Agent-Based Model for Simulation of COVID-19 Spread

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outbreakmodel

Terminus Example Output
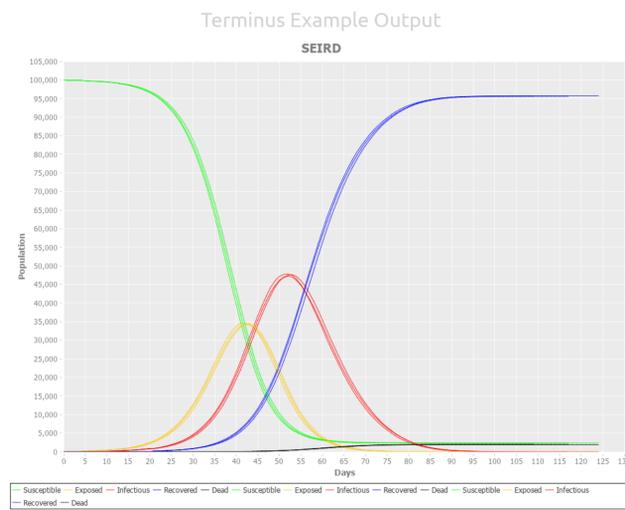
Overview: Here we present *Terminus*, a new Agent Based Model for modeling the spread of infectious disease through a population. In contrast to more mathematical approaches to epidemic modeling, Terminus trades processing speed and simplicity for a greater fidelity to the dynamics of disease transmission. It is highly configurable, capable of simulating various diseases across millions of people. Development on Terminus began during the COVID-19 pandemic in Spring of 2020 using the Clojure language. The source code for the model, along with instructions on its use, is freely available in an effort to help others further understand COVID transmission and the effect of policy decisions.

Methodology: Terminus uses agents to represent individuals within a city; locates them within a household; gives them an age, sex, and susceptibility; and links them with other agents to form social networks through school, work, worship, and more. It is through these networks that the agents spread the disease. To model transmission, for each contagious agent, for each location they go, a group of secondary agents who also visit that location are randomly selected and considered exposed with a probability dependent upon the type of location and mitigation policy currently in effect. After all contagious agents have been processed for a given day, the new exposures are enacted and the policy transition rule is evaluated, and the cycle begins again. Policies take the form of a probability of transmission for a given location type; policy transition rules can depend upon the daily and cumulative counts of agent state transitions, modeling reduced interactions at certain location types with "social distancing" measures in place. Exposed agents are assigned dates of contagiousness, illness, isolation, recovery, hospitalization, discharge, and/or death all dependant upon the agent susceptibility and empirically-derived duration distributions. Each of these parameters can be determined by studies of disease spread and/or chosen to best match observed data for the location being modeled. Due to the stochastic nature of the model, multiple runs should be aggregated to determine the range of likely outcomes. Perturbations to the policy can be made across successive runs in order to account for the uncertainty in their values.

Results: We first demonstrate the applicability of Terminus to epidemic modeling. In Fig A, we present a graph of the compartments by day of three distinct simulations. Each line on the graph bears the characteristic shape of an SEIR(D) model. Given the widespread use of SEIR models in epidemiology, we assert that such similarity shows that Terminus can likewise be used to model outbreaks. Furthermore, the self-similarity of the three simulations demostrates that when using the same initial conditions, Terminus produces nearly identical outputs.

Next we used Terminus to model the spread of COVID-19 in the metro Atlanta area, making predictions on the actual number of exposures, and cumulative and peak hospitalizations and deaths. By adjusting the incubation period distribution within the reported bounds and the transmission rates as different policies went into effect, we were able to achieve curves very similar to the observed hospitalizations in the area, along with the possible future outcomes from simulations that were consistent with the available data to date. We demonstrate that maintanence of the state-wide "stay-at-home" order, effective April 3, 2020, should limit the peak hospitalizations below levels the city hospitals are capable of handling. Calibrating the model to match the available data took less than 3 hours computational time, while the final execution of 256 simulations completed in 1 hour.

Conclusions: We believe that the explanatory power of the Terminus model is worth the added computational time and configuration provided sufficiently accurate data on the dynamics of the disease are available. We hope that other researchers will use Terminus to explore the implications of policy changes and the demographic impact of COVID and other diseases in the future.

Code:

1) Terminus