Escaping an epidemic: Movement optimization via Minority Game

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We study an optimal movement strategy of agents during an ongoing epidemic among the (D) states of a country having various levels of infection spreading. Given that a fraction of the agents have the 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 follow a stochastic strategy, used in the Minority Game, for their movement decisions. 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. 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.

During the ongoing global crisis since the outbreak of the COVID-19 pandemic [1], 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 given an influx of population, some of whom could be a carrier of the disease, to a relatively less infected region can increase the infection rate in those regions. Therefore, a region which was initially had low infections, could become a less viable option in the subsequent times, due to movements of population there from other higher infected regions. Furthermore, if a country has D states with different rates of infection, one person may have a rather limited option in terms of the number of states in which they can live for a long time. Also, in a given state, different persons will have their options distributed between the rest $D-1$ states. 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 agents. Due to the inherent coupling arising out of the possible parallel choices of one state by agents from multiple other states, the problem finding 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 [2]). 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) [3–6], where an odd number ($N = 2M + 1$) of agents try to be, through repeated and parallelly 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.

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 [5]. A stochastic strategy [7], on the other hand, can reduce the fluctuation to the minimum possible value ($\Delta \sim 1$) in a very short time ($\tau \sim \log \log N$). 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 ($\tau \sim \log N$) when $\Delta(t)$ is not exactly know to the agents but a guess value is supplied through an appropriate annealing schedule [8].

In the usual Minority Games, the variations in the target variable i.e., the populations in the two choices, take place due to the movements or switching of choices between the two options. In this work, we study the situation where D number of total choices exists, but one agent tries to be in the minority group in terms of the infection number, by moving between only two choices. The two choices for the N agents are random. Therefore, the infected population in a given region can change due to (a) movements of agents from the other $D-1$ regions and (b) due to the evolution of the epidemic within the region. The evolution of epidemic in our case follow the dynamics of a Susceptible (S)- Infected (I)- Recovered

(R) model. Given that the target variable for minimizing fluctuation (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 a stochastic strategy for switching choices, with a restriction on the total number of allowed switches, can reduce the total infected number compared to a temporary ban on inter-state movements. Furthermore, it is the agents opting for switching of their choice who are less likely to be infected. This shows an individual incentive exists for a strategy which is good for the whole population.

To establish the utility of the stochastic strategy, we first study the dynamics of the parallel Minority Game without an epidemic, where the objective is the usual minimization of the fluctuations in the populations among the choices. As there are D choices, the problem reduces to $D/2$ decoupled Minority Games, if the agents in a pair of choices are completely non-overlapping with the agents of any other pair of choices. The strategy that has proved to be the most efficient [7] in reducing fluctuations in such cases is that agents in the majority choice 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, 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 (α-th) agent in the majority at a given instant to be $p_+(t) = \frac{(P_i^\alpha - P_j^\alpha - 1)/2}{P_i^\alpha}$, where P_i^α is the population at the i-th choice of the α-th agent, P_j^α is the population at the location of the other choice assigned to the agent α and $P_i^\alpha(t) > P_j^\alpha(t)$. 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(b) we show the variation of the fraction of this majority locked agents with time as D is increased. 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(c)). 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 variations of that which does not change such scaling but

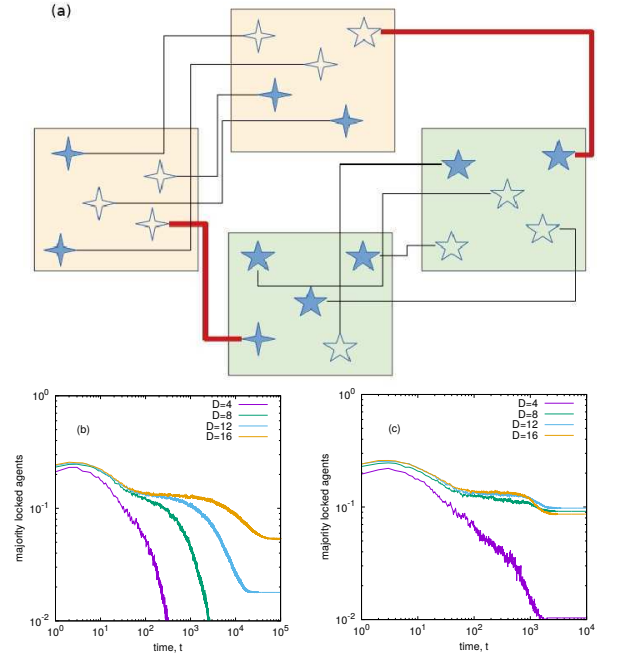only reduces the fluctuation by a constant factor at best.

