

EPIDEMIC SPREAD OVER CELLUAR AUTOMATA

Computational Biology

ex1

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Abstract:

A global epidemic is an interesting research field, and in our exercise, we simulate it over cellular automata, looking for some statistics and behaviors of a virus who's aim is to hit each cell over the CA (Cellular Automata).

The Model:

The model consists 200x200 cells over a grid, each cell resembles to human cell. We have N viruses who moving between cells in a uniform distribution. Each virus can be infected at some time, even the source (the virus that started it all) can be infected during the time (generations). An infected virus has a probability P of infecting other viruses, only those who are its neighbors. The model can even simulate a immune system, with parameter K who define the number of protected cells around a virus, so an infected virus can't infect those cells (no meter what its probability).

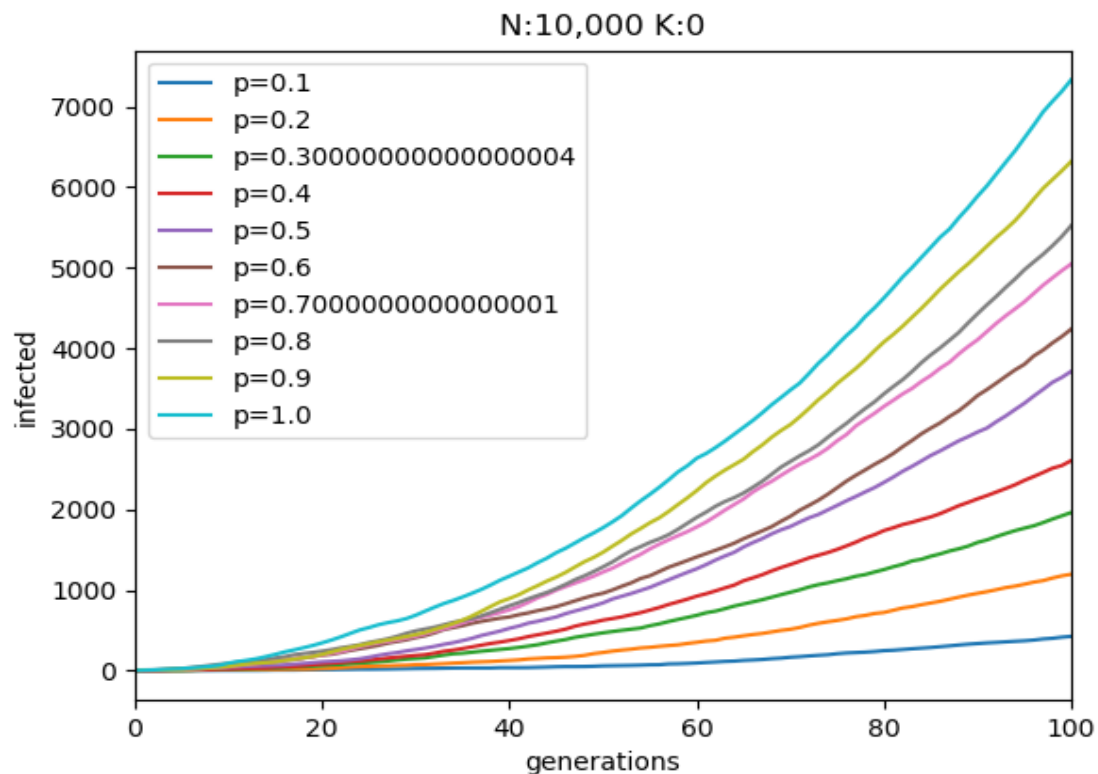
Parameters:

- P – probability of virus to infect a neighbor cell
- K – number of protected cells from infection. 0 means without protection.
- N – number of viruses move around the grid.

Results:

