Introduction to Wright-Fisher Simulations

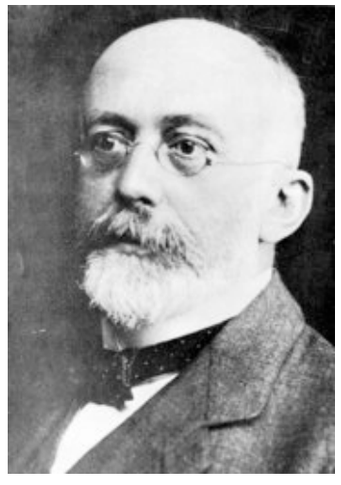
Ryan Hernandez

Goals

- Simulate the standard neutral model, demographic effects, and natural selection
- Start with single sites, and build in multiple sites

Hardy-Weinberg Principle

Godfrey H. Hardy:
1877-1947



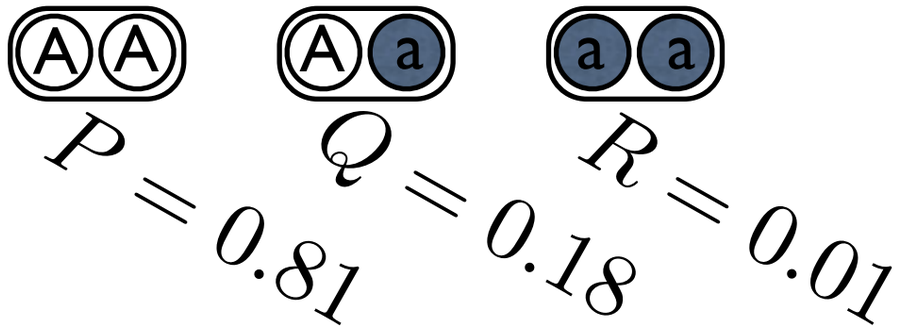
Wilhelm Weinberg:
1862-1937

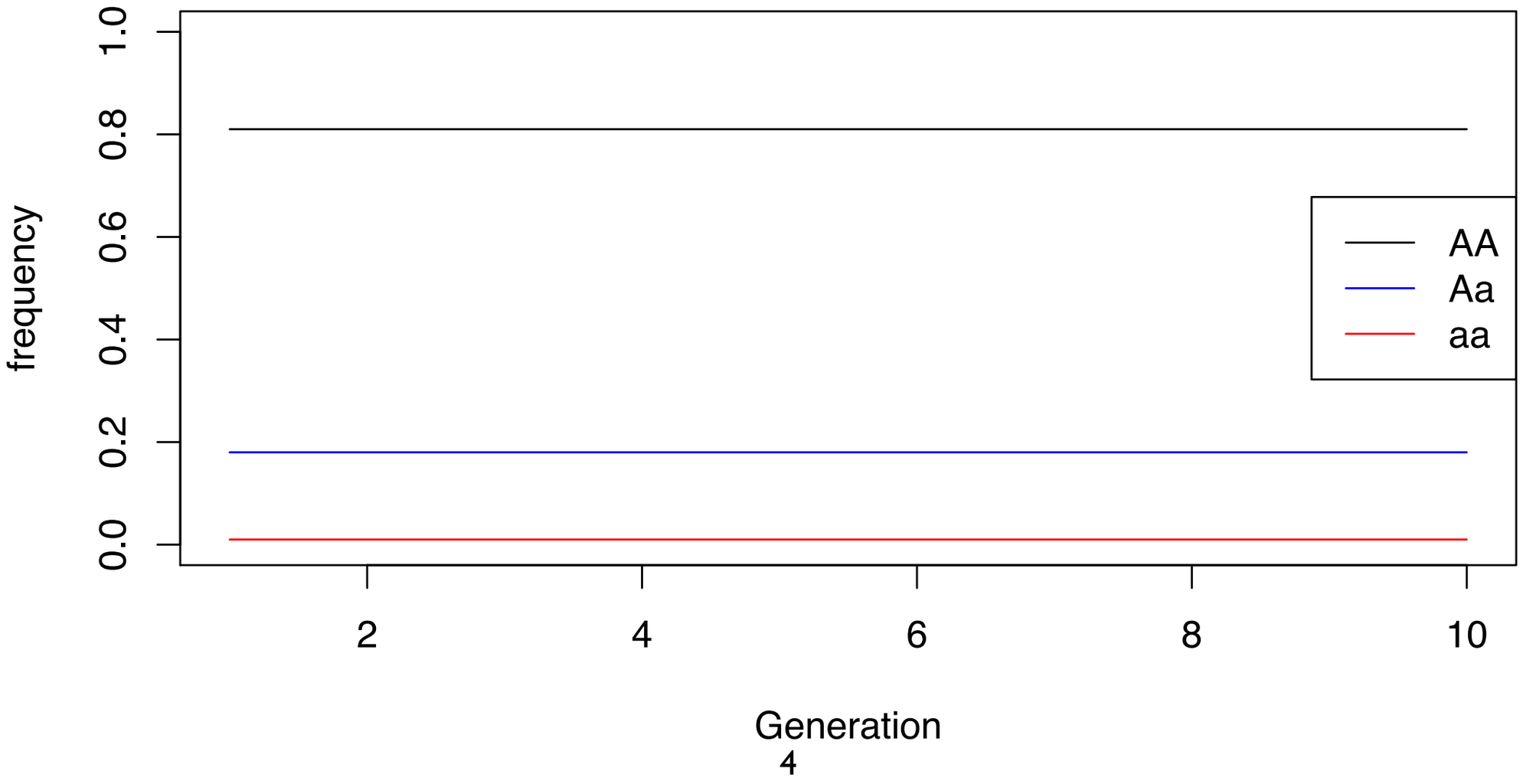
- **Assumptions:**
  - Diploid organism
  - Sexual reproduction
  - Non-overlapping generations
  - Only two alleles
  - Random mating
  - Identical frequencies in males/females
  - Infinite population size
  - No migration
  - No mutation
  - No natural selection
- **Conclusion 1:**
  Both allele AND genotype frequencies will remain constant at **HWE** generation after generation... forever!

