Vicious walker

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1 Introduction

The vicious walker is an algorithm that can be used to model chemical reactions. In this model we what we call walkers, in an n-dim space ($n = 1, 2, 3, \dots$) that each step in time from a time $t \to \Delta t$ with Δt the time step, the vicious walker walks moves to a random neighboring tile. In this project we will consider two types of vicious walkers, a standard vicious walker vicious walker and a "friendly" vicious walker which instead of mimicking reactions could be said to mimic how a population behaves.

2 Methods

2.1 Standard vicious walker

We start with an n-dim box ($n = 1, 2, 3, \dots$) with an integer side length l. The volume V of the box is then l^n. Now we select n random numbers $R_i \in [1, l]$ ($i = 1, 2, \dots, l$) and if the position in our box $\mathbf{X} = R_1\hat{\mathbf{x}}_1 + R_2\hat{\mathbf{x}}_2 + \cdots + R_n\hat{\mathbf{x}}_n$ is not occupied, place a walker there, otherwise generate new random numbers and check the position again and repeat until all the desired number of walkers have been placed. Then for each time step we move each walker into a random neighboring tile by choosing a random number $R \in [1, n]$ and going in the $\hat{\mathbf{x}}_{\mathbf{R}}$ direction. If moving in this direction leads to the walker leaving the box, we reject the move and go to the next walker (closed box) or it teleport to the opposite side (open box). If two walkers walk into the same tile they annihilate. For long times in 1, 2, and 3 dimensions, the average density $\langle\rho\rangle$=$\langle N/V\rangle$ with $N \to \infty$ and $V \to \infty$ in the box should follow at large t [1]

$$\langle\rho\rangle \propto \begin{cases} t^{-1/2}, & \text{1D} \\ t^{-1}\log(t), & \text{2D} \\ t^{-1}, & \text{3D.} \end{cases} \tag{1}$$

2.2 Friendly vicious walker

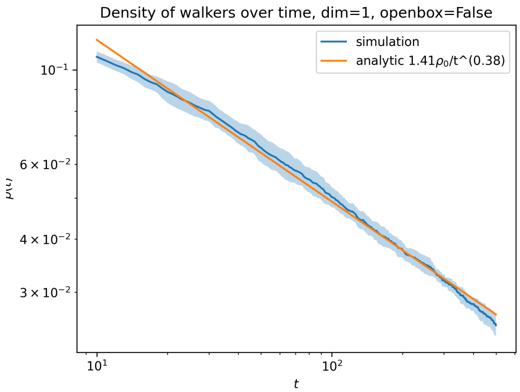
First we make the same initial steps as with the standard vicious walker. Now, instead of walkers annihilating each other when they meet, the have a probability $p_{\text{fertility}}$ to make a new walker at that position and move the parent walkers to their previous position. To have a chance at making a new walker, both walkers must have a lived through $n_{\text{producing}}$ time steps. Each walker also has a probability $p_{\text{die}}^{\text{age}}$ to die each time step. We also introduce a food system with some starting food and each turn the food regenerates by a specific amount. Each walker eats one food each step and if there is no more food to go around the walkers that did not get food all die of starvation. Hence we limit the maximum amount of walkers in our box (which is not the volume of our box). To make it a bit more interesting, we later introduce infections with a starting amount of the initial walkers being infected and each time step, there is a probability for any walker to be infected. If a walker is infected, it in turn has a probability die each turn $p_{\text{die}}^{\text{infection}}$.

3 Results and discussion

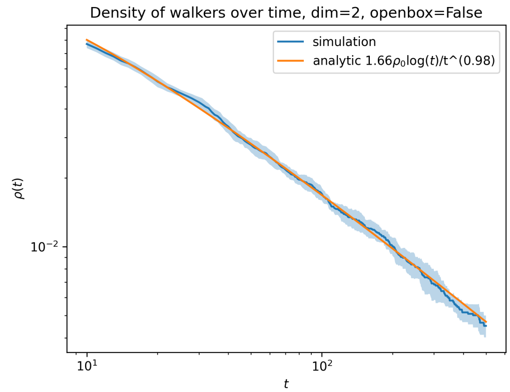
In this section we will display all of our results and the parameters used for each model and plot starting with the standard vicious walker.

