Wright-Fisher Model

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This simulates the Wright-Fisher Model of selection and random genetic drift for an as exual 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</pre>
```

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.

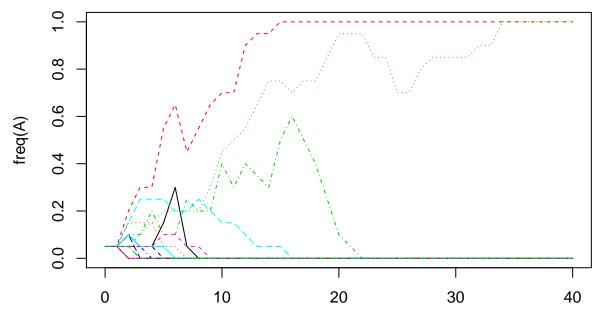
```
j=matrix(init.num,gens+1,reps)
```

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)
    }
}</pre>
```

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="1",ylab="freq(A)",xlab="generation")



generation