Exercises 9

Yongqi WANG, Hangjia ZHAO

Problem 1

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 of 1000×1000 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.

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) so it only represent the sampling difference at a snapshot. On the other hand, if the grid space was pre-occupied with S_1 uniformly, two approaches differs slightly.

```
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

  candidate <- sample(1:num_has_space, 1, prob =
                          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')
```

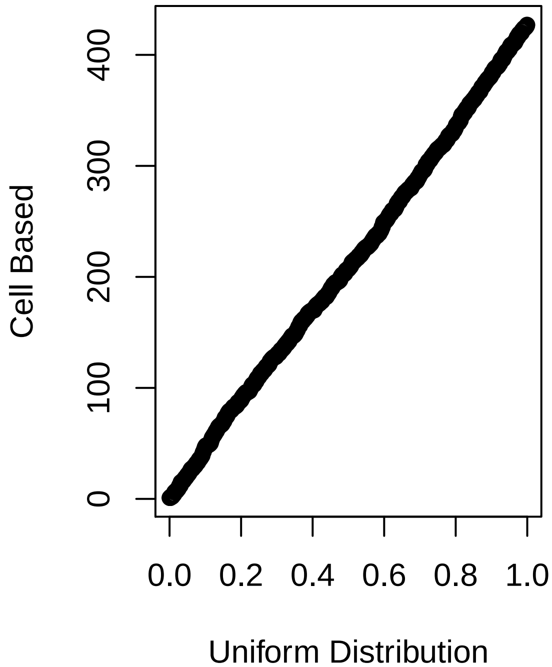


Figure 1: Sampling result using simulation Bond Focus

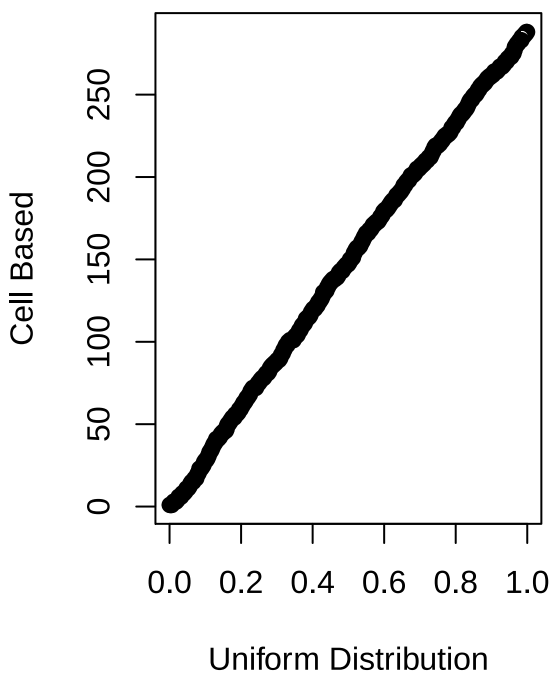
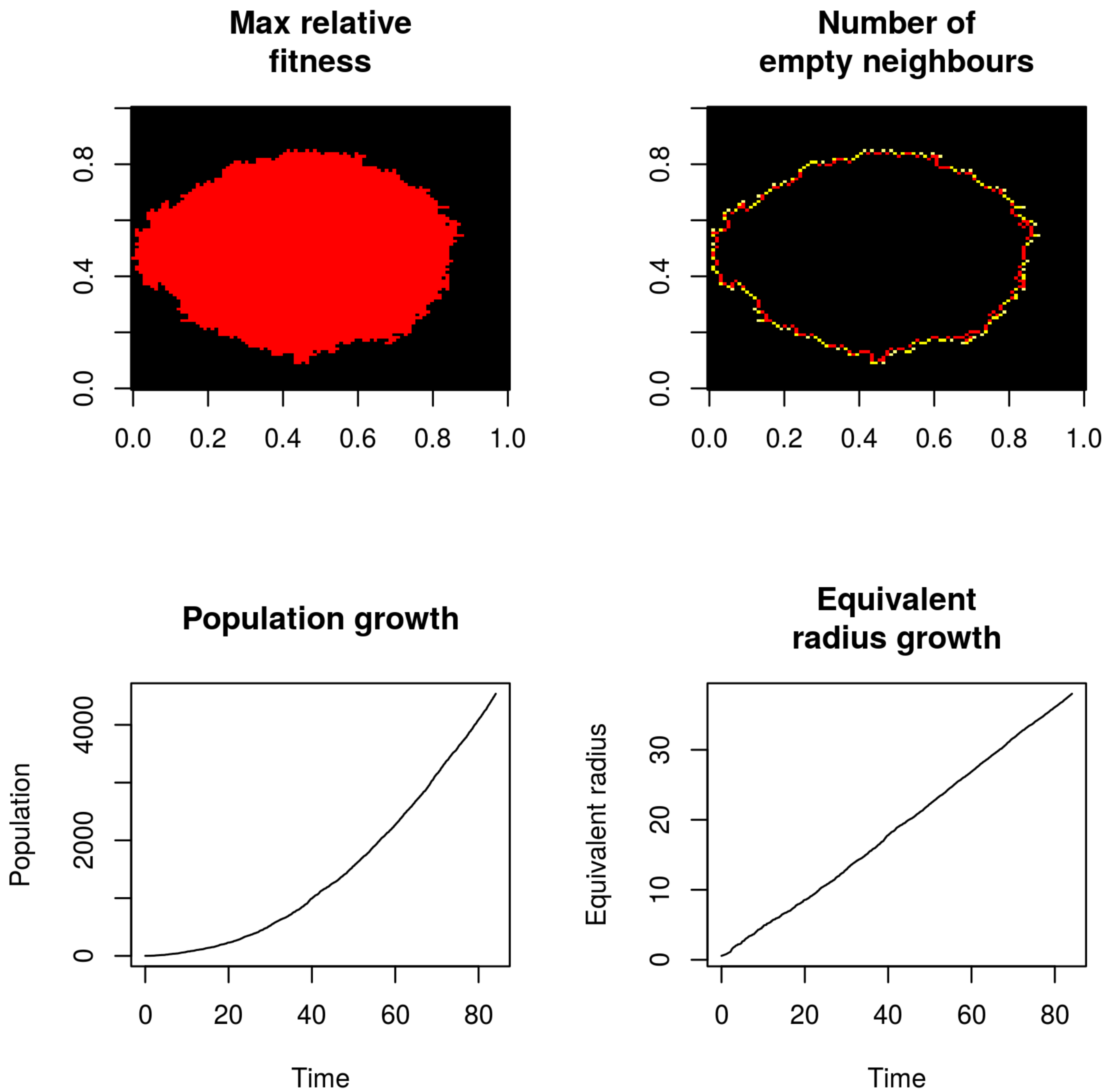
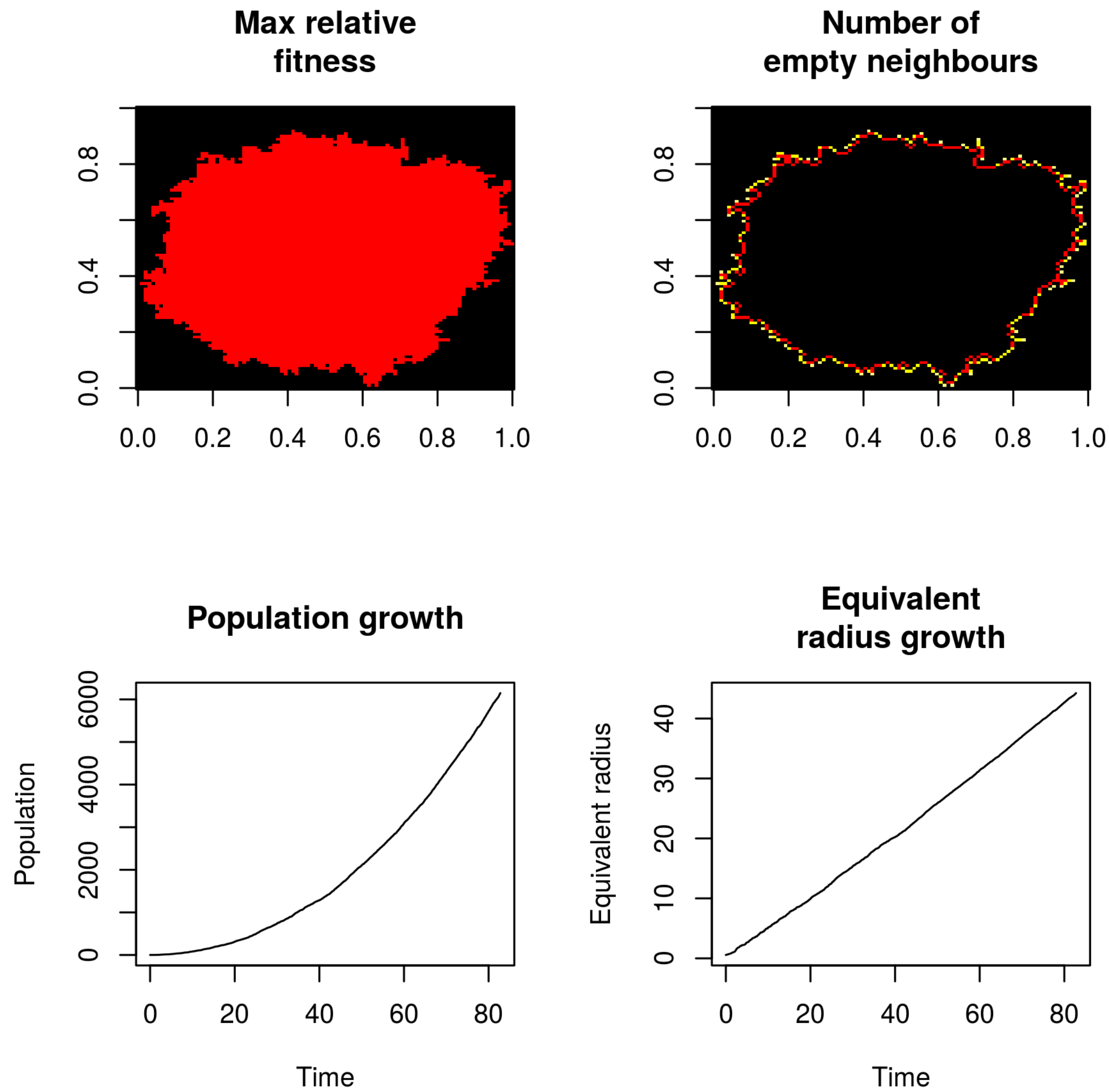


