as positive. Such interventions are likely to reduce the required frequency of undirected asymptomatic surveillance. Also, we hypothesize that testing everyone on a deterministic schedule (each person is tested once every 5 days) will outperform testing randomly, though our model assumes random testing to simplify computation.

- Toward the goal of quantifying uncertainty, we are continuing efforts to estimate parameters, provide ranges of plausible parameter values against which we should plan, and investigate

the impact of modeling assumptions. This effort is supported by a literature review being conducted by the Cornell library and a set of reviews provided by experts both within and outside Cornell on a previous version of this report.

- In parallel, we are using the model to investigate the impact of having vulnerable individuals stay away from campus and modifications to student housing. We are also adding the capability to differentiate student from faculty/staff populations.

Contents

1 An Overview of Methods and Results

This document presents a mathematical modeling framework for COVID-19 at Cornell. The framework is designed to support decision making for university leadership as they consider whether and how to bring students back for a residential fall semester. It is not intended to support decisions about how to initiate research reactivation, as those decisions are moving on a faster timeline. This section is intended for a broad audience and provides an overview of the methods and results. Later sections go into much more detail.

Epidemic Modeling is Fundamentally Imperfect: It is tempting to believe that a model can predict the future. In the case of epidemic modeling, however, accurate prediction is not an attainable goal. While we have done our best to include the most salient aspects of reality and to estimate the parameters that govern them well, epidemics are notoriously difficult to estimate, including this one.

Indeed, estimates for outcomes are sensitive to parameters. Moreover, while each sensitivity analysis plot shows the sensitivity to only one parameter as we hold the others fixed at nominal values, in reality our estimates might *all* need adjustment simultaneously, potentially by quite a bit. Thus, while a strategy might be robust to errors in a single parameter, it might not necessarily be robust to the full uncertainty we face. Further uncertainty is introduced by structural assumptions that do not hold in reality. Hence, with our current knowledge, we are only moderately confident in our ability to say whether a particular strategy will achieve a desired level of risk.

Modeling Methodology and Implementation: Our modeling approach has two components: an Excel model of initial testing for students returning to campus and a stochastic compartmental simulation of the on-campus population, implemented in Python.

The Excel model of initial testing estimates the number of students isolated before and after travel to campus, as well as the number of infected individuals missed by the initial tests. The fraction of individuals missed by this protocol is the initial prevalence for our compartmental simulation. (This is an approximation, discussed below, as it assumes that the people already on campus have the same initial prevalence.) The compartmental model does not account for individuals that were detected through this initial testing. Therefore, these people are not included in the figures of this document, though we do include them in the captions.

The compartmental simulation models the number of people in each of a number of states over time. States describe the course of the disease in an individual in a detailed way that builds on a standard SEIR epidemic model; see, e.g., (24) with random durations in disease states. To this SEIR backbone our model adds more detailed accounting of when an individual becomes PCR positive, includes asymptomatic but infectious individuals, and models how an individual's age influences the severity of their symptoms.

Individuals that report symptoms are tested and isolated, resulting in contact tracing and quarantining identified contacts. Asymptomatic surveillance is conducted and contacts are traced on positive cases that are identified. We include parameters for the number of contacts a person has per day and the probability of infection for each contact. These parameters provide a mechanism for modeling the impact of social distancing and other transmission mitigation measures like masks.

With one replication the model generates one possible future. Results from one such replication are shown in Figures 1 and 2. Many replications yield ensemble forecasts of the future as illustrated in Figures 3 and 4.

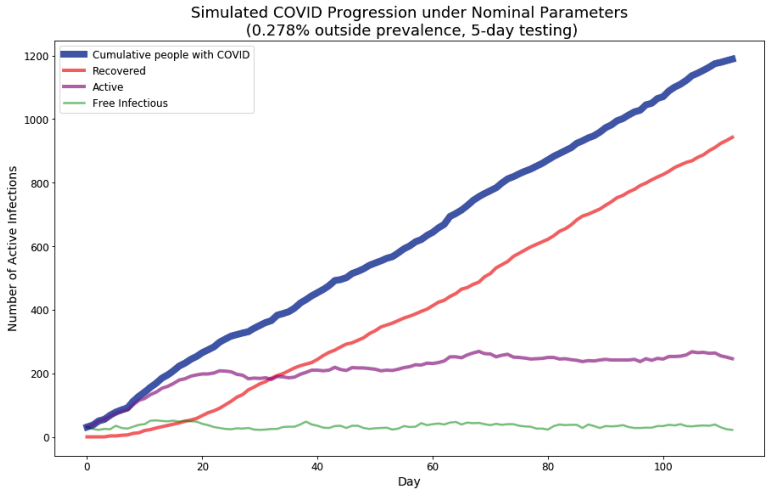

Figure 1: One possible future from our simulation for the fall semester with asymptomatic testing once every 5 days under nominal parameters, beginning just after move-in. At this point, we assume 0.09% of the population (roughly 31 people) are infected and unknown to health authorities. This initial prevalence is obtained from the entry model assuming a 2% prevalence among returning students prior to the two rounds of testing they undergo; testing fails to detect a few infected students. Roughly 200 people who are infected but identified by on-return testing and isolated immediately are not pictured. As they infect others, the number of active infections (purple line) grows. At the same time, many of these infectious cases are identified through asymptomatic screening, symptomatic self-reporting, and contact tracing, and then quarantined or isolated. This causes the number of free infectious people (green line) to be smaller than the number of active infections. Over time, the number of free-infectious and the number of active individuals approach steady levels, representing the counteracting effect between disease spread and quarantine/isolation as well as the constant stream of new infections introduced from outside. The red line represents people who have recovered, and the blue line represents the total number of people who have been infected at any point. Both increase linearly in time due to the constant stream of outside infections.

We believe that this simulation model captures most phenomena determining growth of a COVID-19 epidemic, but like any model it has limitations. Moreover, due to the need to deliver answers quickly, an explicit decision was made to accelerate development through carefully considered approximations in two key aspects: contact tracing and risk groups. These are discussed in detail below in a subsection on limitations.

Parameters: We obtain parameters from the literature. Unfortunately, the literature is fragmented with an incomplete understanding of several important aspects of disease dynamics. Our work continues in collaboration with the Cornell Library to refine parameter estimates using data from the literature, the Tompkins County Health Department, and from Cornell. Where it is not possible to narrow down the value of important parameters, we explore the impact of each parameter over a plausible range. Parameters are discussed in detail in Section 2.

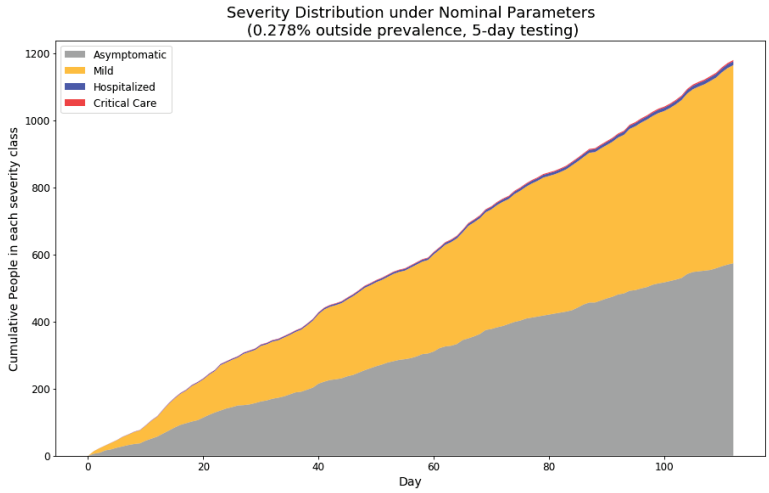

Figure 2: For the same simulated future as in Figure 1, cumulative infections that have passed beyond the time when they would become symptomatic, broken out by severity of symptoms, versus the number of simulated days. Grey represents individuals that remained asymptomatic through the course of their infection, orange represents individuals whose worst severity was mild, blue represents individuals that required hospitalization but not critical care, and red indicates individuals that required critical care. The vast majority of infected cases are asymptomatic or mild. The number of people represented at any given point in this figure is slightly smaller than the cumulative number of people with COVID in Figure 1 because it does not include people who are early in their disease and have not yet reached the time when they would become symptomatic. As in Figure 1, about 200 people who are identified and isolated through test-on-return are not pictured.

Testing Upon Return: We use a spreadsheet-based (Excel) model to study the impact of two PCR tests for students returning to campus — one local test prior to student departure, and a test upon student arrival — on the initial prevalence.

The local test is assumed to be an individual test, performed 5 days prior to student departure. Students are assumed to be isolated in their original location if they test positive. Upon arrival, all returning students are tested using a group testing protocol. Students are isolated immediately if they test positive. By screening students both prior to departure and upon their arrival to campus, we greatly reduce the initial prevalence among the non-isolated campus community.

The model allows for infection of students between the pre-departure and on-arrival tests. There is a small per-day infection probability prior to departure reflecting effective social-distancing measures, and a larger per-day infection probability during travel. The travel duration and the likelihood that students use public transportation (with an associated elevated daily infection probability) depends on the geographic origin of students.

Quarantine Capacity: Because each quarantine and isolation must last at least 14 days, we expect the peak quarantine capacity usage to occur approximately two weeks after move-in. Accordingly, to estimate this peak usage, we use our simulation framework to identify all people that

would need quarantine or isolation in the first 18 days of the fall semester following move-in. This population consists of two parts: (a) those who test positive upon arrival and are isolated immediately (as obtained by the Excel model), and (b) those quarantined/isolated over the subsequent 18-day period through contact tracing, self-reporting or asymptomatic surveillance (as obtained from the Python simulation model).

Contact Tracing: In all scenarios, we assume that contact tracing is performed on individuals that test PCR positive after the test-on-return protocol, whether these individuals were identified through self-reported symptoms or asymptomatic surveillance.

Since we assume that individuals identified as positive in the return-to-campus testing are identified immediately, we do not model contact tracing on these individuals.

We do not currently consider antibody tests because of the lack of clarity surrounding their accuracy and the elevated risk of noncompliance associated with a blood test instead of a saliva test. Still, one can imagine their use for better measuring prevalence and disease progression.

Asymptomatic Screening with Group Testing: In the fall semester, we propose and study the use of regular asymptomatic screening of the Cornell population. When applying asymptomatic testing in our baseline setting, we test 1/5 of the entire campus population every day. In our simulation, for ease of computation, testing is modeled by assuming that each individual independently has a 1/5 chance of being tested on any day. In reality it is likely better to test according to a fixed rotation where each person is tested exactly once every 5 days. We include a sensitivity analysis examining the effect of more or less frequent screening, including testing 1/7 of the population per day.

Feasibility and cost-effectiveness of this frequency of testing is likely to require group testing, discussed in detail below in Section 5.3. There we discuss ongoing work to develop a group testing protocol in collaboration with Drs. Diego Diel and Jeff Pleiss. This requires regulatory approval for group testing at the ADHC. Work is underway to enable this.

While laboratory work must be conducted to estimate sensitivity and specificity parameters that would inform a protocol design, we assume for our nominal parameters that a false negative rate comparable to individual testing would be achieved through a relatively small pool size of 5 and by increasing the reaction volume to mitigate dilution effects. This would require roughly 1400 PCR tests per day.

We are also considering group testing protocols with larger pool sizes that would have more significant cost savings and could plausibly retain a low false negative rate, especially if viral load is highly variable and seldom falls in the gap in the limits of detection between pooled and unpooled tests.

While we study a simple fixed screening strategy in which all members of the campus community are tested equally often, we envision that there is significant value in testing in a more targeted way: e.g., testing all residents of a dorm floor when one resident tests positive; testing those with more contacts or more frequent contact with high-risk individuals; testing a dorm based on the results of PCR analysis of wastewater.

Outside Infections: We have extended the simulation model to allow for "outside" infections that arise from interactions with the non-Cornell local community, in addition to within-campus infections. In our model, each member of the Cornell community has a probability of being infected by some non-Cornell local person every day. This *daily outside-infection probability* depends linearly

on the assumed prevalence in Tompkins County. Each day, a random number of outside infections arise, modeled as a binomial random variable with parameters the number of susceptible people on campus, and the daily outside-infection probability.

In the simulation results, the initial number of infectious cases is given by an assumed initial on-campus prevalence, and then evolves to a level that is non-zero and larger when the outside prevalence is larger. When we have fast-enough asymptomatic testing to control clusters of infectious cases, cumulative cases do not grow exponentially. Rather, cumulative cases grow linearly, with a daily increment equal to roughly 2 to 3 times the expected number of active infections due to interactions with the outside. This factor of 2-3 arises because each new imported case from outside infects 2-3 others before we can control the cluster. For example, assuming asymptomatic testing every 5 days and an outside prevalence of 0.1%, in one simulated future approximately 100 outside infections arise over the first 20 simulated days, during which cumulative cases grow from 85 to about 250. Thus, the magnification factor in this example is about $(250 - 85)/100 \approx 2$.

Scenarios Analyzed: We use our methodology to analyze two scenarios, both focused on the fall semester:

- Fall Semester, Residential Semester: 20,000 students return to Cornell's Ithaca campus in the fall semester. In this scenario, 1/5 of the campus population (faculty/staff/students) is tested each day in regular asymptomatic screening, and a test-on-return policy additionally tests students once before they leave home and once again when they arrive in Ithaca. Infections arrive on campus at the start of the semester due to cases missed during test-on-return and also arrive through the semester due to infection from the outside community. We assume that half[1] of students arrive early and are also tested through the test-on-return protocol and subject to asymptomatic screening before move-in weekend.

- Fall Semester, Virtual Instruction: We also consider what happens if we bring no students back for a residential fall semester. In this scenario, we suppose that a substantial fraction of students, ranging across 35%, 45%, and 55%, are present in Ithaca where they have already signed leases and receive virtual instruction while living in the area. The remaining 65%, 55%, and 45% of students are assumed to not return to Ithaca. We also suppose that faculty, staff, and a subset of graduate and professional students continue to live in Ithaca and work on campus. We assume that test-on-return is not conducted and that asymptomatic surveillance is conducted only for faculty and staff.

We study these scenarios under a nominal set of parameters. We also consider two other sets of parameters, one more optimistic than the nominal parameters and one more pessimistic. The optimistic and pessimistic sets of parameter values were constructed by taking several parameters *simultaneously* to either the optimistic or pessimistic end of plausible ranges. Thus, they represent extreme cases. We describe these parameters in detail in Section 2.

Here, "pessimistic" was chosen to be pessimistic in terms of the number infected rather than the number hospitalized. While most parameters influence both outcomes in the same way, changing

[1]Results are not sensitive to this fraction. This is because most isolations resulting from positives found in test-on-return happen at a student's home. It is also because the prevalence of the population in Ithaca before move-in is similar to the post-test prevalence of the free returning students (both near 0.1%, as we explain later), allowing us to model the two as the same, as we explain below. This means that reducing the population of one and increasing the other has no impact on infectious cases.

the fraction of cases that have asymptomatic disease can decrease hospitalizations (because those that become infected are less likely to get sick and need hospitalization) while increasing overall infections (because infectious individuals spend longer in the general population infecting others). Thus, the pessimistic settings can produce *fewer* hospitalizations than the nominal ones when we do not perform asymptomatic testing, and only slightly more when we do.

While we study a fixed asymptomatic screening frequency, with transmission rates and number of contacts per day corresponding to fixed social-distancing measures, we underscore the need to be nimble and react to facts on the ground. We envision that one would monitor prevalence based on results from asymptomatic screening and adjust the screening frequency and social distancing measures to control the virus while also reducing costs and supporting an enjoyable campus life.

Performance Measures: We examine three performance measures.

1. The number of members of the Cornell community that undergo serious negative health effects from COVID-19 requiring hospitalization by the end of the simulated period of 16 weeks (112 days).