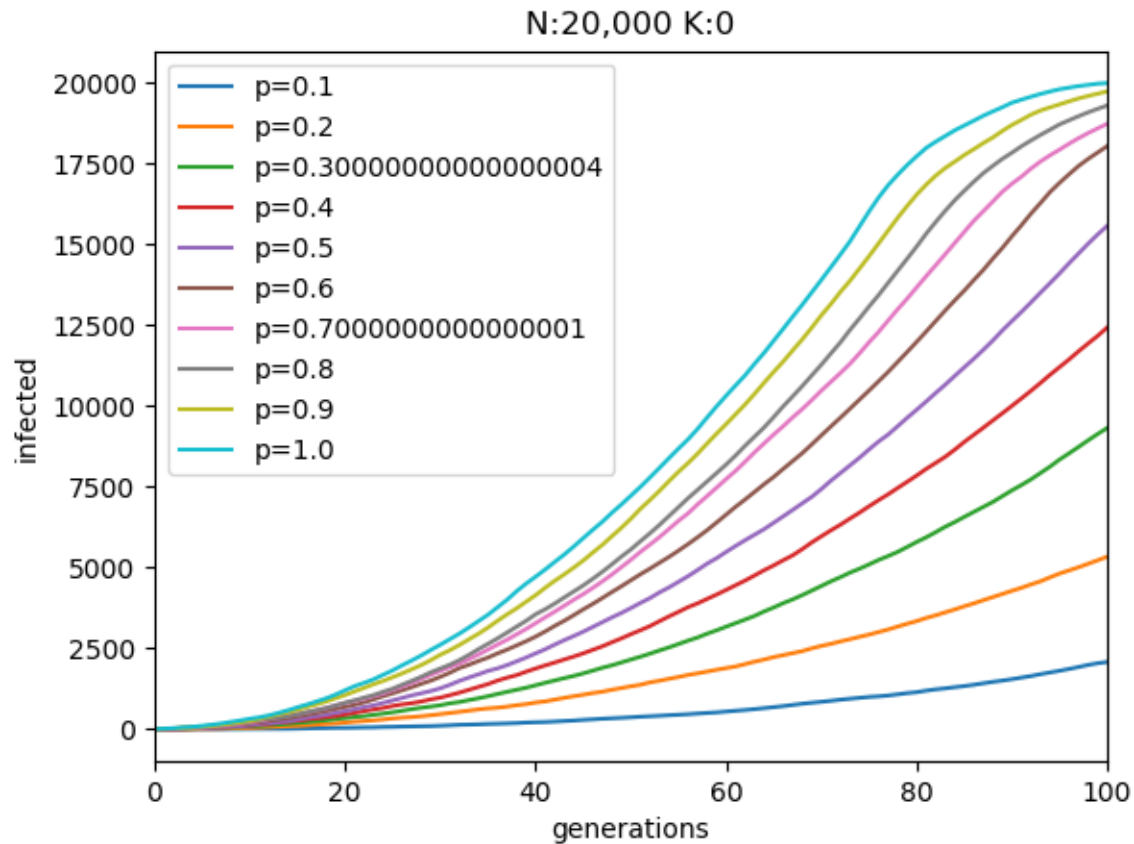
We done our experiments with ensemble of parameters. 10 experiments for each ensemble of parameters.

K=0 N=10000



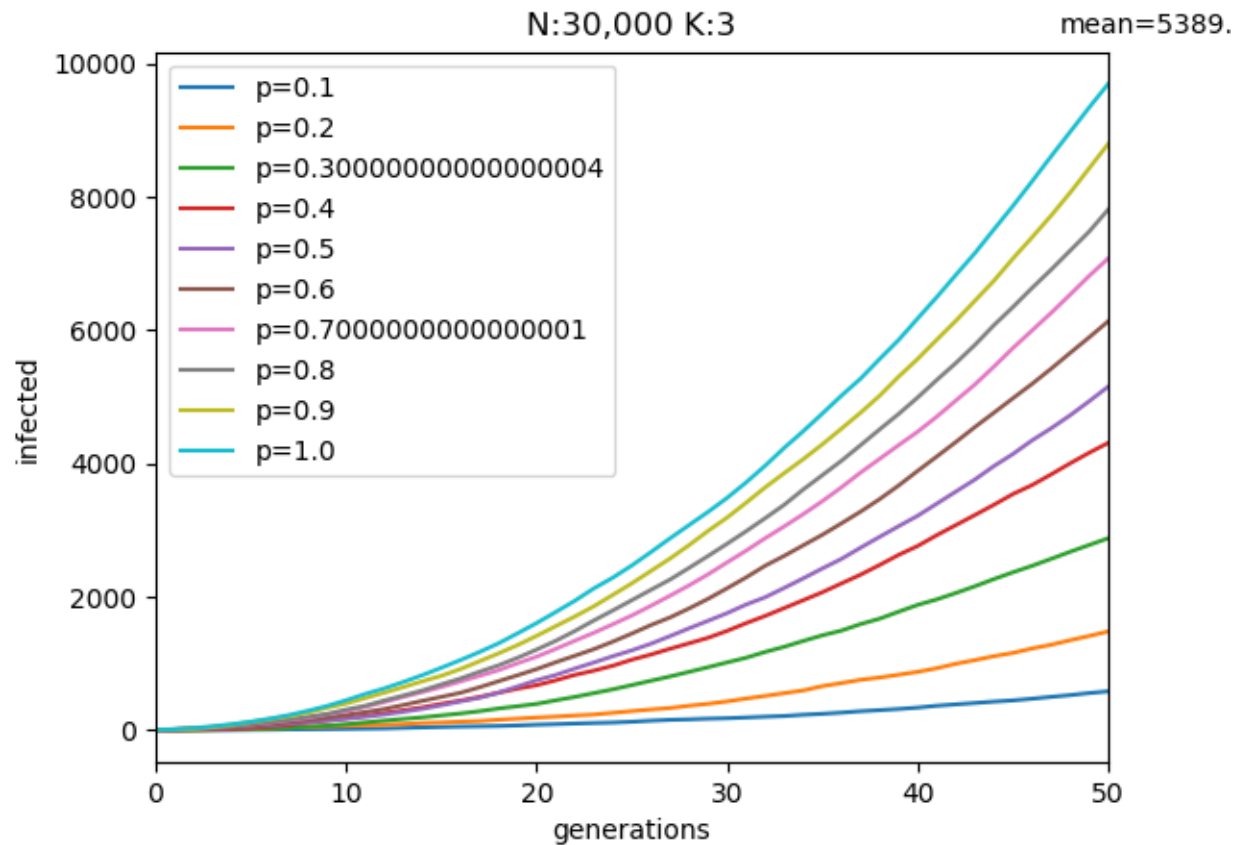
We can see an experiment with 10,000 viruses, 0 cells with protection, means that the model has no immune system, over a 10 probabilities between 0.1-1, when the first spreading virus is infected from the beginning. It's clearly that the curve with $p=1$ is the sharpest. We can see that the curves with $p=0.7$ and $p=0.8$ are very close to each other. See n10000k0 folder to watch animations of the model.

