An Agent-Based Model in Activity-Driven Network of COVID-19 Epidemic using Mobility and Infection Data in Tokyo 2020

Suggesting Practical Vaccine Strategies and Vaccine Passport

Kazumoto Takayanagi [1], Setsuya Kurahashi [1]

[1] *Graduate School of Science and Technology. University of Tsukuba(Japan)*
Contact email: **k.takayanagi1882@gmail.com**

University of Tsukuba

IARIA

Kazumoto Takayanagi

Kazumoto Takayanagi received the master's degree in business administration from the University of Tsukuba, Japan in 2015. He is currently a doctoral student majoring in risk engineering at the Graduate School of Science and Technology, University of Tsukuba.

His research interest lies in the intersection of artificial intelligence(particularly, deep learning), network theory, and social simulation(especially, agent-based modeling).

1. Aims and contributions of our paper

In our paper, we aimed at:

1. developing a useful and reliable model for predicting the epidemic of COVID-19, and
2. comparing the effectiveness of various vaccine strategies using this model.

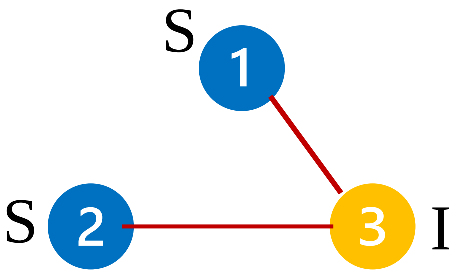
Contributions of our study are threefold:

1. we made an agent-based model with activity-driven networks fitted to mobility data provided by Google,
2. we estimated parameter values by approximate Bayesian computation using observed infection data, achieving as high as 0.99 in correlation coefficient, and
3. we suggested a promising vaccine strategy via simulations under various conditions.

2. 1 Agent-based SEIR model

- ➤ Each agent is in one of four statuses at each timestep [2].
- ➤ Agents change their statuses probabilistically as timestep progresses .

$$\text{Susceptible} \xrightarrow{P = Tr * s} \text{Exposed} \xrightarrow{\beta} \text{Infectious} \xrightarrow{\gamma} \text{Recovered}$$



