The model is based on an SEIR model, which has four populations: Susceptible, Exposed, Infectious, and Recovered (with the assumption the Recovered won’t be reinfected). Our model adds populations for Hospitalized, Critical, and Deceased. Each county population is treated independently, and when age is also modeled, there are seven bins for age, making for a total of nearly 4,000 simultaneous ordinary differential equations that must be solved. Without age binning, they are given by:

Si is the suspectible population for the ith county. Rt is the reproduction rate at time t, depending on whether or not there is an intervention in place. Mij is the transmission from the jth county to the ith county. Ni=Si+Ei+Ii+Hi+Gi+QI+Ri+Di.

Ei is the exposed population. Tinc is the incubation period, i.e., the duration that the population remains in this box.

Ii is the infectious population. Rhosp is the rate of hospitalization per infectious person. Chosp,I is a comorbidity factor for hospitalization, explained below. Tinf is the duration of being infectious (i.e., of remaining in the I box). Individuals who leave the I box can go either to the R or H box. Thosp is a duration for a stay in a hospital that ends in recovery.

Hi is the hospitalized population (including the critically ill). Rdeath is the death rate per infectious person. . Tdeath is time in the hospital leading to death.

Ri is the recovered population, Di is the deceased population, Gi+Qi is the critically ill population.

Comorbidity factor is given by

Where fk is the effect of the comorbidity on the rate R of either hospitalization or death and Pk is the percentage of the population with that comorbidity.