$$P=p^2$$
$$Q=2p(1-p)$$
$$R=(1-p)^2$$

Hardy-Weinberg Principle

- Imagine a population of diploid individuals





Hardy-Weinberg Principle

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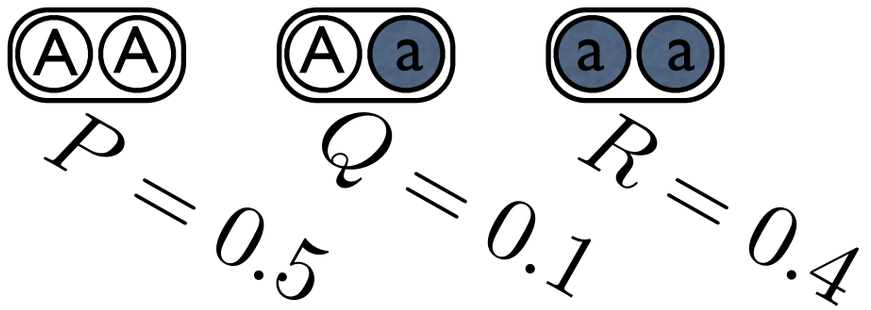
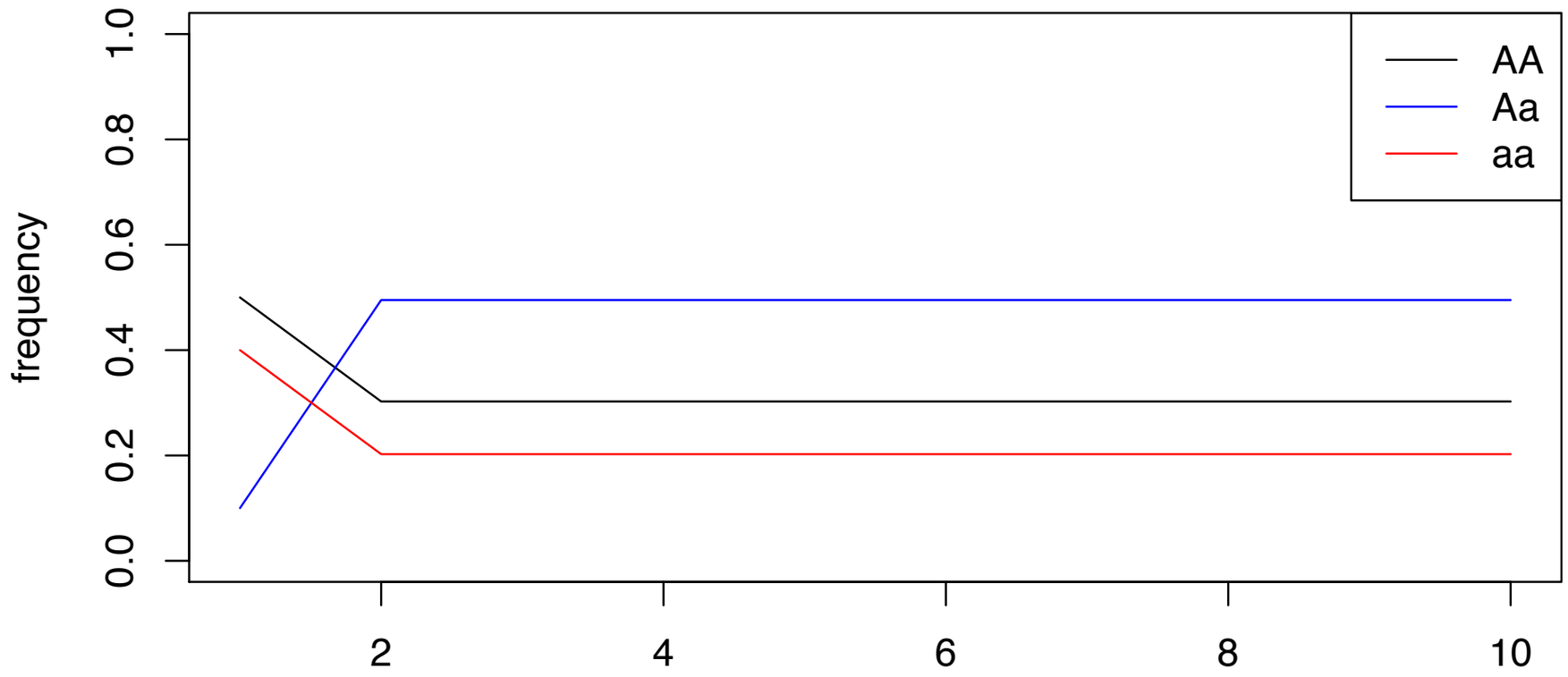


$$p = P + Q/2 = 0.55$$