Tr: transmission rate

s: susceptibility to virus

β: rate of becoming infectious

γ: recovery rate

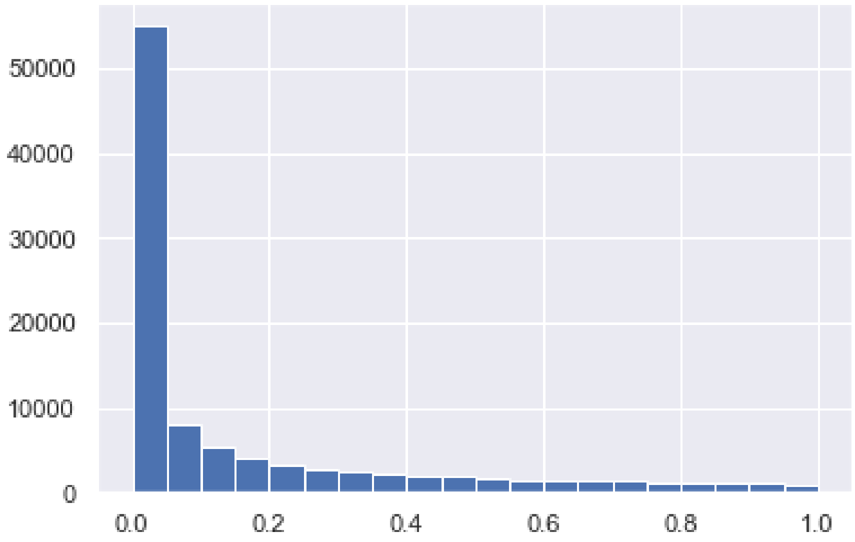
2. 2 Heterogeneity among agents

Susceptibility & Activity of agents are *heterogeneous* among individuals

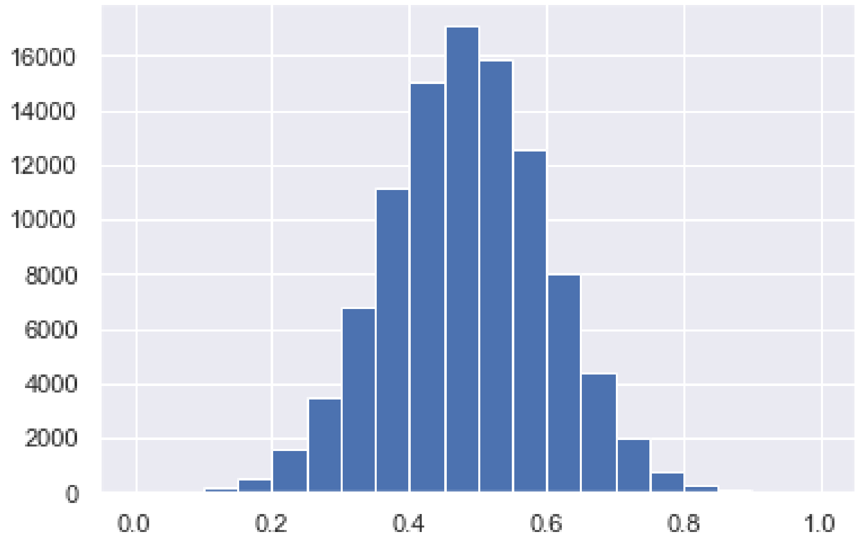
Prior to simulations,

1. Susceptibility to the virus (strength of immune response) is assigned to each agent according to Gaussian distribution [20].
2. Activity in the network is allocated to agents based on power law distribution [14].

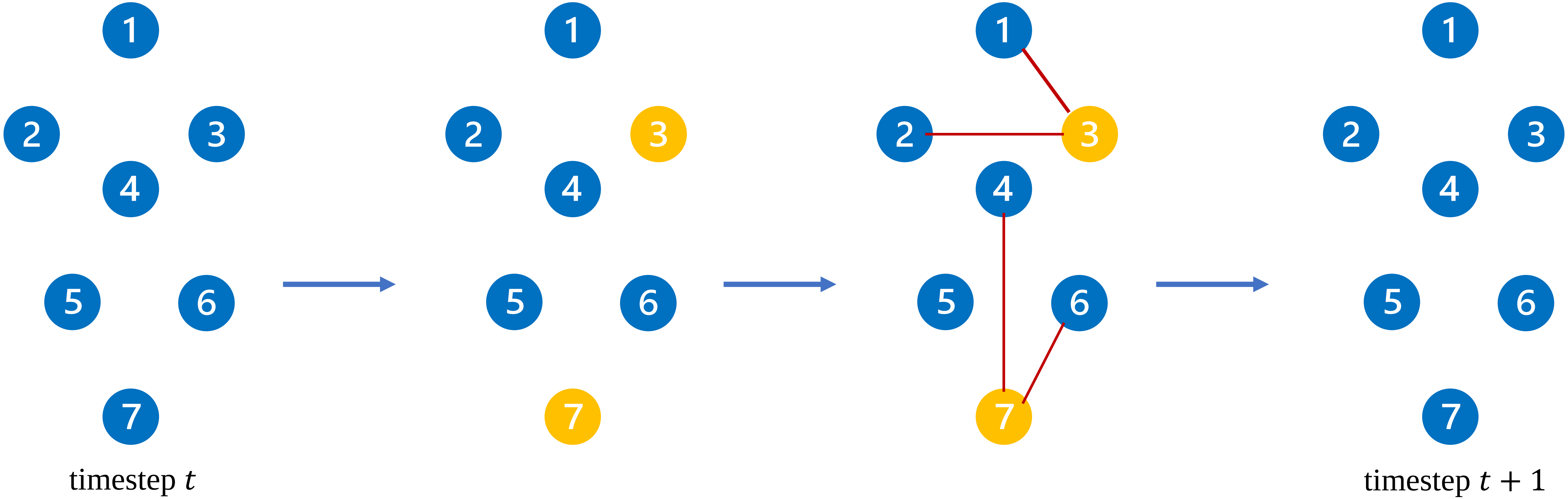
Activity
~power law $F(\alpha) = B\alpha^{-\gamma}$



Susceptibility
~ Gaussian



3. 1 Activity-Driven Networks



1. All agents are initially disconnected at timestep t.
2. Each agent i becomes active by probability a_i.
3. and creates m(e.g., 2) links with other agents.
4. At timestep t+1, all links are deleted and the process restarts [14] [21].

