

Wright-Fisher Model

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This simulates the Wright-Fisher Model of selection and random genetic drift for an asexual organism with two alleles and no mutation. The population size is $2N$ and the coefficient of selection for the A mutant type is s .

First, store parameters and initial values:

```
s <- 0.01      # selection coefficient of the mutant type
init.num <- 1  # initial number of the mutant A type
N <- 10       # population size is 2N
reps <- 15    # number of replicate simulation runs
gens <- 40    # generations of evolution to simulate for each replicate run
```

Create a matrix called `j` with `gens+1` rows and `reps` columns whose every entry is the initial number of mutants. Below, we will replace entries 2 through `gens+1` of each column with simulated numbers of mutants in each replicate run.

```
j=matrix(init.num,gens+1,reps)
```

Now write code for loops that execute the replicate simulations. This code uses the simplified form of the post-selection expected frequency $q^* = j(1+s)/[j(1+s) + (2N-j)] = j(1+s)/(js + 2N)$.

```
# "outer" loop over the number of replicate runs
for(k in 1:reps){
  #inner loop to simulate W-F model starting with init.num mutants
  for(i in 2:gens+1) {
    #compute the post-selection expected frequency, given j
    q.star <- j[i-1,k]*(1+s)/(j[i-1,k]*s + 2*N)
    #generate next j as a single binomial random variable with parameters 2N and q.star
    j[i,k]=rbinom(1,2*N,q.star)
  }
}
```

Show the results as mutant frequencies (i.e., plot each mutant count divided by $2N$). Display all the replicate runs on a single plot.

```
matplot(0:gens,j/(2*N),type="l",ylab="freq(A)",xlab="generation")
```

