Predictive modelling of disease propagation in a mobile, connected community

Ishant Tiwari, Pradeep Sarin and P. Parmananda

Department of Physics, Indian Institute of Technology, Bombay

(Dated: March 23, 2020)

We present numerical results obtained from the modelling of a stochastic, highly connected and mobile community. The spread of attributes like health, disease among the community members is simulated using cellular automata on a planar 2 dimensional lattice. With remarkably few assumptions, we are able to predict the future course of propagation of such disease as a function of time and the fine-tuning of parameters related to the interaction among the automata.

FIG. 1. Lattice Model of cellular automata of two types \( \text{R} \) and \( \text{B} \) (represented by colors Red and Blue respectively). Initial state shown with \( N_{\text{R}} = 1 \) (highlighted with a red circle) and occupancy \( O = 0.17 \).

MODEL CONSTRUCTION AND EVOLUTION RULES

The concept of cellular automata placed on a matrix of sites, with rules defining their evolution as a function of time has been very popular since John Conway’s proposal\[1, 2\].

Here we define a system of cellular automata system of two types \( \text{R} \) and \( \text{B} \). Figure\[1\] shows a visualisation of our system in its initial state on a square lattice in 2 dimensions with 100 \( \times \) 100 sites.

The following set of rules define the evolution of the system:

1. Each automaton can be one of two types \( \text{R} \) or \( \text{B} \). A single automaton may change its type as a function of time.

2. The automata are mobile. At every time step, each automaton must move as directed by a combination of two forces: (a) a uniformly randomized force in 2-D producing a movement by 1 lattice site in \( \pm x, \pm y \) and (b) a force whose direction is weighted by its ‘connectedness’ to other automata in the system as described below. A combination of these two forces results in movement to points in the 2-D space that are not necessarily on the square lattice sites of the initial condition. We do not assume periodic boundary conditions: when an automaton reaches the space boundary, its choice of movement directions is restricted.

3. The system is connected. At any time, each automaton has access to information of the type of all automata in the system. The probability distribution of which vacant site an automaton chooses to jump to, is based on the availability of this information.

   (a) The probability of a \( \text{B} \) jumping to any of the allowed nearby vacant sites is 1, weighted with a Yukawa-like potential function:

   \[
   \frac{C}{r} e^{-\frac{r}{L_s}}
   \]

   \( C \) is a ‘social distancing factor’ and \( L_s \) is the length scale over which the effect of \( \text{R} \) is felt. In this sense \( L_s \) is the length scale over which the system is connected and the individual automata can get information about their neighbours. We calculate the Yukawa ‘force’ exerted on a \( \text{B} \) by evaluating its distance \( r \) to all the \( \text{R} \) in the system. The vector sum of all these Yukawa forces with magnitude capped at 1 determines the probability of \( \text{B} \) jumping in that direction. Thus \( \text{R} \)’s far away from a \( \text{B} \) hardly affect its jumping direction, while nearby \( \text{R} \)‘s strongly influence the probability of \( \text{B} \) to jump away from them.

   (b) We set the probability of \( \text{R} \) moving in all directions as equal, with an absolute value of 0.02 i.e. \( \text{R} \) have less of a tendency to move, compared to \( \text{B} \).

4. After every time step, if a \( \text{R} \) and \( \text{B} \) are within a radius \( r = \sqrt{2} \) of each other, the \( \text{B} \) turns into \( \text{R} \) : \( \text{B} \rightarrow \text{R} \) with a probability 0.5. The reverse transition \( \text{R} \rightarrow \text{B} \) is forbidden.
5. The system is initialized with $N_0 = N_R + N_B$ automata spread uniformly over the lattice. For convenience, we set the initial locations of the automata on a regularly spaced $100 \times 100$ grid. $N_0$ is conserved during the system’s evolution.

**INITIAL CONDITIONS AND MODEL ASSUMPTIONS**

The following assumptions are made to simplify and speed up computations:

1. We start with the initial condition that $N_R = 1$ and $N_B = N_0 - 1$ as shown in Figure 1. The site for placement of the lone $N_R$ is also chosen at random in 2 dimensions.

2. The background space on which the automata move is assumed to remain pristine throughout the simulation, i.e., a site occupied by $R$ or $B$ does not retain any ‘memory’ of the occupant after the automaton has moved away.