3. 2 Fit model to Google's mobility data

Google COVID-19 community mobility reports
how visitors to or time spent in *'categorized places'* change over time [15].

We made agents' activity values decrease and increase in accordance with the change of average of reported mobility values.

Tokyo from Feb 15 to Jun 30 (137 days)

4.1 Approximate Bayesian computation

- We estimated parameter values by approximate Bayesian computation(ABC) [16][17][18].

Parameters to be estimated are,

- transmission rate *Tr*,
- probability of becoming infectious α, and
- recovery rate β.

Algorithm of ABC is,

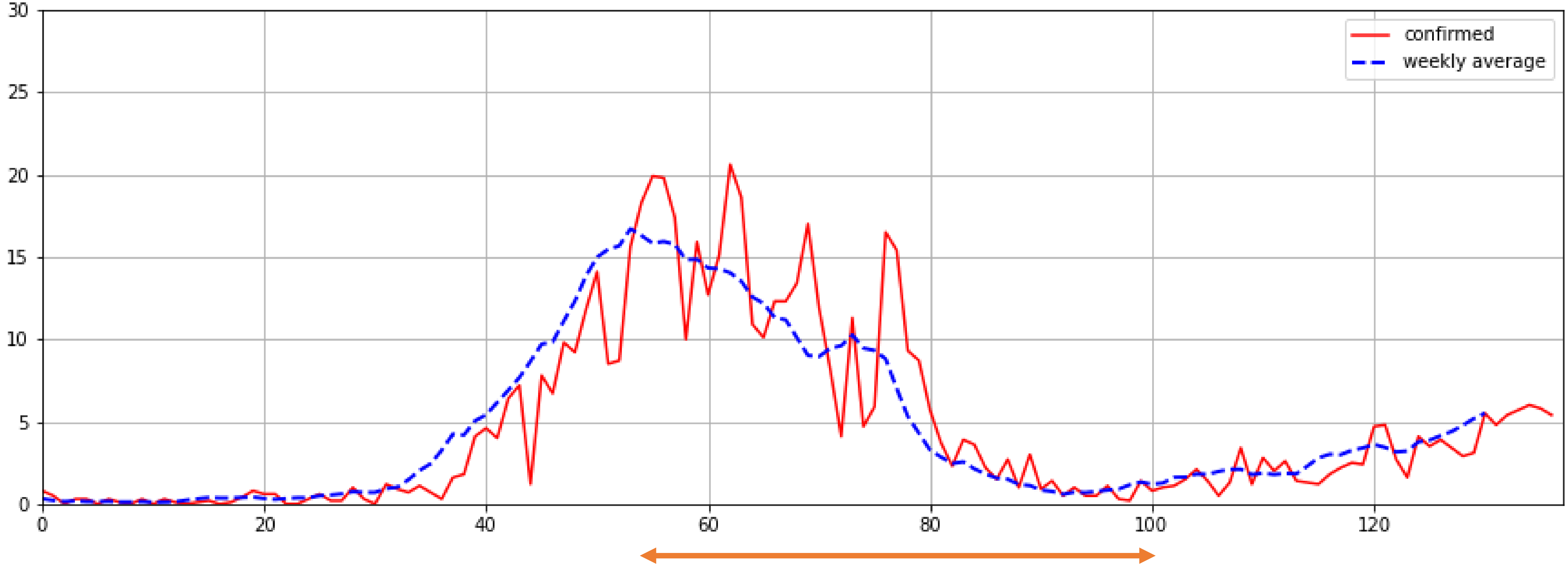
1. Sample parameter θ_i from prior $\pi(\theta)$,
2. Simulate $f(\theta_i)$ by running simulator f with θ_i,
3. Reject θ_i based on the metrics of comparison between $f(\theta_i)$ and observed data X,
4. Repeat 1-3 until a sufficiently large number of samples are obtained.

- We performed 105,000 simulations with 100,000 agents.

- We used Mean Squared Error(MSE) as a metrics to score the result of simulation.
- Top 1% results were accepted to infer the posterior of parameters.

4.2 Observed infection data

- The figure shows the course of the number of positive cases in Tokyo from February 15 to June 30, 2020(for 137 days) [25].

