

# COVID-19 Near-Term Epidemic Risk Assessment for Georgia

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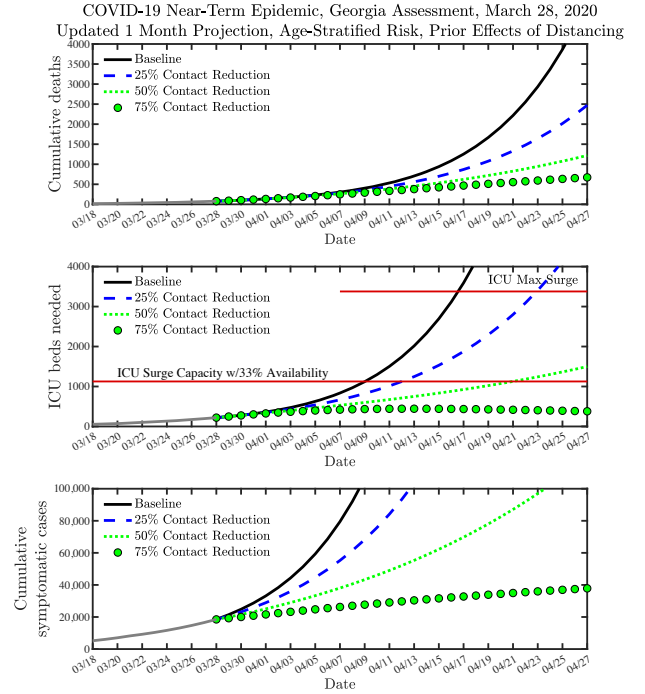
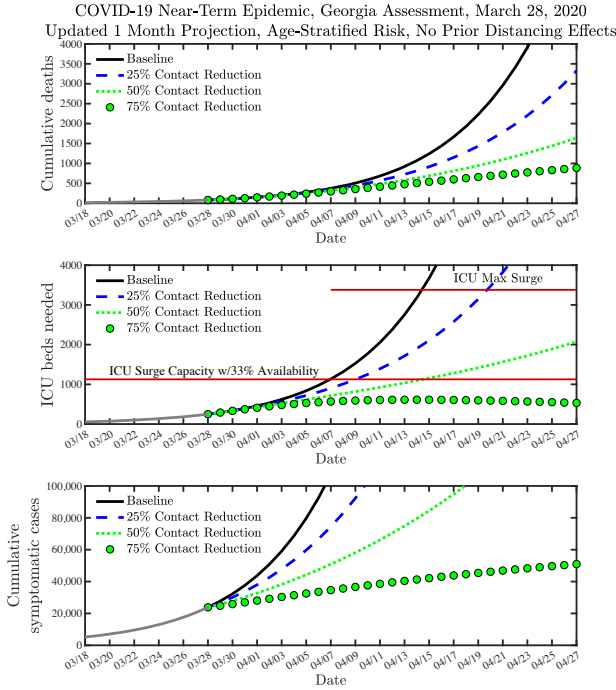
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(Dated: March 29, 2020)

## Summary Findings:

An epidemic model of COVID-19 was developed to include transmission and progress of disease, including estimates of hospitalization, acute ICU beds needed, and total fatalities – following standard approaches to compartmental epidemic models and GA demographic data. Given uncertainty in case counts, the “current” condition was estimated via matching a free-running epidemic simulation to recent, cumulative case reports of hospitalizations and deaths in Georgia. Given evidence of an approximately 3-day doubling period of laboratory confirmed infections, hospitalizations and deaths, simulations project that even with sustained, severe reduction of contacts (to 75%) the total number of deaths may rise near to or above 1000 in the next month. Yet, the alternative is significantly worse. **As guidance, hospital intake and new ICU beds needed is likely to double every 3-4 days for the next 10 days. Re-evaluation of projections is needed on a near-term basis given that there is significant uncertainty in underlying mechanisms and effectiveness of ongoing social distancing – which varies throughout the state.** Notably, “nowcasts” imply that there is a significant pool of undetected cases in the state, perhaps by a factor exceeding 10:1 relative to laboratory reported cases. However, inference of total unreported cases must be taken cautiously, given that infection mechanisms related to asymptomatic transmission highly influence this result and remain poorly characterized. Severe restrictions could buy time for implementation of viral testing via PCR to prevent transmission, serological testing to identify recovered individuals, and follow-up isolation and treatment. Figures below denote estimates assuming impacts of social distancing begin now (left) vs. assuming impacts of social distancing led to a 25% reduction in transmission effective one week ago (right).



