EEC289Q Project Proposal

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Abstract

Epidemiology modeling and it's high-performance implementation have been a popular field of research in parallel processing. However, interactions between large populations of agents and humans inside the system complicate the simulation process. Variables such as incubation time, mortality rate, forced infection between humans and agents, population size, etc. also contribute to how a specific disease spread. During each time step it is necessary to have a well-synchronized and parallel approach to ensure accurate predictions for transmission. In this project, we are trying to design a parallel algorithm using Cuda that simulates the spread of an infectious disease using an agent based model that incorporates disease transmission pathways in the form of a network of potential interactions.

Previous works

There are two disease transmission models commonly used for epidemiology simulation, agent based methods and compartmental methods [1], [2], [3], [4]. An agent based model for disease transmission looks at a host and tracks how an infectious disease spreads to individuals that the host come into contact with. A compartmental method on the other hand, uses differential equations to model the spread of diseases by vectorizing inputs into classes of susceptible, exposed, infected, and recovering patients. This method analyzes the population as a whole and treats the problem analogous to a kind of fluid diffusion.

While agent based models provide a fine-grained granularity for considering how the disease affects individuals within a population, they are computationally expensive to assess. As a result, hybrid algorithms have been proposed in some other works [1], [3] to combine the compartmental and agent based models at the cost of granularity.

In [1] the hybrid model was focused on runtime and computations and generalized an infectious disease to characterize the performance on a CPU vs GPU. Various hybrid models were used to to illustrate the trade offs between runtime and performance with various population sizes. In [3] the Zika virus was modeled using host-agent interactions in variable

population sizes. Both population of humans and mosquitoes were used as variables when calculating the spread of the disease.

Most of the research done in this area is based on the probability of infection due to spatial relations between potential hosts and carrier. However, they miss the actual dynamics of disease transmission path for human based on their sexuality, social network, and habits.

An agent based approach is proposed in [4] to consider the humans interactions with more details. The disease spread has been modeled in this work as a complex network with different contact patterns and features for each agent. This complex network contains several smaller network layers, each responsible for representing one particular path of infection. However, a suitable GPU implementation for this model has not been proposed.

Algorithm Design

The agent based approach for modelling disease transmission looks at individual properties of the agent in order to calculate the probability that they are transitioning from one state into another. The possible states available to an agent are the ones used in a compartmental population model: susceptible, exposed, infected, or recovering. The probabilities are calculated by looking into the possible network of transmissions which are classified as sexaul behavior *Se()*, social behavior *So()*, and habits *Ha()* of agents *a* in the set of all agents *A* so that $\{Se_i(a), So_i(a), Ha_i(a) \in A\}$. So. Initially, two individuals I_x , I_y are selected at random and if they belong to the same network their transition probability is calculated so that the propagation through the network can be determined. If they don't belong to the same network the probability that they will form a relationship is calculated based on their traits.

The dispersion of a population of agents is based on geographical regions. All agents interactions are calculated through a window that slides over the entire region and selects an initial I_x in the current window. An I_y is selected randomly and if that agent doesn't belong to the current window it's information about the transaction is saved and updated when the window reaches that area of I_y.Once the window covers the entire map that can be considered one time step and the the process is repeated for *x* number of time steps.

In order to parallelize this algorithm, all information about networks and geographical location will be stored as additional traits of an agent. Instead of siding across geographical windows, all agents will be given their own thread and processed at the same time. The calculations for probable infections will be modified to represent a gather approach by looking at

the possibility of getting infected from another agent instead of the probability of infecting another agent.

Milestones

In this project, a parallel design and implementation of [4] will be provided. Following steps are required for satisfying the goals of this project:

1) Creating the network for a specific disease transmission and setting the parameters
2) Translating the agent model into a parallel algorithm
3) Apply the algorithm to the disease network

Evaluation and Deliverables

We want to deliver a model that has tunable parameters for a given disease and estimates the rate of infection over a population. To evaluate the efficacy of our model, the effect of tuning the parameters can be monitored. Tracking the disease over a given time period, population size, and geographic location will show the sensitivity of the disease transmission to each variable changes. We want to be graded based on completeness of the parallel design that we provide for a detailed model.

References

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[3] C. J. Kuhlman, Y. Ren, B. Lewis and J. Schlitt, "Hybrid Agent-based modeling of Zika in the united states," *2017 Winter Simulation Conference (WSC)*, Las Vegas, NV, 2017, pp. 1085-1096. doi: 10.1109/WSC.2017.8247857.

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