FIG. 1. (a) The schematic diagram for the agents and their choices in four regions. A filled shape represents a site occupied by an agent and a similar empty shape, connected by black line, represents their alternative choice. Here all agents have an alternative choice. 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 Game. However, the games are coupled when an agent has two choices between two types of regions, marked by red lines. (b) The fraction of majority locked agents (see text) are shown with time for different numbers of regions. The fraction decreases with time, but with a time scale that grows exponentially with D. The number of movements by any given agent is completely unrestricted. (b) The fraction of majority-locked agents are shown when a restriction of only one switch of choice is imposed on the agents. The decrease in the fraction is low, but almost independent of D.

We then proceed with this stochastic strategy of movement to apply in the case where an epidemic dynamics is present in the D states (see e.g., [11–14] for very recent works on the COVID-19 spreading and its effects). We consider the sites of a square lattice ($L \times L$) to represent possible locations for agents in one state. The simplest possible case where a parallel Minority Game could be defined is when $D = 4$, which we take here. We take $L = 160$ and each state is initially occupied with 10000 agents i.e., an occupation fraction of about 0.39. This is less than the site percolation threshold [9], 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 [10] (see Supplemental Materials Fig. for variations of infec-

tion with occupation fraction). The agents are in one of three states: Susceptible (S), Infected (I) or Recovered (R). At any instant, one infected agent can infect its neighboring 8 agents (nearest neighbors and diagonal neighbors) with probability β, provided the neighbors are in S-state. An infected agent remains infected for a period $\tau = 14$ days and then recovers. Given that the reproduction rate R_0 for the COVID-19 pandemic is about 2.28 [15], we keep the infection probability $\gamma = 2.28/(\tau z) \approx 0.02$, as $\tau = 14$ and $z = 8$. While this gives a correct order for the infection probability, this is by no means a precise estimate, which will vary due to the clustering of the locations, immunity variations of the agents and so on.
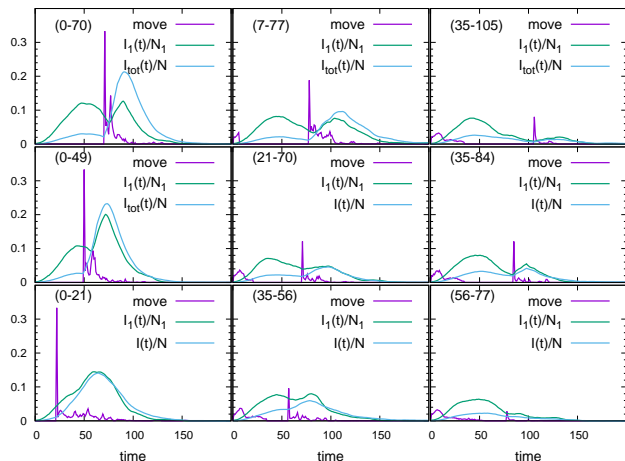

FIG. 2. The time evolution of the total fraction of agents moved, the infected fraction in region 1 and the total infected fraction, each independently normalized (see text) and plotted for various duration and start times of lock down. The lock down start and end times are indicated in each figure. Inevitably, a spike in the movement is noted immediately following the lifting of lock down. This almost in all cases results in a second peak for the total infected fraction. When the effect of lock down is minimal (very late imposition), the restricted movements following the strategy mentioned in Eq. (1) seems to minimize the total infection.

