Regional model of COVID-19 in Colorado with mobility
Technical Description and Model Equations

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1 Model Structure and Equations

We consider two separate models within the state of Colorado. The statewide *LPHA Model* partitions the state into $n_r = 11$ regions, each overseen by its own local public health agency (LPHA):

1. Central
2. Central Mountains
3. East Central
4. Metro
5. Northeast
6. Northwest
7. San Luis Valley
8. Southcentral
9. Southeast
10. Southwest
11. West Central Partnership

Within each region, the population is divided into the following four *fixed* age categories (in that we do not allow individuals to age out of one category into the next):

1. Age 0 to 19
2. Age 20 to 39
3. Age 40 to 64
4. Age 65 and above

Age categories are referenced by subscripts $i, j = 1, 2, 3, 4$, while regions are referred to by parenthetical superscripts $(u, v) = 1, ..., n_r$. For example, $X_i^{(u,v)}$ would denote the number of individuals of age i from region u visiting region v whose status with respect to COVID-19 is X at time t.

Disease transmission and progression is modeled by a system of differential equations, wherein individuals from a given region transition between a set of compartments describing their status with respect to COVID-19. Individuals from region u and of age i are classified as either:

1. Susceptible ($S_i^{(u)}$)
2. Exposed ($E_i^{(u)}$)
3. Infectious (Symptomatic) ($I_i^{(u)}$)
4. Asymptomatic Infectious ($A_i^{(u)}$)
5. Hospitalized ($H_i^{(u)}$)
6. Recovered, symptomatic ($RI_i^{(u)}$)
7. Recovered, asymptomatic ($RA_i^{(u)}$)
8. Vaccinated ($V_i^{(u)}$)
9. Deceased ($D_i^{(u)}$).

Summing over all age categories and disease compartments within a given region is equal to $N^{(u)}$, the total population of region u.

1.1 Incorporating Mobility

In conjunction with the compartment structure within each region, we include inter-regional travel and the additional pathways for disease transmission this brings about; these features are included following the model presented in [1]. Individuals leave their home region u at a per capita rate $\sigma^{(u)}$. Given that an individual leaves region u, the probability that they travel to region v is $\nu^{(u,v)}$. We require $\nu^{(u,u)} = 0$, and $\sum_{v=1}^{n_r} \nu^{(u,v)} = 1$. The per capita rate of return by residents of u from region v, $\rho^{(u,v)}$, is the reciprocal of the average time (in days) residents of u spend visiting region v. The rate of travel from one region to another is scaled by a single mobility factor $M \in (0, 1]$ across all regions.

Each of these rates of travel are approximated from mobility data provided by xmode. Parameters $\sigma^{(u)}$ and $\nu^{(u,v)}$ are estimated from the total number of devices observed traveling from region u to region v, divided by the total number of devices available to xmode and categorized as residents of region u. The average time a resident of region u spends visiting region v is estimated from the total number of hours spent by all residents of region u in region v over a given week, divided by the number of residents of region u observed to have traveled to region v over that same week. This average visit time is then converted to a fraction of a day, and it's reciprocal is the estimate used for $\rho^{(u,v)}$. The average visit time from one Metro LPHA county to another is generally between 5 and 8 hours; whereas the average visit time from one LPHA region to another is generally between 8 and 11 hours. Weekly estimates for travel parameters are interpolated so that changes in the population spatial distribution occur on the same days that a new rate of transmission takes effect.

1.2 Derivation of Model Equations for Disease Transmission

The region-specific transmission rate $\beta^{(u)}(t)$ represents the fraction of interactions between susceptible and infectious individuals which result in exposure to the virus. Higher β values are expected in more densely populated areas, and decrease with interventions such as, social distancing or mask wearing. Susceptible individuals may come in contact with infectious individuals from any region whether the susceptible individual remains in their home region, i.e., in the $S_i^{(u,u)}$ compartment, or is visiting another region, i.e. in the $S_i^{(u,v)}$ compartment. We assume that these interactions adopt the transmission rate of the region in which the contact occurs.

