**Stochastic Simulation**

Simulation

To begin with, let us first understand what a simulation is. According to Merriam Webster dictionary, Simulation is an imitative representation of the functioning of one system or process using functioning of another.' In other words, a simulation replicates an ongoing process or system that works in the real world. Simulations are represented with the help of models. A model simply shows the main features of a system, but a simulation shows how this model changes through time under specific circumstances.

[ <https://en.wikipedia.org/wiki/Simulation> ]

The simulations are typically computer-based, using software-generated models to assist the engineer's decision-making. Additionally, simulations are employed throughout training. Simulation approaches to aid in learning and aid in research because the developed models are interactive and graphic. When a real system is unavailable, too dangerous to evaluate, or is still in the design or theoretical stages, simulation can also be used.

The information that is utilized to create the simulation model is essential to any simulation, and methods for the verification and validation of models are continuously being studied and improved, especially in relation to computer simulation. Simulation creates a visual mock-up of a process using user-friendly simulation software. To effectively represent the real-world process, this visual simulation should incorporate information about timings, rules, resources, and limitations.

System understanding has always been aided by simulations. For instance, in this thesis, we are simulating the disease COVID 19. This approach employs an individual-based framework in which each person experiences discrete-time state changes. In each of the aforementioned scenarios, it is clear that doing a real-world experiment would be quite expensive. The simulation process has always been a means to reduce costs if a process requires a lot of resources. The process is also simulated using a mathematical model. In the case of biological or ecological processes, this is complete. Since many elements will have an impact on the system. In this study, we model the spread of the illness within a fictitious grid lattice using the Python programming language.

Advantages

* Financial risk is lower – Testing theories of actual systems may incur expenditures such as those related to switching to an unproven procedure, hiring personnel, or even purchasing new equipment. Simulated experiments are less expensive than actual ones. Through simulation, you may test hypotheses and steer clear of costly errors in the real world.
* Frequent Testing - This implies that you can rigorously evaluate and contrast several views without deviating. A simulation enables you to repeatedly test various hypotheses and inventions under the same conditions.
* Observe Long-Term Influences - By precisely simulating the effects of years of use in only a few seconds, a simulation that allows you to look into the future can be produced. The ability to see both immediate and long-term effects enable you to confidently make smart financial choices today that will pay off for years to come.
* Understanding of Process Progress - The advantages of simulation are not just realized at the project's conclusion. By putting various theories to the test, improvements can be incorporated throughout the entire process.
* Evaluate Random Trials - You can evaluate random occurrences like an unanticipated employee absence or supply chain problems using simulations.
* Assess Distributions that Are Not Standard - Instead of needing to repeat only the predetermined parameters, a simulation can accommodate for varying and non-standard distributions. A simulation can better represent reality by accounting for changing parameters.
* Promotes Critical Thinking - It is possible to develop ideas or innovations by carefully considering a process or procedure without even using the final simulation. Solutions can even be found in the process of constructing a simulation and choosing the various parameters.
* Increase Stakeholder Support - Additionally, a visual simulation can aid in increasing stakeholders' and partners' buy-in. Visualizing the outcomes of any process modifications and how they were accomplished would increase attention from potential customers and may even allow for a sales pitch based on simulation.

[ <https://www.capsim.com/blog/advantages-of-simulation-based-learning> ]

In several fields, simulation has always made it easier to understand and duplicate processes. Determining the parameters and factors affecting the system will aid in a thorough understanding of it. making future selections using the factors that have been recognized. Some of the most popular simulations include flight simulators, which allow users to simulate the sensation of flying an airplane. The airlines have mandated that pilots log a minimum number of hours in simulation.

Limitations

The following are important difficulties in modeling and simulation:

* Finding reliable sources of information about the appropriate selection of important traits and behaviors required to develop the model.
* The model's use of simplifying assumptions and approximations.
* The accuracy and reliability of the simulation results.

An ongoing area of academic study, elaboration, research, and advancement in simulation technology or practice, notably in the work of computer simulation, is procedures and protocols for model verification and validation.

