Escaping an epidemic: Movement optimization via Minority Game

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We study an optimal movement strategy, for a population during an ongoing epidemic, among the \((D)\) states/regions of a country having various levels of infection spreading. If a fraction of the agents in the population have a choice of staying in any two given states, we show that the total infected population in the country could be as low as that achieved with a complete stoppage of inter-state movements for a prolonged period, provided that the agents instead follow a stochastic strategy, used in the Minority Game, for their movement decisions between their two choices. Due to the random (but fixed in time) choices of the agents, the system essentially forms a set of \(D/2\) coupled Minority Games, played simultaneously. The objective for an agent is to stay in the lower infected state between their two choices. We further show that it is the agents moving once between any two states, following the stochastic strategy, who are less likely to be infected than those not having (or not opting for) such a movement choice, when the risk of getting infected during the travel is not considered. This shows the incentive for the moving agents to follow the stochastic strategy. For the non-moving agents, the strategy is still helpful, as a complete random movement of the moving group results in a significantly higher total infection.

During the ongoing global crisis since the outbreak of the COVID-19 pandemic, many countries around the world have imposed varying degrees of restrictions on international as well as their domestic travels. At times when such restrictions are fully or partially lifted, an inevitable question for a significant fraction of the population would be to change their locations in order to escape the regions of higher infections. But due to difficulties in detecting the disease, an influx of population to relatively less infected regions can increase the infection rate in those regions. Therefore, a region which initially had low infections, could become a less viable option in the subsequent times. Furthermore, if a country has \(D\) states/regions with different rates of infection, one person may have a rather limited option in terms of the number of regions in which they can live for a long time. Also, in a given region, different persons will have their options distributed between the rest of the \(D - 1\) regions. We can consider the relatively safer places from the perspective of one agent as a limited resource that is being sought by a large number of other agents. Due to the inherent coupling arising out of the possible parallel choices of one region by agents from multiple other regions, the problem of distributing the said resource of safe locations can now become a cooperative, multi-agent, complex optimization process with emergent statistical properties.

A large number of agents competing for limited resources is a generic problem appearing in a wide range of situations such as in economics, in sharing natural resources to allocating internet bandwidth and so on. There have been many attempts to address these problems from a game theoretic perspective (see e.g., congestion games). When the number of choices for an agent is limited to two, the resource allocation problem generally falls within the category of the Minority Game (MG), where an odd number \((N = 2M + 1)\) of agents try to be, through repeated and parallely decided autonomous choices, in the minority group, thereby winning a higher share of the (conserved) resources, or in the language of game theory, a positive pay-off. Clearly, the Nash equilibrium state for the problem is when the populations \(P_1\) and \(P_2\) in the two choices are \(M\) and \(M + 1\), such that one agent cannot benefit by their own action alone provided that the others stick to their respective choices. The objective is to reach this state of minimal fluctuation \(\Delta = |P_1 - P_2|\) between the two choices in the least possible amount of time, through autonomous and parallel decisions by the agents.

While a complete random decision would keep the population difference between the two choices very high \((\Delta \sim \sqrt{N})\), a deterministic cooperative learning mechanism with the past memory of winning choices can reduce it by a constant factor. A stochastic strategy, on the other hand, can reduce the fluctuation to the minimum possible value \((\Delta \sim 1)\) in a very short time \((t_{\text{sat}} \sim \log \log N)\). But this strategy requires the additional input of the fluctuation in the previous step to be supplied to the agents, where traditionally they are supplied only with the sign of the fluctuation i.e., the winning choice. However, the stochastic strategy still performs quite well \((t_{\text{sat}} \sim \log N)\) when \(\Delta(t)\) is not exactly know to the agents but a guess value is supplied through an appropriate annealing schedule.

Here, we consider a population distributed in \(D\) states/regions within a country, where an ongoing epidemic is spreading within the population. We simulate the epidemic using a standard Susceptible (S)-Infected (I)-Recovered (R) model. Most agents do not have a choice to switch between the regions. Only a fraction of the agents have a choice to move to only one of the other
Here all agents having an alternative choice are shown. In the model, there are other agents who participate in the epidemic spreading but do not have choice to move. If only similar agents and their alternative choices exist between a pair of regions, say the yellow or green regions, then the problem reduces to a pair of decoupled Minority Games. However, the games are coupled when an agent has two choices between any two regions are completely non-overlapping with the group of agents having choices between the other two regions, then the problem reduces to a pair of decoupled MG. In the absence of the epidemic, the strategy that has proved to be the most efficient in reducing fluctuations (population difference) in such cases is that the agents in the majority choice (having larger population) at an instant $t$ will switch with a probability

$$p_+(t) = \frac{(\Delta(t) - 1)/2}{M + \Delta(t) + 1}$$

and the agents in the minority will not switch ($p_-(t) = 0$).