The main parameters and dynamically tracked quantities in our model calculation are:

1. $N_R(t)$ the total number of $R$ automata present in the system at every time step. It is easy to see that $N_R$ asymptotically reaches $N_0$ with the basic assumptions stated above. The dynamics of $N_R(t)$ at intermediate times show interesting features.

2. Social distancing factor $C$ used to calculate the weighting factor $C e^{-\frac{r}{L_s}}$ in deciding the probabilistic direction of movement of $B$. $L_s = 10$ is fixed for this study.

**NUMERICAL RESULTS**

We have implemented the rule sets in MATLAB, and run the model calculations for 4 sets of parameters for $t_{\text{max}} = 7000$ time steps, or complete population inversion (i.e. $N_B = 0$, whichever occurs earlier).

1. $C = 0$: the automata $B$ don’t take into account the distance other $R$ ’s, and jump to all adjacent neighbor sites with equal probability

2. $C = 1, C = 5, C = 10$ represent increasing ’social
distancing effect in the determining the movement of the automata. A representative snapshot of the system state at an intermediate state for $C = 5$ is shown in Fig 2. The results for $N_R(t), N_B(t)$ at different values of $C$ are shown in Fig 3. The asymptotic approach to $N_R \to N_0$ is borne out in all cases. However the intermediate time dynamics in each case show remarkable features. As the social distancing is increased to a non-zero value, the rate of infection first increases: at $C = 0$, the asymptotic value $N_R = N_0$ is reached at $t \approx 2000$, but at $C = 1$ the asymptote is arrived at a much earlier time $t \approx 1500$. In both cases the slope of the rising $N_R(t)$ is rather sharp, starting at a non-zero value already at $t = 0$. Only for much larger values of $C$ does one observe a gradual rise of $N_R(t)$ followed by eventual saturation.

DISCUSSION AND FUTURE WORK

The cellular automata model discussed here is representative of the spread of a disease in a highly connected, mobile system. At every time step, since each automaton is forced to move to a neighboring site, its attributes $R$ or $B$ are bound to propagate throughout the system asymptotically. Furthermore, the system has been setup in such a way that every automaton is able to compute its ‘distance $r$ to $R$ ’s through an implied top-down information availability (as explicitly implemented in our computation) or through a distributed information sharing network. In both cases, it is necessary at each time step for each automaton to instantaneously know its identity $R$ or $B$ - this simplification in our toy model does not map to a real world disease propagation scenario where the ‘diagnosis’ of the character $R$ or $B$ may occur with some time lag. Such a time lag can be implemented in our model with extra computational cost incurred by storing extra ‘hidden’ variables attributed to each automaton that evolve in parallel and effect hopping decisions in a non-linear fashion. Another aspect of the system dynamics we have not modelled in our closed system study, is to remove the constraint on conservation of $N_0 = N_W + N_R$. Removing this constraint, i.e. adding new automata to the system of type $R$ or $B$ as a function of time could lead to interesting results.

With the reverse transition $R \to B$ ‘curing $R$ to $B$ ’ forbidden in our toy model, the only possible asymptotic condition is $N_R \to N_0$. By allowing such curing process, an asymptotic value $N_R < N_0$ can be reached. In our model all automata, including $R$ are forced to move at every time step (albeit $R$ with much lower, but non-zero probability). By hard quarantine of $R$ ’s in space (assuming a hidden variable can ‘diagnose’ the identity of $R$ since the identity of $R$ may be known only with a time lag), perhaps an asymptote of $N_R < N_0$ can also be reached. This aspect requires further study.

To summarize, we have analyzed the dynamics of properties (here $R$ and $B$ ) attributed to automata which are fundamentally mobile and connected. It is trivial to see that if all the automata are restricted from motion (i.e. we set the probability value=0 for performing any jump), the system will not evolve at all - there is no mobility, and hence no need for connectivity, apart from the few interactions put in by the initial state. In this sense, the mobility and connectivity of the automata are correlated parameters.

CITATIONS

[1] Martin Gardner. Mathematical Games. Scientific American, 223(4):120–123, 1970.
[2] S. Hoya White, A. Martín del Rey, and G. Rodríguez Sánchez. Modeling epidemics using cellular automata. Applied Mathematics and Computation, 186(1):193–202, 2007. ISSN 00963003. doi:10.1016/j.amc.2006.06.126

ACKNOWLEDGMENTS

We are grateful for support provided by DST grants EMR/2016/000275 (P.P.), SR/MF/PS-02/20014-IITB (P.S) and CSIR (I.T.). This work was supported by the Department of Physics, IIT Bombay.