Technical Document for COVID-19 Community Spread Model

Andrea Allen[1]

1 Vermont Complex Systems Center, The University of Vermont, Burlington VT

This document is the technical appendix for a deterministic model of the spread of COVID-19 in ICE facilities and the surrounding community. It's use is to fit a model to existing data on COVID-19 cases in ICE detention and data on the surrounding county, to estimate or predict levels of employee infection rate over a fixed duration of time, and vary initial conditions that may have led to the levels of cases we see in the data.

Our approach follows an SEIR model from [1]. This model is largely based off of their existing work, but altered to reflect what we know about ICE facilities, and simplified from their original model. The various parameters the model takes can be tuned depending on the size of the community, facility, initial outbreak size, and other known parameters and data.

Code for the model is available on GitHub here [6].

1   SEIR Model

We use a standard SEIR model of disease spread, a model in which individuals belong to one of four compartments at all times: Susceptible (S), Exposed (E), Infected (I), and Recovered/Removed (R).

Model Compartments:

S	Susceptible population
E	Exposed to COVID-19, becoming contagious, but not exhibiting symptoms
I	Infectious and exhibiting symptoms
R	Recovered, or Removed from access to the susceptible population (via recovery, complete isolation, or death)

We then split the general population into subpopulations, corresponding to detainees inside the facility, the community population, and then staff (any individuals who regularly move between the facility and the community on a day to day basis). These subpopulations

are denoted by:

Population Compartments:

D	People living in the detention center
C	People living in surrounding community
O_C, O_D	Employees or officers living in surrounding county, working in detention center

Model Parameters:
All the following parameters have default values set, where the values are specific to COVID-19 and are taken from the literature. Then there are facility and community-specific parameters relating to population and infection counts, and those can/should be set as appropriate for the population under study.

COVID-19 Related Parameters:
(Covid-Related Parameters taken from [1] and from data from [2]:)

β	0.4	Contact-based transmission rate: average number of people an infected individual infects per day. Re-scaled later in section 1.1
σ	0.5	Average affect on transmission rate β during the Exposed period, a person is not contagious for 2 days after, but becomes fully contagious in the last few days before becoming symptomatic
γ_{EI}	1/5.1	Incubation period: Rate exposed individuals begin to show symptoms
γ	1/10	Rate an infected individual recovers
$\hat{\gamma}$	1/6.7	Asymptomatic case recovery rate

Environment-Related Parameters:

ψ_D	3	officer work shift: (1 shift per 8 hrs = 1/3 of a day, so $1/(1/3) = 3$ as a rate per day)
ψ_C	1.5	officer home shift: solve from ψ_D, e.g. $1/(2/3)$ of day = 3/2 rate
α	.0001-.0006 (varies)	arrest rate bringing new individuals from community into detention. Should be set to (number people arrested per day)/(community population) for example: arrest rate of .0001 corresponds to a rate of 2 people per day of a county of 20,000 people.
ρ	1/ALOS	average length of stay in days, for specific detention facility under study

1.1   Calibrating the parameters to real data

Deterministic models of disease spread are driven by the parameter β, which is the per-contact transmission probability. However, β is defined on an arbitrary scale. The model relies on the assumption that each subpopulation is fully mixed, i.e. that every member of a subpopulation is in possible contact with every other member. In order to have the model accurately calibrated to the realistic number of infections per day per subpopulation, the β value must be defined relative to each subpopulation, determined by population size and the other disease-related parameters. Following [1], we calibrate using the population values to estimate what fraction of the susceptible population someone infects per day (for the model).

We define c_0 as an arbitrary calibration parameter that will be used to adjust the β values so they are specific to the sub-populations of community (C) and detention (D). While the person-to-person transmission rate β is the same at the individual level between

the populations, deterministic SEIR models assume that the entire population is in contact, or that every individual is in contact with everyone else. We know this is not true in real life, so we need to adjust β_C to get a realistic rate of how many infections an infected individual will actually cause amongst the rest of the population. We do the same for the detention rate, β_D, except we also want to use c_D, a constant that increases β_D from β_C because we know that environmental factors of being inside a detention facility make for a higher rate of transmission between individuals. So, to calibrate β_C and β_D, following [1], we compute

$$\beta_C = \frac{c_0 \times \beta}{pop_C + pop_O}$$

$$\beta_D = c_D \times \frac{c_0 \times \beta}{pop_D + pop_O}$$

In [1], the value for c_0 is chosen such that the disease outbreak would infect 80% of the community population without intervention. Here, we find a value for c_0 such that the model fits the prevalence data that we have available, for both the community and the ICE facility. Depending on the reliability of the data and any other environmental factors that are known, c_0 can be manipulated alongside c_D, as one can see from the above that they play a similar role in terms of affecting β_D.