[<https://www.bbc.co.uk/bitesize/guides/zyqfr82/revision/3#:~:text=Disadvantages%20of%20modelling%20and%20simulation&text=The%20cost%20of%20a%20simulation,not%20be%20realistic%20or%20reliable>. ]

Stochastic simulation

Various simulations applied in various disciplines were developed primarily separately. A more systematic understanding of the concept has emerged as a result of studies in systems theory and cybernetics, as well as the widespread use of computers in all those domains. When a simulation of a system uses a variable that can change stochastically with probabilities then it is called stochastic simulation. Stochastic is defined as random, more particularly as involving a random variable.

These random variables are created as realizations and added to a system model. After recording the model's results, the procedure is repeated using new random data. Until enough data is collected, these processes are repeated. Finally, the distribution of the outputs displays the most likely estimates together with a range of expectations for the values that the variables are more or less likely to fall inside.

Due to the understanding that continuous models are not necessarily a suitable depiction of what is, at the molecular level, a fundamentally discrete process, stochastic simulation has gained great interest in the last 10 to 20 years. Probabilities are used in stochastic simulations. A number of important publications written by Gillespie in the 1970s served as the foundation for the creation of useful stochastic simulation techniques.

[ <https://www.sciencedirect.com/topics/neuroscience/stochastic-simulation> ]

If used enough times, the stochastic model will produce results that are almost identical to those of the comparable deterministic model. We must consider individual molecule behavior fluctuations if they have an impact on the system. Therefore, stochastic models are necessary.

Approaches

The fact that too many events occur in large systems and cannot all be considered in a simulation is a general problem of stochastic simulations. By making some estimates, the following techniques can significantly speed up simulations.

1. τ Leaping method

The SSA method's high temporal complexity makes it impractical to implement for some applications since it maintains track of each transition. The tau-leaping approach leaps from one subinterval to the next, approximating how many transitions occur within a particular subinterval, as opposed to taking incremental steps in time and keeping track of X(t) at each time step as in the SSA method. It is assumed that the value of the leap, τ, is negligibly tiny such that the value of the transition rates over the subinterval [t, t + τ] does not significantly change. The jump condition is the name for this circumstance. Thus, the tau-leaping method has the benefit of simulating numerous transitions in a single leap without significantly reducing accuracy, which shortens the computational time.

1. Conditional Difference Method

By considering only the net rates of the opposing events in a reversible process, this approach approximates reversible processes (which include random walk/diffusion processes). The key benefit of this approach is that it can be applied with a straightforward if-statement, replacing the model's old transition rates with new, efficient ones. Thus, the replacement transition rates model can be solved, for example, using the traditional SSA.

[<https://en.wikipedia.org/wiki/Stochastic_simulation#:~:text=A%20stochastic%20simulation%20is%20a,a%20model%20of%20the%20system>. ]

**Gillespie algorithm**

The method that resulted in the algorithm acknowledges a number of crucial milestones. The differential equations, now referred to as Kolmogorov equations, were first presented by Andrei Kolmogorov in 1931 and correspond to the time-evolution of stochastic processes that advance via jumps. The circumstances under which the Kolmogorov equations permitted probability as solutions were discovered by William Feller in 1940. In his Theorem I, he proves that the likelihood of the following event is proportional to the rate and that the time before the next jump was exponentially distributed. As a result, he demonstrated the connection between stochastic processes and Kolmogorov equations. In 1977, Gillespie uses a physical argument to obtain the algorithm in a unique way.

[ <https://en.wikipedia.org/wiki/Gillespie_algorithm> ]

When the reaction probability is known, the Gillespie algorithm in probability theory is utilized to calculate the expected path for the stochastic equation system. Dan Gillespie used this algorithm, which is more than seven decades old, to mimic the chemical and biochemical systems, which led to its popularity. The approach could be utilized in increasingly more complex systems as computational costs increase over time.

Imagine that we want to simulate a specific chemical reaction. To represent the process using a deterministic technique, we may set up a family of linked differential equations. In effect, we will "ignore" any microscopic behavior by doing this and instead focus on the reaction system's "high level" behavior. This may cause us to lose out on a lot of the reaction's "detail" that we would have found interesting.