3.1 Standard vicious walker

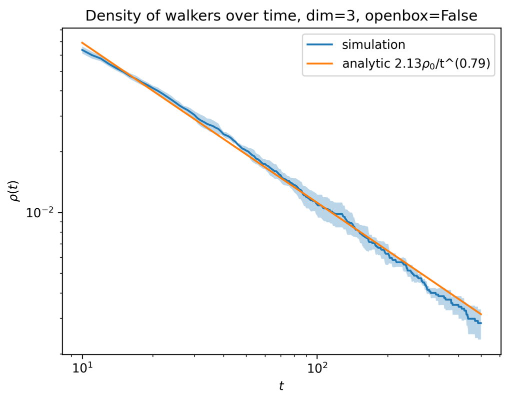
In figure 1 we see the density of the number $\rho(t)$ walkers as a function of time for the simple vicious walker. All of the figures have the exact same initial conditions, with the only difference being the number of dimension that the walker can move in. Note that the figures display the mean result (blue line) for 5 simulations and the blue fill represents 1 standard deviation. The first ten steps have been taken out to avoid division by zeros when comparing making the best fit for the simulation (orange line).



(a) Vicious walker density as a function of time in with D = 1, Starting density = 0.2, Initial walkers = 1100, Volume = 5500.0.



(b) Vicious walker density as a function of time in with D = 3, Starting density = 0.2, Initial walkers = 1100, Volume = 5500.0.

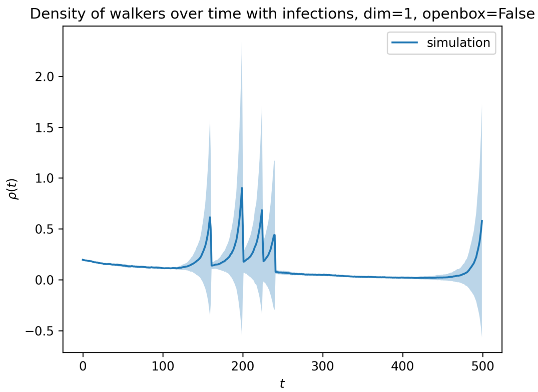


(c) Vicious walker density as a function of time in with D = 3, Starting density = 0.2, Initial walkers = 1100, Volume = 5500.0.

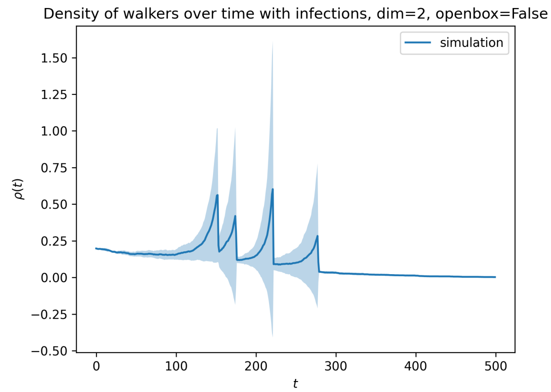
Figure 1: The average density of walkers in time in 3,2 and 1 dimensions.

So as we can see, comparing our results for the best fit with the thermodynamic limit of equation (1), we see that only for 2 dimensions, this seems to match (see figure 1b). For dimensions 1 and 3, we see that the rate at which the density decays is slower than in the thermodynamic limit. Why this is the case only for 1 and 3 dimensions, could be that there simply is not enough data (only averaged over 5 runs) or that the the number of initial walker and volume are too small (the thermodynamic limit holds for $N \to \infty$ and $V \to \infty$). However this argument should also hold for 2 dimensions. There could also be some bug in the code that for some reason does not show up in two dimensions but only for 1 and 3 although unlikely since the only difference in the code is just adding or removing a direction.

