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Report #2

1) For Game of Life:

a) I would use Discrete Space for the model. In that model we can observe such types of agents: patches, turtles and links. The properties of agents in the model are as follows: grids, states, neighborhood and rules. The state of patches is constituted by grids and states, whereas turtles and links – by grids, states, neighborhood and rules. Grids perform the number of dimensions, states represent is cell alive or dead (0 or 1), neighborhood shows us what direction turtle-agents can move, rules are sets of instructions for link-agents. For each agent we need to update its state according to the initial set of rules until it reaches the desirable amount of iterations. Between two subsequent simulation steps the state of each agent updates as follows: 1) any live cell with two or three live neighbors survives; 2) any dead cell with three live neighbors becomes a live cell; 3) all other live cells die in the next generation (similarly, all other dead cells stay dead).

2) For the model of epidemic:

a) This model simulates the spread of an infectious disease in a closed population. Individuals wander around the world in random motion. Individual gets a chance to be infected when it is located in any of the eight surrounding neighbors of the infected person or in the same area or being in contact with an infected person. An infected person has a probability of recovering after reaching their recovery time period. The colors of the individuals indicate the state of their health: white individuals are uninfected, red individuals are infected, green ones - recovered. Once recovered, the individual is permanently immune to the virus. The graph infection and recovery rates show the rate of change of the cumulative infected and recovered in the population. It tracks the average number of secondary infections and recoveries per tick. To provide some useful insight we should consider such aspects: initial amount of people in a population (initial-people), a chance of being infected (infection-chance), a chance of recovery (recovery-chance) and an average recovery time (average-recovery-time). Nevertheless, some aspects of the real phenomenon can be omitted in the model. For example, transmission of an infectious disease may occur through several pathways: by means of contact with infected individuals, by water, airborne inhalation, etc. However, in the model the direct contact of susceptible individuals with an infected one will be considered as the main transmission medium of contagious diseases. Apart from that, we do not consider the condition and capability of each person immune system, we always take an average value of each parameter we use, which is not fully correct in terms of real life. The model assumes a closed population, meaning there are no births, deaths, or travel into or out of the population. It also assumes that there is homogeneous mixing, in that each person in the world has the same chance of interacting with any other person within the world. In terms of the virus, the model assumes that there are no latent or dormant periods, nor a chance of viral mutation. That aspects are omitted due to the impossibility of knowing the data we need about each person, therefore, we are forced to consider an average value of it. That inclusion leads only to an approximate scenario of infection spreading consequences.

b) I would use Continuous Space for the model. In that model we can observe such types of agents: observer, turtles and links. The properties of agents in the model are as follows: initial-people, infection-chance, recovery-chance and average-recovery-time. Initial-people parameter represents the total number of individuals in the simulation, determined by the user; infection-chance parameter shows us a probability of disease transmission from one individual to another; recovery-chance parameter depicts a probability of an infected individual to recover once the infection has lasted longer than the person's recovery time; and average-recovery-time shows us an average recovery time for an individual. For each agent we need to update its state according to the initial set of rules until it reaches the desirable amount of iterations or until all population will be proposed as recovered.

Between two subsequent simulation steps the state of each agent updates as follows: first of all, the program checks the color of the particular individual. If it is white and there are no infected individuals around it – it will be kept white. If it is white but there is at least one infected individual in the near – it will be assumed as infected as well by the program that consequently will change its color to the red one. For each newly infected individual it will check the time for recovery. In case it ends but that individual is still infected, the program starts calculating its chance to recover. If a green turtle faces red one, the program should check the infection-chance parameter in order to know will it be infected again or not. If not – it will be kept as green till the end of algorithm work. If it is proposed as again infected – the cycle for red individuals repeats. During the algorithm work each individual is free to move. The program finishes its work when all the supplied turtles is considered recovered.