Using a stochastic "discrete event" model is an alternative strategy in which we describe individual reactions separately as discrete events taking place across time. This is consistent with our physical sense of how reactions happen: we wait for a reaction to happen just before the reactants "bump" against each other in the proper way. This can be quantitatively summarized by using a "master equation," for example.

[ <https://lewiscoleblog.com/gillespie-algorithm> ]

The master equation can therefore be written in the following form:

Graphical user interface

Description automatically generated with low confidence

The probability distribution of the states at time t is represented by the vector Pt, which is hidden by the notation. This is a Kolmogorov reverse equation for jump processes, which anyone with a mathematical or probabilistic background will be able to recognize.

In the sciences, a multi-state jumping system—that is, a system that "jumps" between various states over time—is represented by a master equation that captures its time evolution characteristics (in contrast a "diffusion system" varies gradually). Due to the stochastic nature of the system in question, we are interested in tracking how the state distribution changes over time. For instance, given a certain beginning condition, what is the likelihood that the system will be in a specific state within the next X seconds/minutes/years?

The time evolution of any spatially homogenous mixture of molecular species that interact through a specific set of linked chemical reaction channels may be numerically calculated using an exact method that is presented within the context of the stochastic formulation of chemical kinetics. The technique is a condensed Monte Carlo simulation process that is computer-based. It should be especially helpful for modeling the transient behavior of well-mixed gas-phase systems where several molecular species take part in numerous chemical processes that are highly linked.

The Gillespie Algorithm, in which objects are observed to change their state along a temporal axis, is one of the well-known techniques for mimicking a Markovian process. In this approach, each object's state at a discrete-time step solely depends on the state that came before it. No reliance on other states exists. Plan to carry out the reaction with a probability at each time step (Stochastic simulation of epidemics).

This algorithm is one kind of dynamic Monte Carlo. It is mainly used in cases where the change of state is within a cell. As it is a stochastic simulation the results are not supposed to be the same after each simulation.

Pseudo Algorithm

1. **Initialization** of the system with the context of reaction and Poisson ratio. Initialization of the parameters and state of the cells.
2. **Monte-Carlo** -
   1. Applying the reaction on the basics of randomly picked value and Poisson rate defined for each reaction.
3. **Update** - Store the value of the current state of the population.
4. Repeat 2 and 3 until the feasibility of the transition is available.

Project Algorithm

1. Initialize the grid lattice, Poisson ratio for global and local transmission, infection rate, vaccination rate, and the recovery rate are defined. Initial infected people are also defined.
2. Events occur according to the randomness defined while initialization.
   1. Location of the Neighbours are stored which is called while infecting locally.
   2. With respect to the drawn event the infection happens in either global transmission or local transmission.
   3. Vaccination and Recovery are carried out with a prefixed probability.
3. Population demography is carried out wherein the number of susceptible, infected, and recovered is identified.
4. Next time step is carried out by repeating 2. and 3. until the last person is recovered.

The SIR model (susceptible-infected-removed model), a well-known method for explaining the spread of infectious diseases in the presence of immunity, is a staple of mathematical epidemiology, a branch of theoretical biology. According to the explanation provided below, it is named after the population's classification into three groups: Susceptible (S), or contagious, Infected (I), and People Removed from the Infection Process (R). By including individuals who are exposed, or those who are infected but not yet contagious, the SEIR model broadens the SIR model's scope.

[ <https://de.wikipedia.org/wiki/SIR-Modell> ]

Algorithm of SIR model

1. An array is used to represent the population in a grid lattice where 0,1 and 2 represent the susceptible, infected, and recovered respectively.
2. Beta and gamma are the propensity value for a single cell to cause a transmission (infection or recovery).

In local transmission following are the steps considered:

* Getting cartesian pair value of the cell with value '1'.
* Getting the set of neighbors to the above list who has the value '0'. Set is considered to avoid repetition.
* Assigning value 1 or 0 to variable 'rand1' with a probability of beta propensity for each iteration with respect to values in the set (susceptible neighbors) and adding this variable 'rand1' to the cell. Thus, the randomness of transmission is wrt to the propensity value.
* Same is done for the global transmission. The number of iterations for global transmission is with respect to the number of infected cells.

