Evolutionary Dynamics Homework 9

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Problem 1: Eden model dynamics

Consider a two-dimensional Eden growth model with von Neumann neighborhood

(b) Simulate different update rules

Consider the R code at https://git.io/vF0KH. What is the update implemented in the code? Modify the code to simulate the other two update rules from question (a) and then explain the difference between the spatial boundaries of the pouplation obtained for the different evolutionary dynamics.

Update rule implemented in the code

The update rule code is implemented in the following block:

It basically selects a cell that will divide in this iteration, with a probability that depends on both the number of empty spaces in the neighbourhood and the fitness of the cell itself. This implementation is most similar to the *bond focused* update rule in question (a), where we randomly choose an S_1 (occupied) site with probability proportional to the number of adjoining S_0 (empty) sites.

Simulate the other two update rules

Available site-focused

• Available site-focused update rule: randomly choose an S_0 that adjoins at least one S_1 site, and switch it from S_0 to S_1 .

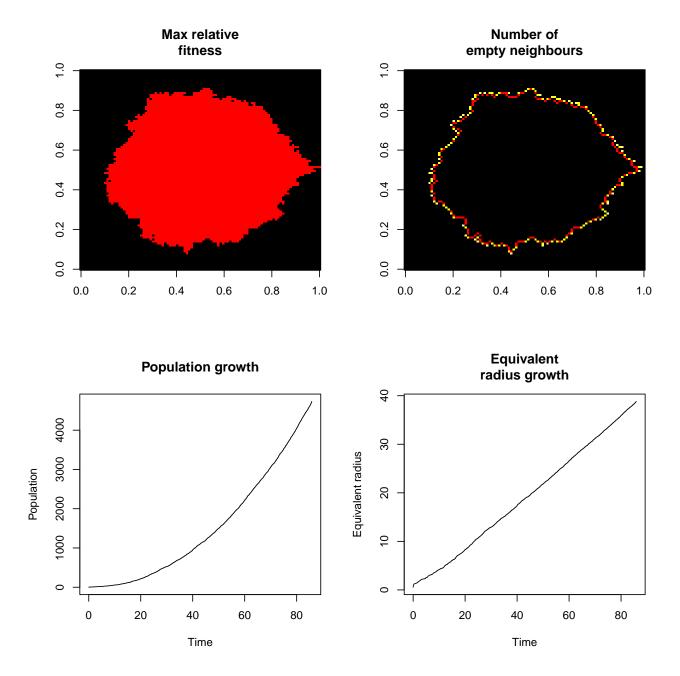
```
# TODO
```

Cell-focused

• Cell-focused update rule: randomly choose an S_1 site that adjoins at least one S_0 site, then sample uniformly an S_0 neighbour and switch it to S_1 .

Basically just remove the scaling using how_many_spaces in the sample function.

```
candidate <- sample(1:num_has_space, 1, prob = sapply(has_space, function(e)
sites[e[1], e[2]]))</pre>
```



Problem 2: Diffusion approximation of a spatial Moran model

Consider the spatial Moran model for a mutation spreading through an infinite row of demes. Let μ denote the death rate, s the fitness advantage of the mutant, m the dispersion probability, and N the number of individuals per deme. Assume initially that $n_i=N, \forall i\leq 0$ and $n_i=0$ otherwise, where n_i is the number of mutants in deme i. The rate at which mutants in a deme die is μn_i . Once an individual has died, it is replaced by the offspring of a wild type individual of its own deme with probability

$$P_1 = \frac{N-n_i}{(1+s)n_i + (N-n_i)} \approx \frac{N-n_i}{N},$$

and it is replaced by the offspring of a wild type individual from any of the neighbouring demes with probability

$$P_2 = \frac{m(N-n_{i-1})}{2N} + \frac{m(N-n_{i+1})}{2N} \approx \frac{m(2N-(n_{i-1}+n_{i+1}))}{2N}.$$

(a) Using these results, show that the rate for the number of mutants in deme i decreasing by one individual is as follows:

$$W_i^-(\mathbf{n}) = \frac{\mu}{N} n_i \left((N - n_i) - \frac{m}{2} n_i'' \right)$$

where $n_i'' = n_{i-1} + n_{i+1} - 2n_i$.

Proof. $W_i^-(\mathbf{n})$ is basically $\mu n_i((1-m)P_1+P_2)$. The following process show proves the result:

$$\begin{split} W_i^-(\mathbf{n}) &= \mu n_i \left((1-m) \cdot \frac{N-n_i}{N} + \frac{m(2N-(n_{i-1}+n_{i+1}))}{2N} \right) \\ &= \frac{\mu n_i}{N} \left(N-n_i - m(N-n_i) + \frac{m(2N-(n_{i-1}+n_{i+1}))}{2} \right) \\ &= \frac{\mu n_i}{N} \left(N-n_i - m \frac{2N-2n_i - 2N+n_{i-1}+n_{i+1}}{2} \right) \\ &= \frac{\mu n_i}{N} \left(N-n_i - \frac{m}{2} (n_{i-1}+n_{i+1}-2n_i) \right) \\ &= \frac{\mu}{N} n_i \left((N-n_i) - \frac{m}{2} n_i'' \right) \end{split}$$

 \end{proof}

(b) Show that the rate of expectation of the number of mutants in deme i is as follows: In general,

$$\frac{d\mathbb{E}[n_i]}{dt} = \mathbb{E}\left[W_i^+(\mathbf{n}) - W_i^-(\mathbf{n})\right]$$

where $\mathbb{E}[X]$ denotes the expected value of a random variable X. Using the expression of $W_i^+(\mathbf{n})$ given in the lecture and applying the approximation $\mathbb{E}[n_i n_k] \approx \mathbb{E}[n_i] \mathbb{E}[n_k]$ (called the *mean-field approximation*), show that

$$\frac{d\mathbb{E}[n_i]}{dt} = \frac{\mu m}{2}\mathbb{E}[n_i''] + \frac{s\mu}{N}(N - \mathbb{E}[n_i])\left(\mathbb{E}[n_i] + \frac{m}{2}\mathbb{E}[n_i'']\right)$$

Proof. From lecture, we know that

$$W_i^+(\mathbf{n})$$

(c) See below.

(d) See below.

(e) See below.

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