However, in our case, the two groups are not disjoint, and cross-linking of choices, indicated by thick red lines in Fig. 1(a), make the games coupled. Even in the absence of the epidemic spreading, finding the optimal choice for each agent is non-trivial, especially when $D$ is large. Nevertheless, for the case without epidemic, we can define a switching probability analogous to Eq. (1) (see Supplemental Materials). We ensure the initial condition such that a given region is a possible choice for $2M + 1$ agents. Therefore, a global minimization of fluctuation is achieved when $D/2$ locations have population $M$ and the other $D/2$ locations have population $M + 1$. However, due to the random assignment of choices between the agents, a given agent can end up with two choices, both having populations $M + 1$. We call that a ‘majority locked’ agent. The stochastic strategy ensures the global minimization of fluctuation. However, the fraction of the majority-locked agents remain finite for large $D$, and the time taken to reach that minimum value of the majority-locked fraction grows exponentially with $D$. An additional constraint that the agents can switch at most once during their entire time, keep the fraction of majority locked agents to a low value (higher than the minimum possible), which is achieved in a time almost independent of $D$ (see Fig. 4 in the SM). Therefore, the stochastic

$D - 1$ regions than their current residence. The objective of the agents, who have a choice of shifting, is to be in the minority group in terms of the number of infected people. In the usual Minority Games, the variations in the target variable (i.e., populations in the two choices), take place due to the switching of choices of the agents. In our case, the target variable is the number of infected people. In a given region, it can change due to (a) movements of agents from the other $D - 1$ regions/states and (b) due to the evolution of the epidemic within the region itself. Given that the target variable for minimizing fluctuation (difference in the infected population) is not a conserved quantity, an equilibrium state is not defined. However, a well defined quantity is the total infected population in the country after the end of the epidemic. We show here that if the agents having the choice to switch adopt a stochastic strategy in deciding such switches, the total infected number in the country could be lower compared to a random movement of the agents or for the most cases of a temporary ban on inter-state movements. Furthermore, it is the agents opting for switching of their choices following this strategy who are less likely to be infected. This imply that neither of the moving or non-moving groups get benefited if the former group abandons the stochastic strategy.

In Fig. 1(a), we show a schematic representation of the coupled MG with four regions/states. Only the agents having options to switch are shown. There are other agents, not shown in the figure, who do not have such choices but they contribute to the epidemic spreading. In the limit when the group of agents having choices between any two regions are completely non-overlapping with the group of agents having choices between the other two regions, then the problem reduces to a pair of decoupled MG. In the absence of the epidemic, the strategy that has proved to be the most efficient in reducing fluctuations (population difference) in such cases is that the agents in the majority choice (having larger population) at an instant $t$ will switch with a probability

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strategy with the constraint of maximum one move for the agents, is an effective scheme for the coupled MG. We proceed with this scheme of optimized movement for the case where epidemic dynamics is also present and the objective for the agents now is to be in the choice with lower infection rather than lower total population.

There has already been a multitude of attempts in simulating the COVID-19 pandemic with varying degree of realistic features and also analysis of the available data (see e.g., [12–16] for very recent works on the COVID-19 spreading and its effects). However, our aim here is to look for a generic strategy for optimized movement between various regions for some of the agents to avoid infection. This should be independent of the details of the epidemic model. Therefore we keep the epidemic spreading and its effects. However, our aim here is to look for a generic strategy for optimized movement between various regions for some of the agents to avoid infection. This should be independent of the details of the epidemic model. Therefore we keep the epidemic spreading and its effects. However, our aim here is to look for a generic strategy for optimized movement between various regions for some of the agents to avoid infection. This should be independent of the details of the epidemic model. Therefore we keep the epidemic spreading and its effects.