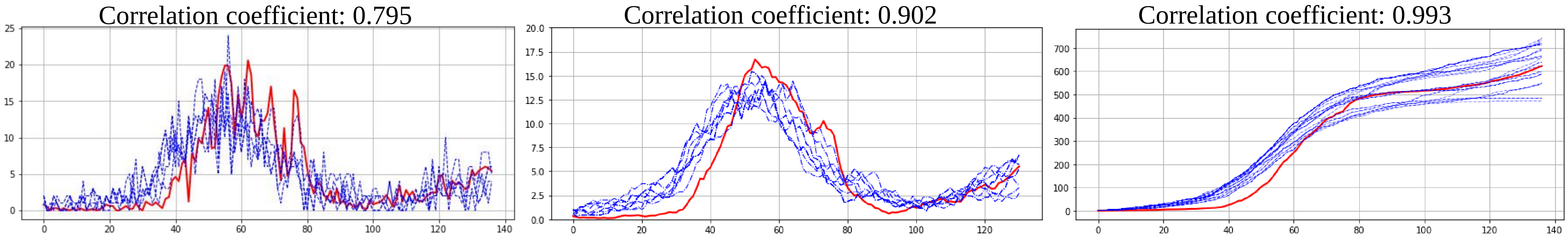


‘State of Emergency Declaration:
from April 7 to May 24(48days)

4.2 Evaluation of results

Top 10 results(blue, dashed) scored by MSE using observed data(red), daily(left), 7-day average(center), cumulative(right).

In terms of cumulative number of infected agents, we achieved as high as 0.99 in correlation coefficient.



Parameter values identified to represent the observed data,

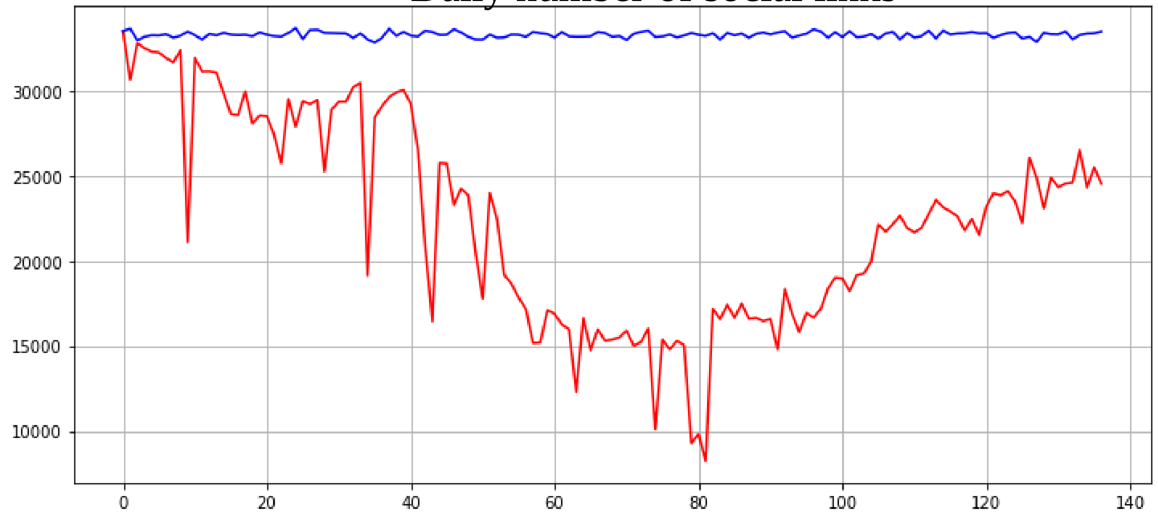
- transmission rate Tr: 0.99,
- probability of becoming infectious α: 0.26, and
- recovery rate β: 0.31.