1. Each infected cell is located first. Propensity value beta is used as the probability of infecting the respective neighboring cell or another global person.
2. Infected persons are changed to recovery with the propensity value gamma with time.
3. p valuelue denotes the probability of local transmission. Probability of Global transmission is calculated as (1-p).

**Cellular Automata**

The term cellular automata are plural. A discrete model of computing investigated by automata theory is the cellular automaton. Tessellation automata, homogeneous structures, cellular structures, tessellation structures, and iterative arrays are other names for cellular automata. Applications for cellular automata can be found in many fields, such as theoretical biology, microstructure modeling, and physics. A cellular automaton is a group of cells arranged in a grid with a predetermined shape, where each cell changes state over time in accordance with a predetermined set of rules that are influenced by the states of nearby cells.

A model of a system of "cell" objects with the properties listed below is called a cellular automaton.

* The cells are arranged in a grid. Any finite number of dimensions can support the existence of a cellular automaton.
* A state exists in every cell. Typically, there are only a limited number of possible states. The two alternatives in the most basic example are 1 and 0 (sometimes known as "on" and "off" or "alive" and "dead").
* There is a neighborhood for each cell. This can be described in a variety of ways, but commonly it is a list of cells that are close to one another.

[ <https://natureofcode.com/book/chapter-7-cellular-automata/> ]

A picture containing text, electronics, calculator

Description automatically generated

Outside of the geographic sciences, cellular automata have also been employed in a range of social scientific applications, largely because of how well they simulate geography.

While working together at Los Alamos National Laboratory in the 1940s, Stanislaw Ulam and John von Neumann made the initial discovery of the idea. Although some people explored it in the 1950s and 1960s, it wasn't until Conway's Game of Life, two-dimensional cellular automata, appeared in the 1970s that interest in the topic grew outside of academia. One-dimensional cellular automata, or what Stephen Wolfram refers to as elementary cellular automata, were the subject of his methodical study in the 1980s; research assistant Matthew Cook demonstrated that one of these rules is Turing-complete.

[ <https://www.sciencedirect.com/topics/earth-and-planetary-sciences/cellular-automata> ]

A set of data manipulation rules is said to be Turing-complete or computationally universal in computability theory if it can simulate any Turing machine. A cellular automaton, a programming language, or a series of computer instructions could all serve as the rules for manipulating data. This indicates that this system is capable of identifying or selecting different rule sets for data manipulation. The strength of such a data-manipulation rule set is expressed in terms of Turing completeness. Turing-complete programming languages are essentially universal nowadays.

[ <https://en.wikipedia.org/wiki/Turing_completeness> ]

Abstract computers can be made from cellular automata. Von Neumann, who built a two-dimensional cellular automaton that can replicate any Turing machine, made the initial observation of this. A Turing machine is a theoretical representation of ad hoc computing systems, such as the universal Turing machine, which served as the inspiration for the design of contemporary digital computers.

The von Neumann neighborhood and the Moore neighborhood are the two most prevalent types of neighborhoods. The von Neumann neighborhood is made up of the four orthogonally adjacent cells and is named for the pioneering cellular automaton theorist. The Moore neighborhood comprises the four diagonally neighboring cells as well as the von Neumann neighborhood.

Chart

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The blue cell's von Neumann neighborhood is represented by the red cells. The pink cells are also included in the range-2 "cross neighborhood".

A red and white flag

Description automatically generated with low confidence

The Moore neighborhood for the blue cell is shown by the red cells.

Insofar as they contain a finite number of states and are entirely controlled by their local functions, which are maps between finite sets, cellular automata are finite machines.