Figure 2: Sampling result using simulation Cell Focus


Max relative fitness
0.0
0.4
0.8
0.0 0.2 0.4 0.6 0.8 1.0
Number of empty neighbours
0.0
0.4
0.8
0.0 0.2 0.4 0.6 0.8 1.0
Population growth
Population
0
2000
4000
0 20 40 60 80
Time
Equivalent radius growth
Equivalent radius
0
10
20
30
0 20 40 60 80
Time



Problem 2

(a)

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

$$p = \frac{1 - r^{-1}}{1 - r^{-N}} \tag{1}$$

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

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

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

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

(b)

$$\begin{aligned}
W_i^{+}(\boldsymbol{n}) - W_i^{-}(\boldsymbol{n}) &= \frac{\mu(1+s)}{N}(N-n_i)[n_i + \frac{m}{2}n_i''] - \frac{\mu n_i}{N}[(N-n_i) - \frac{m}{2}n_i''] &(4)\\
&= \frac{\mu}{N}\left[(1+s)(N-n_i)[n_i + \frac{m}{2}n_i''] - n_i(N-n_i) + n_i\frac{m}{2}n_i''\right] &(5)\\
&= \frac{\mu}{N}\left[s(N-n_i)n_i + (1+s)(N-n_i)\frac{m}{2}n_i'' + n_i\frac{m}{2}n_i''\right] &(6)\\
&= \frac{\mu}{N}\left[s(N-n_i)n_i + s(N-n_i)\frac{m}{2}n_i'' + N\frac{m}{2}n_i'' - \cancel{n_i\frac{m}{2}n_i''} + \cancel{n_i\frac{m}{2}n_i''}\right] &(7)\\
&= \frac{\mu}{N}\left[s(N-n_i)(n_i + \frac{m}{2}n_i'') + N\frac{m}{2}n_i''\right] &(8)
\end{aligned}$$

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

$$\begin{aligned}
\frac{\mathrm{d}\langle W_i^{+}(\boldsymbol{n}) - W_i^{-}(\boldsymbol{n})\rangle}{\mathrm{d}t} &= \langle \frac{\mu}{N}\left[s(N-n_i)(n_i + \frac{m}{2}n_i'') + N\frac{m}{2}n_i''\right]\rangle &(9)\\
&= \frac{\mu m}{2}\langle n_i''\rangle + \frac{s\mu}{N}(N - \langle n_i\rangle)(\langle u_i\rangle + \frac{m}{2}\langle n_i''\rangle) &(10)
\end{aligned}$$

(c)

The differential equation above can be rewritten as:

$$s(1-\frac{1}{N}\langle n_i\rangle)(\frac{1}{N}\langle u_i\rangle) + \frac{\mu m}{2}\langle n_i''\rangle + s(1-\frac{1}{N}\langle n_i\rangle)(\frac{m}{2}\langle n_i''\rangle) \tag{11}$$

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

Therefore, the differential equation can be rewritten as:

$$\begin{aligned}
\frac{\partial u}{\partial t} &= \frac{\mu m}{2}l^2\frac{\partial^2 u}{\partial x^2} + s\mu(1-u)(u - \frac{m}{2}l^2\frac{\partial^2 u}{\partial x^2}) &(12)\\
&= \frac{\mu m}{2}(1+s(1-u))l^2\frac{\partial^2 u}{\partial x^2} + s\mu(1-u)u &(13)
\end{aligned}$$

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