As indicated before, not every agent has the choice of relocating to a different state for a long time. We assign a fraction $g = 0.04$ of the agents with a 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 the location with higher infections i.e., to remain in the minority group in terms of the infected population. However, the infected population at any location will vary due to the epidemic dynamics as well as the due to movements from other locations. We apply a similar stochastic strategy i.e., one agent (α) in the higher infected region (say,

i-th region) will move with a probability

$$p_+ = \frac{(I_i^\alpha - I_j^\alpha)/2}{gP_i^\alpha/(D-1)}, \qquad (1)$$

where I_i^α is the i-th choice for the α-th agent, P_i^α is the population at the i-th choice of the α-th agent and $I_i^\alpha(t) > I_j^\alpha(t)$. The agents already in the lesser infected region compared to their other alternative 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 $(I_i^\alpha - I_j^\beta)/2$ to the j-th region. 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 before.

The initial condition of the simulation is each region has equal population (10000) and all but a small fraction of agents in only one of the regions are initially infected. We keep 15 infected agents in $D = 1$ and all remaining agents everywhere are in S-state. At every time step, one update attempt to all agents, first the epidemic dynamics is carried out and then the movements are made following the strategy mentioned in Eq. (1).

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 region 1 (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 (three, seven and ten weeks) 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 induces a second peak in the total infected fraction. Clearly, this is due to deconfinement and spreading of infections among the different regions. Indeed, the total infected fraction becomes rather limited, when the imposed lock down is very late, which basically amounts to only following the restricted movement rules mentioned above.

To quantify the effects of movements on the travel restrictions, in Fig. 3(a) we show the movement, infected in region 1 and the total infected fractions when no stoppage of inter-state travels is imposed. But the agents
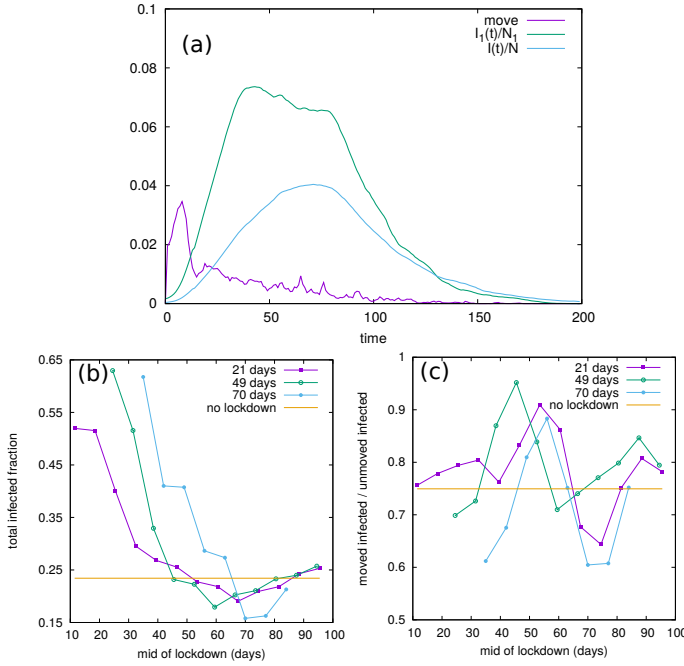
FIG. 3. (a) The time evolution of the movement fraction, infected fraction in region 1 and the total infected fraction, each independently normalized, are show when there is no stoppage imposed in the inter-state movements. But the movements always follow the strategy mentioned in Eq. (1). (b) The fraction 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. A small initial lock down is least effective. Comparisons should be made with the infected fraction for no imposition of inter-state movement, shown in the vertical line. This seems to work better in almost all cases. (c) 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 always less than 1, the population opting for the switching following Eq. (1) are less likely to be infected, where we did not consider the chance of getting infected during the travel.

can switch only once, following the stochastic strategy in Eq. (1). We then compare the total infected fraction, at the end of the epidemic dynamics, for various duration of lock downs with that when no stoppage is imposed. We see that the stochastic strategy performs better almost in all cases (see Fig. 3(b)). Also, if the ratio of the infection probability is calculated for the agents opting for a switch in their choices following Eq. (1) and the same for the agents who did not switch, we see that the ratio is always less than 1, indicating on average a lower risk of infection for the agents making the switch (Fig. 3(c)). This indeed indicates a stability of the strategy itself, as the agents following it gets benefited, while also benefiting (although by a lesser amount) all the remaining agents.