An example result of performing this calibration is using $c_0 = 500$ with a county poopulation of about $20,000$, a detention facility population of 600, and obtaining $\beta_C = 0.06$ and $\beta_D = 4.2$, which can be interpreted as the rate of growth of the infected proportion of each sub-population. This is further explained in the equations governing the model in the next section.

Calibration and Population Parameters:

c_D	2.0-4.0 range	coefficient to scale β to account for higher contact rate inside Detention facilities. From Lofgren et al. in [1]
c_0	varies	calibration parameter for adjusting β values for mean field models
pop_C	varies	arrest rate bringing new individuals from community into detention. Should be set to (number people arrested per day)/(community population)
pop_D	varies	detention facility population
pop_O	varies	number of employees working in detention facility
init community infections	varies	Should be set to number of active cases currently on day "1" of the model (not day 1 of the pandemic, but whenever you start the model from)
init detention infections	varies	Same as above, for initial infections in the facility on day 1 of the model.

1.2   Ordinary Differential Equations

The following ODE's govern the behavior of the model. Each term of the form S_C, E_D, I_C^O, etc., refers to the *proportion* out of total population in that compartment. So, $S_C :=$ number of current susceptible people in the community / total population. All of the terms at each time t must sum together to equal 1. Also, each term is in shorthand, for brevity, but each term should technically read $S_C(t)$ to denote that this is the value at time t.

The equations making up the model will involve the terms such as S_D and S_D^O; these refer to

the proportion of susceptible individuals in the detention center (S_D) and the proportion of susceptible staff members who are currently inside the detention facility (S_D^O). For example, if there are 94 susceptible individuals inside the facility, and the population is 100, then we would have $S_D = .94$.

Ordinary Differential Equation Variables:

S_D	Fraction of population in detention center who are susceptible
E_D	Fraction of population in detention center who are exposed
I_D	Fraction of population in detention center who are infected
R_D	Fraction of population in detention center who are recovered
S_C	Fraction of population in community who are susceptible
E_C	Fraction of population in community who are exposed
I_C	Fraction of population in community who are infected
R_C	Fraction of population in community who are recovered
S_D^O	Fraction of employee population at work in detention who are susceptible
E_D^O	Fraction of employee population at work in detention who are exposed
I_D^O	Fraction of employee population at work in detention who are infected
R_D^O	Fraction of employee population at work in detention who are recovered
S_C^O	Fraction of employee population at home in community who are susceptible
E_C^O	Fraction of employee population at home in community who are exposed
I_C^O	Fraction of employee population at home in community who are infected
R_C^O	Fraction of employee population at home in community who are recovered

Detention Residents ODE's

$$\frac{dS_D}{dt} = -\sigma\beta_D(S_D E_D) - \beta_D(S_D I_D) - \sigma\beta_D(S_D E_D^O) - \beta_D(S_D I_D^O) + \alpha(S_C)$$

$$\frac{dE_D}{dt} = \sigma\beta_D(S_D E_D) + \beta_D(S_D I_D) + \sigma\beta_D(S_D E_D^O) + \beta_D(S_D I_D^O) - \gamma_{EI} E_D - \hat{\gamma} E_D + \alpha(E_C)$$

$$\frac{dI_D}{dt} = \gamma_{EI} E_D - \gamma I_D - \rho I_D + \alpha(I_C)$$

$$\frac{dR_D}{dt} = \gamma I_D + \hat{\gamma} E_D + \alpha(R_C)$$

Community ODE's

$$\frac{dS_C}{dt} = -\sigma\beta_C(S_C E_C) - \beta_C(S_C I_C) - \sigma\beta_C(S_C E_C^O) - \beta_C(S_C I_C^O) - \alpha(S_C)$$