5. Simulation under virtual conditions

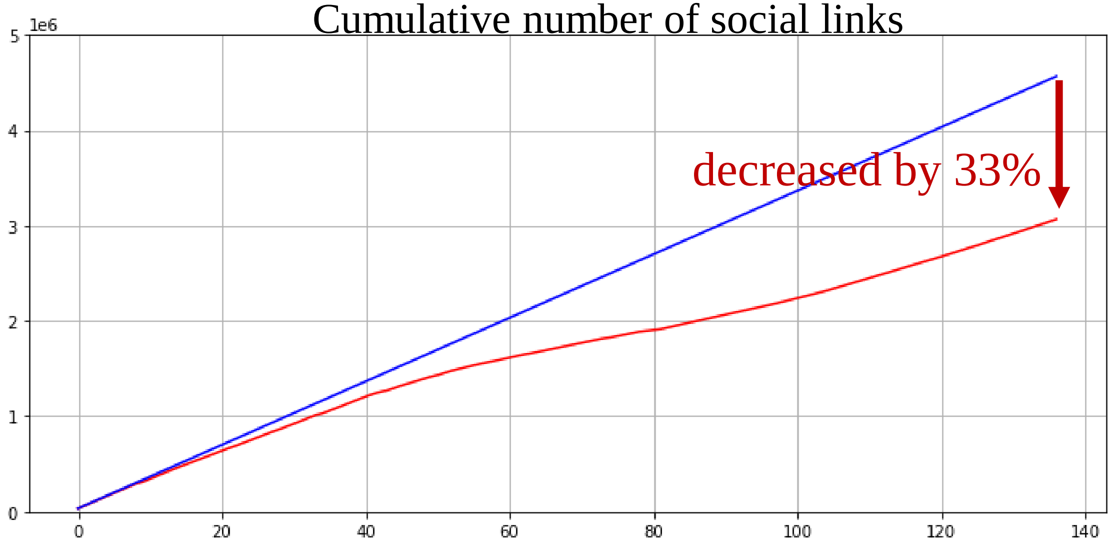
We predicted epidemic with estimated parameter values in case of no restriction on social activity.

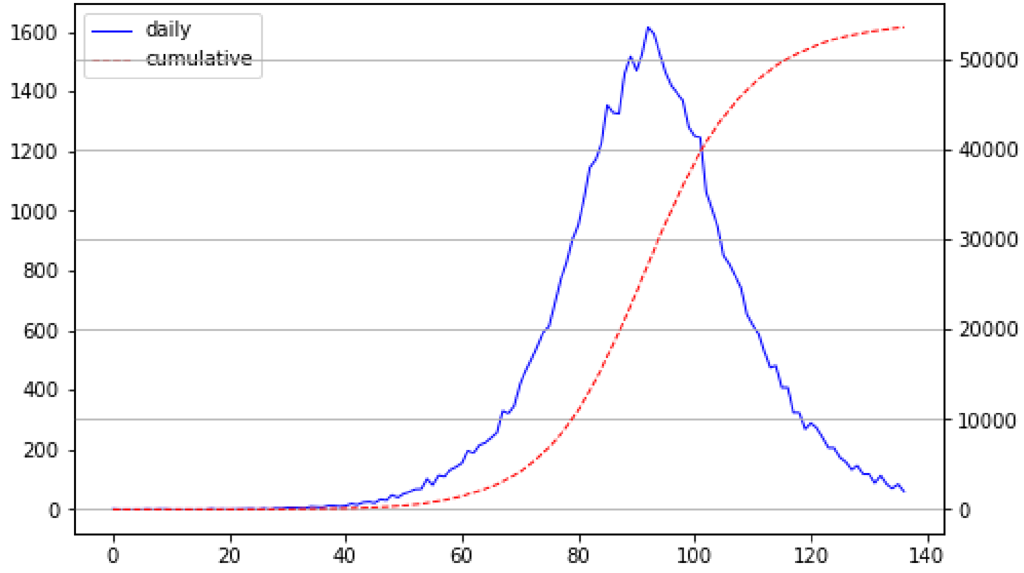
- Number of daily infected would have exceeded 150,000
- Herd immunity may have been realized.

Daily number of social links



Cumulative number of social links





6.1 Vaccine strategies

We examined following 3 vaccine strategies:

✯ Random: vaccinating randomly chosen agents every timestep.

✯ Priority for highly susceptible people, e.g., *elderly*:
preferentially vaccinating highly susceptible people(30%), then randomly.

✯ Priority for individuals relatively *active* in social networks:
preferentially vaccinating people with high activity(30%), then randomly.