In conclusion, we have posed the problem of movements of agents among various infected regions as an op-

timization problem similar to a set of coupled Minority Games played in parallel. We study the effects of various ranges of travel restrictions and find that only the movements following a stochastic strategy described in Eq. (1) and an additional restriction of the agents being allowed to switch only once between the two choices given to a fraction of them, reduces the overall infection considerably. We also show the stability of the strategy in the sense of a reduced infection rate among the agents opting for a switch in their choices.

SUPPLEMENTAL MATERIALS

Details of movement due to stochastic strategy:
An intuitive way to further elaborate on Fig. 1 is to plot the relative risk of region 1, with respect to the average risk in the remaining three regions. A measure of such a risk is the difference between the number of infected agents in region 1 and the average number of infected agents in the remaining regions. In Fig. 4 we plot the relative risk, with the changes in the population in region 1 from its starting value 10000 for various duration of lock downs and their starting times. There is a symmetric oscillatory pattern in the population change in region 1, when the total infected fraction is high. For lower total infection, the symmetric property vanishes. We show in Fig. how does the curve vary for the case without a lock down.
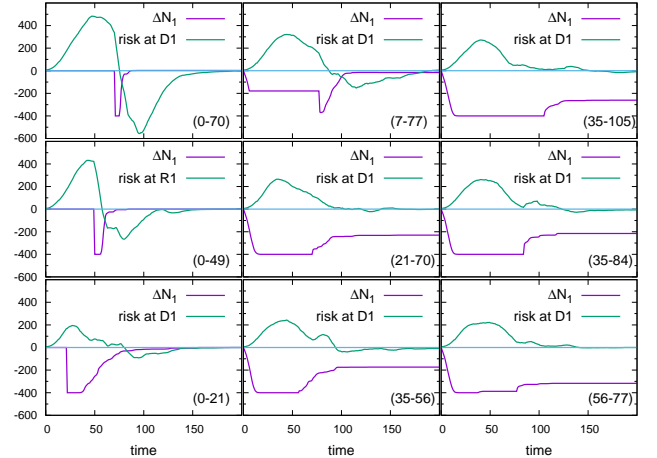

FIG. 4. We plot the time evolution of the relative risk at region 1 with respect to the average risk in the remaining regions. The change in the population in region 1, is anti-correlated with the risk (see text for details).

We also show that the total infected fraction is a monotonically increasing (almost linear) single valued function of the number of infected agents moving during the entire epidemic dynamics (see Fig. 5). This is true irrespective of the lock down duration and the starting point, or even
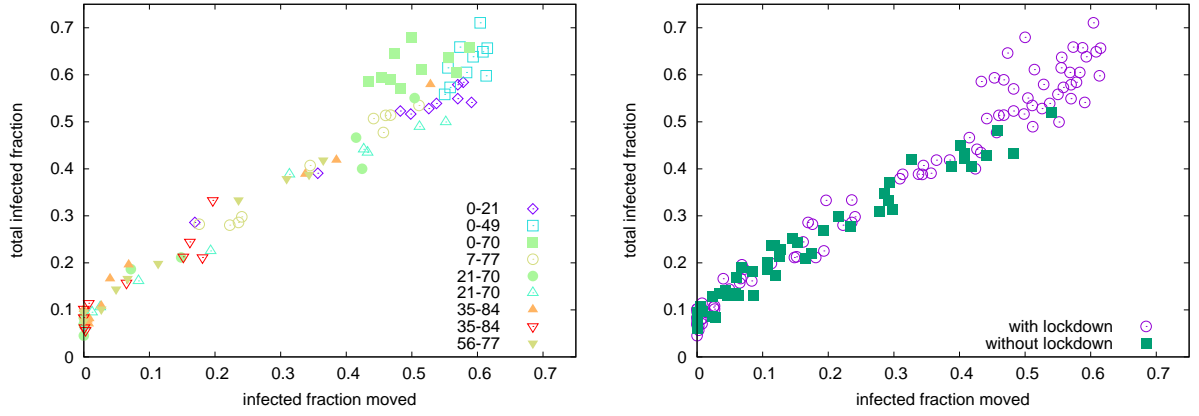
FIG. 5. The top figure shows the variation of the total infected fraction with the number of infected agents moved for various lock down duration and starting times. The bottom figure shows the same variation for both with and without lock down.

without a lock down. This implies that the epidemic dynamics and the movement strategies are largely independent. It is only the total infected people moving that affects the total infected fraction.