The rate of change in the number of susceptible individuals of age i from region u remaining

in region u at time t is formulated by,

$$\begin{aligned}
\frac{d}{dt}S_i^{(u,u)} &= (\text{number of susceptible residents of age } i \text{ returning home}) \\
&\quad - (\text{number of susceptible residents of age } i \text{ leaving}) \\
&\quad - (\text{newly exposed by infectious residents of } u \text{ at home}) \\
&\quad - (\text{newly exposed by infectious residents of } v \text{ visiting } u \text{ at time } t) \\
&\quad - (\text{vaccinated}) + (\text{temporarily immune becoming susceptible again}) \\
&= \sum_{v \neq u}^{n_r} \rho^{(u,v)} S_i^{(u,v)} - \sigma^{(u)} S_i^{(u,u)} - \left(\frac{\beta^{(u)}(t)}{\tilde{N}^{(u)}}\right) S_i^{(u,u)} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(u,u)} + A_j^{(u,u)}\right)\right] \\
&\quad - \left(\frac{\beta^{(u)}(t)}{\tilde{N}^{(u)}}\right) S_i^{(u,u)} \sum_{v \neq u}^{n_r} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(v,u)} + A_j^{(v,u)}\right)\right] - \left(\frac{vac_i^{(u)}}{\bar{N}_i^{(u)}}\right) S_i^{(u,u)} \\
&\quad + \left(\frac{1}{dImmuneI}\right) RI_i^{(u,u)} + \left(\frac{1}{dImmuneA}\right) RA_i^{(u,u)} + \left(\frac{1}{dVac}\right) V_i^{(u,u)}.
\end{aligned} \tag{1}$$

Similarly, the rate of change in the number of susceptible individuals of age i from region u visiting region v at time t is given by,

$$\begin{aligned}
\frac{d}{dt}S_i^{(u,v)} &= (\text{number of susceptible residents of } u \text{ of age } i \text{ arriving in region } v) \\
&\quad - (\text{number of susceptible residents of } u \text{ of age } i \text{ returning home from } v) \\
&\quad - (\text{newly exposed by infectious residents from } \textbf{any} \text{ region } w \text{ in region } v \text{ at time } t) \\
&\quad + (\text{temporarily immune becoming susceptible again while visiting } v) \\
&= \sigma^{(u)} \nu^{(u,v)} S_i^{(u,u)} - \rho^{(u,v)} S_i^{(u,v)} - \frac{\beta^{(v)}}{\tilde{N}^{(v)}} S_i^{(u,v)} \sum_{w=1}^{n_r} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(w,v)} + A_j^{(w,v)}\right)\right] \\
&\quad + \left(\frac{1}{dImmuneI}\right) RI_i^{(u,v)} + \left(\frac{1}{dImmuneA}\right) RA_i^{(u,v)} + \left(\frac{1}{dVac}\right) V_i^{(u,v)}.
\end{aligned} \tag{2}$$

The total number of individuals present in region u at time t is $\tilde{N}^{(u)}$,

$$\tilde{N}^{(u)} = \sum_{i=1}^{4} \left[\left(Ih_i^{(u)} + Ic_i^{(u)} + D_i^{(u)}\right) + \sum_{v=1}^{n_r} \left(S_i^{(v,u)} + E_i^{(v,u)} + I_i^{(v,u)} + A_i^{(v,u)} + RI_i^{(v,u)} + RA_i^{(v,u)} + V_i^{(v,u)}\right)\right].$$

Not to be confused with $\bar{N}_i^{(u)}$, the number of individuals of age i eligible to be vaccinated,

$$\bar{N}_i^{(u)} = N_i^{(u)} - \left(Ih_i^{(u)} + Ic_i^{(u)} + D_i^{(u)} + V_i^{(u)}\right).$$

1.3 Equilibrium Assumption

Formulating the model in this way accounts for all possible pathways of disease transmission. However, it requires that each age-specific disease status compartment (not including hospitalized and deceased) be divided into n_r compartments to keep track of the location of all individuals. (That's 3,675 compartments for the full LPHA model!) Including so many compartments makes parameter fitting exceedingly slow, but we can significantly reduce the number of compartments (to 443) by assuming that the number of individuals in each region reaches equilibrium instantaneously.