2. The number of infections, both because it is an important measure of health impact and because it is indicative of the required isolation / quarantine capacity.

3. The number of individuals that would need to be isolated or quarantined, including those that are not infected but would need to be quarantined because they are a close contact of someone who was.

Recall that our simulation consists of two models: an Excel model of move-in weekend and a stochastic compartmental simulation, implemented in Python, that models the rest of the semester. Although it is most natural to combine estimates across the two models, due to time constraints we sometimes report the numbers separately.

For the stochastic compartmental simulation we also report 10% and 90% quantiles, reflecting the range of potential futures our simulation model produces under the nominal choice of parameters. We use Monte Carlo simulation, using 100 replications for both the no-reopen plots reported in this section and the sensitivity analysis plots reported in Section 4. The use of Monte Carlo simulation creates some errors when estimating these outcome measures, which could be reduced by running more simulation replications. The bulk of the uncertainty arises from uncertainty about parameters and the structure of the simulation model itself rather than from Monte Carlo error.

Summary of Results: We first run our simulation under the nominal, optimistic and pessimistic sets of parameters for the two scenarios described above: a residential fall semester; and virtual instruction only.

Since our model produces random potential futures, the outcome variable is also random. Figures 3 and 4 show histograms of outcomes (infection counts and hospitalization counts, respectively) under our two scenarios, residential ("reopen") and virtual instruction ("no reopen") across multiple replications with and without testing under the three different sets of model parameters. The plot does not include an additional 202 infectious students identified and isolated during the test-on-return protocol for the residential fall campus scenario, 180 of which would be identified at home and 22 in Ithaca. For simplicity, the virtual-instruction scenario is assumed to have the same initial

prevalence numbers as the residential-instruction scenario, despite the lack of any on-return testing for this subpopulation. Absent this assumption there would only be higher initial prevalence numbers, and the resulting gap between the reopen and no-reopen scenarios would be even wider. In addition, all three simulations (fall-reopen, no-reopen-students, no-reopen-faculty/staff) use the same rate of outside infections. A more detailed description of the parameters and assumptions for this analysis is provided in Section 5.1.

Importantly, not reopening actually results in *more* infections and hospitalizations than reopening. This arises because the students returning to campus in the reopen scenario undergo test-on-return and asymptomatic surveillance, which controls epidemic spread within this population. In contrast, in the no-reopen scenario, returning students are not subject to the University's asymptomatic surveillance testing protocols, allowing infections to grow rapidly in this group.

The virtual instruction "no-reopen" simulations are not fully developed. For example, the model assumes that faculty/staff do not interact with students, but in reality there would be cross-interaction and thus infection could spread between the groups.

For sensitivity analysis, for each of several parameters we run other simulations varying that single parameter while holding the other parameters fixed at their nominal values. An example plot (Figure 5) shows how our outcome variable (percentage of the population requiring hospitalization due to COVID-19) varies with one of the parameters in our model. The plot shows the estimated median, 10% quantile and 90% quantile of the percentage of individuals requiring hospitalization vs. the probability that a symptomatic individual reports their symptoms on a given day. When an individual is more likely to self-report symptoms, infectious cases are identified, isolated, and contact traced sooner, resulting in better control of the disease.

Plots are shown for the nominal, optimistic and pessimistic scenarios. A full complement of these plots are given in Section 4.

In examining these plots, we emphasize the sensitivity of the outcomes to parameters. Moreover, in Figure 5 and the other figures in Section 4, only *one* parameter is varied at a time.

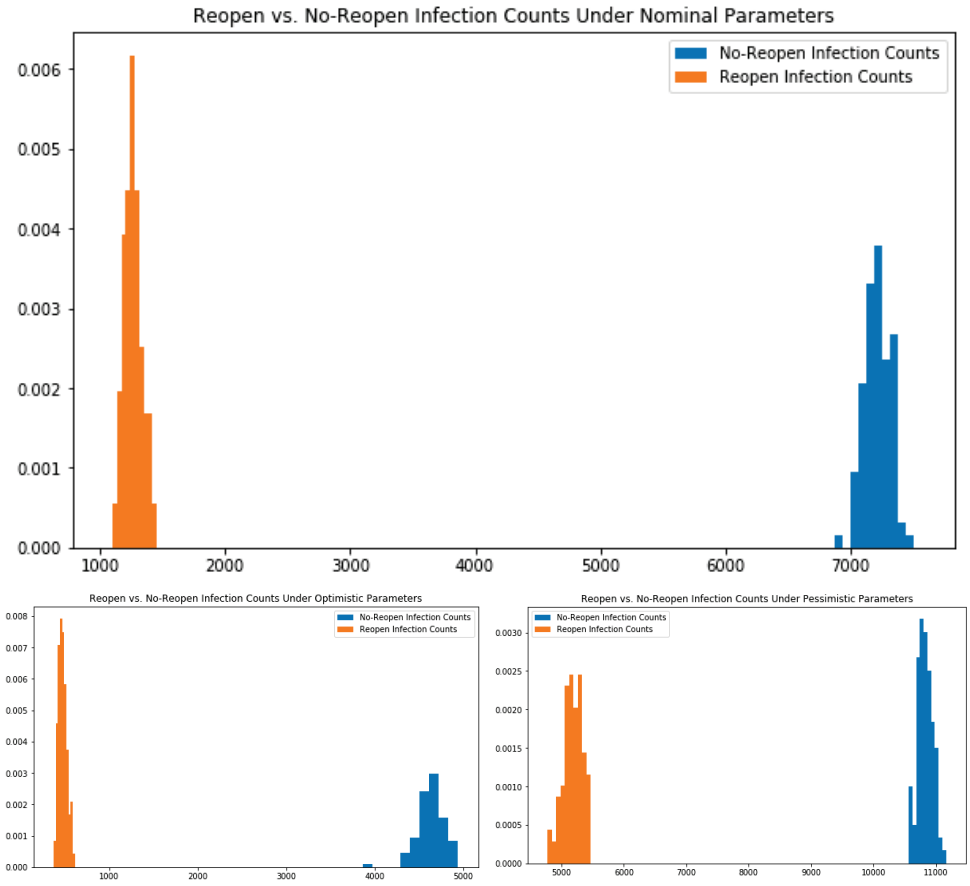

Figure 3: Histograms showing the number of *infections* in the fall semester, comparing the "reopen" (i.e., fall residential campus) vs. "no reopen" (i.e., virtual instruction only) under nominal, optimistic, and pessimistic parameters. Plots do not include an additional 202 infected students identified and isolated through test-on-return in the reopen scenario. For simplicity, the no-reopen scenario uses the same post-test initial conditions as the reopen scenario, despite the fact that this round of testing would not occur in practice. Despite the erroneously low initial infection numbers at the start of the no-reopen scenario, more infections occur in the no-reopen analysis. This is largely because of a lack of asymptomatic testing for students who are living in Ithaca but not subject to university interventions.

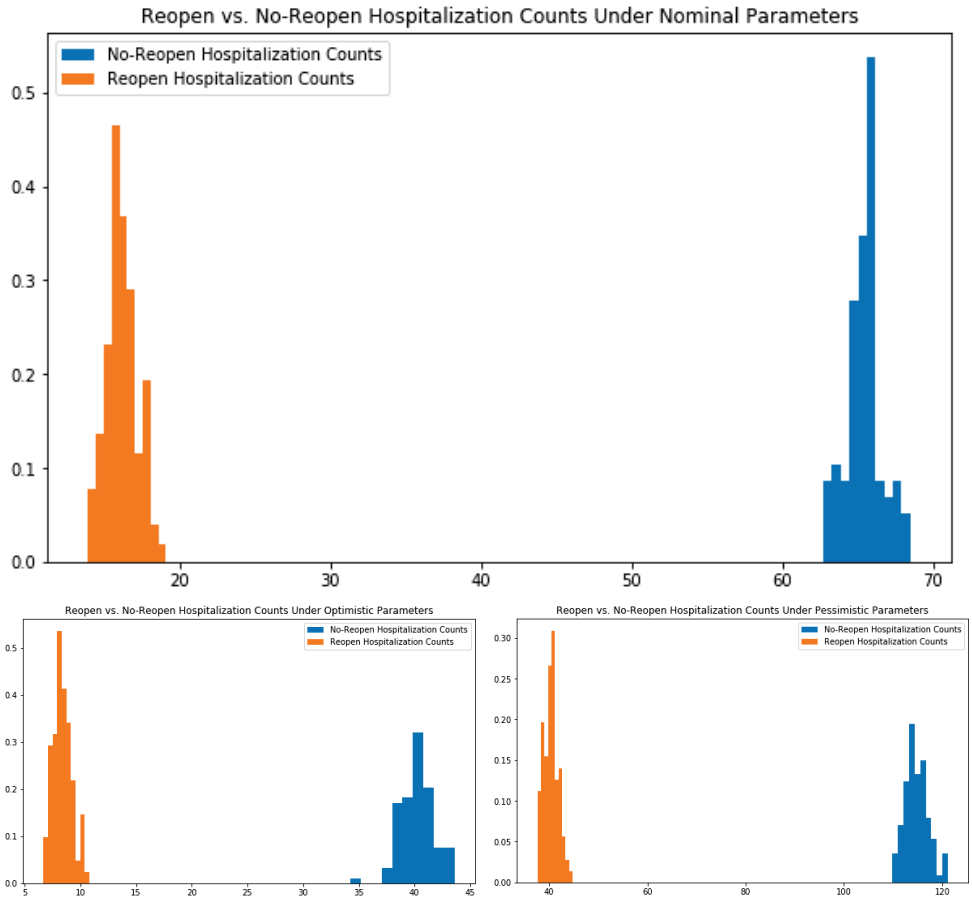

Figure 4: Histograms showing the number of *hospitalizations* in the fall semester under nominal, optimistic, and pessimistic variants of the Reopen vs. No-Reopen alternatives. More hospitalizations occur in the no-reopen scenario, largely because of a lack of asymptomatic testing for students who are living in Ithaca but not subject to university interventions. Outside infections also continue to result in hospitalization of faculty and staff on campus.

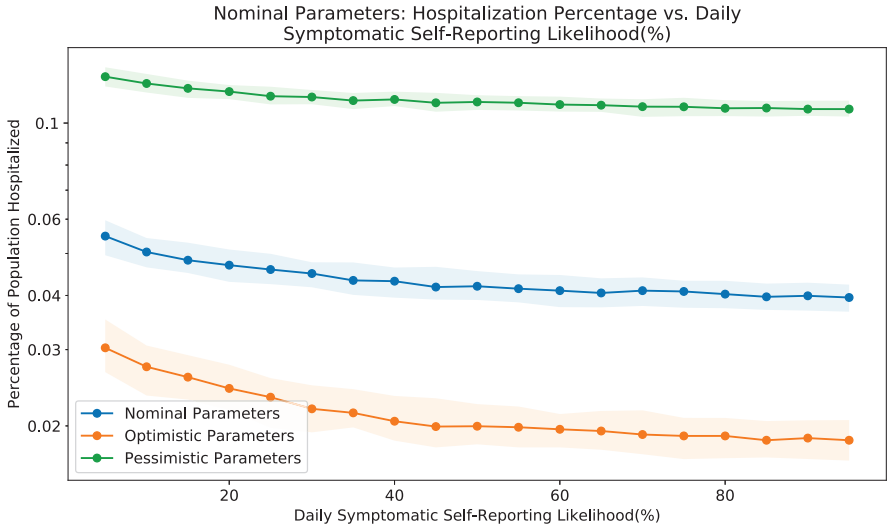

Figure 5: Plot depicts the distribution of hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the daily likelihood that a symptomatic individual self-reports their infection status. The nominal value of this parameter is 18% based on the mean time to report (5).

Current Limitations of the Simulation Model: While we believe that our model captures most aspects of the real world that play a first-order role in the growth or control of a COVID-19 epidemic, there are several aspects we do not model that may materially alter the results.

1. We use an approximation when choosing the prevalence immediately after move-in at the start of the stochastic python-based simulation. At that time, two groups of people are combined: returning students who were not isolated or quarantined by test-on-return; and unquarantined/unisolated faculty/staff/students already on campus. While it would be best to use the results of a summer simulation to estimate the fraction of people on campus that are free and infectious, we instead assume it is the same as the fraction among the post-test returning students. This is discussed in more detail in Section 3.3.

2. Interactions are assumed to be homogeneous across the entire Cornell population and no local community structure such as friendship networks or different interactions for faculty or staff compared to students is assumed or leveraged. Accounting for this may influence outcomes since we anticipate higher contact rates among students vs. staff/faculty may lead to higher infection rates in students and lower rates in staff/faculty. This may reduce the number of severe infections, since high-risk individuals are more concentrated among faculty and staff.

3. In our model, infectiousness does not vary once the infectious period begins, i.e., once the initial exposure period ends.

4. Infectiousness does not vary across individuals: mild cases are assumed to be just as infectious as severe cases. Similarly, after a person becomes infectious, their infectiousness does not vary over time. In reality, asymptomatic cases are less infectious than infectious ones, which may reduce the impact of undetected asymptomatic individuals infecting others.

5. We do not model travel outside of the area.

6. The model of contact tracing is imperfect: within the context of a population-level simulation model, it is difficult to model contact tracing in a way that is robust across a wide range of parameter settings. For example, we model contact tracing by supposing that quarantined contacts are all in the pre-infectious exposed state (if enough such individuals exist). This is likely accurate for small contact tracing delays (and we believe that in reality these are small), but becomes inaccurate for large contact-tracing delays. More work is needed (see Section 6) to understand and improve the accuracy of our model of contact tracing.

7. We model the impact of age and its effect on the distribution of infection severity in an imperfect way. For example, we model the age group 18-45 as a single unit, and assume that the probability of hospitalization for an individual in this group is 0.8%. However, this number is likely driven by individuals aged 35-45, whereas the majority of individuals in this age group in the Cornell community are students aged 18-25 years, who likely have much lower rates of hospitalization.

Several of the limitations are addressable given more time, as discussed in Section 6.

In addition, the simulation model is only as accurate as the parameter estimates it uses. While it is possible to estimate some parameters reasonably accurately, significant uncertainty remains about others. Sensitivity analysis plots in Section 4 give some information about the influence of key parameters on outcome metrics. Within Section 6, we call out ongoing workstreams aimed

at better estimating important parameters. We also hearken back to the need to be adaptive: by modifying our strategy (especially, asymptomatic surveillance) based on up-to-date information, we can hope to create a strategy that is robust to parameter uncertainty.

History and Future of this Document: This document is a living document. Multiple versions have been shared and we plan to continue updating it as modeling work continues. Section 7 contains a detailed history of this document and Section 6 a description of work underway. In that work underway, we specifically call out two efforts. First, detailed reviews of the May 31 version of this document were obtained from several individuals, both at Cornell and outside the institution. These reviews identified several opportunities for improvement, which we are working to address. Second, the Cornell library has begun providing a more detailed literature review to support parameter estimation. We are working through those references now.

2 Parameters

This section describes the parameters used within our simulation model. For each parameter we have chosen a nominal (baseline) value, and up to two other values that represent optimistic and pessimistic settings, based on the literature or data where possible.

We begin by discussing parameters that describe the progress of the disease in an individual in Section 2.1, then epidemiological parameters that describe the disease and its spread at a population level along with our interventions in Section 2.2. Section 2.3 discusses contact tracing and Section 2.4 discusses how symptom severity is modeled. Section 2.5 supplies a calculation of the R_0 value implied by a particular parameter setting, to support comparisons to the literature. Section 2.6 describes how we model infections from the Ithaca community while Section 2.7 discusses the testing protocol that students will go through before returning to campus. Finally we summarize nominal values and state optimistic and pessimistic parameter settings for each scenario in Section 2.8.

