

Peer review file

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Comment 1: The Authors make use of a SEIR model to describe the spread of the virus in a simplified network-based population. Instead of estimating the transmission by solving the differential equation of a traditional SEIR model, the authors describe the dynamics with a CA. The resulting CA-SEIR model seems to successfully describe the spread in the simplified scenario and allows to verify how impactful are the adopted countermeasures. There are few things about the model that should be clarify:

Reply 1: First we would like to thank your positive feedback on our work and please find below our itemized responses to your comments and questions (highlighted in blue color). Besides, we have carefully proof read the whole paper, while other mistakes are highlighted in red color.

Comment 2: How is the infection probability P_{ik} chosen? Please, add some explanations on how this is developed or refer to the previous work where this has been done.

Reply 2: As per your advice, we have revised the relevant text as follows (please see Page 8, line 294-297).

Changes in the text: “The form of p_{ik} is similar to the PR in PageRank algorithm [18], where the k^{th} individual assigns its infection effect to all adjacent nodes including the i^{th} individual.”

One reference is added: Page L, Brin S, Motwani R, et al. The PageRank citation ranking: Bringing order to the web. Stanford InfoLab, 1999.

Comment 3: Is it p_{ik} or P_{ik} , please be consistent.

Reply 3: We have modified it as P_{ik} to ensure the consistency (please see Page 8, line 288).

Please note the changes in the text: $P_{ik} \rightarrow p_{ik}$

Comment 4: Every term in equation at line 269 should be explicitly explained, e.g., what is lik ? What is I_x and what is the parameter x that I_x depends to? should not it be I_i or I_k ?

Reply 4: Yes, we have explained the meaning of the parameters lik and I_k (as we changed the I_x to I_k) (please see Page 8, line 290-291)

Changes in the text: where lik is the infection probability when the i th individual contacting with the k th individual; I_k is the infection intensity corresponding to the state of the k th individual.

Comment 5: The model's parameters are fixed to some values and then they are modified one by one to see the effects on the numbers of infected people.

a. Please, comment a bit more on the rationale of the initial parameter's values. Also, varying the parameter one by one allows the author to show the effect of a specific measure. But what if two or more parameters change at the same time? Could not this be a relevant test for modelling the spread? For instance, with an isolation rate of 0, do the other parameters still influence the virus spread or do they become neglectable? Please, comment on that.

Reply 5: Experiment with zero isolation rate has been included (see Page 9, Figure 4) and we have added some explanation (see Page 9, line 334-335). Further, we have added a joint isolation rate and medical level experiment result (see Page line 436-442 and Figure 9), and also experiments with two variable parameters are included (see Page 10, line 347 2) Contact number).

Changes in the text:

The subgraph of Figure 4 shows that the other parameters still can affect the virus spread with an isolation rate of 0.

6) Joint isolation rate and medical level variation

Here, the isolation rate and medical level varied simultaneously are considered, where it is assumed that the medical level is positively correlated with the isolation rate.

Therefore, three pairs of the parameters are set and the results demonstrates that the number of the death under zero isolation and poor medical condition is larger than the other two cases. Furthermore, compared the results of Figure 7 and Figure 9, it can be seen that the isolation rate plays more vital role in the pandemic development.