The total number of individuals from a given region is the sum of individuals from that region remaining in the region at time t, and those visiting other regions at time t:

$$N^{(u)} = N^{(u,u)}(t) + \sum_{v \neq u} N^{(u,v)}(t). \tag{3}$$

Since the total population of a given region does not change over time,

$$\frac{dN^{(u)}}{dt} = 0 \quad \Rightarrow \quad \frac{dN^{(u,u)}(t)}{dt} + \sum_{v \neq u} \frac{dN^{(u,v)}(t)}{dt} = 0,$$

we can make the assumption that each derivative $\frac{dN^{(u,\cdot)}}{dt}$ is equal to zero as well, and arrive at the following system of equations:

$$\begin{aligned} \frac{dN^{(u,u)}}{dt} &= \sum_{v \neq u} \rho^{(u,v)} N^{(u,v)} - \sigma^{(u)} N^{(u,u)} \\ \frac{dN^{(u,v)}}{dt} &= \sigma^{(u)} \nu^{(u,v)} N^{(u,u)} - \rho^{(u,v)} N^{(u,v)}. \end{aligned}$$

Setting these equal to zero, we get from the $N^{(u,v)}$ derivative that

$$N^{(u,v)} = \left(\frac{\sigma^{(u)} \nu^{(u,v)}}{\rho^{(u,v)}} \right) N^{(u,u)}. \tag{4}$$

Inserting this expression into (3) gives,

$$\begin{aligned} N^{(u)} = N^{(u,u)} + \sum_{v \neq u} N^{(u,v)} &= N^{(u,u)} \left(1 + \sum_{v \neq u} \left(\frac{\sigma^{(u)} \nu^{(u,v)}}{\rho^{(u,v)}} \right) \right) \\ \Rightarrow N^{(u,u)} &= N^{(u)} \left(1 + \sum_{v \neq u} \left(\frac{\sigma^{(u)} \nu^{(u,v)}}{\rho^{(u,v)}} \right) \right)^{-1}. \end{aligned} \tag{5}$$

Let $\eta^{(u,v)} = \dfrac{\sigma^{(u)} \nu^{(u,v)}}{\rho^{(u,v)}}$, and $\theta^{(u)} = \left(1 + \displaystyle\sum_{v \neq u} \left(\frac{\sigma^{(u)} \nu^{(u,v)}}{\rho^{(u,v)}} \right) \right)^{-1} = \left(1 + \displaystyle\sum_{v \neq u} \eta^{(u,v)} \right)^{-1}$, so that we may express the number of individuals in each region in terms of the constant total population

as follows

$$\begin{aligned}
N^{(u,u)} &= \theta^{(u)} N^{(u)} \\
N^{(u,v)} &= \eta^{(u,v)} N^{(u,u)} \\
&= \eta^{(u,v)} \theta^{(u)} N^{(u)} \\
\tilde{N}^{(u)} &= N^{(u,u)} + \sum_{v \neq u} N^{(v,u)} \\
&= \theta^{(u)} N^{(u)} + \sum_{v \neq u} \eta^{(v,u)} \theta^{(v)} N^{(v)} \\
\bar{N}^{(u)} &= N^{(u,u)} - \left(D^{(u)} + Ih^{(u)} + Ic^{(u)} + V^{(u)} \right) \\
&= \theta^{(u)} N^{(u)} - \left(D^{(u)} + Ih^{(u)} + Ic^{(u)} + V^{(u)} \right).
\end{aligned}$$

Repeating the above arguments with $N^{(u)}$ replaced by the sum over all age categories and disease compartments in all locations shows that we can similarly express the regional distribution of each disease compartment in terms of the total. For example, if $S_i^{(u)}$ is the total number of susceptible individuals of age i from region u, then,

$$S_i^{(u,u)} = \theta^{(u)} S_i^{(u)}, \text{ and } S_i^{(u,v)} = \eta^{(u,v)} \theta^{(u)} S_i^{(u)}.$$

To be clear, the transition parameters $\sigma^{(u)}$ and $\nu^{(u,v)}$ which form $\eta^{(u,v)}$ and $\theta^{(u)}$ change every seven days. The assumption we make is that when these parameters change, we reach equilibrium instantaneously. In making this assumption, we sacrifice continuity in $\tilde{N}^{(u)}$ for model simplicity. Plotted below are comparisons of the two model approaches.