2.1 Individual Disease Progression

Our simulation assumes that the disease progresses through several stages in each infected individual, represented in Figure 6.

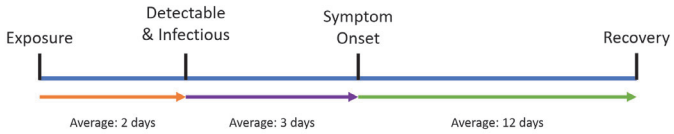

Figure 6: Timeline of disease progression in an infected individual.

In the period after exposure, the individual is infected but not yet detectable by a PCR test. They also cannot infect another person during this period. After the exposure period, the individual becomes infectious and detectable by a PCR test but is not yet symptomatic. Then, the individual enters a symptomatic period during which the severity of their symptoms falls into one of two groups: either an extremely mild set of symptoms that the patient would not notice (we refer to this briefly as being "asymptomatic"); or a more noticeable and perhaps even severe set of

symptoms (we refer to this as being "symptomatic"). Individuals who are symptomatic self-report their illness to a healthcare provider with a given probability each day while individuals who are asymptomatic do not self-report.

Parameters for the length of these windows are given in Table 1.

Table 1: Parameters for disease progression in an individual.

Parameter Description	**Nominal Parameter Value(s)**	**Sources**
Time from exposure to detectable & infectious	Poisson(2)	(23); (35); (2); (39)
Time from detectable & infectious to symptom onset	Poisson(3)	
Time in symptomatic state	Poisson(12)	(40)
P(self-report each day | asymptomatic)	0	Conservative assumption
P(self-report each day | symptomatic)	0.18	CDC planning scenario

Choice of time in the "exposed" and "detectable and infectious" states: (23) does a pooled analysis and finds the median incubation period to be 5.1 days, with a confidence interval of 4.5 to 5.8 days. (39) and (35) find that transmissions can occur 2-3 days before symptom onset. Thus we set the time in the detectable and infectious state to be Poisson(3), and subtract it from the incubation period to get a mean of 2 days for the exposed state.

The probability of self-reporting each day for symptomatic patients was chosen to match the average time from symptom onset to hospitalization for influenza-like illness (ILI) according to the CDC (5), which is based on (3). The latter paper reports that

- 35% of symptomatic individuals seek care in ≤ 2 days,
- 47% of symptomatic individuals seek care in $3-7$ days,
- 18% of symptomatic individuals seek care in ≥ 8 days.

We model this as a random number of days that is conditionally uniform(0,2) with probability 35%, conditionally uniform(3,7) with probability 47%, and conditionally uniform(8,12) with probability 18%. The resulting mean of this distribution is $.35 \times 1 + .47 \times 5 + .18 \times 10 = 4.5$ days. The daily probability of self-reporting for symptomatic individuals is then chosen to be $1/4.5 \approx 0.22$ so that the mean time to self-report, $1/0.22 = 4.545$, approximately matches this value.

Unfortunately, a rounding error in the CDC translation of (3) led us to use the distribution $(35\%, 50\%, 25\%)$ instead of $(35\%, 47\%, 18\%)$ in our calculations so far. This set of probabilities is incorrect as the entries sum to 110%. This caused us to compute a larger time-to-report of $0.35 \times 1 + 0.5 \times 5 + 0.25 \times 10 = 5.35$ days and a daily self-report probability of $1/5.35 \approx 0.18$. Work is underway to correct this error. From sensitivity tests, we observe that results are somewhat insensitive to the self-report probability (e.g., see Figure 5). So for the sake of consistency, we continue to use 0.18 in this version of the report, and will adjust it to 0.22 in future versions.

Other limitations of our approach include:

- The population of individuals considered in (3) differ in age, socioeconomic status, and access to healthcare from Cornell's population.

- Societal opinions and marketing campaigns encouraging the seeking of care may influence individuals to self-report symptoms more quickly than in (3). Conversely, fear of isolation may cause individuals to self-report less frequently.
- Different definitions of "symptomatic" between (3) and those used to estimate severity probabilities.
- Although the distribution from which we compute the mean is consistent with the cdf reported in (3), other distributions with different means are also consistent. While the mean could be substantially different if the upper bound of the final uniform were significantly bigger than 12, regular asymptomatic screening at a frequency near 12 days or smaller would reduce the impact of this assumption.

There may be an opportunity to improve our estimates: (3) reports values broken out by age and occupation (including student).

Another limitation of our model is that we assume that the time to report symptoms is geometrically distributed (i.e., constant probability of self-report per day, given that an individual has not yet self-reported). However, the data in (3) are not consistent with this distributional assumption.

2.2 Epidemiology and Intervention Measures

Next we examine the parameters for epidemiology (how the disease spreads through people's daily interactions) and intervention measures other than contact tracing (asymptomatic testing and isolation/quarantine). The parameter values are presented in Table 2.

Table 2: Parameters for epidemiology and intervention measures.

Parameter Description	**Nominal Parameter Value(s)**	**Sources**
Initial prevalence	0.25%	
Contacts per day (for each non-quarantined / isolated person)	8.3	See text
P(infection transmission | susceptible -infectious contact)	2.6%	(28)
Testing false negative rate	0.1	(20); (36); see Section 5.3 for explanation
Testing false positive rate	0.001	
P(an isolated individual recovers each day)	0.05	
P(a quarantined individual is released each day)	0.3	

We choose the number of contacts per day to cause our implied R_0 (calculated in Section 2.5) to match the nominal value of 2.5 recommended by the CDC (5).

2.3 Contact Tracing

In our simulation, each positive case identified through symptomatic self reporting or asymptomatic screening initiates a contact trace. We assume that each such contact trace results in a deterministic number of contacts identified by the health department. We take this number to be 7 based on data from the Tompkins County Health Department (29). All such contacts are modeled as either quarantined or isolated.

We also assume that, among these cases quarantined or isolated, the number that are infectious is deterministic given the reason for contact trace initiation: symptomatic self-reporting; or asymptomatic screening. Traces resulting from symptomatic self-reporting are modeled as having a higher number of infectious cases among those contacts identified by the health department because these cases will tend to have been infecting others for a longer period of time.

We assume that contact traces are not initiated for cases isolated as a result of other contact traces. The Tompkins County Health Department does not currently test contacts and so would not know that a contact was positive. Moreover, while a quarantined case could become symptomatic and initiate a contact trace, the fact that this individual had been in quarantine or isolation would dramatically reduce the number of contacts they would have had. The assumption that contact tracing is not done on positives that result from another contact trace nevertheless present a limitation because in the fall additional testing might be performed on contacts.

Here we describe the computation of the two undiscussed contact tracing parameters: the number of infectious cases identified per symptomatic self-report and the number identified per positive identified with asymptomatic screening.

For each positive case newly identified because of self-reporting, we assume that the individual had n contacts while they were infectious but before they were isolated, where the number of contacts $n = ct$, where c is the average number of contacts per day and t is the average time a person was infectious before self reporting. (Here, we use the term "contact" in the sense of potentially leading to an infection, rather than the more restrictive sense required by the Tompkins County Health Department for quarantine.)

Given that the individual self-reported, they must be symptomatic (since the asymptomatic self-reporting rate is assumed to be 0), and so t is the sum of the means of the time in the infection & detectable state ("ID", below) and the time in the symptomatic state. (Under our nominal parameters, this is $t = 3 + 1/.18 = 8.56$ days.)

As described above, each contact is assumed to be infected with probability p, the transmission probability from an interaction. We assume that the process of recalling contacts, and in particular the infected contacts, is imperfect: each infected contact is recalled with a probability r (the infected contact recollection probability). In total, then the expected number of contact-traced infected contacts is $N = ctpr$. Under our nominal parameters, $ctp = 8.3 \times 8.56 \times 0.026 = 1.85$. Then, at $r = 0.5$, $ctpr = 0.92$.

We then multiply this number of contact-traced infected contacts per self-reported case by the number of self-reporting cases, and round down to the nearest integer. We model the actual number of contact-traced infected contacts overall as deterministic and equal to this value. All of these identified and positive cases go into isolation (QI). They are pulled from the E, D, and ID states, in that order of precedence.

The remaining $7 - N$ cases quarantined per self-report are pulled from the susceptible (S) state and enter quarantine (QS).

Note that $ctr = 8.3 \times 8.56 \times 0.5 = 35.5$ contacts is much larger than 7 under our nominal parameters: This is because 7 models only those contacts that meet the more stringent guidelines

required for quarantine while *ct* is the larger number of contacts that could potentially result in transmission. This is also because the 7 contacts quarantined are *unique* contacts, while many of the 35.5 contacts would include multiple contacts with the same person.

Positive cases identified through asymptomatic surveillance follow a similar contact tracing process, but with a smaller number of infectious contacts identified because individuals identified through screening should tend to be identified earlier in the course of their disease at which point they would have infected fewer people. A parameter less than 1 determines the ratio of infectious contacts identified through a positive identified by asymptomatic screening to those identified by a symptomatic case.

Our model of contact tracing has a number of limitations. Perhaps the most important is that it may not accurately capture the expected number of *new* infectious contacts identified through each contact trace. In particular, an infectious contact recalled may have already been identified (through symptomatic self-reporting, asymptomatic screening, or another contact trace) by the time the trace is completed.

Table 3: Parameters for contact tracing.

Parameter Description	**Nominal Parameter Value(s)**	**Sources**
Fraction of contacts identified and traced	0.5	
# Quarantined / isolated per contact trace	7	(29)
Contact tracing delay	1 day	(29)
(Isolations per screening positive) / (isolations per self-report)	0.5	
(Implied) New isolations per self-report contact trace	0.92	Calculation in text

2.4 Severity of Symptoms

Our simulation model separates symptomatic from asymptomatic individuals. Over the course of the simulation, symptomatic individuals self-report each day with some probability, while asymptomatic individuals do not self-report. Symptomatic infections can be of different levels of severity, ranging from mild pneumonia symptoms to critical life-threatening conditions. More granularity in the symptomatic group gives a better understanding of the simulation outcomes. Thus we further divide the symptomatic individuals into three different severity levels. In total, we consider four different severity levels, defined as follows:

- Severity level 1: patient is asymptomatic.
- Severity level 2: patient shows mild symptoms, but does not require hospitalization.
- Severity level 3: patient needs to be hospitalized, but does not require intensive care.
- Severity level 4: patient requires intensive care.

At the end of each simulated period, we allocate the symptomatic individuals to severity levels 2-4 with certain proportions. These proportions are estimated from data as explained below. Once an individual is assigned to a severity level they remain there; further transitions between severity levels are not modeled.

Let $P(\text{sev } i)$ be the probability that, as a result of a single contact with an infected person, an individual becomes infected and falls within severity level i. Thus the sum of these probabilities over $i = 1, 2, 3, 4$ is the probability of infection as a result of a single contact. Then, the probabilities that as a result of a single contact an individual becomes infected and asymptomatic, respectively infected and symptomatic, are

$$P(\text{asymptomatic}) = P(\text{sev } 1), \text{ and}$$
$$P(\text{symptomatic}) = P(\text{sev } 2) + P(\text{sev } 3) + P(\text{sev } 4).$$

We want to find $P(\text{sev } i)$ for the population while considering age-based factors. Specifically, we model how the severity of the disease varies with age, and that older age groups are more likely to become infected after an interaction with an infectious person. To that end,

$$P(\text{sev } i) = \sum_{\text{age}} P(\text{sev } i|\text{infected, age})P(\text{infected}|\text{age})P(\text{age}), \text{ where}$$
$$P(\text{infected}|\text{age}) = P(\text{infected}|\text{contact, age})P(\text{contact}|\text{age}) \propto P(\text{infected}|\text{contact, age}).$$

The proportionality in the second equation comes from the assumption of a homogeneous well-mixed population. Therefore, the distribution of the age of contacts is the distribution of the age of the population.

Severity Calculation Part 1: Severity and Infection given Age We obtain values for the probability of infection as a function of age from (28), which reports the probability of infection through a close contact for different age groups among 4941 close contacts traced from early cases in Guangzhou, China. These estimates are given in the first row of Table 4.

Later, we will estimate the age distribution ($P(\text{age})$) for Cornell's fall reopen.

Table 4: Parameters for age-stratified infection probability and severity level distribution. Sources: (28; 7; 13; 4; 25).

	Age grp 1 (0-17)	Age grp 2 (18-44)	Age grp 3 (45-64)	Age grp 4 (65-74)	Age grp 5 (75+)
P(infection | age)	1.8%	2.2%	2.9%	4.2%	4.2%
P(sev 1 | infected,age)	17.0%	52.0%	31.0%	13.0%	13.0%
P(sev 2 | infected,age)	81.6%	47.2%	65.9%	80.6%	80.6%
P(sev 3 | infected,age)	1.1%	0.6%	2.2%	4.7%	4.7%
P(sev 4 | infected,age)	0.3%	0.2%	0.9%	1.7%	1.7%

The severity level distribution for each age stratum is estimated from a combination of data sources. These data sources are fragmented and partially contradictory. Accordingly, our fitting procedure is far from ideal, but the best we have been able to do given this data.

We first estimate $P(\text{sev } 1|\text{infected, age})$, the asymptomatic rate for each age group, as follows.

1. Fix the asymptomatic rate for the 75+ age group, $P(\text{sev } 1|\text{infected, age grp } 5)$ to 13%. The 13% figure comes from (19), where a nursing home in Seattle had 3 asymptomatic cases out of 23 confirmed cases. Note the extremely small sample size.

2. To estimate the asymptomatic rate of the remaining four age groups, we attempt to match the following data points by minimizing the sum of squared errors. In doing so, we assume that the asymptomatic rates decrease over Age Groups 2 through 5.

   (a) The CDC estimates that the population asymptomatic rate in the USA is 35% (Source: (5)). Weighting our age-stratified asymptomatic rates by the age distribution for the US population we should obtain something close to 35%. (Sources for age demographics: (6) and (18).) We are weighting by the age distribution for the entire US population, but it would have been more accurate to weight by the *infected* US population.

   (b) The Diamond Princess cruise ship had an estimated 17.9% asymptomatic rate (Source: (30)). Exactly as we did for the CDC US-population rate, we use age strata for the infected passengers on the Diamond Princess to attempt to match the 17.9% rate.

   (c) A study of 78 infected patients from Wuhan had the following age profile for the 33 asymptomatic patients: 25^{th} percentile: 26 yrs, 50^{th} percentile: 37 yrs, 75^{th} percentile: 45 yrs (Source: (41)). We attempted to match these percentiles. We use the age demographics of China for this purpose. (Source: (32).)

To this point then, we have estimated the asymptomatic rate for each of the 5 age groups, P(sev 1|infected, age). We next divide the remaining probability within each age group into severity levels 2, 3 and 4 using CDC numbers for hospitalization rates and ICU rates in the nominal planning scenario (5). By our definition, hospitalization includes both severity levels 3 and 4, and ICU corresponds to severity level 4. The three equations we need for the three unknowns (probability of each of severity levels 2, 3 and 4) are

1. P(symptomatic|infected,age) = P(sev $2, 3, 4$|infected,age) $= 1 - P$(sev 1|infected,age).

2. Given that a patient is symptomatic, the probability they will be hospitalized is

$$P(\text{sev } 3, 4|\text{infected,age})/P(\text{symptomatic}|\text{infected,age}).$$

3. Given that a patient is hospitalized, the probability that they will be admitted to the ICU is

$$P(\text{sev } 4|\text{infected,age})/P(\text{sev } 3, 4|\text{infected,age}).$$

CDC (5) estimates the symptomatic case hospitalization ratio to be 1.7% for age 0-49, 4.5% for age 50-64, and 7.5% for ages 65+. The percent admitted to ICU among those hospitalized is 21.9% for age 0-49, 29.2% for age 50-64, and 29.8% for ages 65+. We recognize that the age cutoffs are slightly different to ours. We match CDC's estimates for age 0-49 to our first two age groups, those for age 50-64 to our second age group, and those for 65+ to our fourth and fifth age groups. The probabilities of severity levels 2, 3, 4 are calculated accordingly to fit these estimates.