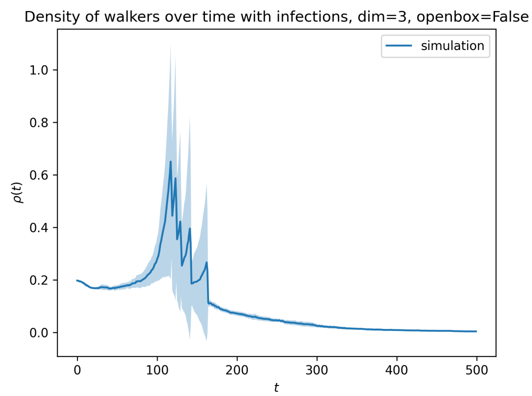
3.2 Friendly walker



(a) Friendly walker with infection density as a function of time in with D = 2, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.



(b) Friendly walker with infection density as a function of time in with D = 2, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.



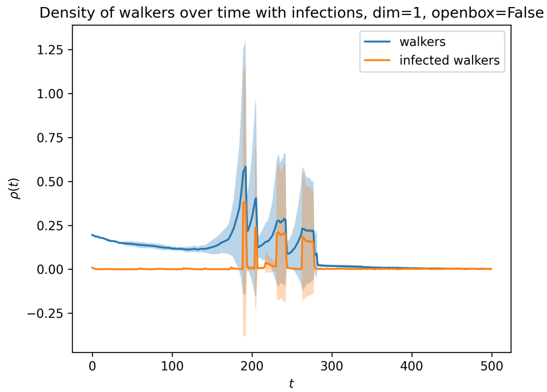
(c) Friendly walker with infection density as a function of time in with D = 3, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.

Figure 2: The average density of walkers in time in 3,2 and 1 dimensions.

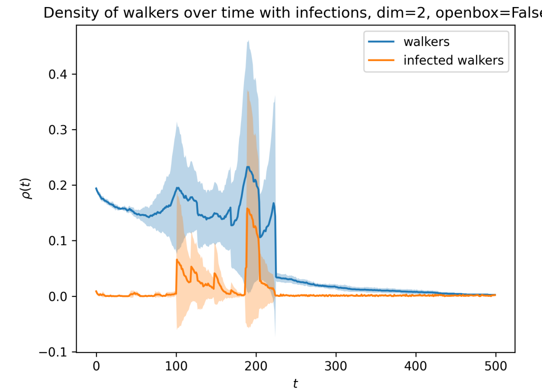
Figure 3 shows the average density for the the friendly walker in 1, 2 and 3 dimensions with all other parameters unchanged without any infections. Same as for the vicious walker, the blue line is the average density over 5 simulations and the blue fill is one standard deviation. The parameters are as follows: $p_{\text{die}}^{\text{age}} = 1/100$, $p_{\text{fertility}} = 1/200$ and $n_{\text{producing}} = 14$, starting food = 200, food regeneration = 200. An important thing to note is that multiple walkers are allowed to be born at the same position. This is a bug in the code from when we move back the walker. If it has already reproduced and then another walker moves into this position, they might produce another walker. But when we move back this walker which has now reproduced twice, it just stays in the same place as the newborn which allows for $\rho(t) > 1$.

As we can see, limiting the food has a large affect on the overall population as we can see with the sharp drop in density for each of the figures in 3. In the beginning of each simulation, there is enough food to go around (200 for 100 walkers) and each step, the food pile gets larger by 200. So when the population reaches 200, the food supply is steadily going down until it reaches zero, at which point there might be 300 walkers. Since we only generate 200 food each step, 100 walkers die of starvation at once.