We performed simulations under 4 different conditions:

✯ Efficacy : effective(reducing susceptibility by 80%), or
moderate(reducing susceptibility by 30%), e.g., variants.

✯ Availability: 1,000(1% of the population) shots per day, or
500(0.5%) shots per day.

Vaccination starts from the 40^{th} day.

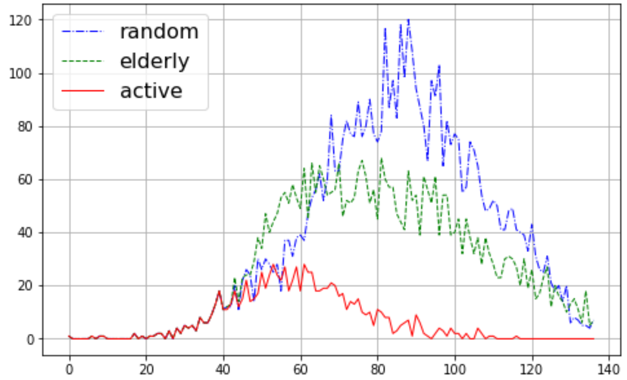
6.2 Comparison of effectiveness

Comparison of the effectiveness of 3 vaccine strategies under 4 different conditions.

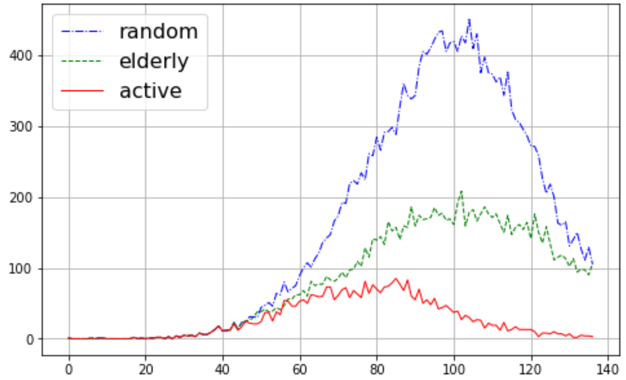
The figure shows the course of the daily number of infected agents.

susceptibility reduced by 80%

(1,000 shots per day)

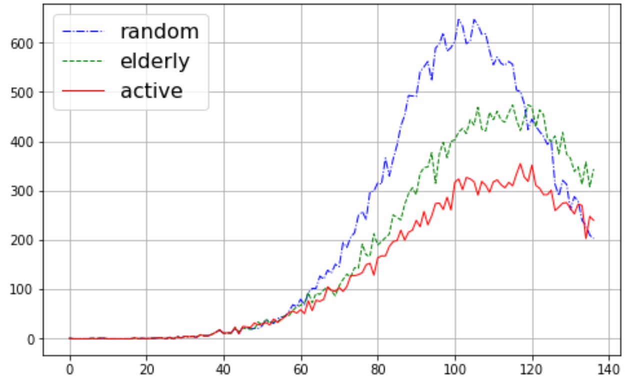


(500 shots per day)

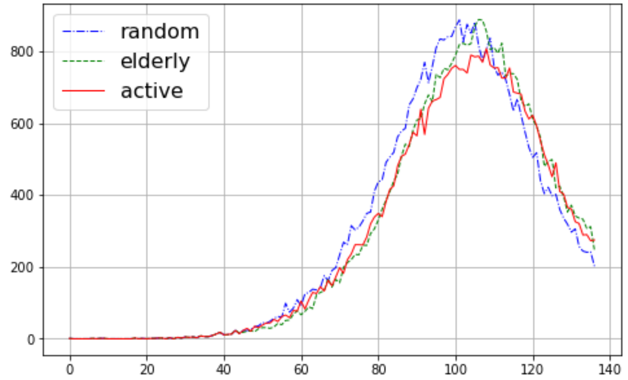


susceptibility reduced by 30%

(1,000 shots per day)



(500 shots per day)



It is observed from the results that,

1. preferentially vaccinating highly active agents in the network is most effective strategy under all conditions,
2. as the speed of vaccination slows down or the efficacy of vaccines against viruses decline,
   the three strategies differ less evidently in their performance.