Severity Calculation Part 2: Age Distribution To complete our severity calculation, we first identify different groups on Cornell's campus and estimate their distribution over the five age groups. The parameter values are given in Table 5.

Table 5: Information for different population groups on Cornell's campus. The size of each group as well as the faculty age distribution are provided by (9); the age distribution for academic professionals, staff, and students are assumed.

	Group size	Age group 1 (0-17)	Age group 2 (18-44)	Age group 3 (45-64)	Age group 4 (65-74)	Age group 5 (75+)
Faculty	1684	0%	33.1%	46.1%	17.9%	2.9%
Academic professionals	1114	0%	90%	10%	0%	0%
Staff	7485	0%	50%	50%	0%	0%
Students	24027	0%	100%	0%	0%	0%

For the fall reopen, we assume everyone is on campus and compute a combined age distribution over all 34,310 people. Results are presented in Table 6.

Table 6: Parameters for age distribution on campus for Fall reopen.

	Age group 1 (0-17)	Age group 2 (18-44)	Age group 3 (45-64)	Age group 4 (65-74)	Age group 5 (75+)
P(age) for Fall reopen	0%	85.81%	13.17%	0.88%	0.14%

Finally, using the age distribution for the fall re-open, we can calculate the severity level distribution using the procedure described above. Results are presented in Table 7.

Table 7: Severity level distribution on campus for Fall reopen under the nominal scenario.

	Severity 1	Severity 2	Severity 3	Severity 4
Fall reopen	47.81%	50.91%	0.94%	0.34%

Sensitivity Analysis The optimistic and pessimistic parameter settings also vary the probability that an infected person is asymptomatic. The CDC gives a range of $20 - 50\%$ with an expected value of 35% (source: planning scenarios given by (5)). For the optimistic parameter, we multiply the nominal probability, $P(\text{sev } 1)$, by 20/35 and for the pessimistic parameter we multiply it by 50/35. We re-scale the other severity probabilities accordingly.

2.5 Implied R_0

To support intuition and comparison to other measurements of disease spread, it is useful to calculate the R_0 implied by a fall scenario with no testing or contact tracing measures. In this scenario, infected individuals are only isolated if they self-report. We estimate R_0 under optimistic, nominal, and pessimistic parameters. We selected our parameters so that our implied $R0$ range is similar to the range suggested in (5), though our pessimistic value is somewhat higher than that range: our value is 3.2 while the CDC uses 3. Our optimistic R_0 matches the CDC at 2.

First, we find the expected time that a case is both infectious and free. This is the sum of the duration of the infectious period before symptom onset (time in ID) and the expected time of being free after symptom onset (time in Sy). For asymptomatic individuals, the latter is the remaining

length of their disease duration because they do not self-report. For a symptomatic individual, who self-reports every day with a fixed probability, the expected number of days that he/she is free after symptom onset is given by inverse of his/her daily self-reporting probability. Then, over each day in the "infectious and free" duration, a free infectious individual comes into contact with a certain number of people and infects them with a fixed probability (2.6% in all three scenarios). Thus, the expression for R_0 is given by

$$\begin{aligned}&(\text{Days infectious pre-symptoms} + \text{Expected days free post-symptoms})\\ &\quad * \text{Contacts / day} * \text{Probability (infection transmissions} \mid \text{contact}),\end{aligned}$$

where

$$\begin{aligned}\text{Expected days free post-symptoms} = {}&\text{percent asymptomatic} * \text{duration of Sy}\\ &+ \text{percent symptomatic} * 1 \text{ / daily self-reporting probability.}\end{aligned}$$

For the three parameter settings, we calculate R_0 according to the procedure above:

- Optimistic: $R_0 = (2.5 + (27.3\% \cdot 10 + 72.7\% \cdot 1/18\%)) \cdot 8.3 \cdot 2.6\% = 2.$
- Nominal: $R_0 = (3 + (47.8\% \cdot 12 + 52.2\% \cdot 1/18\%)) \cdot 8.3 \cdot 2.6\% = 2.5.$
- Pessimistic: $R_0 = (3.5 + (68.3\% \cdot 14 + 31.7\% \cdot 1/18\%)) \cdot 8.3 \cdot 2.6\% = 3.2.$

Note: These numbers might be slight over-estimates because the above calculation assumes that all people an infected person comes into contact with are *distinct*. In reality, a person is likely to have common contacts on different days. Moreover, the contacts of different people might overlap given the small-world network structure of Cornell's campus, as studied by (37), which notes the tight clustering and low degrees of separation among students based on course co-enrollment information alone. Note R_0 is calculated under the assumption that all others are susceptible.

2.6 Outside Infections

To model the effect of interacting with the wider Tompkins county, we specify a parameter that governs the probability that anyone in the Cornell population is exposed to an infectious person from outside Cornell on any given day, which we call the *daily outside-infection probability*. We have developed two methods to estimate this parameter, which yielded estimates that differ by a factor of 3. Here we describe in detail only the first one that yields the larger estimate. We comment briefly on the other estimation method afterwards.

The daily outside-infection probability depends on an assumed prevalence within Tompkins County, the probability of infection as a result of a contact, and the amount of contact that an individual in the Cornell community has with others outside of Cornell.

To estimate these quantities, we break the Cornell population into seven groups based on their daily activity routines and estimate the amount of contact a member of each group has with those outside of Cornell, normalized so that someone with exactly 1 close contact per day would have a value of 1. This is shown in Table 8.

Someone who works at Cornell and lives with a spouse that works outside of Cornell would have a higher amount of contact with the outside due to the possibility of transmission through their spouse, even if that Cornell employee has no other non-Cornell contacts. For this reason, we model

those with school-aged children as having a substantial amount of contact with the outside world, although some (27) have argued that children are actually not a significant vector for COVID-19.

We aggregate the expected number of close contacts per day across all groups and multiply that by outside prevalence and the probability of infection transmission per close contact, which we set to be 2.6%, to get an expected number of daily outside infections in the entire Cornell community. Then we divide the expected daily outside infections by the total Cornell population to approximate the daily outside-infection probability as a single parameter. This figure is 0.055 * outside prevalence. Due to this linear dependence, we typically state results in relation to the assumed outside prevalence value, rather than to the daily outside-infection probability.

Below we explain our reasoning behind group-splitting and parameter estimation in detail.

Table 8: Group division for calculating daily outside-infection probability.

Group Name	Group size	Amount of contact with outside (Normalized so a group with 1 close contact / day / person has value 1)
Faculty/Staff who do not have a spouse or whose SO works at Cornell & no school-age children	4000	3
Faculty/Staff whose SO does not work at Cornell & no school-age children	3000	5
Faculty/Staff with school-age children	3283	10
Undergraduates living on campus	6920	1/7
Undergraduates living off campus	8123	3/7
Graduate/Professional students living in campus housing	988	1/7
Graduate/Professional students living elsewhere	7996	1

We first split the population into students (undergraduate, graduate, and professional students) and non-students (faculty, staff, and academic professionals), because these two groups have quite different daily routines, which result in different levels of interaction with the local community every day. We further subdivide these groups as follows based on factors that significantly influence their frequency of contact with outside:

For members of faculty/staff group, having school-age children is likely their major source of contact with outside, as children gather in classrooms on a daily basis and are relatively less cautious about personal hygiene. Having a spouse that does not work at Cornell also introduces a higher risk of infection from outside. Thus, we subdivide the faculty/staff group into three subgroups based on these factors, as seen in the top three rows of Table 8. The faculty/staff group has 10283 people, according to the University Factbook (9). The sizes of the subgroups and the numbers of daily effective close contacts are estimated based on faculty's experience.

For students, the two important factors for daily interaction with outside are 1) whether the student is an undergraduate or a graduate/professional student, and 2) whether the student lives in campus housing. Being an undergraduate and/or living on campus implies a smaller scope of daily activity mostly within the campus. With this reasoning, we split the student group into four subgroups. The Student and Campus Life (Student and Campus Life) website states that 46%

(6920) of undergraduates live on campus, and Cornell Graduate School website (8) states that 11% (988) of graduate/professional students live on campus. This informs our choice of the subgroup sizes. For students living on campus, we estimate their activity pattern to be such that they have one close contact per week with outside; we estimate this number to be three for undergraduates living off campus, and to be seven (one contact per day) for graduate/professional students living off campus.

We calculate the expected number of total daily close contacts by multiplying the two columns entry-wise and summing across all groups. We then multiply this by the assumed outside prevalence and the probability of transmission per contact (2.6%) and divide by the Cornell population (34,310) to obtain the probability of outside infection per person per day, which turns out to be 0.055 * assumed outside prevalence.

In Table 9 below, we list the critical outside prevalence values and the corresponding outside infection rate. In the simulation, for each day, the outside infection rate is the daily probability a person in state "susceptible" transitions to state "exposed".

Table 9: Outside prevalence and daily outside-infection probability

Outside prevalence	0.1%	0.2%	0.278%	1%	1.25%
Daily outside-infection probability	0.000055	0.00011	0.000153	0.00055	0.0006875

We choose prevalence $0.1\%, 0.2\%, 1\%$ for baseline comparisons. In addition to those, we add 0.278% and 1.25% for the following reasons.

- 0.278% is the result of Cornell vet school CVM testing where the researchers tested one positive out of a sample of 360 people in May 2020. We took this figure as a reliable source estimating outside infection rate where $0.278\% \approx 1/360$.
- 1.25% is approximately the largest prevalence at which we would fail to reject a one-sided test when observing no more than one success from a Binomial distribution with sample size 360. This is our "pessimistic" case.

There is significant uncertainty in these estimates. It is hard to locate data for each group's number of daily contacts with the Tompkins community, so these are estimated based on our experience as members of the Cornell community. In addition, using the test result 1/360 as an estimate of outside prevalence implicitly assumes that the context of the May vet school test would be similar to the Tompkins County condition in the fall semester. However, this is a somewhat bold assumption; moreover, we don't know how the circumstances will change between now and fall, which might further invalidate this estimate.

We conclude this section by briefly explaining the (unused) second method of estimating the daily outside-infection probability. We use the same separation into groups adopted above. However, we break down a person's daily contacts into outside-Cornell contacts and within-Cornell contacts. Faculty and staff with children have significantly more outside-Cornell contacts than do on-campus students. Likewise, Cornell students have significantly more within-Cornell contacts than outside-Cornell contacts. As a consequence of this group-dependent distribution of contacts inside and outside Cornell, each group has both a different chance of outside infection and a different number of follow-on within-Cornell infections should someone from that group become infected. The net effect of our analysis using this more complicated modeling of contacts is that the daily outside-

infection probability is reduced by a factor of approximately 3. For the sake of conservativeness, we do not use this reduced probability in the results presented herein.

2.7 Test-on-Return

The returning population during the move-in weekend is assumed to be 10,000 under the nominal scenario. We envision that a fraction of the undergraduate population may choose to come to Ithaca early, or choose not to come. We do not model students returning over the course of a few days but rather model them as an impulse arriving all at once to estimate the potential quarantine capacity needed in the extreme case. In the nominal scenario, we estimate the prevalence of COVID-19 in students' original locations to be 2%. We consider two tests for each undergraduate that decides to return: one local test performed prior to student departure and a test upon student arrival. The local test is assumed to be an individual test, performed 5 days prior to student departure. Students are isolated in their original location if they test positive. The false negative rate (FNR) of the test is set to 10%. The test upon student arrival uses a group testing protocol, with false negative rate (FNR) and false positive rate (FPR) set to 10% and 0.1%, respectively; see Section 5.3 for explanations. The parameters corresponding to different scenarios in the Test on Return methodology are listed in Table 10.

The model also allows for infection of students between pre-departure and on-arrival tests. The duration between pre-departure test and departure is assumed to be 5 days. Under the nominal scenario, the per-day infection probability prior to departure is assumed to be 0.01%, reflecting effective social-distancing measures. The per-day infection probability during travel is assumed to be 0.1%, reflecting the impossibility of fully effective social distancing during travel. Per-day infection probabilities in Optimistic and Pessimistic scenarios can be found in Table 10.

Table 10: Parameters for Test-on-Return modeling

Parameters	**Optimistic**	**Nominal**	**Pessimistic**
Number of undergraduates returning	8000	10000	12000
Prevalence level at student origin	0.50%	2.00%	4.00%
False negative rate for test before arrival (individual test)	10.00%		
False negative rate for test after arrival (group test)	10.00%		
False positive rate for test after arrival	0.10%		
Probability of getting infected during each day of travel	0.05%	0.10%	0.20%
Probability of getting infected during each day between local test and departure	0.005%	0.01%	0.02%

We divide students into groups based on their geographic origins, estimating the travel duration and likelihood that students use public transportation within each group, as shown in Table 11. We then aggregate these numbers to compute the weighted probability of infection between pre-departure test and departure, and infection during travel.

Table 11: Parameters for modeling infections between two PCR tests. Sources for geographic origin distribution: (10; 11; 12).

	NY + New England + Mid Atlantic	Midwest + South/Southeast	West + Southwest/Mountain	International
Fraction of the undergraduate population	59.56%	13.72%	15.36%	11.36%
Fraction of population using public transportation within the group	50.00%	90.00%	100.00%	100.00%
Fraction of population using public transportation	29.78%	12.35%	15.36%	11.36%
Duration of travel (days)	0.5	1	1	2
Duration between local test and departure (days)	5			

2.8 Parameter Values for Fall Reopen

In addition to the nominal parameters, we consider an optimistic and a pessimistic setting. Table 12 is a comprehensive summary of the parameters we use for all settings.

Table 12: Parameters for optimistic, nominal, and pessimistic settings.

Parameter Name	**Optimistic**	**Nominal**	**Pessimistic**
Time in E	Poisson(2)		
Time in D	0		
Time in ID	Poisson(2.5)	Poisson(3)	Poisson(3.5)
Time in Sy (with and w/o symptoms)	Poisson(10)	Poisson(12)	Poisson(14)
Contacts per day (for each free person)	8.3		
P(infection transmission | susceptible-infectious contact)	2.6%		
Total population	34310		
Student-origin prevalence	0.5%	2%	4%
Ithaca outside prevalence	0.1%	0.278%	1.25%
Prevalence at beginning of compartmental simulation	0.05%	0.09%	0.175%
Asymptomatic rate	27.3%	47.8%	68.3%
P(self-report each day | no symptoms)	0%		
P(self-report each day | symptoms)	18%		
New quarantines+isolations per contact trace	7		
(Implied) new isolations per self-report contact trace	0.92		
(Isolations per screening positive) / (isolations per self-report)	0.5		
Fraction of contacts identified and traced	0.5		
Contact tracing delay	1 day	1 day	2 days
Testing false positive rate	0.1%		
Testing false negative rate	10%		
P(an isolated individual recovers each day)	0.05		
P(a quarantined individual is released each day)	0.3		
Age-severity matrix	(Table 5)		
Implied R_0 w/o intervention	2	2.5	3.2
Simulated time length	16 weeks (112 days)		
Parameters for the Excel model	(Table 10)		

3 Detailed Simulation Model Specification

Our simulation framework has 2 major components:

1. Test-on-return (Excel) - the goal of this component is to estimate the effectiveness of our test-on-return protocol. We use its output to determine the initial prevalence for the compartmental simulation and to estimate the quarantine requirements at the beginning of the semester.

