

Epidemic spreading dynamics

Continuous assessment activity #4

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Explanation:

Software used to work on the networks: NetworkX (Python).

(In the notebook and the following discussion the letters “p”, “b” and “u” stand, respectively, for “ ρ (rho)”, “ β ” and “ μ ”)

I analyzed the following networks:

- ER networks, created with the function I implemented for the Models project (Continuous assessment activity #2) :
 - $N = 500$, $\langle k \rangle = 6$, I studied the behavior for $u = 0.1 / 0.5 / 0.9$
 - $N = 1000$, $\langle k \rangle = 12$, I studied the behavior for $u = 0.5$
- SF networks, created with the function I implemented for the Models project (Continuous assessment activity #2) :
 - $N = 500$, exponent = 2.7, studied for $u = 1$
 - $N = 500$, exponent = 4, studied for $u = 1$
- Real Networks:
 - Airports network ($N = 3618$), studied for $u = 0.1 / 0.5 / 0.9$
 - Erdős collaboration network ($N = 6927$), studied for $u = 0.1$
 - Friend lists on Facebook ($N = 4039$), studied for $u = 1$

For each network the results of the Monte Carlo simulation were compared to the theoretical prediction of the Microscopic Markov Chain Approach (MMCA) model.

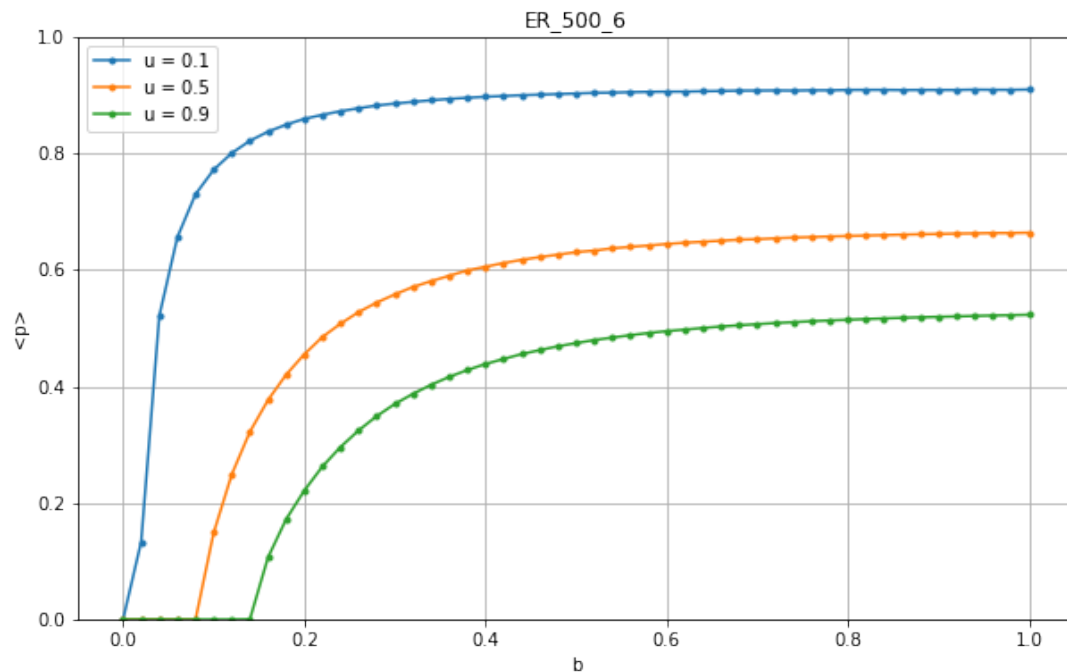
Some simulations were done for 100 repetitions and some others just for 50 because they required too much time otherwise.

To optimize the computing time, for each network, before launching the full simulation, I plotted the simulated evolution of the fraction of infected nodes through the time-steps for some b values to see when the transitional state ends and the stationary state is reached. T_{trans} and T_{max} were adjusted consequently.