1.4 Model Equations

Proceeding with the equilibrium assumption, the previously derived expressions (1) and (2) for $\frac{d}{dt} S_i^{(u,u)}$ and $\frac{d}{dt} S_i^{(u,v)}$, respectively, are added to form the differential equation for $\frac{d}{dt} S_i^{(u)}$.

$$\begin{aligned}
\frac{d}{dt} S_i^{(u)} &= \frac{d}{dt} S_i^{(u,u)} + \sum_{v \neq u} \frac{d}{dt} S_i^{(u,v)} \\
&= \sum_{v \neq u}^{n_r} \rho^{(u,v)} S_i^{(u,v)} - \sigma^{(u)} S_i^{(u,u)} - \left(\frac{\beta^{(u)}(t)}{\tilde{N}^{(u)}} \right) S_i^{(u,u)} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(u,u)} + A_j^{(u,u)} \right) \right] \\
&- \left(\frac{\beta^{(u)}(t)}{\tilde{N}^{(u)}} \right) S_i^{(u,u)} \sum_{v \neq u}^{n_r} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(v,u)} + A_j^{(v,u)} \right) \right] - \left(\frac{vac_i^{(u)}}{\bar{N}_i^{(u)}} \right) S_i^{(u,u)} \\
&+ \left(\frac{1}{dImmuneI} \right) RI_i^{(u,u)} + \left(\frac{1}{dImmuneA} \right) RA_i^{(u,u)} + \left(\frac{1}{dVac} \right) V_i^{(u,u)} \\
&+ \sigma^{(u)} \sum_{v \neq u} \nu^{(u,v)} S_i^{(u,u)} - \sum_{v \neq u} \rho^{(u,v)} S_i^{(u,v)} - \sum_{v \neq u} \left(\frac{\beta^{(v)}}{\tilde{N}^{(v)}} S_i^{(u,v)} \sum_{w=1}^{n_r} \left[\sum_{j=1}^{4} \left(\lambda I_j^{(w,v)} + A_j^{(w,v)} \right) \right] \right. \\
&\left. + \left(\frac{1}{dImmuneI} \right) RI_i^{(u,v)} + \left(\frac{1}{dImmuneA} \right) RA_i^{(u,v)} + \left(\frac{1}{dVac} \right) V_i^{(u,v)} \right)
\end{aligned} \tag{6}$$