2. Compartmental Simulation (Python) - the goal of this component is to model the spread of the disease on campus, and the impact of different interventions such as contact tracing and asymptomatic testing. It tracks population-level counts of individuals across multiple relevant states. As in reality, the dynamics are stochastic. We use Monte Carlo simulation to generate many potential futures starting from a random initial state that reflects an initial prevalence.

Details of combining the initial prevalence Excel estimate with the Python-based simulation can be found in Section 3.3.

3.1 Test-on-Return (Excel)

We use a spreadsheet-based (Excel) model (available here[2]) to study the impact of two PCR tests for students returning to campus — one local test prior to student departure, and a test upon student arrival — on the initial prevalence. The local test is assumed to be an individual test performed 5 days prior to student departure. The individual test is assumed to have a false negative rate of 10% and students that test positive are isolated in their original location. Students that test negative (which consist of infected students not identified by the test and students susceptible to infection) are allowed to return to the campus. We calculate these numbers based on an assumed student-origin prevalence level.

The model then allows for infection of students between the pre-departure and on-arrival tests. There is a small per-day infection probability prior to departure reflecting effective social-distancing measures, and a larger per-day infection probability during travel. The travel duration and the likelihood that students use public transportation (with an associated elevated daily infection probability) depends on the geographic origin of students. We estimate the probability of student infection between the pre-departure and on-arrival tests based on their geographic origin. The fractions of such infections that end up being in exposed (E) state and in infectious and detectable (ID) state upon arrival in Ithaca are calculated accordingly based on a typical duration in the exposed (E) state. Detailed definitions of these infection states can be found in Secion 3.2.1.

Upon arrival, all returning students are tested using a group testing protocol (discussed in Section 5.3). The group test is assumed to have an FNR of 10% and an FPR of 0.1%. Students that test positive (which consist of true positives and false positives) are isolated immediately. The fraction of individuals missed by this protocol is used in two ways:

- It is set as the initial prevalence for our compartmental simulation (Section 3.2). This is an approximation as it assumes that the people already on campus have the same initial prevalence. Detailed discussions of the approximation can be found in Section 3.3.

[2] `https://docs.google.com/spreadsheets/d/1E4hoMIvmHcq819KeVOTf7PyAt826UbBG4G2dnLTv42w/edit?usp=sharing`

- It is set as the initial prevalence for an 18-day simulation run that aims to estimate the peak usage of quarantine capacity in the first 18 days of the fall semester following move-in. The 18-day simulation model has the same structure as the compartmental simulation model but only runs for 18 days. Moreover, it does not allow removal of people from the quarantine states because we want to estimate the peak quarantine usage. The total quarantine or isolation is the sum of the following two figures: (a) those who test positive upon arrival and are isolated immediately (as obtained by the Excel model), and (b) those quarantined/isolated over the subsequent 18-day period through contact tracing, self-reporting or asymptomatic surveillance (as obtained by the 18-day simulation model).

3.2 Compartmental Simulation (Python)

This section summarizes the dynamics of the Compartmental Simulation model that is implemented in python.

3.2.1 Population-Level Dynamics

The states across which individuals are tracked, and a short description of the dynamics governing relevant state transitions, are as follows. These dynamics are depicted in Figure 7.

Susceptible (S) A *susceptible* person does not carry the virus, is not infectious, and tests negative by PCR. A susceptible (S) person becomes exposed (E) with some probability once he/she comes in contact with someone infectious. We describe the assumptions regarding contacts and transmission in more detail below.

Exposed (E) An *exposed* person is infected after previous contact with someone infectious. The person is not yet infectious, detectable, or symptomatic. The person spends a random number of days in the exposed state, and then becomes detectable (D).

Detectable (D) A *detectable* person carries the virus, is potentially detectable by PCR, but is not yet infectious. For our simulation, we assume that 0 time is spent in this state; people go directly from exposed (E) to infectious and detectable (ID).

Infectious and detectable (ID) An *infectious and detectable* person is infectious, i.e. he/she can generate more exposed cases from the currently susceptible population. The person is not symptomatic and does not self-report their illness. The person spends a random number of days in the infectious and detectable state, and then becomes either Symptomatic or Asymptomatic (i.e., they will never have symptoms).

Symptomatic / Asymptomatic The asymptomatic/symptomatic states are the next stage in the disease for those leaving the infectious and detectable state. Asymptomatic people do not report their symptoms. Symptomatic people who have not yet self-reported or been identified in some other way (contact tracing, screening) self-report to the healthcare system with some probability each day. Self-reported individuals enter the quarantine-infected (QI) state. An asymptomatic or a symptomatic person who does not self-report eventually recovers (R).

Recovered (R) The person's disease is no longer infectious. We assume all patients recover and there are no deaths. Indeed, the mortality rate is low and we strive to keep prevalence low, deaths would be exceedingly rare. Recovered patients cannot become susceptible again.

Quarantine-Susceptible (QS) The person is put in quarantine by a test decision, or by the outcome of a contact trace, but does not carry the virus. At the conclusion of quarantine a person returns to the susceptible state

Quarantine-Infected (QI) Someone with the virus is put in isolation or quarantine by a test decision, a contact trace, or by self-reporting. At the conclusion of isolation the person enters the recovered state.

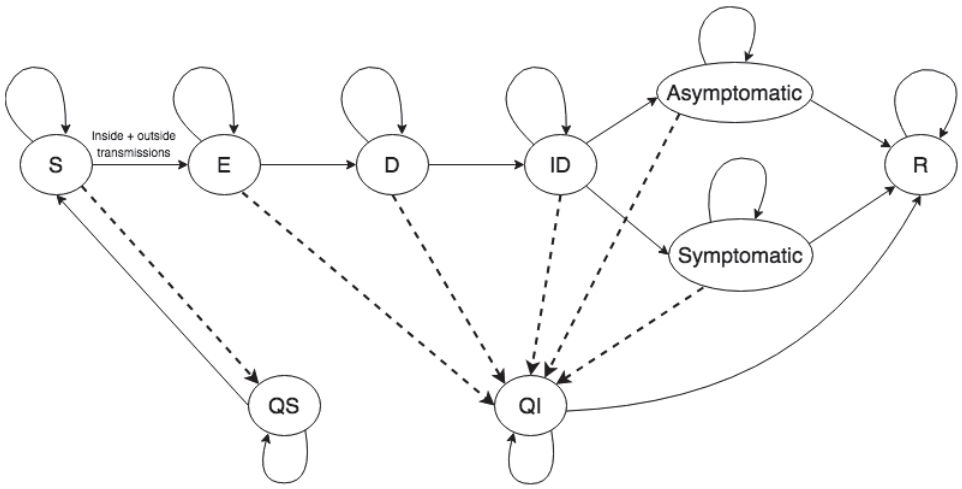

Figure 7: The dynamics between disease and quarantine states over a single time period for the compartmental simulation. "S" = susceptible, "E" = exposed, "D" = detectable, "ID" = infectious and detectable, "R" = recovered, "QS" = quarantined susceptible, and "QI" = quarantined infected. Solid lines represent the epidemiological progressions, outside infections, and people being released at the end of their quarantine; dashed lines represent the effects of intervention measures, including testing, self-reporting, and contact-tracing, which put some of the population into isolation/quarantine. Both on-campus transmissions and outside infections generate new cases that move from the susceptible to exposed state.

3.2.2 Daily Infection Dynamics

In our model, susceptible individuals can become exposed to the virus and transition to the exposed state, depending on daily contacts and an infection-transmission probability. A "contact" is an interaction between two people that has the potential for transmission of the infection. The dynamics are governed by the following values.

1. The expected number of contacts per person per day (c). This is an input parameter.
2. The number of free and infectious individuals, i.e., individuals who have the virus, are infectious, and who are not yet in isolation. The number of free and infectious individuals (F_I) is the sum of the numbers of individuals in the ID, asymptomatic and symptomatic states.

3. The number of free and susceptible individuals, i.e., individuals who are susceptible to the disease and not currently quarantined. The number of free and susceptible individuals (F_S) is simply the number of individuals in state S.

4. The number of free individuals, i.e. the size of the pool of individuals within which interactions can occur. This pool consists of free and susceptible, free and infectious, exposed, detectable and recovered individuals. Hence the number of free individuals (F) is the sum of F_I, F_S, E, D and R.

5. The transmission probability p that gives the probability of transmission during an interaction between an infectious person and a susceptible person.

6. The daily outside-infection probability r.

Every infected individual interacts with a random number of other free individuals each day, modeled as a Poisson(c) random variable. Each of these free individuals is assumed to be susceptible with a probability that is proportional to the number of free susceptibles within the free population, i.e., a contact is a susceptible with probability F_S/F. Thus, the total number of interactions between an infectious person and a susceptible each day is modeled as a Poisson random variable with mean cF_IF_S/F. This simplified model of interactions assumes no overlap between the interactions originating from each infectious person. Finally, each interaction between an infectious person and a susceptible person results in transmission with probability p. Accordingly, the total number of new infections each day due to internal-to-Cornell transmission is modeled as a Poisson random variable with mean cF_IF_Sp/F. In addition, the number of new infections due to outside infection is binomially distributed with parameters F_S (free and susceptible individuals) and r (daily outside-infection probability).

3.2.3 Interventions: Self-Reporting and Contact-Tracing

There are two interventions through which positive cases can be isolated.

1. Self-reporting. Individuals in the symptomatic state have a probability of self reporting each day. If they self report they enter the quarantine-infected state (QI). If they do not self-report and do not recover, then they remain in their present state for another day.

2. Contact tracing. We use a simplified model of contact tracing. A contact trace is initiated when an individual self-reports symptoms or when they are identified as positive through asymptomatic screening. Additional contact tracing is not initiated from positive cases found among contacts traced, as the Tompkins County Health Department does not have a policy of testing contacts.

   Contact tracing is described by 3 parameters: number of people to place into quarantine or isolation with each contact trace; the number among these that are infectious for self-reporting positive cases; and the number that are infectious for cases identified through asymptomatic screening. We set the number of infectious cases identified smaller for those identified through asymptomatic screening because these cases will tend to have been infectious for less time and thus will tend to have infected fewer people. The choice of these parameters is discussed in detail in Section 2.3.

3.3 Approximation when combining test-on-return Excel model and stochastic Python-based simulation

Here we discuss an approximation used when passing the results from the Excel-based model of test-on-return into the stochastic Python-based simulation, and specifically in the fraction of the population that is free and infectious at the start of the simulation.

The way in which we pass results from one model to the other is intended to simulate the fact that, after move-in, two groups of people are combined: returning students who were not isolated or quarantined by test-on-return; and unquarantined/unisolated faculty/staff/students already on campus.

We estimate the prevalence of the unisolated/unquarantined returning students in a reasonable way, by modeling false negatives and the pre-test prevalence.

To estimate the fraction of people already on campus that are infectious, it would be best to run an additional simulation starting earlier in the summer, using the testing interventions that would be in place, and to take the prevalence at the start of move-in. In our simulations, we observe that the fraction of the population that is free & infectious typically converges to a steady state value driven by outside infections and the rate of asymptomatic screening.

However, for expedience, we instead suppose that the fraction of people already on campus that are infectious is equal to the fraction among the post-test returning students.

We can use Figure 1 to understand the level of error in this approximation.

Based on Figure 1, after move-in, the number of people in a population of 34K that are free and infectious has a steady state 40. This is approximately 0.1% of the population. Our simulation dynamics are approximately scale-invariant (if you double the size of the population, you roughly double the number of free and infectious people), which would argue that at the end of the summer the fraction of people in the on-campus population that are infectious would also be 0.1%.

Under the nominal parameters, this happens to be fairly close to fraction free and infectious among the post-test returning students: 0.09%.

4 Sensitivity Analysis: Fall Full-Return

The results below indicate the sensitivity of our model outcomes under perturbations to meaningful parameters for the Fall full-return scenario. The primary sensitivity analysis appears in Section 4.1. Analysis relating to quarantine capacity appears in Section 4.2. Discussion of the results is deferred to 4.3.

4.1 Sensitivity Results for Parameters in the Python Simulation

The sensitivity results consist of multiple plots, each consisting of 3 curves corresponding to the nominal, pessimistic and optimistic settings as given in Table 12. Each curve gives the results as we perturb a single parameter, keeping other parameters fixed to their nominal value for that setting.

The plots give sensitivities for the following list of parameters:

- The daily likelihood of a symptomatic individual self-reporting (Figure 8). This was also shown above as Figure 5.
- The initial prevalence of the infection, stated as a percentage of the total population (Figure 9).

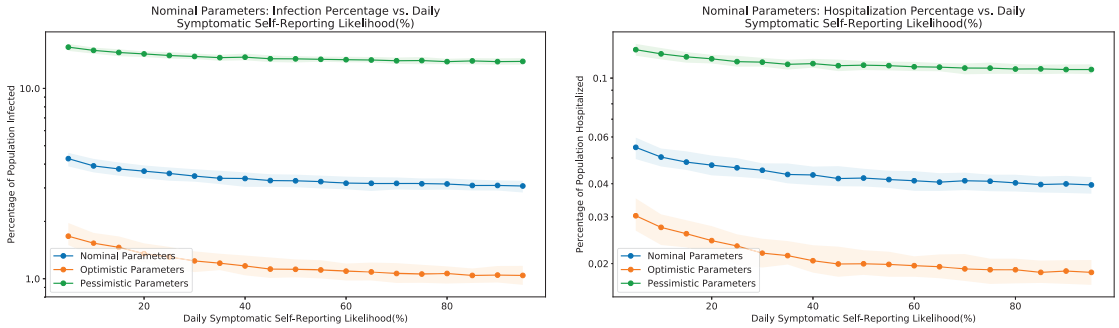

Figure 8: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the daily likelihood that a symptomatic individual self-reports their infection status. The value of this parameter is 18%, for all the nominal/optimistic/pessimistic parameter scenarios.

- The probability of transmission when an infectious individual comes into contact with a susceptible individual (Figure 10).
- The average number of contacts per person per day, for an individual who is not quarantined or isolated (Figure 11).
- The contact trace delay, i.e. the number of days between an individual self-reporting and the resulting quarantine and isolation decisions enacted from that individual's contact trace (Figure 12).
- The number of new positive cases that are identified and isolated for each one individual who undergoes a contact trace (Figure 13).
- The fraction of infections which are are asymptomatic (Figure 14).
- The percentage of the population that is tested for the infection each day (Figure 15).
- The false-negative rate associated with the daily tests (Figure 16).
- The daily probability of an infection from outside interaction (Figure 17).

Each point on each of the sensitivity plots contained in Figures 8—16 is obtained from 100 Monte Carlo replications for the relevant parameter configuration over a time horizon of 112 days or 16 weeks. We do not indicate the Monte Carlo error in these plots; indeed, the Monte Carlo error tends to be very small, except when estimating very small probabilities. The y-axis corresponds to the distribution of hospitalizations at the end of the 16 week time horizon; the main plot depicts the 50th percentile, while the shaded region depicts the 10-90th percentile range.

4.2 Quarantine Capacity Sensitivity Analysis

Table 13 summarizes the peak quarantine capacity needed in a single move-in weekend and the subsequent 18 days of the fall semester, under the optimistic, nominal and pessimistic settings.

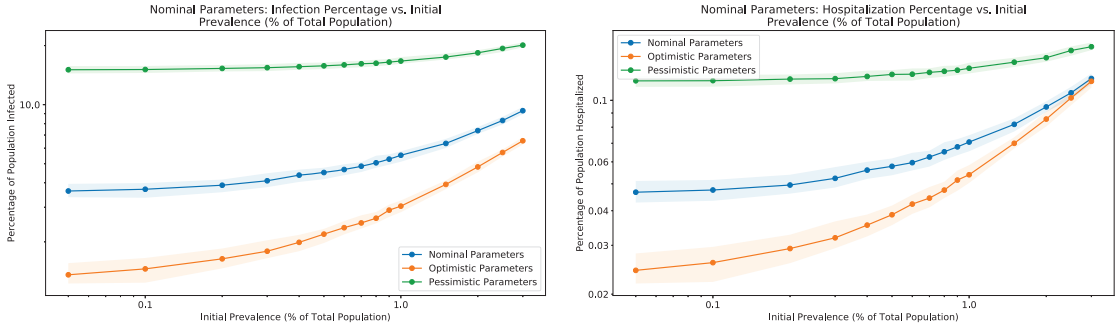

Figure 9: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the initial percentage of infected individuals within the population. The values of this parameter are 0.05%, 0.09% and 0.175%, for the optimistic/nominal/pessimistic scenarios respectively.