In the simplest case where a coupled MG is defined is when $D = 4$. We begin with a mean field version with $D = 4$, where each agent in any region can interact with $z = 4$ randomly selected agents in the same region. There is no interaction between agents belonging to two different regions at a given time. As indicated before, not every agent has the choice of relocating to a different state for a long time. We assign a fraction $g = 0.1$ of the agents with the choice to move to one of the remaining 3 locations only once during entire period of the epidemic dynamics. The remaining question is then the decisions of the agents with movement choices to switch (or not) to their alternative locations. A natural tendency for such agents would be to avoid a region with higher infection i.e., to remain in the minority group in terms of the infected population. However, the infected population at any region will vary due to the epidemic dynamics as well as the due to movements of agents from the other regions. We apply a similar stochastic strategy as in Eq. (2), i.e., one agent ($\alpha$) in a higher infected region (say, $i$-th region) will move with a probability

$$p_{+} = \frac{(I_{i}^{\alpha} - I_{j}^{\alpha})/2}{gP_{i}^{\alpha}/(D-1)},$$

(2)

where $I_{i}^{\alpha}$ and $I_{j}^{\alpha}$ are the numbers of infected populations in the two choices ($i$-th and $j$-th) of the $\alpha$-th agent, $P_{i}^{\alpha}$ and $P_{j}^{\alpha}$ are the respective total populations and $I_{i}^{\alpha}(t) > I_{j}^{\alpha}(t)$. The agents already in the lesser infected region compared to their other alternative choice at an instant do not switch at that instant ($p_{-} = 0$). The factor $(D-1)$ is introduced as the agents can move to any one of the $D-1$ regions, giving an average shift of $(I_{i}^{\alpha} - I_{j}^{\alpha})/2$ to the $j$-th region, which balances the infections in the two regions. Note that as the infected number is not conserved, the total number may not be odd, therefore we remove the $-1$ factor in the numerator, as used in Eq. (2).

The dynamics of the model proceeds as follows: At each time step, first the SIR model is implemented for all agents. Then the movements are made following Eq. (2). A parallel update rule is followed, such that the changes in both the epidemic part and the movement part, are reflected in the following time step (see SM for the algorithm and Ref. [18] for the code used). Furthermore, we study the effect of a lock down period, during which all inter-state movements are stopped. During the lock down period, the SIR model runs, but the movements do not happen. Fig. (1b) shows the variation in the total recovered fraction with time, for various duration of lock down, starting at $t = 0$. At $t = 0$, all agents are in susceptible state, except some of the agents in one region who are infected, which act as the starting seed for the epidemic. We consider a population size of 15000 for each state (total population 60000) and an initial infection for 1000 agents in one region (say, D1). Fig. (1c) shows the variation of infected agents with time, also for various lock down periods ($\tau$). It shows that a primary peak is always present, which is due to the spreading of infected in D1. However, an early lifting of lock down prompts the agents in D1, who have the choice, to switch to the other regions and thereby bringing infection to those regions, resulting in a secondary peak, which is often more prominent. A prolonged lock down (~ 60 time steps), however, reduces and finally eliminates the second peak. However, for a shorter lock down, the total recovered fraction approaches unity in the long time $R_{tot}(t \to \infty) \to 1$, i.e. almost everyone is infected at some pint of time, which is unrealistically high. Although the infection probability for the moving agents are comparatively lower (not shown), the benefit of the stochastic strategy is not clear here due to the overall high infection rate. This is due to the mean field like connectivity among the agents within a region. Therefore, we need to consider a less connected topology.

To do that, the simplest choice is a square lattice ($L \times L$) to represent possible locations for agents in each state. A susceptible agent can get infected from any one of its nearest and next nearest neighbors. We take $L = 173$ and each state is initially occupied with 15000 agents i.e., an occupation fraction of about 0.5, giving an average coordination number $z = 4$. This is close to the site percolation threshold [10], which represents a reasonable
restriction in interactions among the populations in terms of either the imposed social distancing or due to other factors seen in epidemic spreading [11] (see SM Fig. 5 for variations of infection with occupation fraction).

The initial condition, as before, is all but 1000 agents in D1 are susceptible. The epidemic dynamics then follows the SIR model and then the movements are made following the strategy mentioned in Eq. (2). Finally, we also study the effect of a complete lock down of inter-state movements for a period of time. The epidemic dynamics, of course, continue during such a period. Below we report the effects of the various duration and start times of such stoppages of movements on the evolution of the total infected number and other related quantities.