$$p^2 = 0.3025$$
$$2p(1-p) = 0.495$$
$$(1-p)^2 = 0.2025$$



- **Conclusion 2:** A single round of random mating will return the population to HWE frequencies!

Hardy-Weinberg Principle

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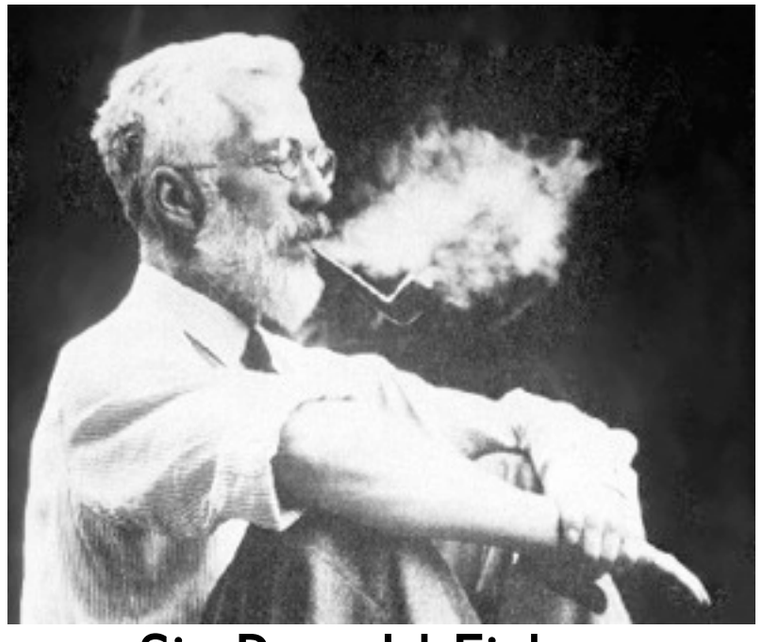
Wright-Fisher Model