K=0 N=20000



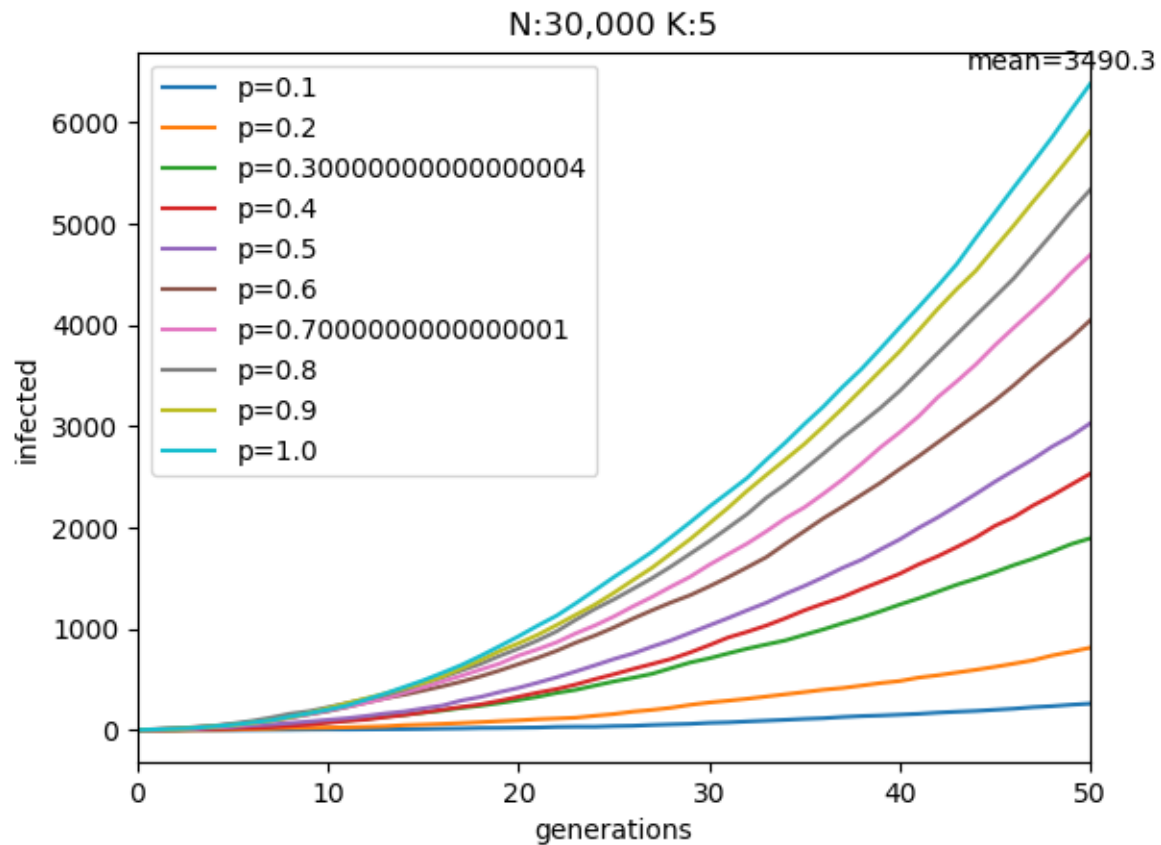
Now we have almost the same as before, but now we examine 20,000 viruses over the grid. We can see two changes from the previous graph - more exponential curves and more infected cells. This is because there are more viruses moving around the grid and cover it, so the first spreading virus has more chances to infecting neighbors. See n20000k0 folder to watch animations of the model.