In Fig. 2 we show the time evolution of the number of agents moving (normalized by the total number of agents having choice of such movement), the fraction of the infected population in D1 (normalized by the instantaneous population at that region \(N_1(t)\)) where the initial infection started and the total infected fraction of all four regions, for various duration of lock downs i.e., complete stoppage of inter-state movements and for various start times of such a lock down. Invariably, a spike in the movement is noticed immediately following the lifting of a lock down, which then subsequently decreases. This is intuitively clear, as a lock down will keep the initially infected region highly infectious and immediately after the lifting of the lock down, agents will move out of it (see SM Fig. 4 for details). Almost in all cases, the lifting of the lock down slows down the recovery rate in the total infected fraction. Clearly, this is due to deconfinement and spreading of infections among the different regions.

To quantify the effects of movements on the travel restrictions, in Fig. 3(a) we show the total infected fractions when no stoppage of inter-state travels is imposed. But the agents can switch only once, following the stochastic strategy in Eq. (2). If the movements are random (agents switch with 50% probability), the infected fraction is 0.197, which is worse than almost all the cases. (b) The relative infection probabilities are shown for the agents opting for switching their location divided by the corresponding probability for the agents who did not switch. Given the ratio is almost always less than 1, the population opting for the switching following Eq. (2) are less likely to be infected, where we did not consider the chance of getting infected during the travel.

FIG. 2. The time evolution of the total fraction of agents moved, the infected fraction in D1 and the total infected fraction, each independently normalized (see text) and plotted for various duration and start times of lock down, for the model implemented in a square lattice. The lock down start and end times are indicated in each figure. Inevitably, a spike in the movement is noted immediately following the lifting of lock down. This almost in all cases results in a slowing down of the total recovery rate.

FIG. 3. (a) The fraction of the total infected population, at the end of the epidemic dynamics, is shown for various duration of lock downs against the mid-point of the lock down period for the model in th square lattice. A small initial lock down is least effective. Comparisons are made with the infected fraction for no imposition of inter-state movement, shown in the horizontal line. This seems to work better than a small period lock down, or equally good as the late imposition of long lock down. The movement strategy, in all the cases, follow Eq. (2). If the movements are random (agents switch with 50% probability), the infected fraction is 0.197, which is worse than almost all the cases. (b) The relative infection probabilities are shown for the agents opting for switching their location divided by the corresponding probability for the agents who did not switch. Given the ratio is almost always less than 1, the population opting for the switching following Eq. (2) are less likely to be infected, where we did not consider the chance of getting infected during the travel.
ments of agents among various infected regions as an optimization problem similar to a set of coupled Minority Games played in parallel. We show that a restricted movement (agents can move only once) of the agents following a stochastic strategy described in Eq. 2 performs better than a random movement, or even with most cases of short lock downs. Irrespective of the topology of the underlying lattice and the parameter ranges studied for the epidemic model, the moving agents are less likely to be infected, giving a stability in the strategy, where neither of the moving and non-moving groups are benefited if such a strategy is discarded in favor of random movements.

SUPPLEMENTAL MATERIALS

A: Parallel Minority Games, without epidemic spreading:

When a group of agents try to be in the minority choice between their two choices, but the choices of the individuals are distributed randomly between \(D-1\) options, the formulation of the MG gets modified to a set of coupled MGs. Here we describe the dynamics of the parallel MG without an epidemic, where the objective is the usual minimization of the fluctuations in the populations among the choices. As there are total \(D\) choices, the problem reduces to \(D/2\) decoupled MGs, if the agents in a pair of choices are completely non-overlapping with the agents of any other pair of choices. However, the choices here could be overlapping i.e., the agents in one choice at a given instant may have their other choice distributed between \(D-1\) options (see Fig. 1(a)). We keep the switching probability for a given (\(\alpha\)-th) agent in the majority at a given instant to be

\[
p_{\alpha}(t) = \frac{(P_{\alpha}^i - P_{\alpha}^j - 1)/2}{gP_{\alpha}},
\]