Sewall Wright:
1889-1988



Sir Ronald Fisher
1890-1962

- Suppose a population of N individuals.
- Let X(t) be the #chromosomes carrying an allele A in generation t:

$$P(X(t+1) = j | X(t) = i) = \binom{N}{j} p^j (1-p)^{N-j}$$

$$= \mathrm{Bin}(j | N, i/N) = \binom{N}{j} \left(\frac{i}{N}\right)^j \left(\frac{N-i}{N}\right)^{N-j}$$

Wright-Fisher Model

- A simple R function to simulation genetic drift:

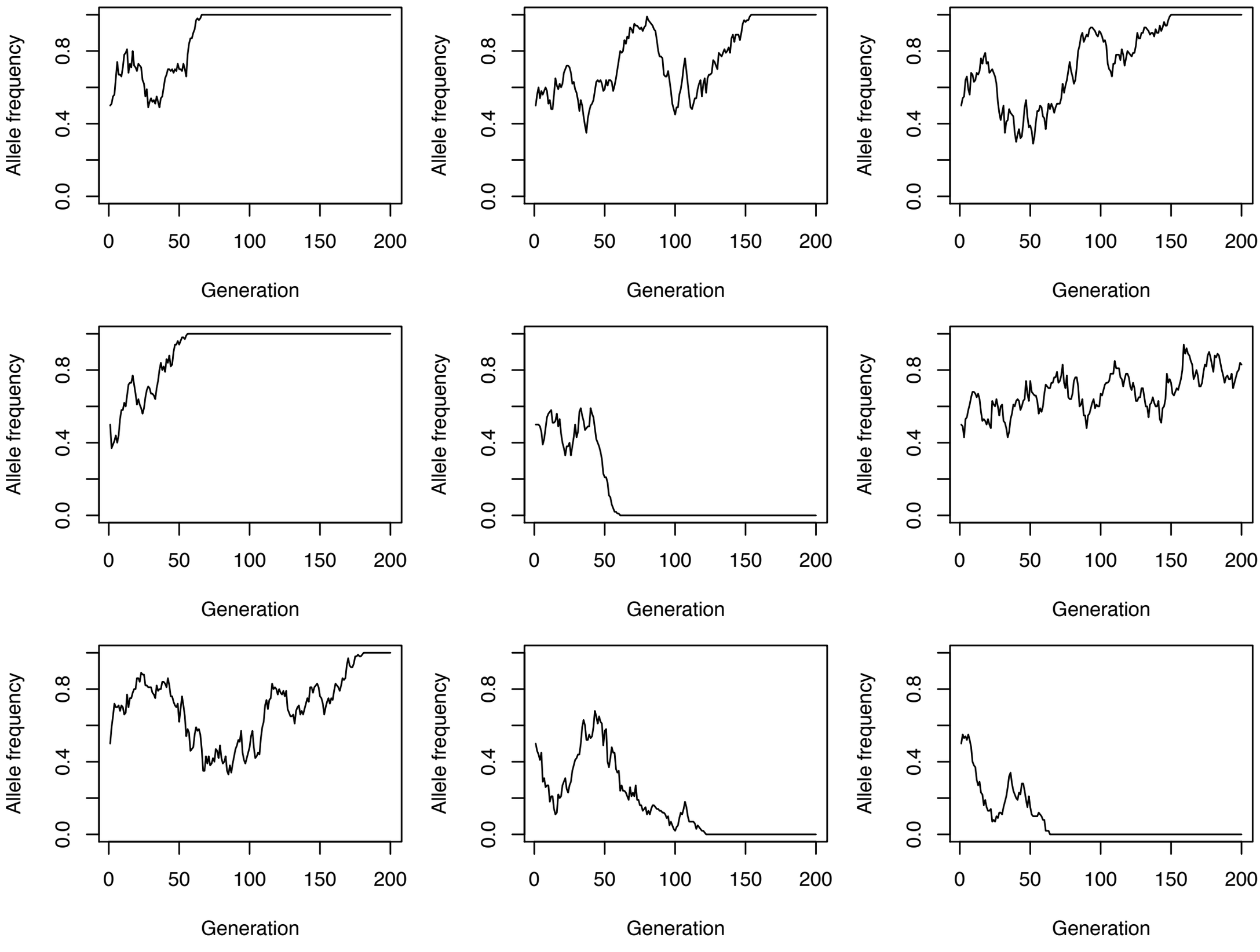
Initial pop size
Starting frequency
number of simulated generations

```
WF=function(N, p, G){
  t=array(,dim=G);
  t[1] = p;
  for(i in 2:G){
    t[i] = rbinom(1,N,t[i-1])/N;
  }
  return(t);
}
```

