Exercises 9

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Problem 1

(a)

In the setting descriped in the script, only one type of occupied state ($S_1 = 1$) and no mutation was allowed during the process. Therefore, each site in the grid space would either be in S_1 occupied state or un-occupied. Following is the brief idea of the evolution process as per the script descrips.

The models described here is **bond-focussed**, explained below.

1. A candidate was randomly sampled from all the sites in the grid space that have been occupied (code) with a probablity **proptional to the number of S_0 sites in its neibours**.
2. A unoccupied neibouring site (S_0) will switched to S_1. Skip if the neibouring sites were occupied (code)
3. Record the time for the proliferation event, which follows an exponetial distribution with the parameters $\lambda \propto \sum_{i,j} \text{neibours}_{i,j}$ (code)
4. Update the sites that has been occupied, the corresponding index list and the list of neibours. (code)

To make the proliferation rate **same** across all cells of more than one S_0 in their neibours, the update rule needs to switch to **cell-focussed** method described in the slides.

(b)

A modification was made during the sampling stage. As indicated by the Q-Q plot below, the sampling in bond foucussed approach clearly derivate from the uniform distribution much more than the cell foucussed one. It should be noted the below Q-Q plot is re-sampling after the simulation (both cell focus and bond focus). On the other hand, if the grid space was pre-occupied with S_1 uniformly, two approaches do not differ in the re-sampling result as expected.

As shown in the simulation results below, the occupied grids in simulation of the cell focus one appears to be more uniform around the edge while the other possess rougher edge. This is probably due to the fact that the **bond-focussed** method gives larges weight to unoccupied sites (S_0) surrounded by multiple occupied ones (S_1). Due to this bias in sampling, unoccupied sites around the corner in the grid space would have been `smoother` in the **cell-focussed** one (as shown in Fig. 1). The effects of the sampling method can be clearly shown by the Q-Q plot below (Fig. 3)

```
source('ex9_1_EdenModelSim.R')
```

```
ITER = 1000
bond_based <- list()
cell_based <- list()

for(iter in 1:ITER) {
  candidate <- sample(1:num_has_space, 1, prob = unlist(how_many_spaces) *
                      sapply(has_space, function(e) sites[e[1], e[2]]))
  bond_based[[iter]] <- candidate
}
```

```
source('ex9_1_EdenModelSimCellBased.R')
```

```
for(iter in 1:ITER) {
  candidate <- sample(1:num_has_space, 1, prob =
```
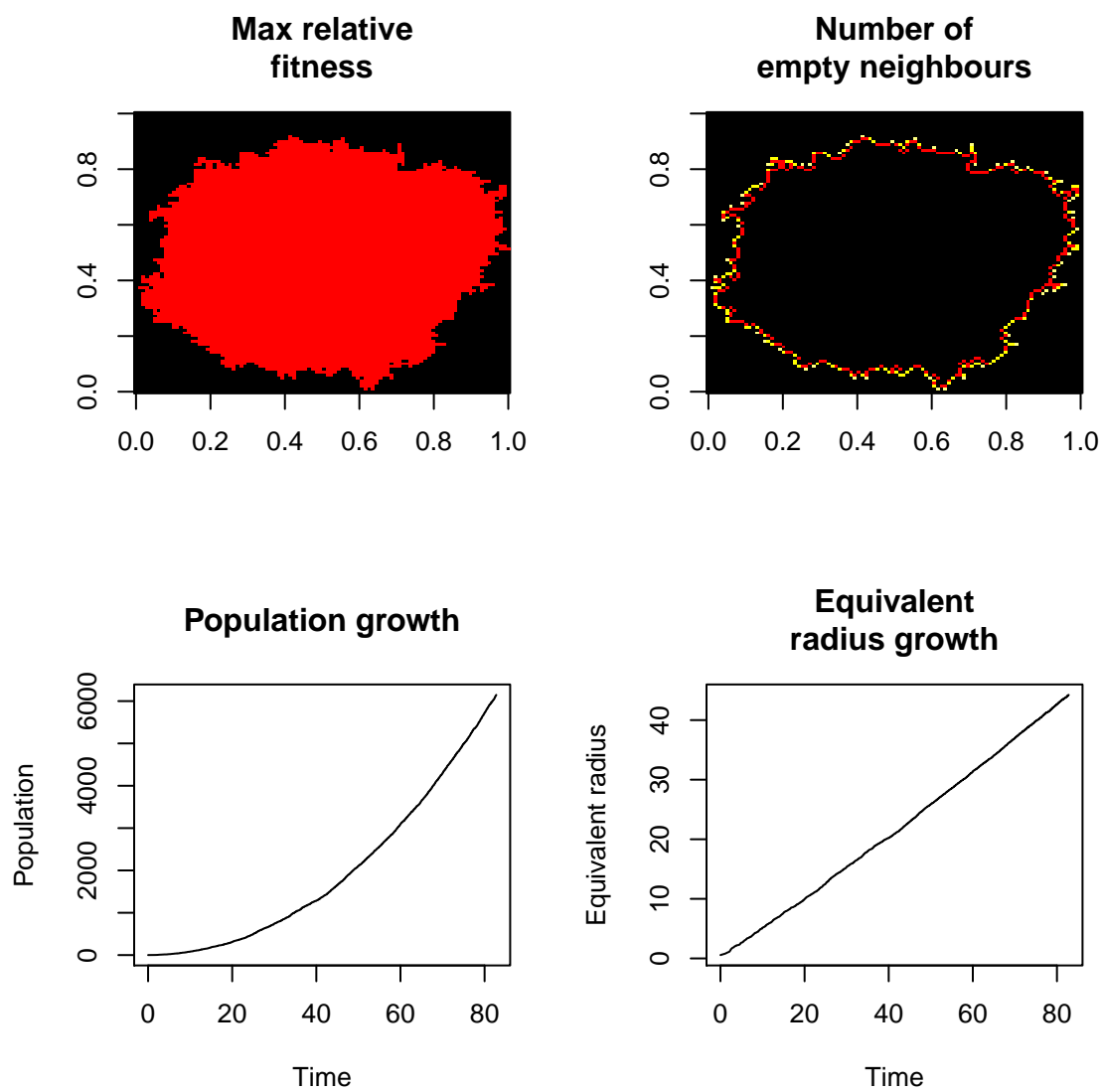
Figure 1: Simulation using bond focus method