where \(P_{\alpha}^i\) is the population at the \(i\)-th choice of the \(\alpha\)-th agent, \(P_{\alpha}^j\) is the population at the location of the other choice assigned to the agent \(\alpha\). \(g\) is the fraction of agents having the choice of movement and \(P_{\alpha}^i(t) > P_{\alpha}^j(t)\). For comparison with the traditional MG, we keep \(g = 1\) here, instead of the realistic case of \(g < 1\) for epidemic dynamics. We ensure the initial condition such that a given region is a possible choice for \(2M+1\) agents. Therefore, a global minimization of fluctuation is achieved when \(D/2\) locations have population \(M\) and the other \(D/2\) locations have population \(M+1\). Nevertheless, due to the random assignment of choices between the agents, a given agent can end up with two choices, both having populations \(M+1\). We call that a ‘majority locked’ agent. In Fig. 1(a) we show the variation of the fraction of this majority locked agents with time as \(D\) is increased, where the agents can switch an unrestricted number of times between their assigned choices. The fraction does not always go to zero, and the time taken to reach a minimum value increases exponentially with \(D\). We then impose a constraint that one agent can switch only once (see Fig. 1(b)). Then the fraction of the majority locked agents still does not go to zero, but a reduction, although comparatively low, can be achieved in a time scale with no significant variation with \(D\) in the rage of the simulations. Therefore, we see that the this movement strategy still works considerably better than a random choice, where fluctuation grows with population involved with \(\sqrt{N}\) or

![FIG. 4.](image-url)
of infected agents (1/15), or a fixed fraction of infected agents (1/15). The three configurations show the susceptible (green), recovered (red) and vacant sites (blue) at the end of the simulation, for occupation fractions 0.167 (b), 0.501 (c) and 0.835 (d), for a fixed number (1000) of infected agents at \( t = 0 \). For the simulations in the text, the half occupancy configuration is used.

C: Details of movement due to stochastic strategy:

An intuitive way to further elaborate on Fig. 2 is to plot the relative risk of \( D_1 \), with respect to the average risk in the remaining three regions. A measure of such a risk is the difference between the fraction of infected agents in \( D_1 \) and the average fraction of infected agents in the remaining regions. In Fig. 6 we plot the relative risk, with the changes in the population in \( D_1 \) from its starting value 15000 for various duration of lock downs and their starting times.

![FIG. 6](image_url)

It is seen that when the lock down periods are smaller, the population in \( D_1 \) gets back to almost its original value, as at that point the infection has spread to other regions substantially. Indeed, it is possible to relate the total number of infected agents’ movement with the final infected fraction. In Fig. 6(a), we show the total infected number with the total number of infected agent movement. For different lock down start time and duration, the infected number seem to depend only upon the infected movement, and not when such movements occurred (or the lock down for that matter). This is true, as long as the stochastic strategy in Eq. (1) is followed. If the movements are random, then the total infection is higher (see Fig. 6(b)) than that following the stochastic strategy, even for a similar number of infected agent movement.

D: Algorithm for the simulations:

Finally, the algorithm used for the simulations is given in Fig. 8.
FIG. 7. (a) The variation in the final infected number is shown with the number of infected agents movement. The total infected number depends upon the total infected agents moved, irrespective of the lockdown periods or even just the movement with stochastic strategy (restricted movement). However, if the stochastic strategy is not followed, and the movements are random (maximum movement per agent is still 1), then even for the similar values of infected agents moved, the total infection is higher. This shows the utility of the stochastic strategy. (b) The same quantities are shown for the three classes of movements, stochastic strategy with lock down, stochastic strategy without lock down and random strategy without lock down.