- Run it in R using:

```
f=WF(100, 0.5, 200)
plot(f)
```

Wright-Fisher Model



Demographic Effects

- Population changes size at a given generation

Wright-Fisher Model

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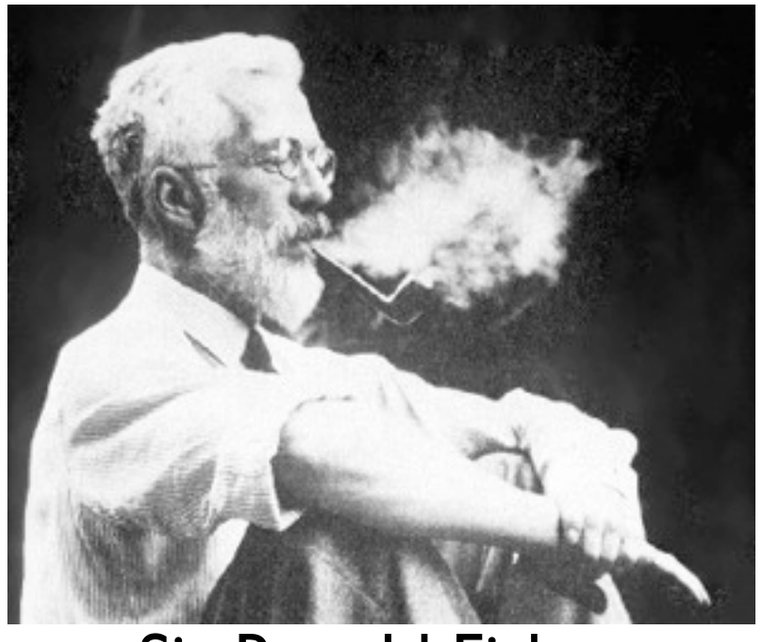

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Wright-Fisher Model

- A simple R function to simulation demographic effects:

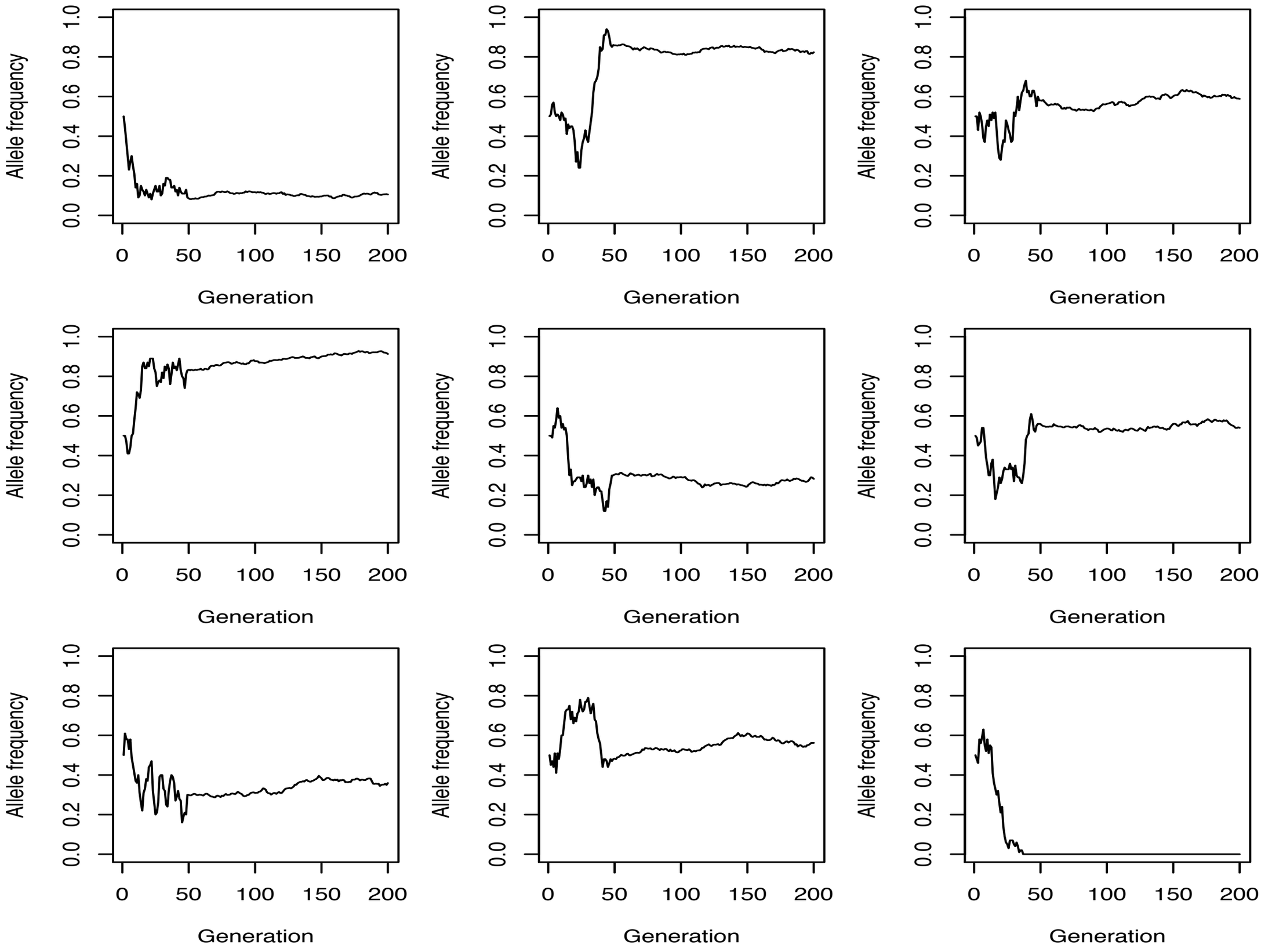
```
WFdemog = function(N, p, G, Gd, v){
    t=array(,dim=G);
    t[1] = p;
    for(i in 2:G){
     if(i == Gd){
         N = N*v;
       }
       t[i] = rbinom(1,N,t[i-1])/N;
    }
    return(t);
}
```

Initial pop size
Starting frequency
Generations to simulate
Gen demographic event happens
Magnitude of size change

- Run it using:

```
f=WFdemog(100, 0.5, 200, 50, 100)
plot(f)
```

Wright-Fisher Model with Expansion



Wright-Fisher Model with Contraction

- Run it using: `WFdemog(100, 0.5, 200, 50, 0.1)`

Wright-Fisher Model with Contraction

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Hardy-Weinberg Principle

- **Assumptions:**
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  - No migration
  - No mutation
  - No natural selection
- What happens when we allow natural selection to occur?
- Alleles change frequency!