**Max relative
fitness**

**Number of
empty neighbours**

Population growth
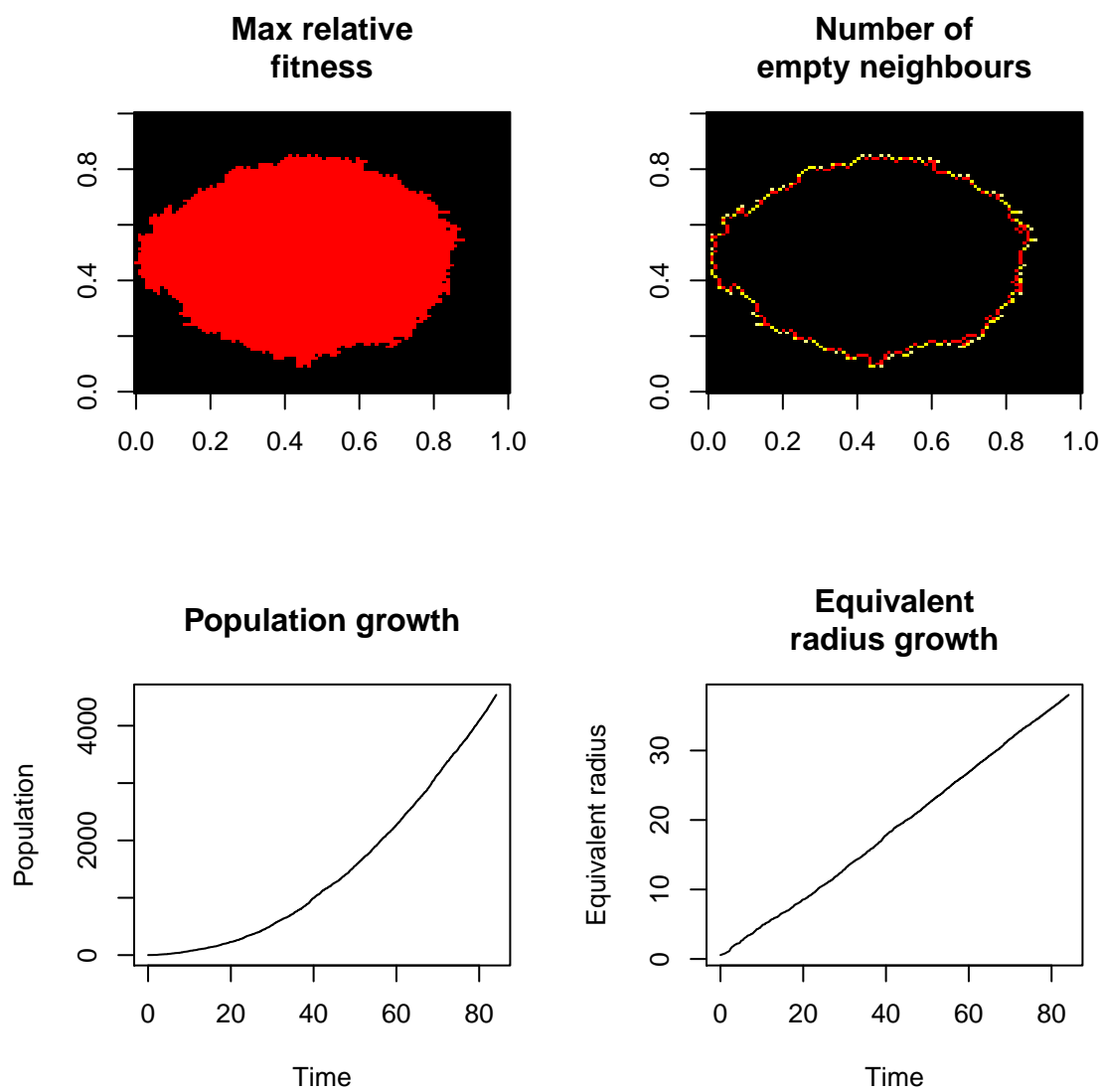
**Equivalent
radius growth**

Figure 2: Simulation using cell focus method
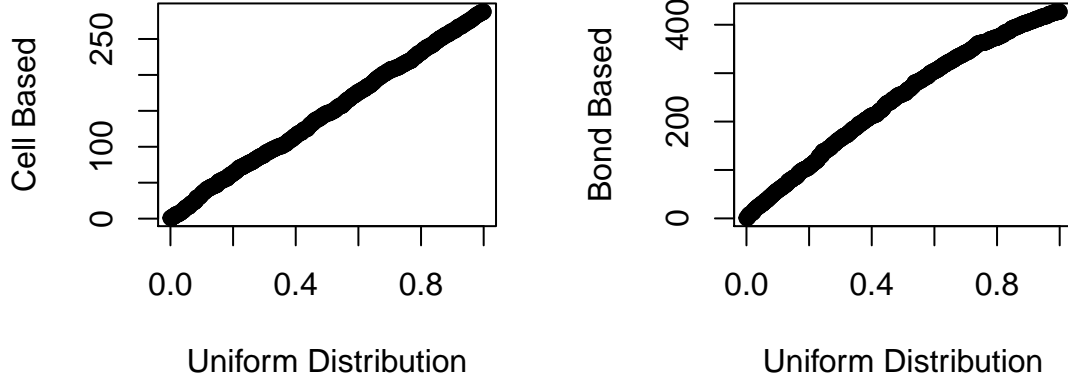
Figure 3: Sampling result using simulation

```
                    sapply(has_space, function(e) sites[e[1], e[2]]))
  cell_based[[iter]] <- candidate
}
```

```
x <- qunif(ppoints(ITER))
par(mfrow = c(1, 2))
qqplot(x=x, y=sort(unlist(cell_based)), xlab = 'Uniform Distribution', ylab='Cell Based')
qqplot(x=x, y=sort(unlist(bond_based)), xlab = 'Uniform Distribution', ylab='Bond Based')
```

Problem 2

(a)