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[1] Zhou P., Yang X-L., Wang X-G., Hu B., Zhang L., Zhang W., Si H-R., Zhu Y., Li B., Huang C.L., Chen H-D., Chen J., Luo Y., Guo H., Jiang R-D., Liu M-Q., Chen Y., Shen X-R., Wang X., Zheng X-S., Zhao K., Chen Q-J., Deng F., Liu L-L., Yan B., Zhan F-X., Wang Y-Y., Xiao G-F., Shi Z-L., A pneumonia outbreak associated with a new coronavirus of probable bat origin, Nature, https://doi.org/10.1038/s41586-020-2012-7.
[2] A. Chakraborti, D. Challet, A. Chatterjee, M. Marsili, Y.-C. Zhang, B. K. Chakrabarti, Phys. Rep. 552, 1 (2015).
[3] R. W. Rosenthal, Int. J. Game Theory 2, 65 (1973).
[4] D. Challet, Y.-C. Zhang, Physica A 246, 407 (1997); ibid Physica A 256, 514 (1998).
[5] D. Challet and M. Marsili, Phys. Rev. E 60, R6271 (1999).
[6] D. Challet, M. Marsili, Y. C. Zhang, Minority Games, Oxford University Press, Oxford (2005).
[7] E. Moro, in Advances in Condensed Matter and Statistical Mechanics, edited by E. Korutcheva and R. Cuerno (Nova Science Publishers, New York, 2004), arXiv:0402651v1; A. De Martino and M. Marsili, J. Phys. A. 39, R465 (2006).
[8] D. Dhar, V. Sasidewan, B. K. Chakrabarti, Physica A 390, 3477 (2011).
[9] S. Biswas, A. Ghosh, A. Chatterjee, T. Naskar, B. K. Chakrabarti, Phys. Rev. E 85, 031104 (2012).
[10] D. Stauffer and A. Aharony, Introduction to Percolation Theory, 2nd ed. (Taylor & Francis, London, 1994).
[11] A. Khauleque, P. Sen, Sci. Rep. 7, 42594 (2017); K. Biswas, A. Khauleque, P. Sen, arxiv:2003:07063 (2020).
[12] A. Martin, M. Markhvida, S. Hallegatte, B. Walsh, arxiv:2005:05945 (2020).
[13] B. Benrengua, H. Moumen, M. A. Merzoug, arxiv:2005:05523 (2020).
[14] S. Khajanchi, K. Sarkar, J. Mondal, M. Perc, arxiv:2005:06280 (2020).
[15] A. Galeazzi et al. arxiv:2005:06341 (2020).
[16] J. Dehning, J. Zierenberg, F. P. Spitzner, M. Wibral, J. Pinheiro Neto, M. Wilczek, V. Priesemann, Science, DOI: 10.1126/science.abb9789 (2020).
[17] S. Zhang, M. Diao, W. Yu, L. Pei, Z. Lin, D. Chen, Int. J. Infect. Dis. 93, 201 (2020).
[18] The code used for the simulations in the square lattices is available at: https://github.com/amitmandalnitdgp/Epidemic/
FIG. 8. The algorithm used for the simulation.

```plaintext
1 Def Person:
2   state           // 1 = Susceptible, 2 = Infected, 3 = Recovered
3   choice          // region id where it can move
4   InitialRegion   // starting region of the person
5   stateWhenMoved // state of the person during movement
6   currStateTimeStep // tracks infection days
7
8 Def Region:
9   regID            // ID of the region
10  population       // total population in the region
11  endTime          // end of days for the simulation
12  initInfectedPopulation // initial infected population
13  infectionProbability // probability of getting infected
14  infectionDuration // duration of infection
15  choiceFraction   // % of people can move
16  Grid prevGrid    // holds the previous state of the region
17  Grid currGrid    // holds the current state of the region
18  susceptibleCounts // susceptible population in the region
19  infectedCounts   // infected population in the region
20  recoveredCounts  // recovered population in the region
21
22 Def State:
23   Person[] grid   // 2D array of persons
24   maxRows         // calculated from population size
25   maxColumns      // calculated from population size
26
27 Function Initialize():
28   // determine size of grids from the total population & population point
29   set initial status to Susceptible: 1;
30   randomly populate prevGrid and currGrid;
31   randomly place the initInfectedPopulation on the grids by changing its state to infected: 2;
32
33 Function Simulate(first, second):
34   currentTime = 0;
35   while currentTime < endTime do
36     for k = 0; k < regionMaxRows; k++ do
37       for i = 0; i < regionMaxColumns; i++ do
38         for j = 0; j < regionMaxColumns; j++ do
39           if person is Susceptible then
40             for all the neighbors of a person in prevGrid do
41               if neighbor is infected in prevGrid then
42                 calculate a randomProbability for the person;
43                 if randomProbability < regionX InfectedProbability then
44                   Marked Person as Infected in currGrid;
45                 if person is Infected then
46                   if currStateTimeStep == infectionDuration then
47                     Marked Person as Recovered in currGrid;
48     if currTime < 50 || currTime > 30 then
49       allowMovement (region, currTime);
50   for all possible inter region (regionX, RegionY) movement do
51     movePrev = getMovementProbability (regionX, RegionY);
52     for each person in regionX do
53       if [choose to move] then
54         calculate a randomProbability for move;
55         if randomProbability < regionX MovementProbability then
56           More that person: regionX -> RegionY;
57
58 Function getMovementProbability(regionX, regionY):
59     prob = (regionX infectedCounts - regionY infectedCounts) / (regionX totalPopulation + (regionX choiceFraction / TotalNoOfRegions - 1));
```

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