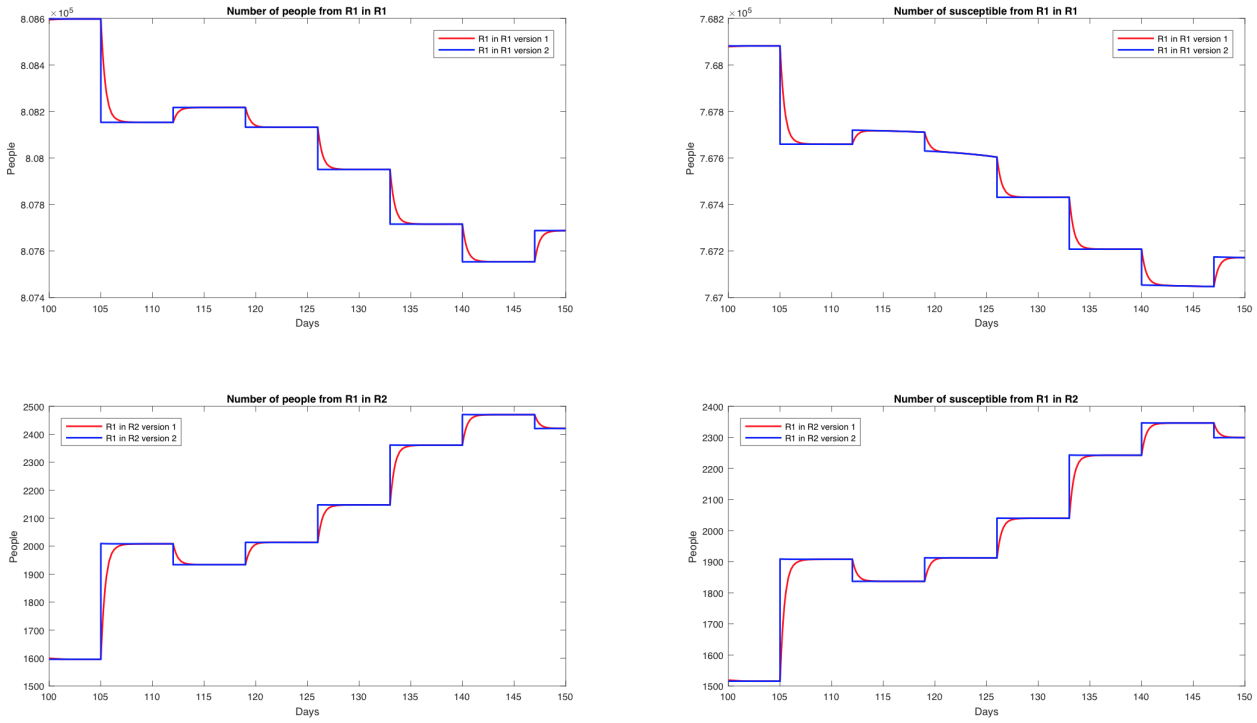

Figure 1: Comparison of changing regional population computed by model version 1 (plotted in red), with regional compartments, and version 2 (plotted in blue), with the equilibrium assumption.

The mobility terms (in blue) cancel, since $\sum_{v \neq u} \nu^{((u,v))} = 1$. Further combining like terms and replacing $S_i^{(u,u)}$ with $\theta^{(u)} S_i^{(u)}$, and $S_i^{(u,v)}$ with $\eta^{(u,v)} \theta^{(u)} S_i^{(u)}$, we arrive at the following full system of model equations.