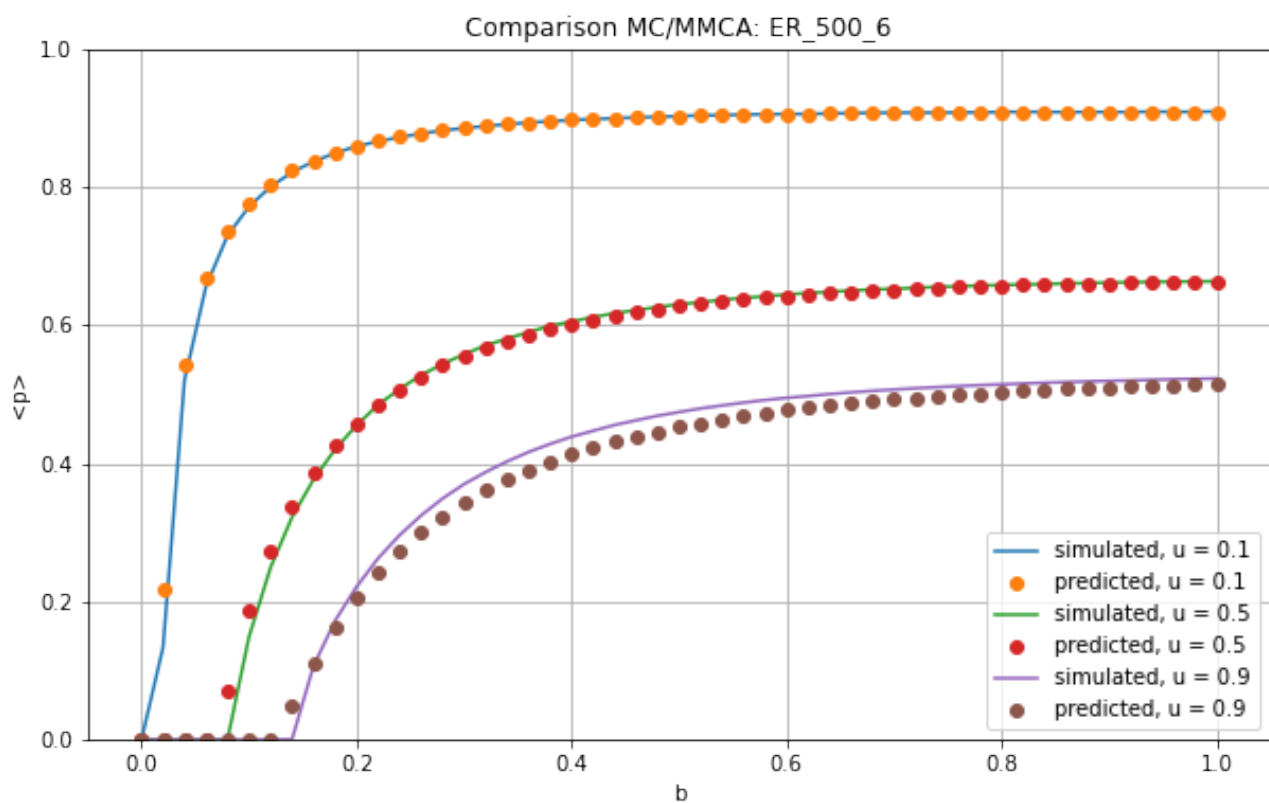
ER networks:

- ER, $N = 500$, $\langle k \rangle = 6$

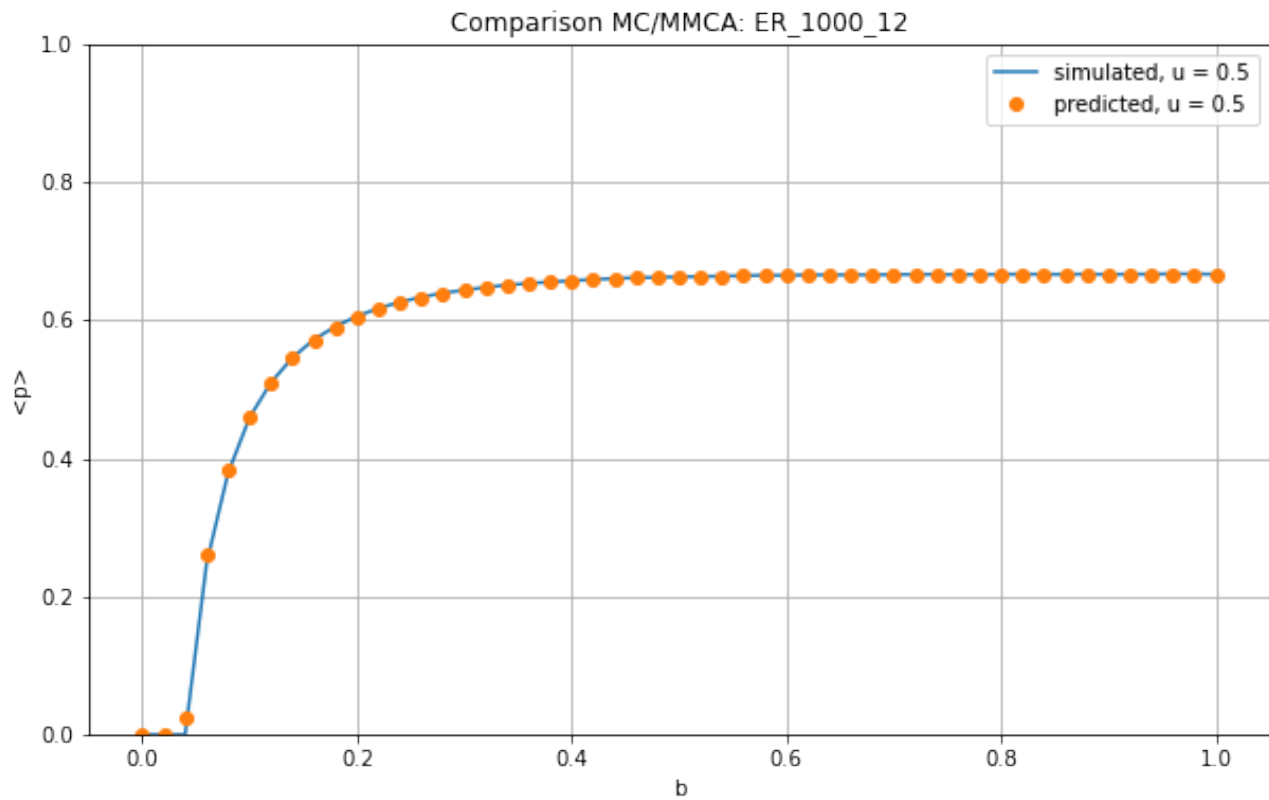
Plot of MC simulation:



Plot of comparison between simulation and theoretical prediction:

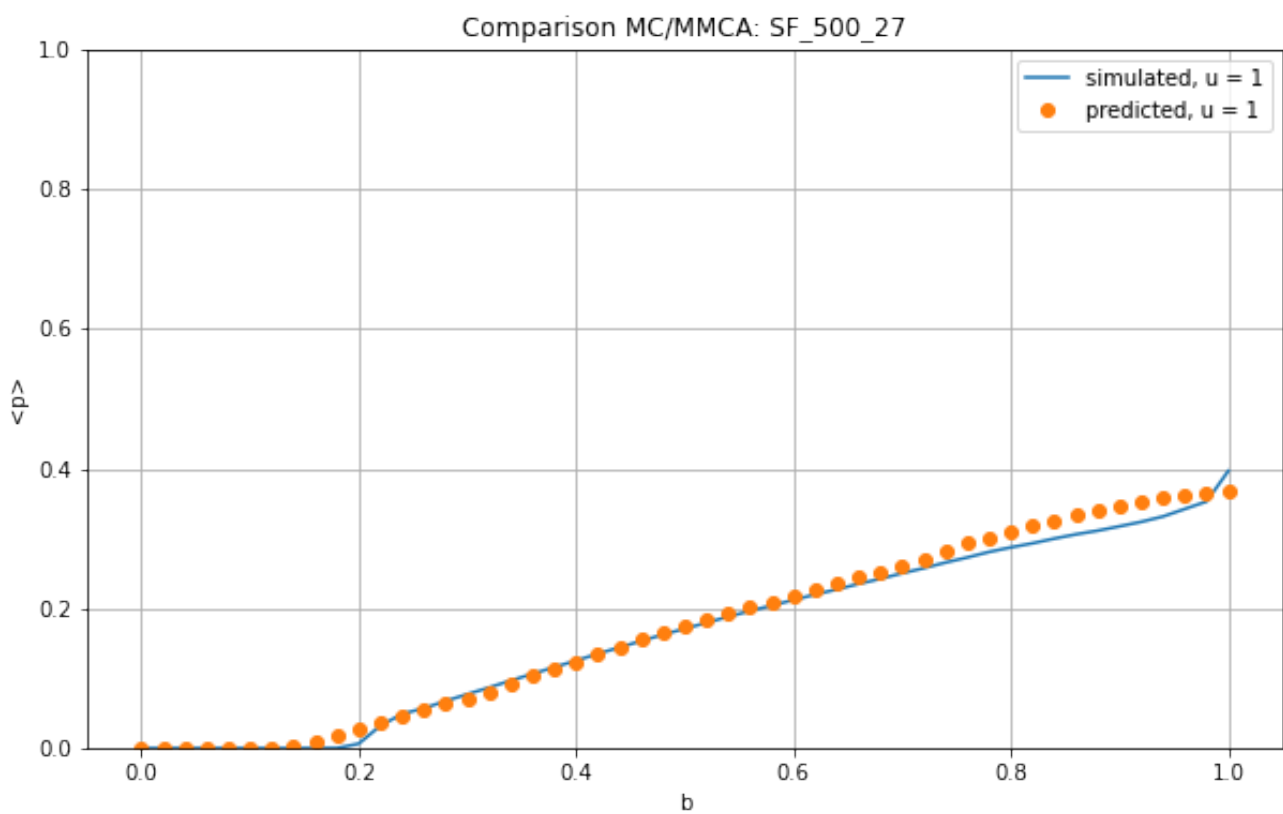


- ER, $N = 1000$, $\langle k \rangle = 12$

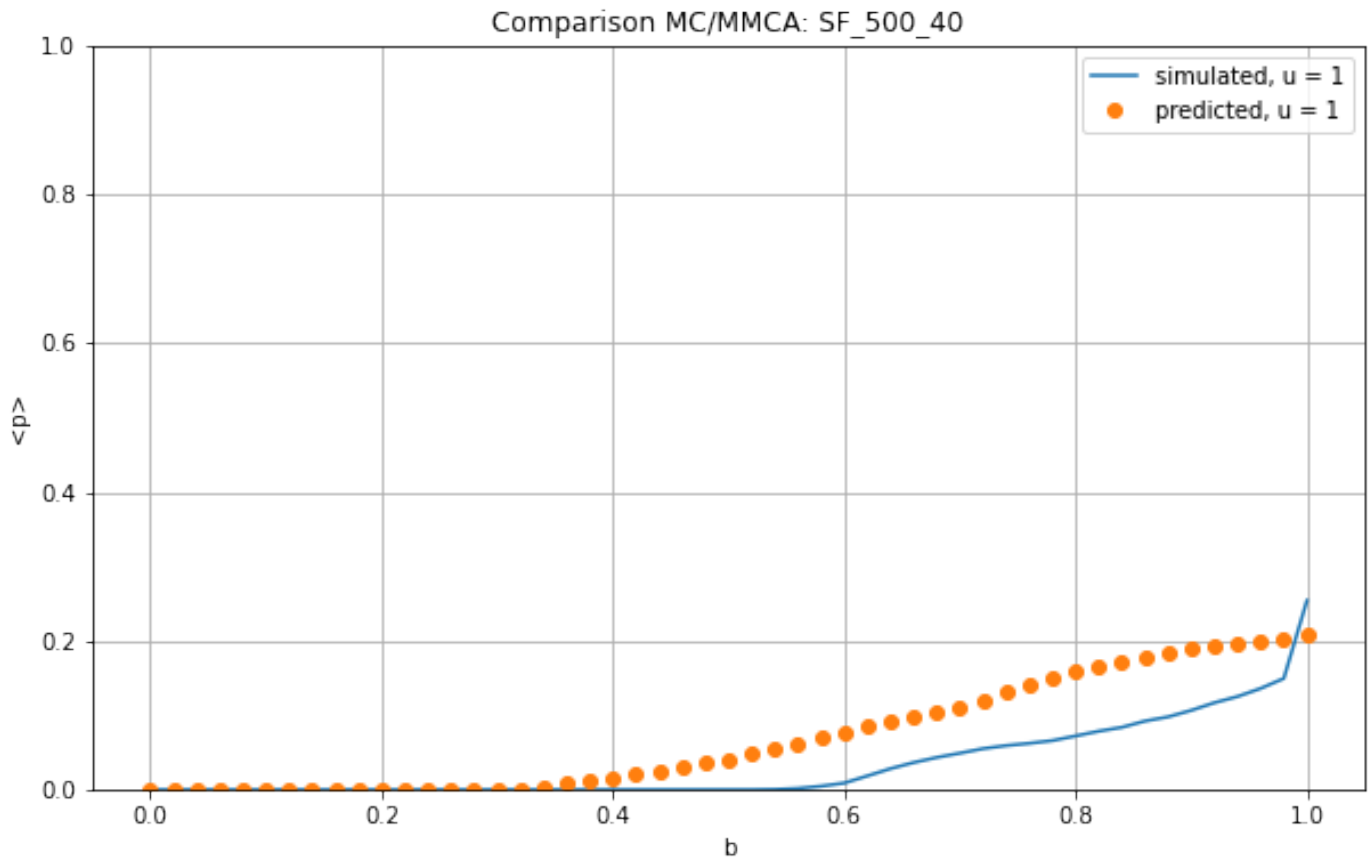


SF networks:

- SF, $N = 500$, exponent = 2.7

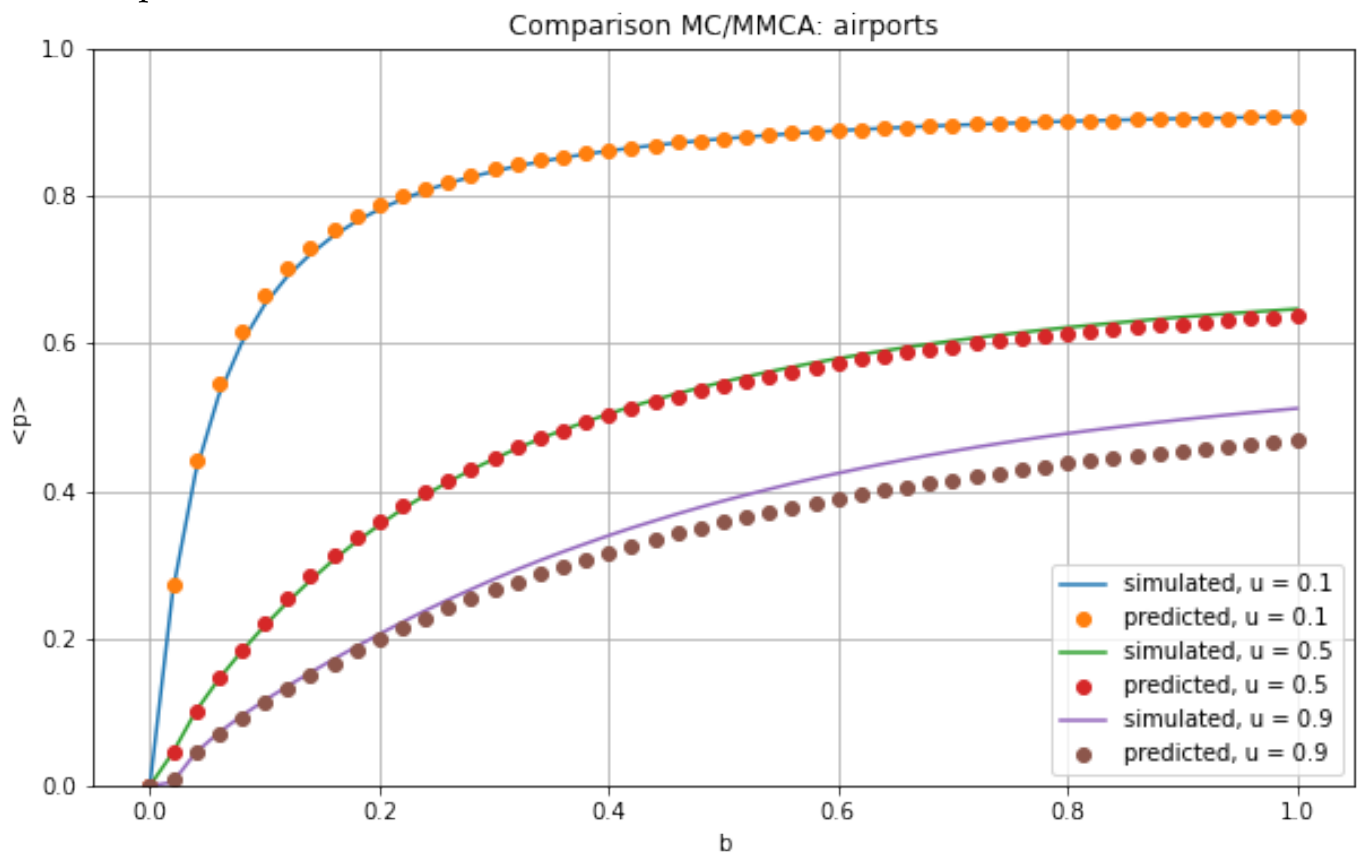


- SF, $N = 500$, exponent = 4.0

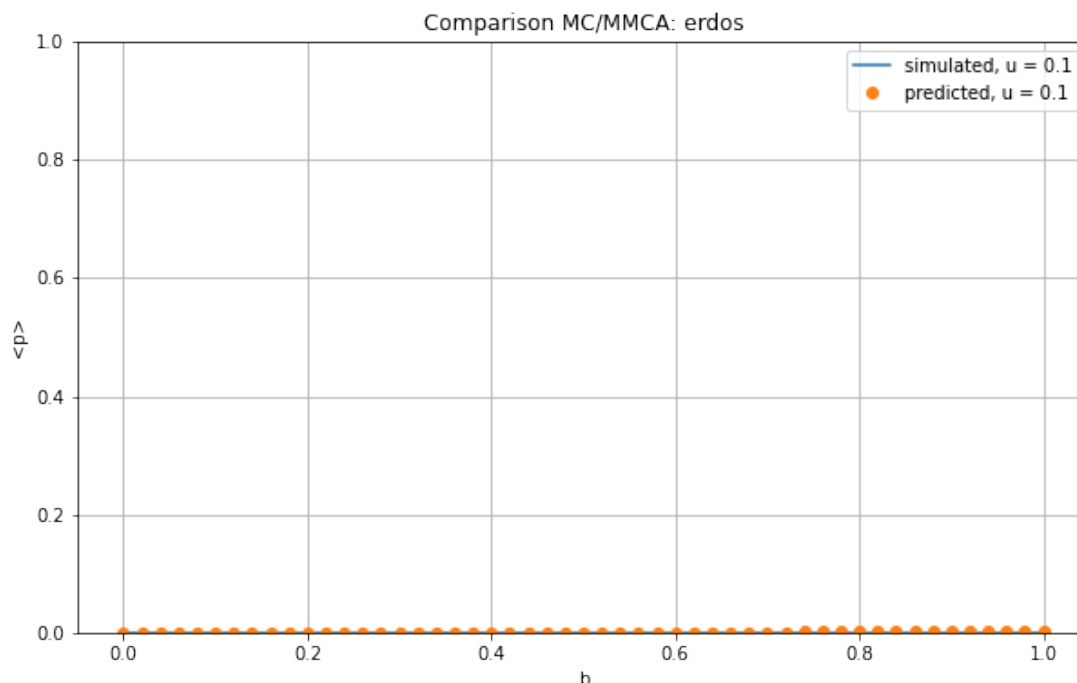


Real networks:

- Airports_UW ($N = 3618$)



- Erdős collaboration network ($N = 6927$)



This network is very sparse (just 574 edges) and the epidemic dies out quickly. I also tried to see the behavior for different u to see if I could find a sort of epidemic threshold for u (a u value such that exist a b that makes the epidemic spread) but even for really small u values the fraction of infected nodes decreases in the log run (in 2000 time steps) without reaching a stationary state. (These plots can be found in the notebook)

- Facebook friends lists ($N = 4039$)