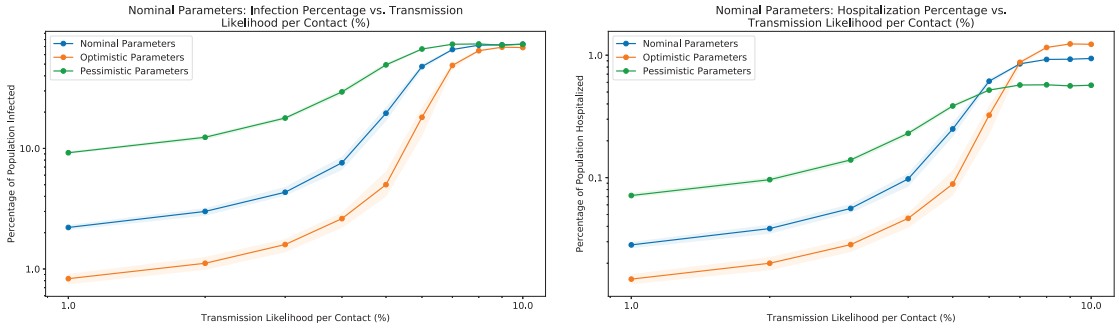

Figure 10: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the likelihood of transmission when a susceptible individual comes into contact with an infectious individual. The nominal value of this parameter is 2.6%, for all the nominal/optimistic/pessimistic parameter scenarios.

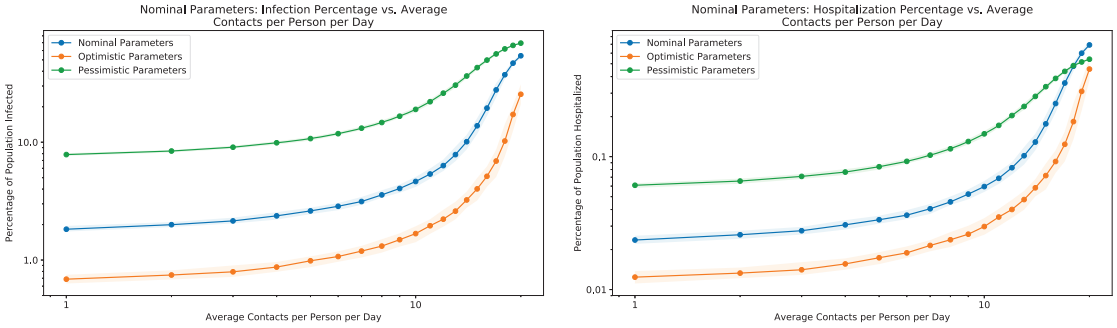

Figure 11: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the average number of contacts that a non-quarantined and non-isolated individual has on any given day. The nominal value of this parameter is 8.3 contacts per day, for all the nominal/optimistic/pessimistic parameter scenarios.

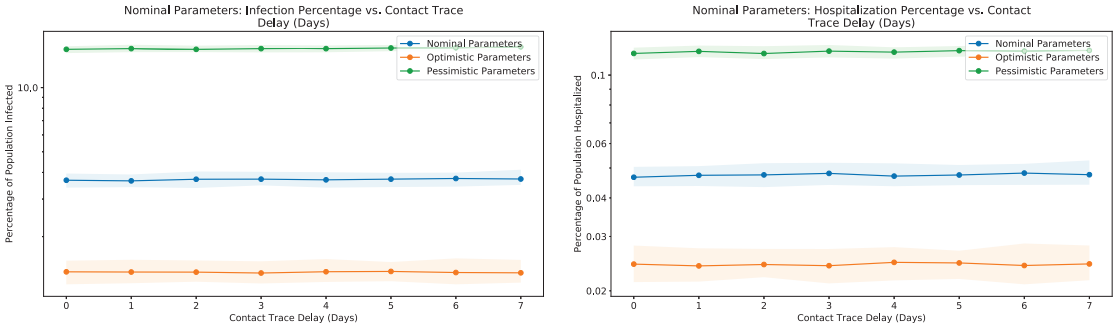

Figure 12: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the delay, measured in days, from identifying a new positive case to isolating their contacts via contact tracing. The nominal value of this parameter is 1 day for the optimal/noministic parameter scenarios and 2 days for the pessimistic parameter scenario.

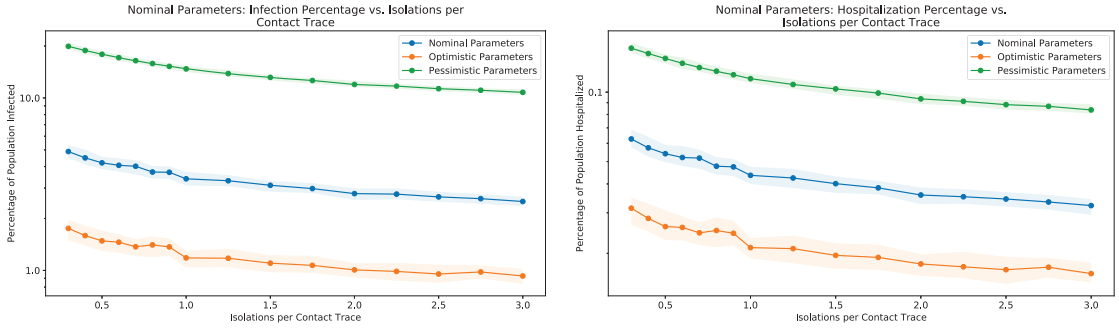

Figure 13: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the number of isolations which occur for each individual who undergoes a contact trace. The nominal value of this parameter is 0.87, 0.92, and 0.98 for the optimistic, nominal, and pessimistic parameter scenarios, respectively.

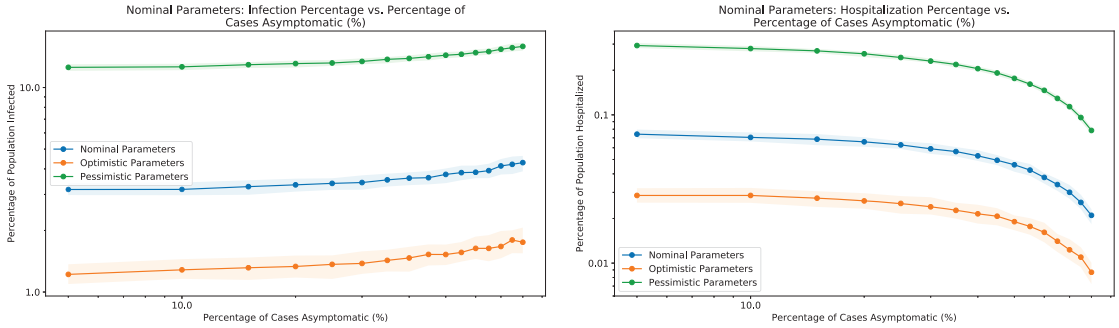

Figure 14: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. fraction of infections which become asymptomatic. The fraction of asymptomatic infections is 27.3%, 47.8%, and 68.3% for the optimistic/nominal/pessimistic parameter scenarios, respectively.

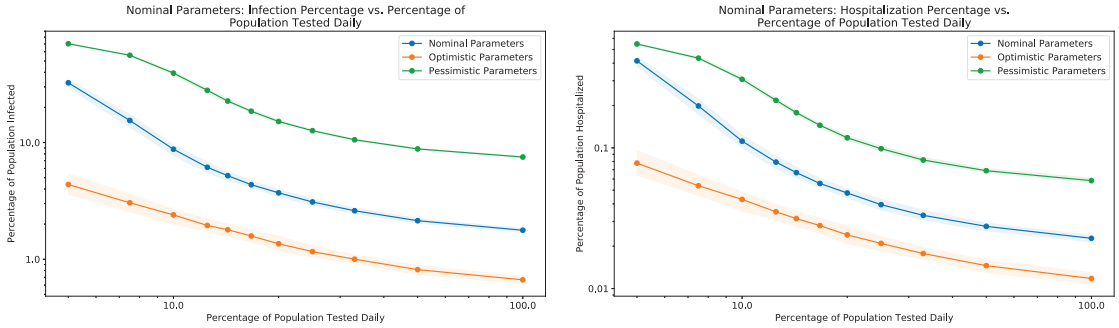

Figure 15: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the percentage of the total population that is tested for the presence of infection each day. The value of this parameter is 20% of the population (across all scenarios), which approximately corresponds to testing the entire population once every 5 days. This was also shown above as Figure 5.

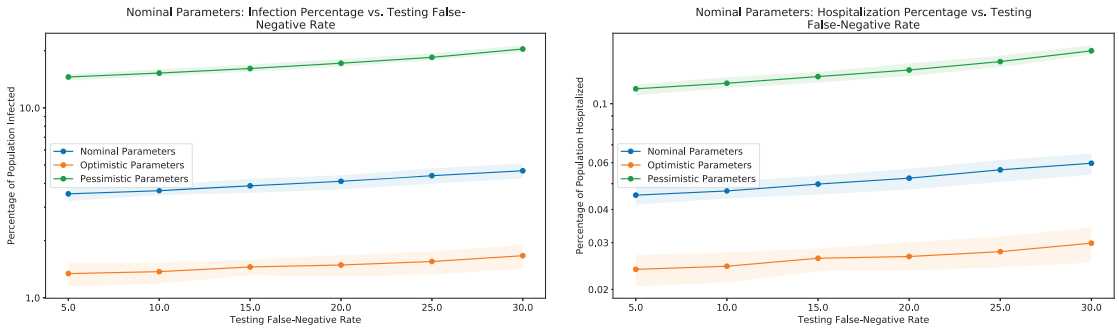

Figure 16: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the false-negative rate used for the daily testing procedure. The value of this parameter across all scenarios is 10%.

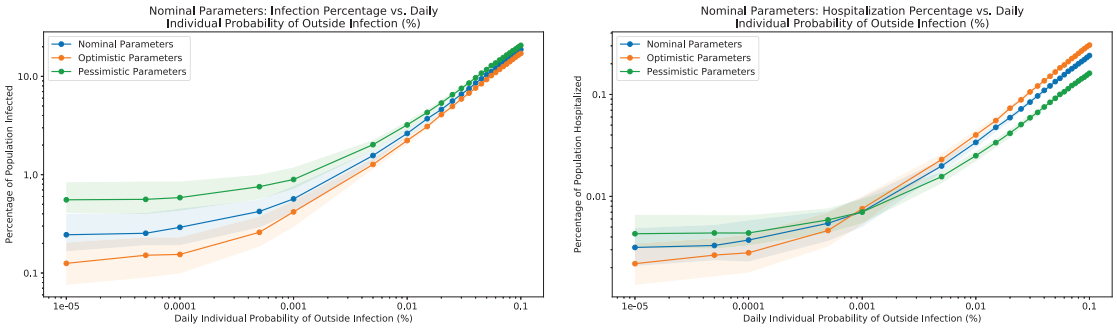

Figure 17: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the daily probability of an individual being infected from outside interaction. The value of this parameter is 0.005%, 0.015%, and 0.069% across the optimistic, nominal, and pessimistic parameter regimes, respectively.

(See Section 2.7). The number of quarantined/isolated cases due to a positive test upon arrival is obtained from the Excel model, while the number of quarantined or isolated cases over the subsequent 18-day period is obtained from the python simulation model using 500 Monte Carlo replications.

These estimates of quarantine needs include members of the Cornell community who could self isolate. Thus the capacity needed to quarantine/isolate students will be smaller.

Table 13: Peak quarantine capacity needed in a single move-in weekend and the subsequent 18 days of the fall semester, under three different scenarios.

	Optimistic	**Nominal**	**Pessimistic**
Students in ID state isolated due to positive test on arrival	5	22	53
Student in S state isolated due to positive test on arrival	8	10	11
(a) Students that test positive upon arrival and are isolated immediately	13	32	64
Number of cases in QI state over the 18-day period	70	172	626
Number of cases in QS state over the 18-day period	288	496	1301
(b) Number of quarantined/isolated cases over the 18-day period	358	668	1927
(a) + (b) Total quarantine capacity needed in the 18-day period	371	700	1991

4.3 Discussion

1. The trends in all plots are intuitive, with the potential exception of Figure 14 depicting infections and hospitalizations as a function of the fraction of infections that become asymptomatic. Overall infections increase due to asymptomatic individuals infecting others throughout the course of their infection until they are tested and isolated. Hospitalizations decrease because asymptomatic individuals do not need to be hospitalized. The horizontal axes range up to 80%. The low sensitivity to this value at the lower end of the scale indicates that the combination of asymptomatic testing and symptomatic self-reporting is sufficient to keep on top of the epidemic.

2. The percentage of infections in all plots is substantially higher than the percentage of hospitalizations, because the unique age demographics of the Cornell community yield a very low hospitalization rate. The nominal level of infection and hospitalization are 3.6% and 0.047% (1254 people and 16 people, respectively).

3. Figure 8 shows a modest but important reduction in infections and hospitalizations as the self-reporting probability increases. While modest, these reductions can probably be readily achieved through an information campaign to encourage people to report and self isolate as soon as they feel any symptoms.

4. Figure 9 shows a small sensitivity of hospitalizations to initial prevalence. In settings where epidemics grow, the role of initial prevalence is largely to get out of an initial phase in which random variation in contact tracing can contain an epidemic, and into uncontrolled growth. As the initial prevalence increases, it is less likely that the epidemic can be contained, but our aggressive asymptomatic testing ensures that the tipping point to uncontrolled growth is at a high level of initial prevalence. On the other hand, Figure 17 depicts a strong dependency of infections and hospitalizations on the likelihood of outside infections. This is to be expected, since this probability is a persistent source of infections, and thus also hospitalizations, over time. The strong dependency suggests that minimizing the risk of infection from interaction with the outside community can go a long way to curbing the spread of the disease in the Cornell community.

5. In virtually all sensitivity plots the results for pessimistic, nominal and optimistic settings are ordered as we would expect. The only exceptions are the hospitalization percentages plotted in Figures 10, 11 and 17. In the first two of these plots, the curves cross at the right-hand end, which is counter-intuitive. We believe this occurs because the settings progressively increase the asymptomatic rate amongst those confirmed with the virus as the settings progress from pessimistic to optimistic. At the right-hand end of these plots, the parameters take values that ensure that the epidemic spreads to essentially the entire Cornell community. In that setting, a high asymptomatic rate is actually an advantage, because it decreases the fraction of people who will need to be hospitalized. In the last of these plots, i.e. Figure 17 depicting sensitivity with respect to daily outside infections, we see that the order of optimistic, nominal, and pessimistic is reversed. This is again due to the higher rates of asymptomatic infections in the pessimistic and nominal parameters. When interpreting this particular plot, it is important to keep in mind that the daily probability of outside infection takes a different baseline value in each of the optimistic/nominal/pessimistic scenarios. Thus, in other sensitivity plots, the effect of asymptomatic infections on hospitalization percentage is mitigated by large discrepancies in the rate of outside infections.

6. The results are highly sensitive to the transmission probability per contact and contacts per day, highlighting the need for measures such as masks to reduce the former, and social distancing to reduce the latter.