Natural Selection

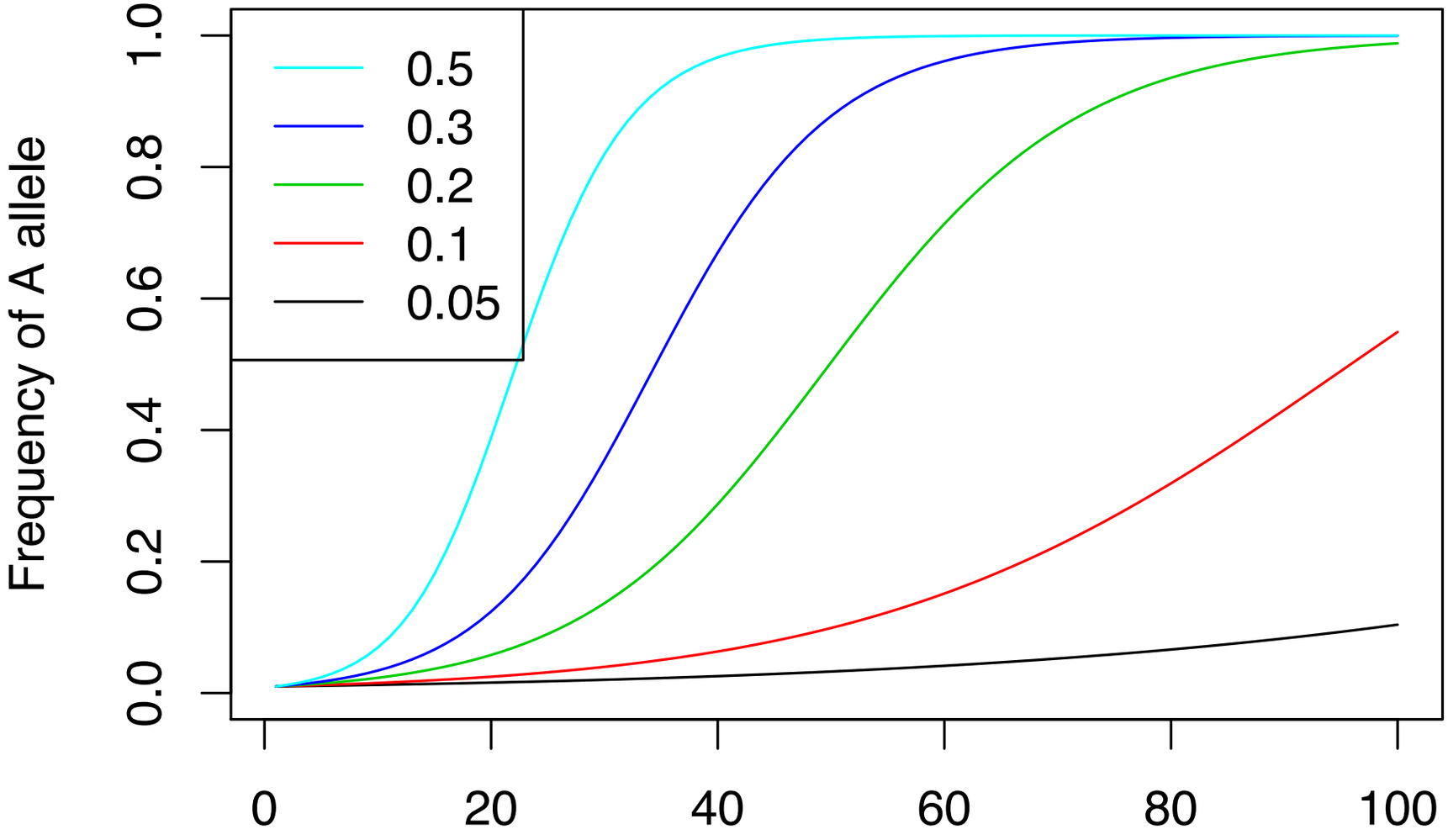
Genotype	AA	Aa	aa
Frequency	p^2	2pq	q^2
Fitness	1	1+hs	1+s

- The *expected frequency* in the next generation (q') is then the density of offspring produced by carriers of the derived allele divided by the population fitness:

$$q' = \frac{q^2(1+s) + pq(1+hs)}{1 + sq(2hp + q)}$$

Natural Selection

- Trajectory of selected allele with various selection coefficients under genic selection (h=0.5) in an "infinite" population



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  - Identical frequencies in males/females
  - Infinite population size
  - No migration
  - No mutation
  - No natural selection
- What happens with natural selection in a finite population?
  - Directional selection AND drift!