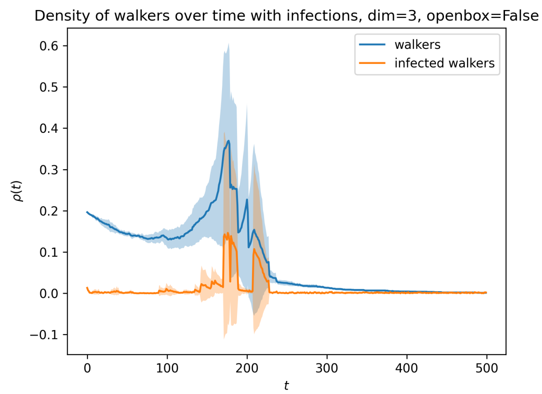
Now one thing of note is that we notice that compared to the vicious walker, we have a much larger



(a) Friendly walker density as a function of time in with D = 2, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.



(b) Friendly walker density as a function of time in with D = 2, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.



(c) Friendly walker density as a function of time in with D = 3, Starting density = 0.2, Initial walkers = 100, Volume = 500.0.

Figure 3: The average density of walkers in time in 3,2 and 1 dimensions.

standard deviation. This is due to the many more parameters and probabilities in the model. Ex. instead of just having two walkers in the same position annihilate, they instead have a probability to reproduce. We also see that as time goes on for all the dimensions (except 1 which requires more time-steps), the conditions for reproducing are not large enough to keep a stable population. This is largely due to the food limitation as discussed above as without it, each simulation would continue to grow (due to the bug allowing for $\rho(t) > 1$). But also due to there just not being enough walkers to reproduce, i.e the probability for them to die of old age is larger than the probability for two walkers to reproduce and two walkers to meet (together with the walkers not being able to reproduce for 14 steps).

3.3 Friendly walker with infection

Now we can move onto friendly walkers with infection spread. All of the figures in figure 2 have the same paramters as with the friendly walkers except for the additional parameters; #initial infected = #initial walkers/10, $p_{\text{die}}^{\text{infection}} = 1/10$, $p_{\text{recover}} = 1/2$ and $p_{\text{infection}}^{\text{start}} = 1/(10\#\text{initial walkers})$.

With these additional parameters, we see that regular triangle shapes in figures 3a and 3c start to disappear and the simulation reaches a steady state (i.e all walkers are dead) faster than in the regular friendly walkers without infections. This is expected since we only make walkers dying more probable. Note that the number of initial infected in our simulation is too small to start a pandemic and instead the infection dies out, but the number of infected walkers also follows population growth. This is because every walker has a probability $p^{\text{start}}_{\text{infection}} = 1/(10\#\text{initial walkers})$ to get infected. So the more walkers the larger the probability to start an infection and also it is more probable that the infected walker will pass on the disease to another walker.

In the future one could add different infections (here they are all the same) with new probabilities of recovering, dying and so on. Another thing to make the system more physical could be to more mimic the $p^{\text{age}}_{\text{die}} = p^{\text{age}}_{\text{die}}(t)$ to an existing curve that is know in nature instead of it being uniform. However the main thing to change would be to make every walker have it's own parameters of $p_{\text{fertility}}$ and $p^{\text{age}}_{\text{die}}$ that they can pass on to their children which could emulate evolution of a species.

4 Conclusion

So as we have seen with the vicious walker, the density of the vicious walker does behave like the thermodynamic limit, however not entirely. Why this is the case could be that the volume and number of walkers are too small in the simulation. We have seen that the density of friendly walkers with the current set of parameters, decrease for all dimensions. However as we increase the number of dimensions the quicker the walkers die out due to old age and we note that there is a population boundary for the walkers not dying out which grows with the number of dimensions. We also note by introducing infections to the friendly walker that the walkers die out faster as expected and that the number of infected walkers closely follows population growth. In the future to simulate a population better, the friendly walkers could have private parameters instead of global ones with a global mean and variance that they could then pass on to their children.

References

[1] Dept. of Astronomy and Theoretical Physics, Lund University, Sweden. FYTN03 Computational Physics: Stochastic Processes, part. PDF, 2017.