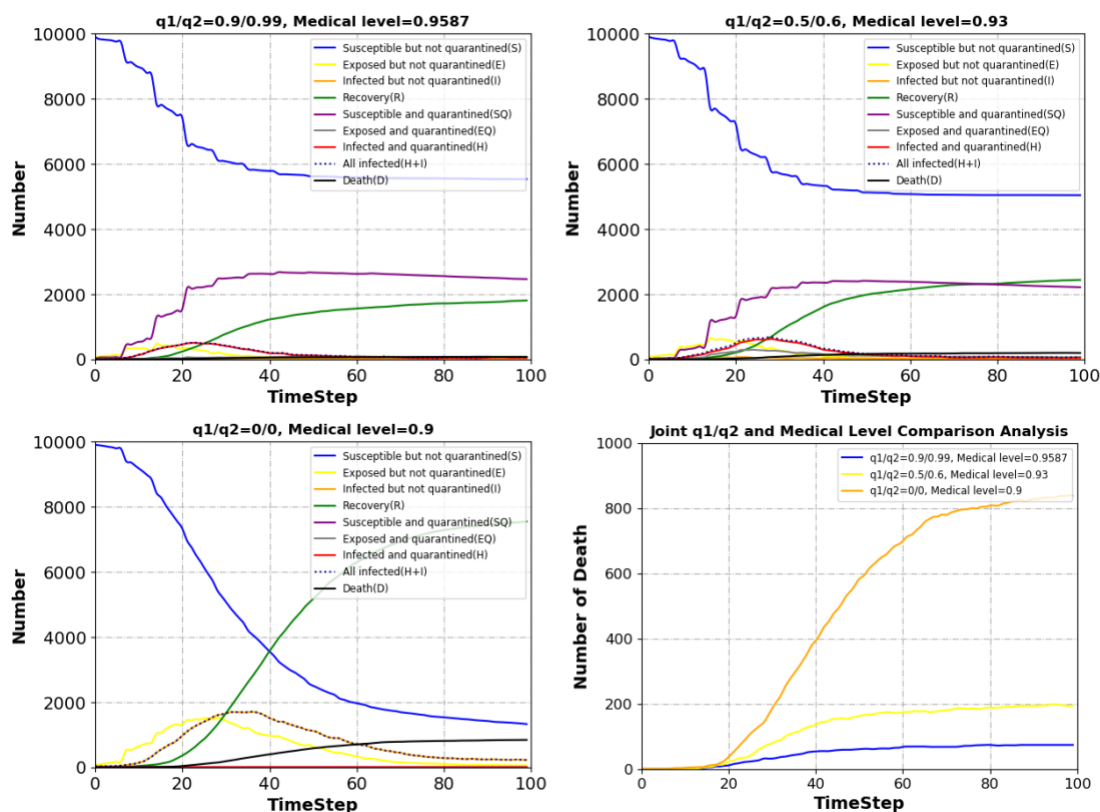


Figure 9: Simulated pandemic under joint isolation rate and medical level variation

Comment 6: Medical level index parameter influences the number of infected people that dies. The higher the index the lower the deaths. This is quite obvious and it does not add a lot to the discussion. What is missing in the analysis of the model (fig. 7) is how a lower medical index and a subsequent bigger amount of deaths influences the spread of the virus. Also in Fig. 7 the tested medical index values are 0.9, 0.9587, ~1, whereas in Table 1, where parameters setting is described, the reported values are 0.001, 0.04 and 0.1 and on line 289 the reported value is 0.4. Please, explain this inconsistency.

Reply 6: The reported value on line 289 was written as 0.4 by mistake, the correct

value is 0.0413, while the values in Table 1 was written by mistake. Actually, these values are used in the program and the correct value would be 0.9, 0.9587, ~1. And the value 0.9 and ~1 are the parameter value of control experiment. (see Table 1)

Changes in the text:

Table 1: Parameters setting of the CA-SEIR model for pandemic development estimation

Parameters	Isolation rate q_1/q_2	normal contact times	gathering contact times	Initial Infected number	Medical level	Number of imported
1	0/0	4	60*(susceptible/all)	100	0.9587	round(rand*3)
2	0.5/0.6	4	60*(susceptible/all)	100	0.9587	round(rand*3)
3	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*3)
4	0.9/0.99	2	60*(susceptible/all)	100	0.9587	round(rand*3)
5	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*3)
6	0.9/0.99	6	60*(susceptible/all)	100	0.9587	round(rand*3)
7	0.9/0.99	4	0*(susceptible/all)	100	0.9587	round(rand*3)
8	0.9/0.99	4	60*(susceptible/all)	50	0.9587	round(rand*3)
9	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*3)
10	0.9/0.99	4	60*(susceptible/all)	150	0.9587	round(rand*3)
11	0.9/0.99	4	60*(susceptible/all)	100	0.9999	round(rand*3)
12	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*3)
13	0.9/0.99	4	60*(susceptible/all)	100	0.9	round(rand*3)
14	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*0)
15	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*4)
16	0.9/0.99	4	60*(susceptible/all)	100	0.9587	round(rand*8)

Comment 7: I think that this model or something similar was used for simulate transmission of other virus like HIV, please report in discussion section literature about this.