Simulation details In Fig. 6 we plot the occupation fraction (by varying L) with total infected fraction. For our simulations, we keep this ratio at about 0.39, which is realistic for a population.
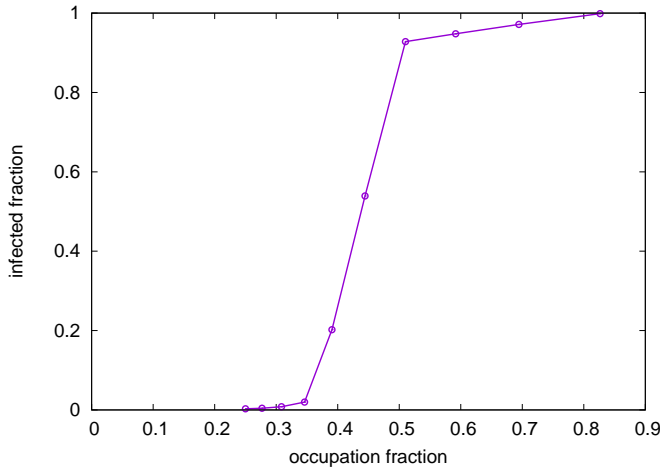

FIG. 6. The total infected fraction is plotted with the variation of occupation fraction. The simulation is done only for one region.

Finally, the outline of the algorithm used for the simulations is shown in Fig. 7

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```
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                          // no 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     recoverCounts                    // Recovered population in the region
21 Def Grid:
22     Person[ ][ ] grid                // 2D array of persons
23     maxRows                          // calculated from population size
24     maxColumns                       // calculated from population size
25 Function Initialize():
26     determine size of grids from the total population & percolation
          point;
27     set initial status to Susceptible : 1;
28     randomly populate prevGrid and CurrGrid;
29     randomly place the initInfectedPopulation on the grids by
          changing its state to infected: 2;
```

```
1  Function Simulate(first, second):
2      ccurrentTime = 0;
3      while currTime != endTime do
4          for k = 0; k < regionCount; k++ do
5              for int i = 0; i < region_K.MaxRows; i++ do
6                  for int j = 0; j < region_K.MaxColumns; j++ do
7                      Person person = prevGrid_k.getPerson(i,j);
8                      if person is Susceptible then
9                          for all the neighbour of a person in prevGrid do
10                             if neighbour is Infected in prevGrid then
11                                 calculate a randomProbability for the
                                     person ;
12                                 if randomProbability >
                                     region_K.infectionProbability then
13                                     Marked Person as Infected in currGrid ;

14                         if person is Infected then
15                             if currStateTimeStep == infectionDuration then
16                                 Marked Person as Recovered in currGrid ;

17                 Store susceptibleCounts, infectedCounts and recoverCounts ;
18         currTime++;
19         if currTime<56 || currTime >126 then
20             AllowMovement (region, currTime);

21 Function AllowMovement(region, currTime):
22     for all possible inter-region (regionX, RegionY) movement do
23         moveProb = getMovementProbability (regionX, RegionY);
24         for each person in rgionX do
25             if have choice to move to regionY then
26                 calculate a randomProbability for movemet ;
27                 if randomProbability > region_K.infectionProbability
                     then
28                     Move that person: regionX → RegionY ;

29 Function getMovementProbability(regionX, regionY):
30     prob = ((regX.infectedCounts −
          regY.infectedCounts)/2)/(regx.totalPopulation *
          (regx.choiceFraction/(TotalNoRegions − 1)));
```

FIG. 7. The algorithm used for the simulation.