For a wild type to die off, the probablity w.r.t. time is:

$$p = \frac{N - n_i}{N}\mu \tag{1}$$

Probablity that a dead individual is replaced by parents of its own deme:

$$W_i^{+(local)}(\boldsymbol{n}) = \frac{1 + s}{N}n_i \tag{2}$$

Probablity that a dead individual is replaced by parents of other demes:

$$W_i^{+(neibours)}(\boldsymbol{n}) = \frac{m}{2} \cdot \frac{\mu(1 + s) \cdot (n_{i+1})}{N} + \frac{m}{2} \cdot \frac{\mu(1 + s) \cdot (n_{i-1})}{N} - \frac{m}{2}\frac{(1 + s)n_i}{N} \tag{3}$$

Thus,

$$W_i^{+}(\boldsymbol{n}) = \frac{N - n_i}{N}\mu\left(\frac{1 + s}{N}n_i + \frac{m}{2} \cdot \frac{\mu(1 + s) \cdot (n_{i+1})}{N} + \frac{m}{2} \cdot \frac{\mu(1 + s) \cdot (n_{i-1})}{N} - \frac{m}{2}\frac{(1 + s)n_i}{N}\right) \tag{4}$$

$$= \frac{\mu(1 + s)(N - n_i)}{N}\left(n_i + \frac{m}{2}(n_{i+1} + n_{i-1} - n_i)\right) \tag{5}$$

$$= \frac{\mu(1 + s)(N - n_i)}{N}\left(n_i + \frac{m}{2}n_i''\right) \tag{6}$$

4

(b)

$$W_i^+(\boldsymbol{n}) - W_i^-(\boldsymbol{n}) = \frac{\mu(1+s)}{N}(N-n_i)[n_i + \frac{m}{2}n_i''] - \frac{\mu n_i}{N}[(N-n_i) - \frac{m}{2}n_i''] \tag{7}$$

$$= \frac{\mu}{N}\left[(1+s)(N-n_i)[n_i + \frac{m}{2}n_i''] - n_i(N-n_i) + n_i\frac{m}{2}n_i''\right] \tag{8}$$

$$= \frac{\mu}{N}\left[s(N-n_i)n_i + (1+s)(N-n_i)\frac{m}{2}n_i'' + n_i\frac{m}{2}n_i''\right] \tag{9}$$

$$= \frac{\mu}{N}\left[s(N-n_i)n_i + s(N-n_i)\frac{m}{2}n_i'' + N\frac{m}{2}n_i'' - \cancel{n_i\frac{m}{2}n_i''} + \cancel{n_i\frac{m}{2}n_i''}\right] \tag{10}$$

$$= \frac{\mu}{N}\left[s(N-n_i)(n_i + \frac{m}{2}n_i'') + N\frac{m}{2}n_i''\right] \tag{11}$$

Therefore, $\frac{d\langle n_i\rangle}{dt}$ can be written as:

$$\frac{d\langle n_i\rangle}{dt} = \langle W_i^+(\boldsymbol{n}) - W_i^-(\boldsymbol{n})\rangle \tag{12}$$

$$= \langle\frac{\mu}{N}\left[s(N-n_i)(n_i + \frac{m}{2}n_i'') + N\frac{m}{2}n_i''\right]\rangle \tag{13}$$

$$= \frac{\mu m}{2}\langle n_i''\rangle + \frac{s\mu}{N}(N - \langle n_i\rangle)(\langle n_i\rangle + \frac{m}{2}\langle n_i''\rangle) \tag{14}$$

(c)

The differential equation above can be rewritten as:

$$\mu s(1 - \frac{1}{N}\langle n_i\rangle)(\frac{1}{N}\langle n_i\rangle) + \frac{\mu m}{2}\langle n_i''\rangle + \mu s(1 - \frac{1}{N}\langle n_i\rangle)(\frac{m}{2}\langle n_i''\rangle) \tag{15}$$

As $\langle n_i''\rangle$ can be interpreted as $\left\langle (n_{i+1} - n_i) - (n_i - n_{i-1})\right\rangle$, which is the epected difference in $l\frac{\partial u}{\partial x}$, $l^2\frac{\partial^2 u}{\partial x^2}$ (since $x = l \cdot i$ and change of variable)

Therefore, the differential equation can be rewritten as:

$$\frac{\partial u}{\partial t} = \frac{\mu m}{2}l^2\frac{\partial^2 u}{\partial x^2} + s\mu(1-u)(u + \frac{m}{2}l^2\frac{\partial^2 u}{\partial x^2}) \tag{16}$$

$$= \frac{\mu m}{2}(1 + s(1-u))l^2\frac{\partial^2 u}{\partial x^2} + s\mu(1-u)u \tag{17}$$

(d)

When $s = 0$, the equation (4) resembles the 1-D heat equation, which has the anlytic solution and can be solved numberically.

