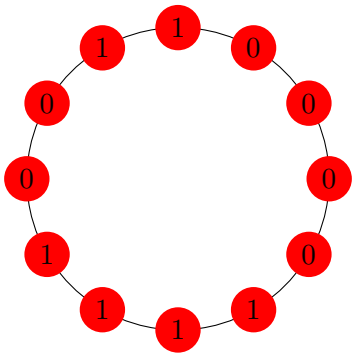
Genetic Homogeneity

Consider the voter model on the lattice $\mathbb{Z}_N = \{0, 1, \ldots, N-1\}$, corresponding to a lattice with periodic boundary conditions and N sites, each with only one neighbor. Assume that the rates of transition between states are still given by the rate 1. The case of $N = 12$ is sketched below, in a random initial state.



As we will soon see, many properties of the 1D voter model are not so hard to obtain. Denote by $\mathrm{P}(x,t)$ the probability that at time t, a site a distance x steps away from a given site has the *opposite* state.

(a) Approximating x as a continuous variable, show that if $x \ll N$,

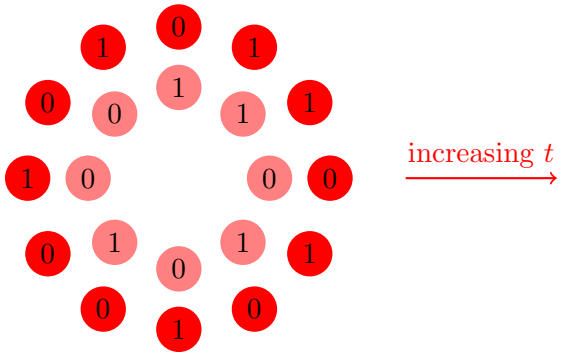
$$\frac{\partial \mathrm{P}}{\partial t} = \frac{\partial^2 \mathrm{P}}{\partial x^2}.$$

(b) Show that, under the appropriate boundary condition of $\mathrm{P}(0,t) = 0$ (thinking of the solution as depending only on $|x| \in \mathbb{R}^+$), the solution of the equation above is

$$\mathrm{P}(x,t) = \frac{1}{2}\mathrm{erf}\left(\frac{|x|}{2\sqrt{t}}\right).$$

(c) How does the time required to reach consensus, T, scale with N?

The voter model in 1D on a graph which is expanding at some rate v can be used to model the spread of alleles in bacteria, growing in a petri dish. The basic idea is as follows: suppose we start with a disk-shaped region, filled randomly with bacteria which either have allele 0 or 1. The bacteria at the edge, with room to divide, can divide outwards, forming a bigger circle.



We can write the effective equation here, using the same logic as above,

$$\frac{\partial \mathrm{P}}{\partial t} = \frac{D}{(R_0 + vt)^2} \frac{\partial^2 \mathrm{P}}{\partial \theta^2}.$$

Here R_0 relates to the initial radius of the circle, related in turn to the initial size of the bacterial colony. Note that we have replaced x with an angular coordinate θ, as here since the radius is time-dependent this is a better description.

(d) Using the same boundary condition and initial condition as in the previous part, find the solution $\mathrm{P}(|\theta|, t)$.

(e) Explain why the expected number of domains, N_d, (corresponding to the number of distinct regions where all nodes of at time t), is given by

$$N_\mathrm{d}(t) = 2\pi \frac{\partial \mathrm{P}(t, 0^+)}{\partial \theta}.$$

(f) Show that in this case, the system does not reach a consensus state as $t \to \infty$. Instead, show that

$$N_\mathrm{d}(\infty) = \sqrt{\frac{\pi R_0 v}{2D}}.$$

Comment on the biological implications.