Reply 7: Yes, we have referred to the following references dealing with HIV infections based on the similar modeling approaches and three references are added (see original Line 213, currently version in Line 237).

Changes in the texts:, which can be used for infectious disease analysis with CS-

SIR modelling.¹⁵ CA based SEIR-IBM (individual based model) model was developed to study the density of population.¹⁶ Besides, CA can be used to simulate the virus in the human body and T cell dynamic transformation process after being infected by HIV.¹⁷

[15] White S H, Del Rey A M, Sánchez G R. Modeling epidemics using cellular automata. *Applied mathematics and computation*, 2007, 186(1): 193-202.

[16] Holko A, Mędrek M, Pastuszak Z, et al. Epidemiological modeling with a population density map-based cellular automata simulation system. *Expert Systems with Applications*, 2016, 48: 1-8.

[17] dos Santos R M Z, Coutinho S. Dynamics of HIV infection: A cellular automata approach. *Physical review letters*, 2001, 87(16): 168102.

Comment 8: Dates are inconsistently reported using abbreviations in some cases whereas the extended month is used elsewhere. I would replace everywhere the abbreviation with the extended month, e.g., “Dec” in line 71 becomes December, “Mar” in line 72 becomes “March”, and so on.

Reply 8: We have changed all inconsistent spellings of dates throughout the revised text.

Comment 9: In the introduction, predictions of the measures that were planned to be taken by the authorities in France do not corresponds to the actual implemented measures. Please update this.

Reply 9: we have updated the measures implemented in France and other countries in the revised Introduction.

Comment 10:

Minor comments per line

6: please remove the point after 2019 (done)

24: In the methods of abstract session SEIR is acronym, please specify. (done)

38-41: specify that ‘the speed of reproductive number, accelerating of the inflection

point etc' is about coronavirus. (changes in the text: ... had the largest positive impact on...in the COVID-19 pandemic development.)

64: Keywords: "Prevension" -> "Prevention" (done)

78: is not virulent disease but virulent agent (done)

85: "Covid-19" -> "COVID-19". Or please, be consistent throughout the whole manuscript. (We changed them in the same form throughout the paper. done)

91-97: this sentence is too long, please rephrased it.

Changes in the text: The coronavirus has the highly contagious nature, which can be spread via person-to-person channel among close contacts between local residents & travellers. Besides, ineffective preventive measures were taken during early stage of the pandemic outbreak by the local authority together with the Chinese Spring Festival transportation.⁵ Therefore, the initial sporadic infections in Wuhan have eventually resulted in the rapid spread of the pandemic cases through entire China within a few weeks, especially within Hubei province.)

94-95: Please remove the text "Journal of Thoracic Disease.)," (done)

105: "case" -> "cases" (done)

105-106: "the 138,000 cases threshold" -> "the threshold of 138,000 people" (done)

Fig. 1 caption: Some numbers are written using commas, some are not. Please, be consistent. (done: comma is added in all numbers.)

137: "outbreak COV19" -> "COVID-19 outbreak" (done)

139: "inventions" -> interventions (done)

169: Please remove "help" and "of virus" (done)

186: "properties COVID-19" -> "properties of COVID-19" (done)

238: SEIR has already been defined (done: removed)

259: "removed" -> "recovered" (done)

435: "AP-SEIR" -> "CA-SEIR" (done)

442: "Covid19" -> "COVID-19" (done)