PDE: $u_t = u_{xx}$, $0 < x < L$

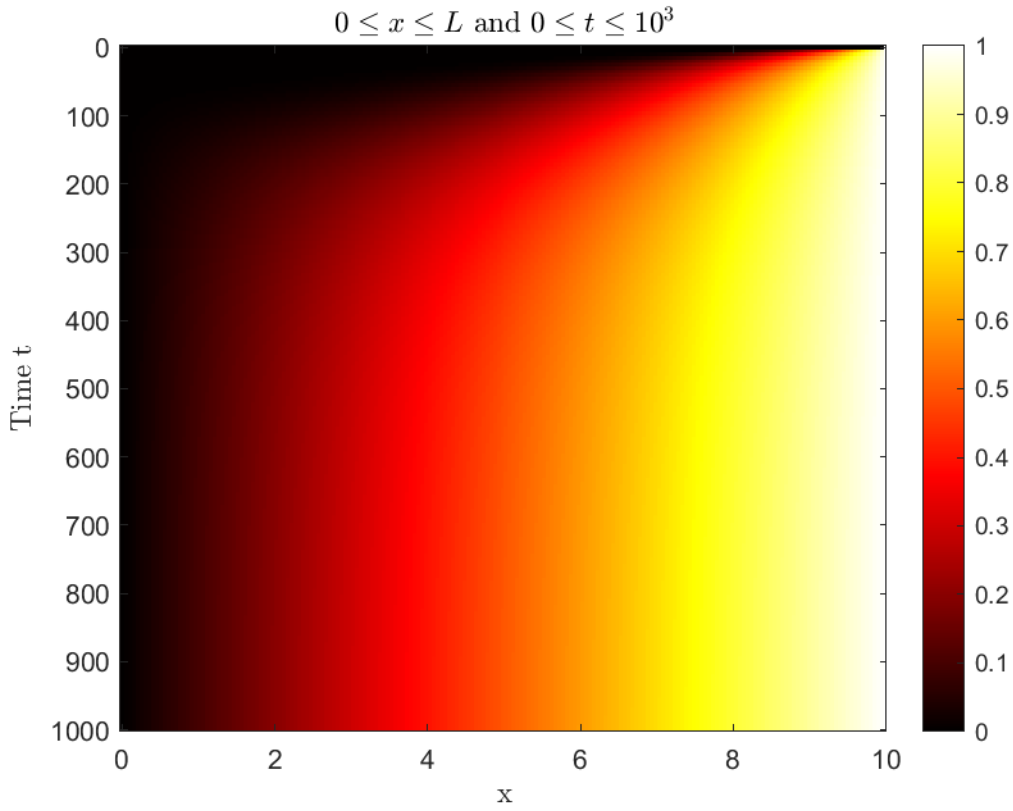IC: $u(x,0) = f(x)$, $0 < x < L$ In this case, it assigns a constant value 0

BC: $u(0,t) = u(1,t) = 0$, $t > 0$

$$u(0,t) + (0 \cdot f) = 0, \tag{18}$$
$$(u(L,t) - 1) + (0 \cdot f) = 0. \tag{19}$$

$$u(x,t) = \sum_{n=1}^{\infty} B_n \sin n\pi x e^{-n^2\pi^2 t}, \quad , B_m = 2 \int_0^1 sin(m\pi x) f(x) dx \tag{20}$$

As shown in the Fig below, the above diffusion equation failed to describe/approximate the spatial Moral model.

Matlab code for generating the figure can be found here

Code is available on github repo: (https://github.com/wyq977/evolutionary-dynamics-2019)