7. Figure 12 indicates almost no dependence on contact tracing delay. As described in Section 1, we believe that our model of contact tracing becomes less accurate as contact tracing delays increase: in reality, for large contact tracing delays, we expect the number of hospitalizations to be significantly larger than those predicted here. Work to address this inaccuracy is called out in Section 6.

8. There is modest but important sensitivity to isolations per contact trace in Figure 13, highlighting the value of quality contact tracing.

9. There is high sensitivity to the percentage of the population tested daily (Figure 15) around the nominal value of 20%. We explore the implications of moving to a lower frequency of 14% corresponding to testing the entire population once every seven days in Section 5.2.

10. There is low sensitivity to the false negative rate in daily testing in Figure 16. We believe this is due to contact tracing, which can lead to isolation of many of those true cases that escape detection.

11. Figures 3 and 4 contrast the full reopen and do-not-reopen scenarios for the fall. Those results are discussed at a high-level in in Section 1, and a detailed discussion is provided in Section 5.1. In essence, the full reopen scenario results are far better due to intervention measures planned by Cornell for the reopen scenario that would not be available to Cornell students who return to Ithaca but not to campus in the no-reopen scenario.

12. All figures do not count infected students who were identified during the test-on-return procedure. This number is very small, relatively speaking, and does not change the overall sense obtained from the plots.

13. The sensitivity analysis for quarantine capacity needs in Section 4.2 is telling. Under the nominal setting, the total number of people that would need to be quarantined or isolated in the peak period following move-in is 700. This result is extremely sensitive to our choice of parameter values. The number of cases imported to the Cornell community and Tompkins County is highly sensitive to the prevalence level at student origin. In addition, outside infections are a significant source of cases for the Cornell community, even over just those first 18 days.

5 Additional Discussion

5.1 Virtual Instruction "No-Reopen" Scenario

While the total infection numbers reported by our simulation may seem large, it is important to think critically about the state of the world if Cornell were not to reopen for the Fall semester. We envision that, for lack of a better option, a meaningful fraction of the student population would still return to Ithaca in the fall. In this case, in light of the decision to not reopen campus, these returning students would be outside the purview of Cornell and would not be subject to repeated

asymptomatic surveillance. We use our simulation model to try quantifying the distribution of infection and hospitalization counts in this setting.

To compare the two alternatives, henceforth referred to as the Reopen and No-Reopen scenarios, we adopt a simulation methodology which assumes that the No-Reopen scenario can be modeled as two distinct communities with zero interaction between one another. The first community reflects the faculty, staff, and graduate students who will be on campus in the fall under both alternatives. Following from the Cornell facts page (9) there are 10283 individuals across faculty, academic professionals, and staff; there are 15043 undergraduate students; and there are 8984 graduate and professional students. We use a population size of 15000 for the first community, to reflect the presence of all faculty, staff, and academic professionals, together with a little over half the graduate student population. For the second community, we take a nominal population size of 9000 students who return to Ithaca but remain outside the purview of Cornell's asymptomatic testing, which we view as comprised mainly of undergraduate students but includes a small number of graduate and professional students as well.

The majority of parameters used in the simulation for the two groups take their optimistic / nominal / pessimistic values as specified in Table 12; for example, both communities use a nominal initial prevalence level of 0.09%. (This assumes optimistically that those in the second community not already in Ithaca would not bring high prevalence with them.) The few parameters which are not copied over from Table 12 are summarized as follows:

- The faculty-staff community has a population size of 15000, which reflects the campus population in the absence of undergraduate students, and includes faculty, staff and some graduate / professional students. The returning student community has a population size of 7000, 9000, and 11000, for the respective optimistic, nominal, and pessimistic regimes.
- The returning student community simulation does not use any asymptomatic testing.
- The age distribution among the faculty/staff/graduate students/professional students on campus is assumed to be 57% in the 18-44 category, 39.8% in the 45-64 category, 2.7% in the 65-74 category, and 0.43% in the 75+ category.
- The returning student age distribution is assumed to be 100% in the 18-44 category.

Figure 18 and 19 depict the distribution of infections and hospitalizations, respectively, across the pessimistic/nominal/optimistic parameter regimes. Across all parameter regimes we see that having a large contingent of students return to Ithaca who are not subject to asymptomatic testing produces worse outcomes than if all students were to return to Ithaca and be subject to asymptomatic testing.

It is important to note that the large number of infections in the no-reopen alternative is largely exacerbated by high rates of asymptomatic infections among the student population, who we assume all fall under the 18-45 age category. As noted in item 7 in the list of model-limitations in Section 1, the hospitalization rate for this age category is assumed to be 0.8%, but this is likely largely driven by the ages 34-45 which are not immediately relevant as the student population consists mainly of individuals aged 18-25 years. However, while the hospitalization rate may be a slight overestimate for this reason, the observed gap in outcomes in Figures 18 and 19 is so wide that this source of error likely has negligible effect.

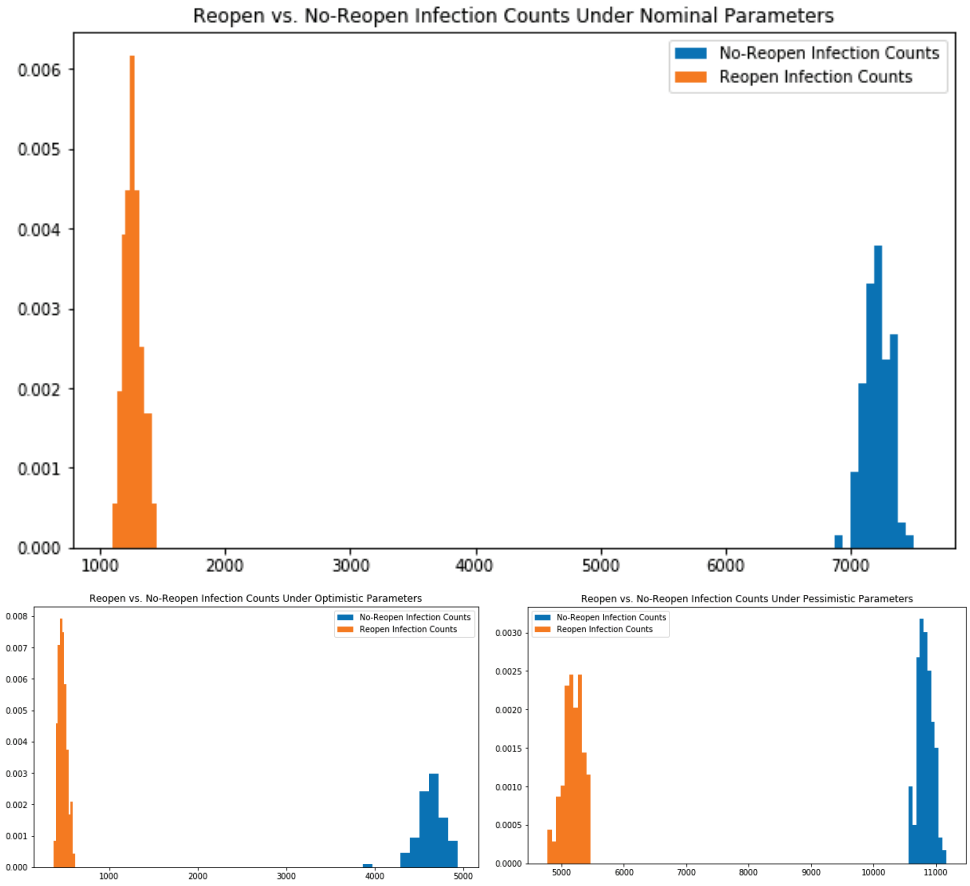

Figure 18: Histograms showing the number of *infections* in the fall semester under nominal, optimistic, and pessimistic variants of the Reopen vs. No-Reopen alternatives.

5.2 Testing Once per Week

One of the proposals that we considered was reducing the frequency of testing from once every five days to once a week (once every seven days). To evaluate the effect of this policy, we can refer to Figure 20 which shows the sensitivity analysis of the testing fraction parameter (inverse of the frequency).

Table 14 below shows the median infections and hospitalizations under both testing regimes. Our simulation model indicates that testing weekly instead of once every 5 days would lead to a 41% increase in infections and hospitalizations.

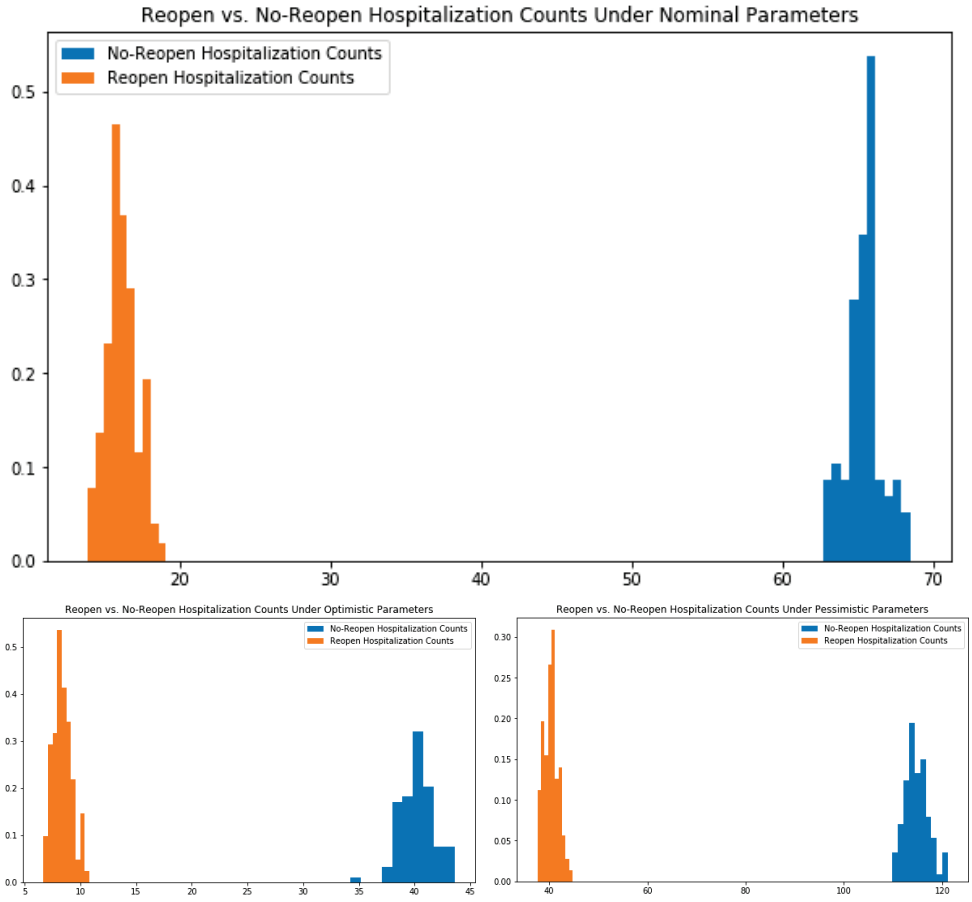

Figure 19: Histograms showing the number of *hospitalizations* in the fall semester under nominal, optimistic, and pessimistic variants of the Reopen vs. No-Reopen alternatives.

Table 14: Median infections and hospitalizations under nominal scenario with testing once every 5 days and once a week.

Testing Frequency	**Infections**	**Hospitalizations**
5 days	1254	16.1
7 days	1778	22.8

5.3 Asymptomatic Screening with Group Testing

We envision group testing as an important component for enabling widespread asymptomatic screening. Group testing pools multiple samples together and tests each pool using a single PCR test. It

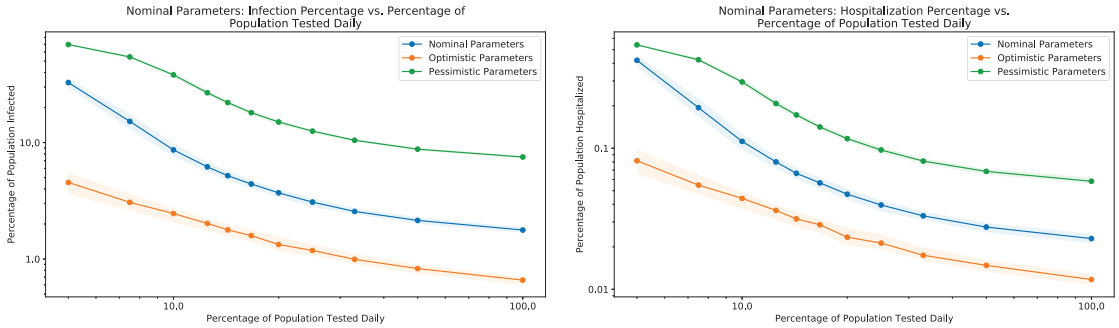

Figure 20: Plot depicts the distribution of infections and hospitalizations (i.e. 50th percentile, with the wider range corresponding to the 10-90th percentile range) vs. the percentage of the total population that is tested for the presence of infection each day. The nominal value of this parameter is 20% of the population, which approximately corresponds to testing the entire population once every 5 days. This was also shown above as Figure 15.

could save a significant amount of testing resources while still ensuring a reasonably high accuracy. The idea of group testing was first proposed by Dorfman (14) as an approach to screening soldiers for syphilis during WWII. Since then, different group testing protocols have been developed and studied. In the context of COVID-19, recent analyses and editorials (17; 21; 22) have called for widespread deployment of group testing because it can greatly expand the testing capacity. In mid May, the city Wuhan screened nine million citizens using pools of 5-10 samples (15). Researchers at Stanford Health Care Clinical Virology Laboratory (16), University of Saarland (26), Nebraska Public Health Laboratory (1), Technion-Israel Institute of Technology (42), and Goethe University Frankfurt (33) examined the efficacy of pooled RT-PCR experimentally and showed that pooled testing is able to preserve high accuracy while saving a significant amount of testing resources.

While larger pool sizes and more sophisticated testing algorithms can conserve more test resources, we adopt the more conservative protocol of one-stage pooled test using pool size 5. The concrete protocol is as follows:

- Collect samples from individuals. Before testing, take two subsamples of equal volume, A and B from each sample.
- Test subsample A's in pools of five.
- For people whose pooled tests are positive, test their subsample B's individually.
- If an individual's subsample B tests positive, he/she is labeled positive and isolated.

We argue that this pooled testing protocol could plausibly achieve a false negative rate of 10%. First, we define two terms: the *viral load* of a sample refers to the amount of viral material present in a sample; the *limit of detection* (LoD) of a PCR test refers to the threshold viral load value such that samples with viral load above LoD will always be detectable and those with viral load below LoD might be undetected.

Given the small pool size and low prevalence, it is highly unlikely that a pool contains more than one positive sample. So, if a pool tests positive, we can safely assume that it contains an

positive subsample A with viral load above LoD. Since the pair of subsamples A and B have equal volumes, they contain roughly the same amount of viral material (under the assumption that the sample is well-mixed). Hence, we assume that the corresponding subsample B also has a viral load beyond LoD and will test positive in the follow-up individual test.

Thus, under the assumptions stated above, if an infected sample is detectable in an individual test, it is detectable in a pooled test. The probability that an infected sample is detectable in an individual test (and pooled test) is given by the individual PCR sensitivity. Both Kojima *et al.* (20) and To *et al.* (36) report a sensitivity for the individual PCR test of roughly 90%, or a false negative rate of 10%. Therefore, it is justified that our group testing protocol can achieve a false negative rate of 10%.

Next we calculate the required test capacity for carrying out the testing protocol under our 5-day testing cycle. Assuming an on-campus prevalence of 0.09% (under nominal scenario), the number of tests required to screen the entire Cornell population of 34,310 once is given by $34310/5 + 34310 \times 0.09\% \times 5 \approx 7016$ tests. The first term is the number of size-5 pooled tests needed; the second term is the expected number of individual follow-up tests needed. Since we test 1/5 of the population per day, we expect to need roughly 1400 tests every day. This is a large number of tests but potentially feasible within the capacity of the Animal Health Diagnostic Center (ADHC).