K=3 N=30000

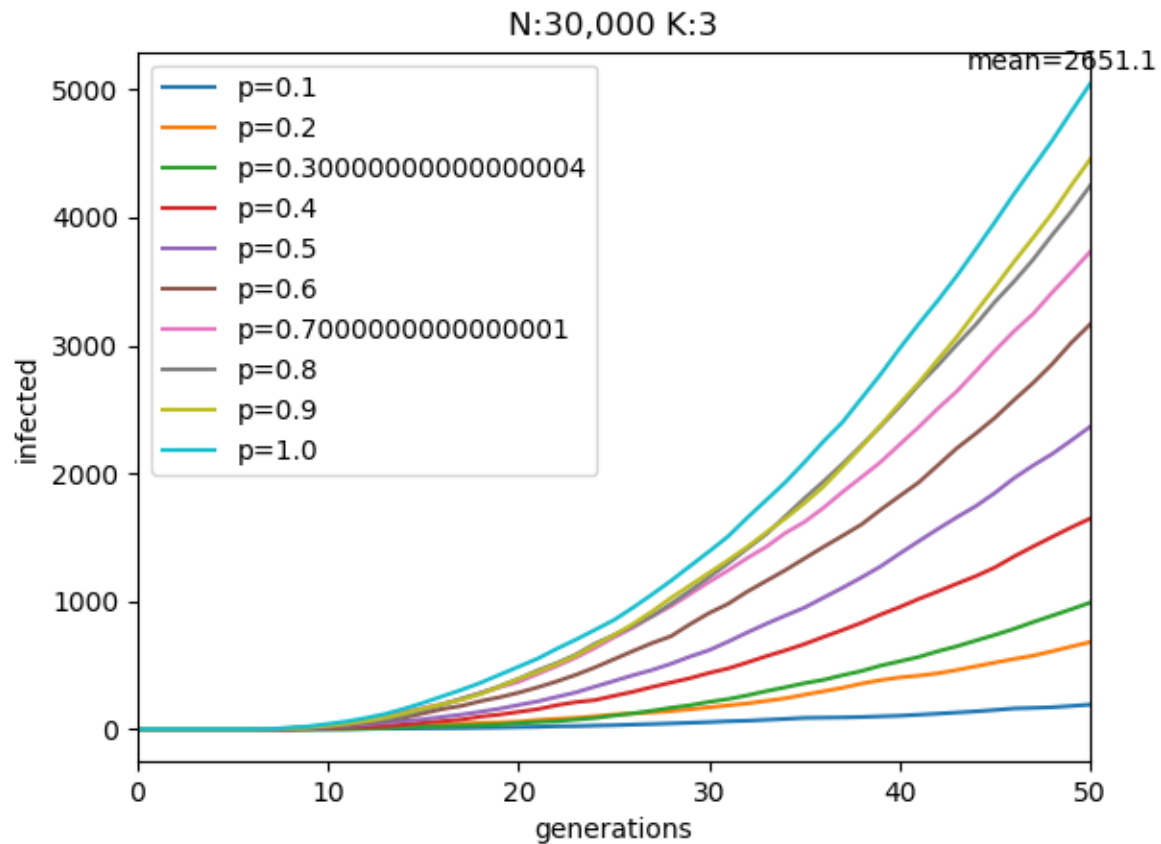


Now, we can see a model with 30,000 viruses moving around the grid – it's three-quarters of the grid, more exponential curves, with protection factor of K=3, it's means that 3 cells around infected virus can't be infected. The model reaches the 10,000 and more cells during 50 generations. The infected cells average of this model is 5389 cells. See n30000k3 folder to watch animations of the model.