[ <https://en.wikipedia.org/wiki/Cellular_automaton> ]

Cellular Automata is time discretized approach to simulating a system. When the system has elements that influence each instance of time this method is highly exploitable. At the time step, each cell has its state which can or can affect the neighboring or the other cells according to the condition defined in the system. It employs a grid that represents the population or set of elements in the play. The grid lattice is usually a finite space i.e., the grid size will be a predetermined size and dimension. This paper uses 2 Dimension grid lattice.

Cellular automata come in a variety of forms. A binary, nearest-neighbor, one-dimensional automaton known as an elementary cellular automaton is the most basic form. The smallest non-trivial class of cellular automata is called an elementary cellular automaton (CA). Cells in this CA can have one of two potential values: 0 or 1. This CA can therefore be represented by a table that specifies the state that a cell will be in during the following generation based on the value of the cell to its left, the cell itself, and the cell to its right.

[<https://www.techtarget.com/searchenterprisedesktop/definition/cellular-automaton#:~:text=A%20cellular%20automaton%20(CA)%20is,the%20states%20of%20neighboring%20cells>. ]

Elementary CA's key traits include the following:

* It only has one dimension.
* There are just two potential values for cells: 0 or 1.
* Any cell on the grid in this instance is dependent upon the cell itself as well as its left and right neighbors.
* Cells' states can change across generations. Starting with the initial state ("generation zero") in the first row, the first generation in the second row, etc., one can visualize the evolution of a one-dimensional CA.

**Global and local transmission**

The covid virus is a highly contagious disease. It was difficult at the beginning of the outbreak to exactly determine how the spread of the virus is happening. There was speculation that virus spread through contacted bodies like metals and objects. It enters the body through the nose and mouth and affects the respiration system of the body. In some people, the case worsens and leads to death. Due to the nature of the disease, it is very important to restrict the movement of the people. And hence the lockdown was brought into action by the government Onsight of the presence of the virus in most countries. Which also lead to a standstill in the daily actions in the country and a huge drop in the economy and life balance of the people. With the implementation of the lockdown, the spread had come down which otherwise will be a highly catastrophic situation. Lockdown and reduced movement of the people implies that the spread of the disease is highly likely through neighbors in the town. Even though the restrictions are brought into effect complete stoppage of mobility will not be possible in order for the country to work. Thus, there will be people at work who will meet others in a different locality. Moreover, public transport is a place where there is a high chance of people having contact with many others in general. This type of transmission is considered Global transmission.

In this stochastic cellular Automaton to simulate the local spread the vertical and horizontal neighbors are considered. For each time step, the list of neighbors is extracted and infected. While in the case of global transmission every susceptible is equally likely to be infected. But one could observe that the spread is never completely global or local. It is most likely that most of the spread is happening through global transmission because the one person if he traveled around the chance of meeting another person is very probable. Hence infecting the other susceptible in the process. It could be that the person was asymptotic and did not know that he was infectious. With the level of restriction, the ratio of the local transmission and global transmission changes. In this master thesis, simulation of the disease spread with a varying change of the transmission ratio from 0 to 1 is one of the focuses. In the reality, we have seen the peak of the number of infected people has prolonged after the implementation of the lockdown in the outbreak of the virus. But after the restriction of mobility was reduced, we have seen a huge spike in the infected people with a sudden increase.

Since there is no vaccination for the disease the virus can infect the same person more than once. Thus, we have seen the tendency of forming peaks at an interval in countries. The number of infected at a point time reaches a time high and comes down for a period of time and then increases in numbers to move on to the next wave. With restrictions coming down with each wave we have seen that the peak number of infected people has increased each time. This study is conducted to identify how the rate of spread of disease changes with the transmission of the virus among neighbors which is termed local transmission or population in general called global transmission. Local transmission implies that an infected person will be infecting the next person which is his immediate neighbor. This can be in compared to the real-life situation of a person being in the building and the chance of him infecting the person living in the same building. And the obvious condition of infecting his household people.

Global transmission is when an infected person is traveling around the place and infecting the person. Meaning he has an equal chance of infecting the entire population. This is the case of the general compartmental model of the Disease spread. The mathematical model of the SIR model considers the infection for the entire population to be the same. This is not entirely true in the case of reality. Global transmission in a way can be related to the community transmission of the disease.