$$\frac{dE_C}{dt} = \sigma\beta_C(S_C E_C) + \beta_C(S_C I_C) + \sigma\beta_C(S_C E_C^O) + \beta_C(S_C I_C^O) - \gamma_{EI} E_C - \hat{\gamma} E_C - \alpha(E_C)$$

$$\frac{dI_C}{dt} = \gamma_{EI} E_C - \gamma I_C + \rho I_D - \alpha(I_C)$$

$$\frac{dR_C}{dt} = \gamma I_C + \hat{\gamma} E_C - \alpha(R_C)$$

Officers/Employees ODE's

$$\frac{dS_D^O}{dt} = -\sigma\beta_D(S_D^O E_D^O) - \beta_D(S_D^O I_D^O) - \sigma\beta_D(S_D^O E_D) - \beta_D(S_D^O I_D) - \psi_D S_D^O + \psi_C S_C^O$$

$$\frac{dE_D^O}{dt} = \sigma\beta_D(S_D^O E_D^O) + \beta_D(S_D^O I_D^O) + \sigma\beta_D(S_D^O E_D) + \beta_D(S_D^O I_D) - \psi_D E_D^O + \psi_C E_C^O - \gamma_{EI} E_D^O - \hat{\gamma} E_D^O$$

$$\frac{dI_D^O}{dt} = \gamma_{EI} E_D^O - \gamma I_D^O - \psi_D I_D^O + \psi_C I_C^O$$

$$\frac{dR_D^O}{dt} = \gamma I_D^O + \hat{\gamma} E_D^O - \psi_D R_D^O + \psi_C R_C^O$$

$$\frac{dS_C^O}{dt} = -\sigma\beta_C(S_C^O E_C) - \beta_C(S_C^O I_C) + \psi_D S_D^O - \psi_C S_C^O$$

$$\frac{dE_C^O}{dt} = \sigma\beta_C(S_C^O E_C) + \beta_C(S_C^O I_C) + \psi_D E_D^O - \psi_C E_C^O - \gamma_{EI} E_C^O - \hat{\gamma} E_C^O$$

$$\frac{dI_C^O}{dt} = \gamma_{EI} E_C^O - \gamma I_C^O + \psi_D I_D^O - \psi_C I_C^O$$

$$\frac{dR_C^O}{dt} = \gamma I_C^O + \hat{\gamma} E_C^O + \psi_D R_D^O - \psi_C R_C^O$$

1.3 Solving the model

Using the `scipy.integrate.solve_ivp` package, we solve the above model by giving it an initial vector of states, corresponding to number of active infections at the time of the model's start. The initial conditions are determined by splitting the initial case counts into both exposed and infected, without loss of generality.

Let $I_D(0)$ and $I_C(0)$ be the number of initial infections in the facility and community, respectively. We let the initial values be defined as

Detention facility:

$$S_D(0) = \frac{pop_D - I_D(0)}{N}, E_D(0) = \frac{0.5I_D(0)}{N}, I_D(0) = \frac{0.5I_D(0)}{N}, R_D(0) = \frac{0}{N}$$

Community:

$$S_C(0) = \frac{pop_C - I_C(0)}{N}, E_C(0) = \frac{0.5I_C(0)}{N}, I_C(0) = \frac{0.5I_C(0)}{N}, R_C(0) = \frac{0}{N}$$

Staff in Detention and Community:

$$S_D^O(0) = \frac{pop_O}{2N}, E_D^O(0) = 0, I_D^O(0) = 0, R_D^O = 0$$

$$S_C^O(0) = \frac{pop_O}{2N}, E_C^O(0) = 0, I_C^O(0) = 0, R_C^O = 0$$

1.4 Choosing the Best Parameters for Data Fit

For choosing the calibration parameter c_0 as well as the initial case counts, we start with the data for each scenario of interest, and run a range of models over all combinations of parameters from a chosen range. We allowed for variation in initial case counts to account for variability in true cases versus reported data. We fit the results of each time series model to the available data, and chose the parameter set that best fit the data using the minimum mean squared error measure. For theoretical scenarios where we predicted ICE cases, we fit the model to the best fit of community cases only.