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## I. MATHEMATICAL MODEL OF COVID-19 – BASELINE CASE

### A. Nonlinear population dynamics

Our population model of COVID-19 includes susceptible  $S$ , exposed  $E$ , infectious asymptotically  $I_a$ , infectious symptomatically  $I_s$ , and recovered  $R$  individuals who are free to move, without restrictions in a 'business as usual' scenario. A subset of symptomatic cases will require hospital care, which we further divide into subacute  $I_{hsub}$ , and critical/acute (i.e., requiring ICU intervention)  $I_{hcri}$  cases. We assume that a substantial fraction of critical cases will die. The model considers these 8 classes of individuals, further stratified by age  $a$ , in 10 categories, from 0-9; 10-19; 20-19, and so on, until 90-99, and avoids the inclusion of birth and death processes (for simplicity). The total number of asymptomatic and symptomatic infected cases are  $I_{tot,a}$  and  $I_{tot,s}$  respectively. The equations retain age structure for all categories.

$$\dot{S}(a) = -\beta_a S(a) I_{tot,a} - \beta_s S(a) I_{tot,s} \quad (1)$$

$$\dot{E}(a) = \beta_a S(a) I_{tot,a} + \beta_s S(a) I_{tot,s} - \gamma_e E(a) \quad (2)$$

$$\dot{I}_a(a) = p\gamma_e E(a) - \gamma_a I_a(a) \quad (3)$$

$$\dot{I}_s(a) = (1-p)\gamma_e E(a) - \gamma_s I_s(a) \quad (4)$$

$$\dot{I}_{hsub}(a) = h(1-\xi)\gamma_s I_s(a) - \gamma_h I_{hsub}(a) \quad (5)$$

$$\dot{I}_{hcri}(a) = h\xi\gamma_s I_s(a) - \gamma_h I_{hcri}(a) \quad (6)$$

$$\dot{R}(a) = \gamma_a I_a(a) + (1-h)\gamma_s I_s(a) + \gamma_h I_{hsub}(a) + (1-\mu)\gamma_h I_{hcri}(a) \quad (7)$$

$$\dot{D}(a) = \mu\gamma_h I_{hcri}(a) \quad (8)$$

The basic reproduction number of this model is

$$\mathcal{R}_0 = p\mathcal{R}_a + (1-p)\mathcal{R}_s \quad (9)$$

where  $\mathcal{R}_a = \beta_a/\gamma_a$  and  $\mathcal{R}_s = \beta_s/\gamma_s$ . Here note that  $\dot{H}_{tot}(a) = h\gamma_s I_s(a)$ , such that  $H_{tot}(t, a)$  keeps track of the cumulative number of hospitalized cases. The total number of ICU beds needed at a given time (see figure, page 1) denotes  $I_{hcri}(t)$ , summed across all ages. Technically this model has 80 ODE-s (all code available via github; of note, the code enables age-structured asymptomatic fraction). The baseline epidemiological parameters, age stratified risk, and population structure are listed in tables at the end of this manuscript, and age-specific outcome estimates are based on the Imperial College London report [1] augmented by information on age-structured asymptomatic fractions [2]. Two cases are considered, one with age-dependent probability of asymptomatic cases  $p(a)$  with an intrinsic, mean generation interval of 10 days with a 4 day incubation period on average.

### B. Identifying “now” position in simulated outbreaks

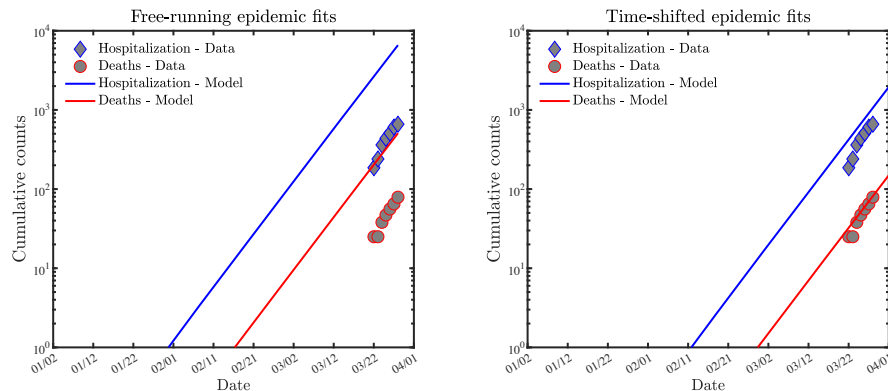
An outbreak is seeded with a single exposed individual, and then simulated until a trigger point of 200,000 total cases out of a population of approximately 10.7 million. This projection extends beyond the current moment in the outbreak. We determine “now” states by identifying a prior time in the simulated outbreak such that features,  $H_{tot}(t)$  and  $D_{tot}(t)$ , in model simulations approach that of observed data  $\hat{H}_{tot}(t)$  and  $\hat{D}_{tot}(t)$ , where we assume that 30% of cases are hospitalized for those before 3/24/20, representative of a local average of recent cases (all other values are via the Georgia Department of Public Health daily report):