K=5 N=30000

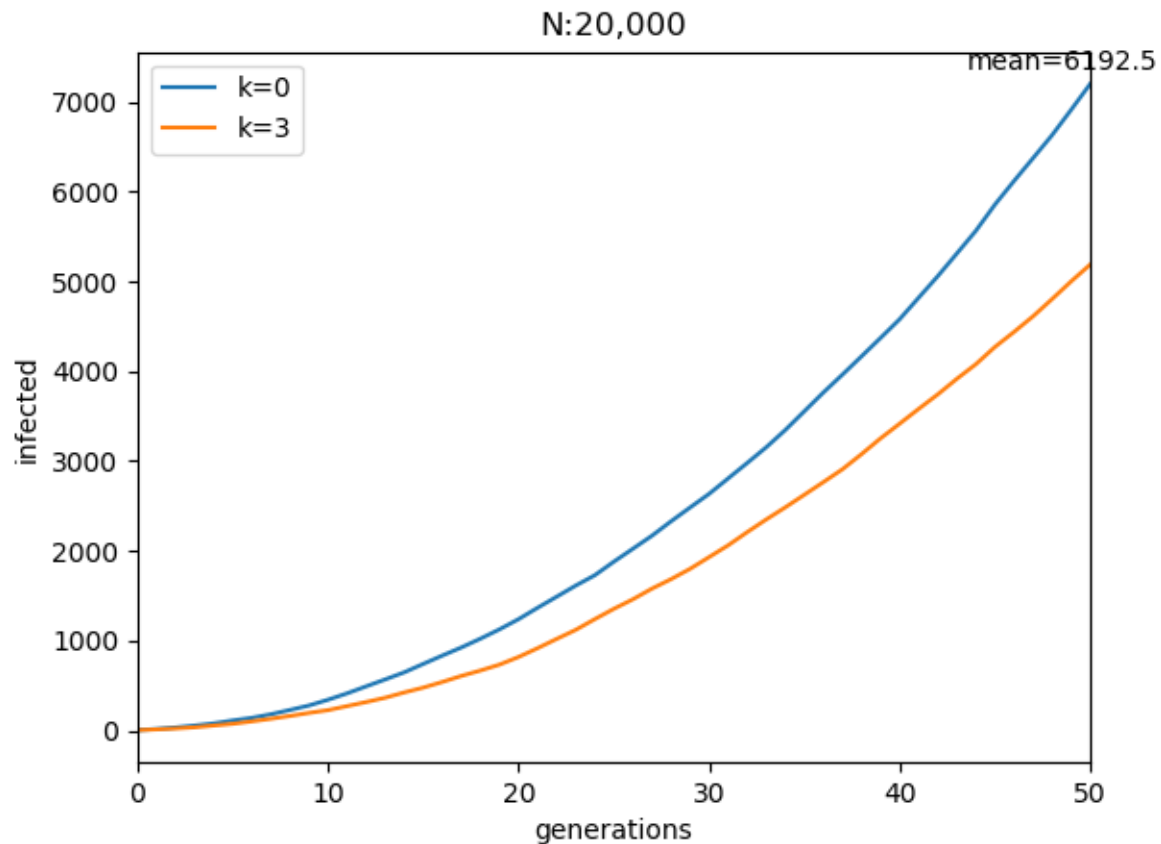


Here we have increased the number of protected cells to 5 cells (more strong immune system) and the average number of infected cells was decreased to 3500 cells, lower than the previous one. See n30000k5 folder to watch animations of the model.



This model has the same parameters as the previous one, but now we let the first spreading virus to be infected only after 6 generations. Due to that, we can see how the beginning numbers of infected cells at each probability measure are very close to each other, during 10 generations. It means that until the first spreading virus were infected, the system was clean, and finally the average number of infected cells has been diminished.

K=0 or 3 N=20000



Here we have tried to compare between two models – one with $k=0$ (no immune system) and the other with $k=3$ (immune system with 3 protected cell around virus). We took a 20,000 viruses and probability of 1 to infection. We can see the differences – the blue curve more exponential from the orange curve, due to their number of protected cells. The average of infected cells is 6200 cells.

Conclusions:

Our model success to mimic a human body system with different difficult levels of an immune system. We have showed how an infected virus can infect other viruses around it, with different probabilities, i.e. for $p=1$ we saw how the infection rate is grow, and how a strong immune system can defend on her cells from being infected.