2 Selected Values for real data

For the scenarios in the article, the following parameters were used from existing data or chosen from the minimum MSE fit.

South Texas Detention Complex - Scenario 1

parameter	value	source
County pop	20,306	county data
Staff pop	120	estimated
Detention pop	650	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	2.5	estimated
c_0	4400	estimated
init county infections	233	[5]
init ICE infections	2	[2]
arrest rate	.0003	estimated
alos	.033	ICE data [2]

South Texas Detention Complex - Scenario 2

parameter	value	source
County pop	20,306	county data
Staff pop	120	estimated
Detention pop	650	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	2.4	estimated
c_0	5000	estimated
init county infections	233	[5]
init ICE infections	0	reduced from data value
arrest rate	.0003	estimated
alos	.033	ICE data [2]
delay	5 days	delay 5 days to fit data

South Texas Detention Complex - Scenario 3

parameter	value	source
County pop	20,306	county data
Staff pop	120	estimated
Detention pop	650	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	1.7	Reduced, to show effect
c_0	5100	estimated
init county infections	233	[5]
init ICE infections	2	from ICE data [2]
arrest rate	.0003	estimated
alos	.033	ICE data [2]

Karnes County Residential Facility - Fit & Scenario 1

parameter	value	source
County pop	15,545	county data
Staff pop	40	estimated
Detention pop	200	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	2.0	estimated
c_0	2300	estimated
init county infections	200	[5]
init ICE infections	4	from ICE data [2]
arrest rate	.0006	estimated
alos	.033	ICE data [2]

Karnes County Residential Facility - Scenario 2

parameter	value	source
County pop	15,545	county data
Staff pop	40	estimated
Detention pop	200	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	2.0	estimated
c_0	2300	estimated
init county infections	200	[5]
init ICE infections	0	from ICE data [2]
arrest rate	.0006	estimated
alos	.033	ICE data [2]
delay	5 days	delay 5 days to fit data

Karnes County Residential Facility - Scenario 3

parameter	value	source
County pop	15,545	county data
Staff pop	40	estimated
Detention pop	200	ICE data [2]
β	0.4	arbitrary, chosen via R_0 from CDC. Is rescaled later per sub-population.
σ	0.6	[1]
γ	1/10	[1]
γ_{EI}	1/5.1	[1, 3]
$\hat{\gamma}$	1/6.7	[1, 4]
ψ_D	3	[1]
ψ_C	1.5	[1]
c_D	1.5	estimated
c_0	2300	estimated
init county infections	200	[5]
init ICE infections	4	from ICE data [2]
arrest rate	.0006	estimated
alos	.033	ICE data [2]

References

[1] Eric Lofgren, Kristian Lum, Aaron Horowitz, Brooke Madubuonwu, Kellen Myers, and Nina H. Fefferman. The epidemiological implications of jails for community, corrections officer, and incarcerated population risks from covid-19. *medRxiv*, 2021.

[2] Sharon Dolovich, Aaron Littman, Kalind Parish, Grace DiLaura, Chase Hommeyer, Michael Everett, Hope Johnson, Neal Marquez, and Erika. Tyagi. UCLA Law Covid-19 Behind Bars Data Project: Jail/Prison Confirmed Cases Dataset. `https://uclacovidbehindbars.org/`, 2020.

[3] SA Lauer, KH Grantz, Q Bi, FK Jones, Q Zheng, HR Meredith, AS Azman, NG Reich, and J. Lessler. The incubation period of coronavirus disease 2019 (covid-19) from publicly reported confirmed cases: Estimation and application. *Ann Intern Med.*, 172(9):577–582, 2020. PMID: 32150748.

[4] Z Hu, C Song, C Xu, G Jin, Y Chen, and X Xu. Clinical characteristics of 24 asymptomatic infections with covid-19 screened among close contacts in nanjing, china. *Sci China Life Sci*, 63(5):706–711, 2020.

[5] The New York Times. Coronavirus (Covid-19) data in the united states. Retrieved may, 2021 from. `https://www.nytimes.com/article/coronavirus-county-data-us.html`, 2021.

[6] Andrea Allen. covid-spread-ICE-SEIR GitHub. `https://github.com/andrea-allen/covid-spread-ICE-SEIR`, 2021.