Date	Hospitalizations	Deaths
3/19/20	85	10
3/20/20	145	14
3/21/20	166	20
3/22/20	186	25
3/23/20	240	25
3/24/20	361	38
3/25/20	438	47
3/26/20	509	56
3/27/20	607	65
3/28/20	660	79

Then, we find an equivalent point  $\hat{t}$  such that the state of the epidemic in the simulated system  $x_p(t)$  for  $\hat{t}-6 \leq t \leq \hat{t}$ , minimizes the distance in feature space to observed case data over the prior week, where  $x_p \equiv (H_{tot}(t), D_{tot}(t))$ . The distance between a local window of case data to observed case data is measured as the distance in log-transformed feature space, i.e.,:

$$\sqrt{\sum_i \left( \log \frac{H_{tot}(t_i)}{\hat{H}_{tot}(t_i)} \right)^2 + \sum_i \left( \log \frac{D_{tot}(t_i)}{\hat{D}_{tot}(t_i)} \right)^2} \quad (10)$$

Current estimates are intended for guidance and not as a robust statistical method; as such we are not providing confidence intervals (which will be influenced by measurement noise, behavior change, ascertainment bias, parameter uncertainty, etc). Given recent case data, the ‘now’ moment is equivalent to forward-dynamics of the nonlinear population model given a seed event. As a result, the current trajectories (nearly) match the speed (i.e., exponential growth rate) and values of both cumulative hospitalizations and deaths. As is evident, the models slightly over-estimate hospitalizations which could reflect differences in hospitalization risk in GA, under-reporting, a reluctance/inability to go to a hospital, or other forms of model error.



### C. Scenarios

Different scenarios are projected forward, conservatively, over a 1 month period by assuming that contact reduction begins to take effect now, by reducing  $\beta_{reduction} = \epsilon \beta_{baseline}$  where  $\epsilon = 0.25, 0.5$  and  $0.75$  (see figure on page 1, left panel). In addition, we evaluate a different set scenarios by assuming that the impacts of social distancing reduced transmission by 25% one week ago, and then use the same  $\beta$  values for forward estimation (see figure on page 1, right panel). Note that effects of prior reduction in contacts will start to appear over the next  $\sim 10$  days, given the time it takes, on average, for impacts of infection reduction on hospitalization and death. The forward projections are then appended to the epidemiological ‘pre-cast’ and ‘now’ state as defined above.

**Acknowledgments and Code:** JSW thanks C. Andris for sharing census data, K. Carden for sharing ICU data (originally from ‘Kaiser Health News analysis of hospital cost reports filed to the Centers for Medicare and Medicaid Services’ - khn.org), as well as J. Drake, J. Dushoff, S.W. Park and the Weitz group for feedback. Mistakes are the fault of the author solely. All code is available at: <https://github.com/jsweitz/covid-19-ga-summer-2020>.

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- 1 Ferguson N, et al. (2020) Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand.
  - 2 Wu J, Leung K, Bushman M, et al. (2020) Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. *Nature Medicine*.

### Assumptions for Age-Structured COVID-19 Model

Parameter	Meaning	Value
$\beta_a$	Asymp transmission	0.4/day (base), 0.3/day (25%) 0.2/day (50%), 0.1/day (75%)
$\beta_s$	Symp transmission	0.8/day (base), 0.6/day (25%), 0.4/day (50%), 0.2/day (75%)
$1/\gamma_e$	Mean exposed period (non-infectious)	4 days
$1/\gamma_a$	Mean asymp period	6 days
$1/\gamma_s$	Mean symp period	6 days
$1/\gamma_h$	Mean hospital period	10 days
Age-stratified $p$	Fraction asymptomatic	[0.95 0.95 0.90 0.8 0.7 0.6 0.4 0.2 0.2 0.2]
$\mathcal{R}_0$	Basic reproduction number	3.09 (base), 2.32 (25%), 1.55 (50%), and 0.77 (75%)

TABLE I: Epidemiological characteristics of scenarios, age-stratified  $p$ .

Age	Hospital Fraction	ICU (given hospitalization) Fraction
0-9	0.001	0.05
10-19	0.003	0.05
20-29	0.012	0.05
30-39	0.032	0.05
40-49	0.049	0.063
50-59	0.102	0.122
60-69	0.166	0.274
70-79	0.243	0.432
80-89	0.273	0.709
90-99	0.273	0.709

TABLE II: Age-stratified risk for COVID-19 [1]. Of note, the model assumes that 50% of ICU cases die.

Age	Fraction of Population
0-9	0.13
10-19	0.14
20-29	0.14
30-39	0.13
40-49	0.13
50-59	0.13
60-69	0.10
70-79	0.06
80-89	0.03
90-99	0.01

TABLE III: Assumed age structure of the GA population based on the 2018 US census with population of approximately 10.7 million individuals.