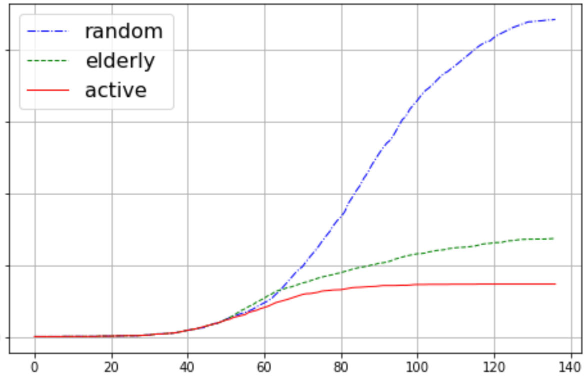
6.3 Comparison of effectiveness

Comparison of the effectiveness of 3 vaccine strategies under 4 different conditions.

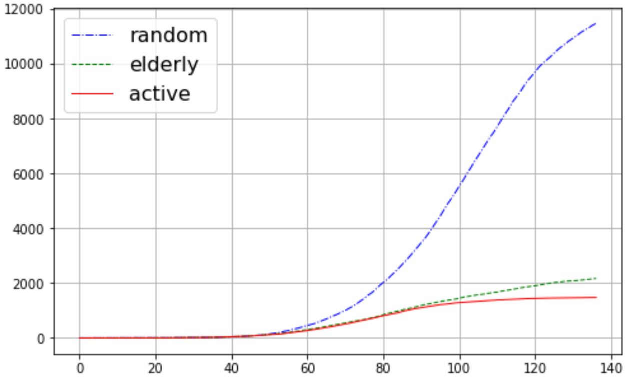
The figure shows the cumulative number of highly susceptible agents who get infected.

susceptibility reduced by 80%

(1,000 shots per day)

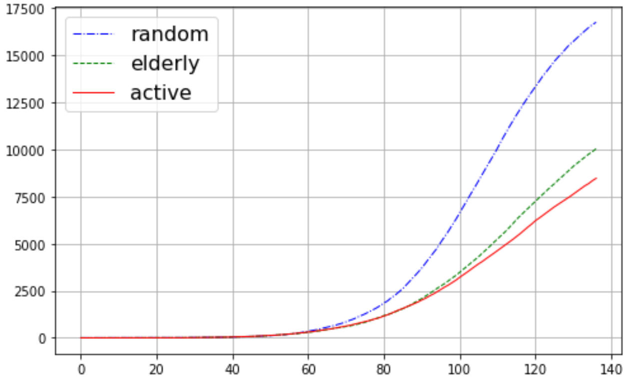


(500 shots per day)

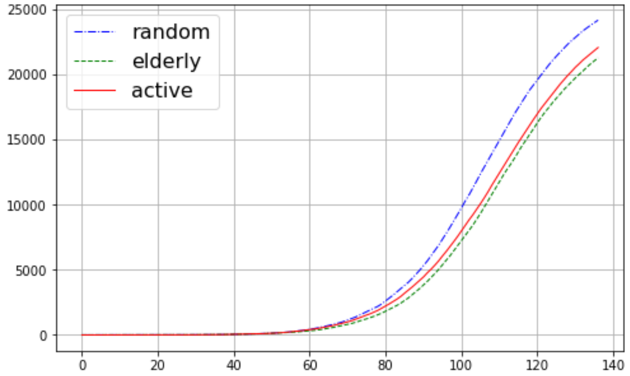


susceptibility reduced by 30%

(1,000 shots per day)



(500 shots per day)



It can be observed that,

1. though it may be counterintuitive, the cumulative number of infected people among highly susceptible group is lower when highly active agents are prioritized, so
2. preferentially vaccinating highly active individuals in the network may be a promising strategy.

6.2 Conclusion and future work

Conclusion:

- We developed an agent-based model of COVID-19 infection with activity-driven networks fitted to actual mobility data provided by Google.
- We inferred the parameter values via approximate Bayesian computation with 105,000 results of simulations.
- We achieved as high as 0.99 in correlation coefficient with the estimated values of parameters.
- Through additional simulations under certain conditions, we examined the effectiveness of several vaccine strategies and suggested a promising one.

Future work:

- We will perform more simulations of our model to examine whether the results in this study are robust under a variety of different conditions.
- We also try to infer posterior of parameters more sufficiently by using deep learning as summary statistics in approximate Bayesian computation.

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