Experimental measurement of pooled test accuracy is being conducted by our collaborators Dr. Diego Diel and Dr. Jeff Pleiss. Work is in progress to estimate the cost of applying the proposed pooling protocol to Cornell campus.

Previously, we also explored a second pooling protocol, the *square-array protocol*, first proposed by Phatarfod and Sudbury (31) and closely analyzed by Westreich *et al.* (38). Under this protocol, we place samples onto a square array and form a pool from each row and each column. A PCR test is run on each pool, providing an indication of whether at least one sample in that pool contains viral material. Samples whose rows and columns are both positive are tested in follow-up confirmatory individual tests. Based on earlier discussions with Dr. Pleiss, the cost of the 24×24 square-array protocol (not including tubes, viral transport media, sample collection, transportation, and IT) would be on the order of 20 cents per sample tested. At the above cadence of 1/5 of the community per day, this roughly costs $34,310/5 \times 0.2$ dollars per day, or about $10K per week.

To provide robustness in the case of equipment failure, it would be important to fall redundant equipment as a fallback.

The additional cost of sample collection could be reduced by asking students and other members of the campus community to collect their own saliva (and potentially also add transport media). In particular, one possible implementation of asymptomatic surveillance would follow the following steps, leveraging the capabilities of the ADHC.

- Student (or staff / faculty) gets a saliva RNA collection kit on a bi-weekly basis;
- Student spits into the tube until the saliva sample reaches a specified volume (indicated on the tube);
- Student adds viral transport media (VTM) that comes with the kit to the tube;
- Student sticks the barcode label to the tube and keeps a photo of the label for future reference;
- Student drops off the saliva sample at specified drop-off locations (e.g. first floor of dorm buildings) throughout the campus;

- Courier collects samples (contactlessly) on the same day and brings them to the vet school lab;
- ADHC uses group testing to identify positive cases.

6 Ongoing Work

This is a work in progress. Here we provide a partial list of improvements that we considered but did not include due to time constraints. To support prioritization of ongoing work, we describe work items below, segmented by the amount of effort required. A small effort (S) is roughly 1-5 person-days, a medium effort (M) is 6-10 person-days, and a large effort (L) is 11-20 person-days. Here, we have roughly 5 people who can each provide 5 person days per week.

- (M) Estimate sustained quarantine capacity. Requires revisiting our assumption about holding times for quarantined susceptible individuals to extend the mean holding time to 14 days
- (M) Estimate impact of telling high-risk individuals not to come to campus
- (L) Group testing protocol design
- (L) Segment populations into groups (enables accuracy improvements & new features)
  - (S) Estimate impact of moving from doubles to singles (requires segmenting populations into groups)
  - (S) Estimate impact of "pod" dorm structure
- (L) Simulations at the individual level (enables accuracy improvements & new features below)
  - (S) Improvement to contact tracing accuracy (requires individual sims)
  - (S) Improvement to risk group accuracy (requires individual sims)
- (M) Parameter estimation of number of contacts based on card swipe and network data from Cornell
- (L) Develop and understand adaptive screening and social distancing strategies, including efforts to identify ranges of plausible parameters over which strategies should be robust.

We also call out two additional efforts.

First, the Cornell Library has been conducting a rapid literature search to support parameter estimation and model-building. The initial results from this literature search (available at this zotero link) are now available at the time of writing. We are reading this papers and plan to update our parameters and model structure with the information contained.

Second, we sent the May 31 version of our report out for informal review both within and outside of Cornell. We received detailed comments from three sets of reviewers:

- Dr. Leah Johnson from Virginia Tech
- Drs. Casey Cazer, Kristina Ceres, and Yrjö Gröhn from the College of Veterinary Medicine
- Drs. Renata Ivanek and Ece Bulut from the College of Veterinary Medicine

We are working through these reviews to respond to the opportunities for improvement that they identified.

7 History of This Document

This is a living document and is being shared periodically with stakeholders even while we refine results. Here we describe this document's evolution.

May 21 version A first and very preliminary version of this document (dated May 21) was shared with a small number of people between May 21 and May 24 to get feedback on methodology and priorities for additional work. It used a single set of nominal parameters and included sensitivity analyses varying one at a time.

May 27 version: This version developed a new set of nominal parameters. It included two additional sets of parameters, an "optimistic" set (which was the same as the May 21 set of parameters) and a "pessimistic" set. It also included a more detailed discussion of group testing, and a number of other edits. This version was shared more broadly, including with Provost Kotlikoff and the President of Boston University, Bob Brown.

May 28 version: We computed Figure 1 (an example trajectory) using the nominal parameters (previously it had been computed using a separate set of parameters and had been intended only as an illustration). We then split the figure into two figures, one showing cumulative cases by severity and the other showing current counts by infection statuses relevant to epidemic growth.

May 31 version: Based on feedback from President Brown and his team on the May 27 version, we reexamined the literature on asymptomatic rates, which led us to make a number of modifications to other parameters that significantly altered the results. These are listed here:

- Significant increase to asymptomatic rate (see 2.4 for details).
- Decrease in probability of hospitalization to conform with CDC numbers
- Reducing self-reporting rate to conform to $\tilde{5}$ days on average across people between becoming symptomatic and self-reporting, based on CDC numbers for influenza-like illness. (We see an opportunity to improve this through an information campaign.)
- Decreased contacts per day so that implied $R0$ equals CDC's baseline estimate of 2.5. Optimistic and Pessimistic scenarios adjusted to reflect the CDC's range for $R0$ of 2 to 3, though our pessimistic value (3.2) is actually above the CDC's range.
- Contact tracing delay in optimistic scenario increased to 1 day

The net effect of the fraction of people asymptomatic, self-reporting rate, and contacts per day on infections are summarized through the implied R_0. Thus, while increasing asymptomatic rate tends to increase infections, the reduction in contacts / day more than compensates for it. As a result, the May 31 parameters predict significantly fewer infections than the May 27 and 28 parameters.

The main additional effect of the parameter change is to reduce the fraction of infected cases hospitalized. These two effects (reduced infections, reduced hospitalization rate) significantly reduces the number of hospitalizations overall.

June 10 version

- Added the ability to model outside infections
- Added an explicit model of test-on-return
- Added a comparison to a "no-return" virtual-instruction-only scenario
- Added a discussion of quarantine.
- Significant update to the writeup.

We were surprised to see that the outside infections had such a large effect on results. Indeed, they are essentially the driving factor in infections.

June 11 version Minor update: fixed a few typographical errors and added some clarifications.

June 15 version Minor update. Clarified details of the no-return analysis, including that it includes some graduate students in the number that are modeled as being on campus in addition to faculty/staff. Also clarified some details of the age-severity distribution calculations. Added a paragraph to the executive summary pointing out that predictions for the no-reopen scenario is sensitive to assumptions, but that the conclusion that no-reopen has worse outcomes appears to be robust across a range of parameter settings.

References

[1] Abdalhamid, B., Bilder, C. R., McCutchen, E. L., Hinrichs, S. H., Koepsell, S. A., and Iwen, P. C. (2020). Assessment of specimen pooling to conserve sars cov-2 testing resources. *American Journal of Clinical Pathology*, 153(6):715–718.

[2] Arons, M. M., Hatfield, K. M., Reddy, S. C., Kimball, A., James, A., Jacobs, J. R., Taylor, J., Spicer, K., Bardossy, A. C., Oakley, L. P., et al. (2020). Presymptomatic sars-cov-2 infections and transmission in a skilled nursing facility. *New England Journal of Medicine*.

[3] Biggerstaff, M., Jhung, M. A., Reed, C., Fry, A. M., Balluz, L., and Finelli, L. (2014). Influenza-like illness, the time to seek healthcare, and influenza antiviral receipt during the 2010–2011 influenza season—united states. *The Journal of infectious diseases*, 210(4):535–544.

[4] CDC COVID-19 Response Team (2020). Severe outcomes among patients with coronavirus disease 2019 (covid-19)—united states, february 12–march 16, 2020. *MMWR Morb Mortal Wkly Rep*, 69(12):343–346.

[5] Centers for Disease Control and Prevention (2020). Covid-19 pandemic planning scenarios.

[6] Central Intelligence Agency (2020). The world factbook - united states.

[7] China CDC (2020). The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (covid-19)—china, 2020. *China CDC Weekly*, 2(8):113–122.

[8] Cornell Graduate School (2020). Housing for graduate students. https://gradschool.cornell.edu/admissions/admitted-students/living-in-ithaca/housing/.

[9] Cornell Institute for Research and Planning (2019). Cornell university factbook. http://irp.dpb.cornell.edu/university-factbook/employees.

[10] Cornell University (2017). Class of 2021 student profile. http://irp.dpb.cornell.edu/wp-content/uploads/2017/08/Profile2017-Freshmen.pdf.

[11] Cornell University (2018). Class of 2022 student profile. http://irp.dpb.cornell.edu/wp-content/uploads/2018/08/Profile2018-Freshmen2.pdf.

[12] Cornell University (2019). Class of 2023 student profile. https://admissions.cornell.edu/sites/admissions.cornell.edu/files/ClassProfile%202023b.pdf.

[13] Dong, Y., Mo, X., Hu, Y., Qi, X., Jiang, F., Jiang, Z., and Tong, S. (2020). Epidemiological characteristics of 2143 pediatric patients with 2019 coronavirus disease in china. *Pediatrics*.

[14] Dorfman, R. (1943). The detection of defective members of large populations. *The Annals of Mathematical Statistics*, 14(4):436–440.

[15] Fan, W. (2020). Wuhan tests nine million people for coronavirus in 10 days. https://www.wsj.com/articles/wuhan-tests-nine-million-people-for-coronavirus-in-10-days-11590408910.

[16] Food, U., Administration, D., et al. (2020). Stanford health care clinical virology laboratory sars-cov-2 test eua summary.

[17] Gollier, C. (2020). Optimal group testing to exit the covid confinement. Technical report, Technical report, Toulouse School of Economics.

[18] Kaiser Family Foundation (2018). Us population distribution by age.

[19] Kimball, A. (2020). Asymptomatic and presymptomatic sars-cov-2 infections in residents of a long-term care skilled nursing facility—king county, washington, march 2020. *MMWR. Morbidity and mortality weekly report*, 69.

[20] Kojima, N., Turner, F., Slepnev, V., Bacelar, A., Deming, L., Kodeboyina, S., and Klausner, J. D. (2020). Self-collected oral fluid and nasal swabs demonstrate comparable sensitivity to clinician collected nasopharyngeal swabs for covid-19 detection. *medRxiv*.

[21] Kotlikoff, L. (2020). Daily testing of all americans is the only answer.

[22] Kotlikoff, L. and Kotlikoff, M. (2020). How to get the economy safely back to work in just 2 weeks.

[23] Lauer, S. A., Grantz, K. H., Bi, Q., Jones, F. K., Zheng, Q., Meredith, H. R., Azman, A. S., Reich, N. G., and Lessler, J. (2020). The incubation period of coronavirus disease 2019 (covid-19) from publicly reported confirmed cases: estimation and application. *Annals of internal medicine*, 172(9):577–582.

[24] Li, M. Y., Graef, J. R., Wang, L., and Karsai, J. (1999). Global dynamics of a seir model with varying total population size. *Mathematical biosciences*, 160(2):191–213.

[25] Li, R., Pei, S., Chen, B., Song, Y., Zhang, T., Yang, W., and Shaman, J. (2020). Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (sars-cov-2). *Science*, 368(6490):489–493.

[26] Lohse, S., Pfuhl, T., Berkó-Göttel, B., Rissland, J., Geißler, T., Gärtner, B., Becker, S. L., Schneitler, S., and Smola, S. (2020). Pooling of samples for testing for sars-cov-2 in asymptomatic people. *The Lancet Infectious Diseases*.

[27] Ludvigsson, J. F. (2020). Children are unlikely to be the main drivers of the covid-19 pandemic–a systematic review. *Acta Paediatrica*.

[28] Luo, L., Liu, D., Liao, X.-l., Wu, X.-b., Jing, Q.-l., Zheng, J.-z., Liu, F.-h., Yang, S.-g., Bi, B., Li, Z.-h., et al. (2020). Modes of contact and risk of transmission in covid-19 among close contacts. *medRxiv*.

[29] McMullen, S. (2020). Covid-19 isolation and quarantine discussion with tompkins county health department.

[30] Mizumoto, K., Kagaya, K., Zarebski, A., and Chowell, G. (2020). Estimating the asymptomatic proportion of coronavirus disease 2019 (covid-19) cases on board the diamond princess cruise ship, yokohama, japan, 2020. *Eurosurveillance*, 25(10):2000180.

[31] Phatarfod, R. and Sudbury, A. (1994). The use of a square array scheme in blood testing. *Statistics in Medicine*, 13(22):2337–2343.

[32] PopulationPyramid.net (2020). 2019 china population.

[33] Schmidt, M., Hoehl, S., Berger, A., Zeichhardt, H., Hourfar, K., Ciesek, S., and Seifried, E. (2020). Fact- frankfurt adjusted covid-19 testing- a novel method enables high-throughput sars-cov-2 screening without loss of sensitivity. *medRxiv*.

[Student and Campus Life] Student and Campus Life. Cornell housing. `https://scl.cornell.edu/residential-life/housing`.

[35] Tindale, L., Coombe, M., Stockdale, J. E., Garlock, E., Lau, W. Y. V., Saraswat, M., Lee, Y.-H. B., Zhang, L., Chen, D., Wallinga, J., et al. (2020). Transmission interval estimates suggest pre-symptomatic spread of covid-19. *MedRxiv*.

[36] To, K. K. W., Tsang, O. T. Y., Leung, W. S., Tam, A. R., Wu, T. C., Lung, D. C., Yip, C. C. Y., Cai, J. P., Chan, J. M. C., Chik, T. S. H., Lau, D. P. L., Choi, C. Y. C., Chen, L. L., Chan, W. M., Chan, K. H., Ip, J. D., Ng, A. C. K., Poon, R. W. S., Luo, C. T., Cheng, V. C. C., Chan, J. F. W., Hung, I. F. N., Chen, Z., Chen, H., and Yuen, K. Y. (2020). Temporal profiles of viral load in posterior oropharyngeal saliva samples and serum antibody responses during infection by SARS-CoV-2: an observational cohort study. *The Lancet Infectious Diseases*, 20(5):565–574.

[37] Weeden, K. A. and Cornwell, B. (2020). The small world network of college classes: Implications for epidemic spread on a university campus. *Manuscript under review. http://osf. io/t7n9f*.

[38] Westreich, D. J., Hudgens, M. G., Fiscus, S. A., and Pilcher, C. D. (2008). Optimizing screening for acute human immunodeficiency virus infection with pooled nucleic acid amplification tests. *Journal of clinical microbiology*, 46(5):1785–1792.

[39] WHO (2020a). Coronavirus disease 2019 (covid-19) situation report - 73. `https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200402-sitrep-73-covid-19.pdf`.

[40] WHO (2020b). Report of the who-china joint mission on coronavirus disease 2019 (covid-19). `https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf`.

[41] Yang, R., Gui, X., and Xiong, Y. (2020). Comparison of clinical characteristics of patients with asymptomatic vs symptomatic coronavirus disease 2019 in wuhan, china. *JAMA Network Open*, 3(5):e2010182–e2010182.

[42] Yelin, I., Aharony, N., Shaer-Tamar, E., Argoetti, A., Messer, E., Berenbaum, D., Shafran, E., Kuzli, A., Gandali, N., Hashimshony, T., et al. (2020). Evaluation of covid-19 rt-qpcr test in multi-sample pools. *medRxiv*.