Model Equations

$$
\begin{aligned}
\frac{d}{dt}S_i^{(u)} &= -\frac{\beta^{(u)}}{\tilde{N}^{(u)}}\theta^{(u)}S_i^{(u)}\left(\sum_{j=1}^{4}\left(\lambda\theta^{(u)}I_j^{(u)}+\theta^{(u)}A_j^{(u)}\right)+\sum_{v\neq u}\left[\sum_{j=1}^{4}\left(\lambda\eta^{(v,u)}\theta^{(v)}I_j^{(v)}+\eta^{(v,u)}\theta^{(v)}A_j^{(v)}\right)\right]\right)\\
&\quad-\sum_{v\neq u}\left(\frac{\beta^{(v)}}{\tilde{N}^{(v)}}\eta^{(u,v)}\theta^{(u)}S_i^{(u)}\right)\sum_{w=1}^{n_r}\left(\sum_{j=1}^{4}\left(\lambda\eta^{(w,v)}\theta^{(w)}I_j^{(w)}+\eta^{(w,v)}\theta^{(w)}A_j^{(w)}\right)\right)\\
&\quad-\left(\frac{vac_i^{(u)}}{\bar{N}_i^{(u)}}\right)\theta^{(u)}S_i^{(u)}+\left(\frac{1}{dImmuneI}\right)RI_i^{(u)}+\left(\frac{1}{dImmuneA}\right)RA_i^{(u)}+\left(\frac{1}{dVac}\right)V_i^{(u)}\\
\frac{d}{dt}E_i^{(u)} &= \frac{\beta^{(u)}}{\tilde{N}^{(u)}}\theta^{(u)}S_i^{(u)}\left(\sum_{j=1}^{4}\left(\lambda\theta^{(u)}I_j^{(u)}+\theta^{(u)}A_j^{(u)}\right)+\sum_{v\neq u}\left[\sum_{j=1}^{4}\left(\lambda\eta^{(v,u)}\theta^{(v)}I_j^{(v)}+\eta^{(v,u)}\theta^{(v)}A_j^{(v)}\right)\right]\right)\\
&\quad+\sum_{v\neq u}\left(\frac{\beta^{(v)}}{\tilde{N}^{(v)}}\eta^{(u,v)}\theta^{(u)}S_i^{(u)}\right)\sum_{w=1}^{n_r}\left(\sum_{j=1}^{4}\left(\lambda\eta^{(w,v)}\theta^{(w)}I_j^{(w)}+\eta^{(w,v)}\theta^{(w)}A_j^{(w)}\right)\right)-\frac{1}{\alpha}E_i^{(u)}\\
\frac{d}{dt}I_i^{(u)} &= \frac{pS_i}{\alpha}E_i^{(u)}-\gamma I_i^{(u)}\\
\frac{d}{dt}A_i^{(u)} &= \left(\frac{1-pS_i}{\alpha}\right)E_i^{(u)}-\gamma A_i^{(u)}\\
\frac{d}{dt}H_i^{(u)} &= \gamma(chosp_i)I_i^{(u)}-\left(\frac{1}{chlos_i}\right)Ih_i^{(u)}\\
\frac{d}{dt}RI_i^{(u)} &= \gamma(1-chosp_i-dnh_i)I_i^{(u)}+\left(\frac{1-dch_i}{chlos_i}\right)H_i^{(u)}-\left(\frac{1}{dImmuneI}\right)RI_i^{(u)}\\
\frac{d}{dt}RA_i^{(u)} &= \gamma A_i^{(u)}-\left(\frac{1}{dImmuneA}\right)RA_i^{(u)}\\
\frac{d}{dt}V_i^{(u)} &= \left(\frac{vac_i^{(u)}}{\bar{N}_i^{(u)}}\right)\theta^{(u)}S_i^{(u)}-\left(\frac{1}{dVac}\right)V_i^{(u)}\\
\frac{d}{dt}D_i^{(u)} &= \gamma(dnh_i)I_i^{(u)}+\left(\frac{dch_i}{chlos_i}\right)H_i^{(u)}
\end{aligned}
\tag{7}
$$

Description of Parameters

Parameter	Description
$\beta^{(u)}$	Regional transmission rate
λ	Difference in infectiousness: symptomatic/asymptomatic
α	Incubation period
γ	Recovery Rate
pS_i	Fraction of symptomatic cases
$chosp_i$	Fraction of cases requiring hospitalization (non-ICU and ICU)
$chlos_i$	Length of hospital stay (non-ICU and ICU)
dch_i	Death rate for hospitalized patients (non-ICU and ICU)
dnh_i	Death rate for non-hospitalized individuals
$dImmuneI$	Period of immunity for an individual recovered from a symptomatic case
$dImmuneA$	Period of immunity for an individual recovered from an asymptomatic case
$dVac$	Period of immunity from vaccination
$\bar{N}_i^{(u)}$	Individuals of age i from region u eligible to be vaccinated
$vac_i^{(u)}$	Vaccination rate for individuals of age i from region u
$\tilde{N}^{(u)}$	Total number of individuals present in region u at time t
$\sigma^{(u)}\nu^{(u,v)}$	Probability that a resident of region u travels to region v
$\rho^{(u,v)}$	Rate of return for residents of region u visiting region v
$\theta^{(u,v)}$	The fraction of residents of region u remaining in region u at time t
$\eta^{(u)}$	The ratio of residents of region u visiting region v and those remaining in region u at time t
$\eta^{(u,v)}\theta^{(u,v)}$	The fraction of residents of region u visiting region v at time t
$\theta^{(u)}X_i^{(u)}$	Individuals of disease status X and age i from region u in region u at time t
$\eta^{(u,v)}\theta^{(u)}X_i^{(u)}$	Individuals of disease status X and age i from region u in region v at time t
M	Mobility scaling. This term does not appear in the model equations (since it is often set to one), but each η is implicitly multiplied by M

References

[1] Lisa Sattenspiel, Klaus Dietz, et al. A structured epidemic model incorporating geographic mobility among regions. *Mathematical biosciences*, 128(1):71–92, 1995.