Simulating Natural Selection

- First write an R function for the change in allele frequencies:

initial freq
dominance
fitness

```
fitfreq = function(q, h, s){
  p=1-q;
  return((q^2*(1+s) + p*q*(1+h*s))/( 1 + s*q*(2*h*p+q)));
}
```

- Now use this in an updated WF simulator:

pop size
initial freq
dominance
fitness
gens to simulate

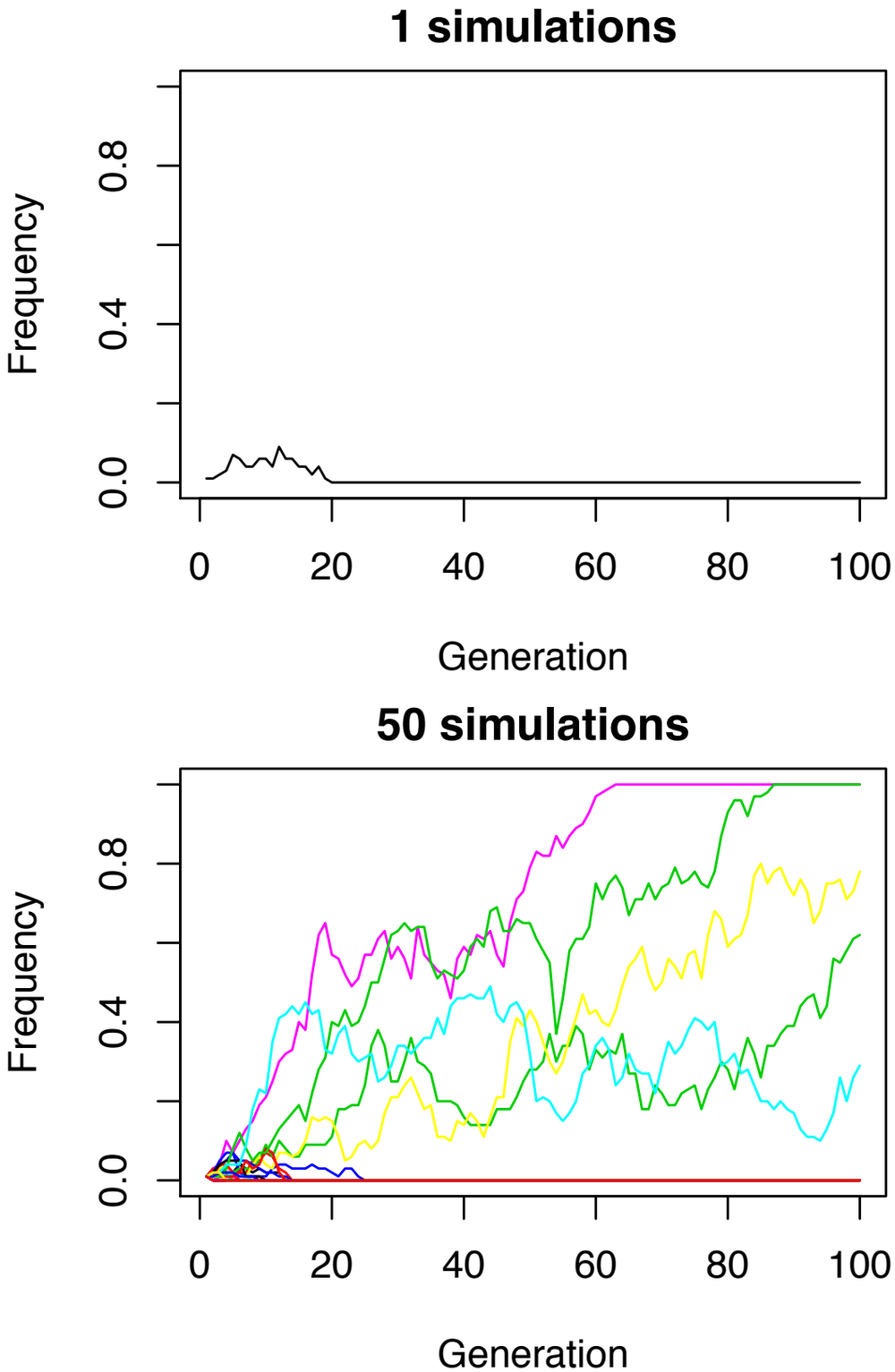
```
WF.sel=function(N, q, h, s, G){
  t=array(,dim=G);
  t[1] = N*q;
  for(i in 2:G){
    t[i] = rbinom(1,N,fitfreq(t[i-1], h, s))/N;
  }
  return(t);
}
```

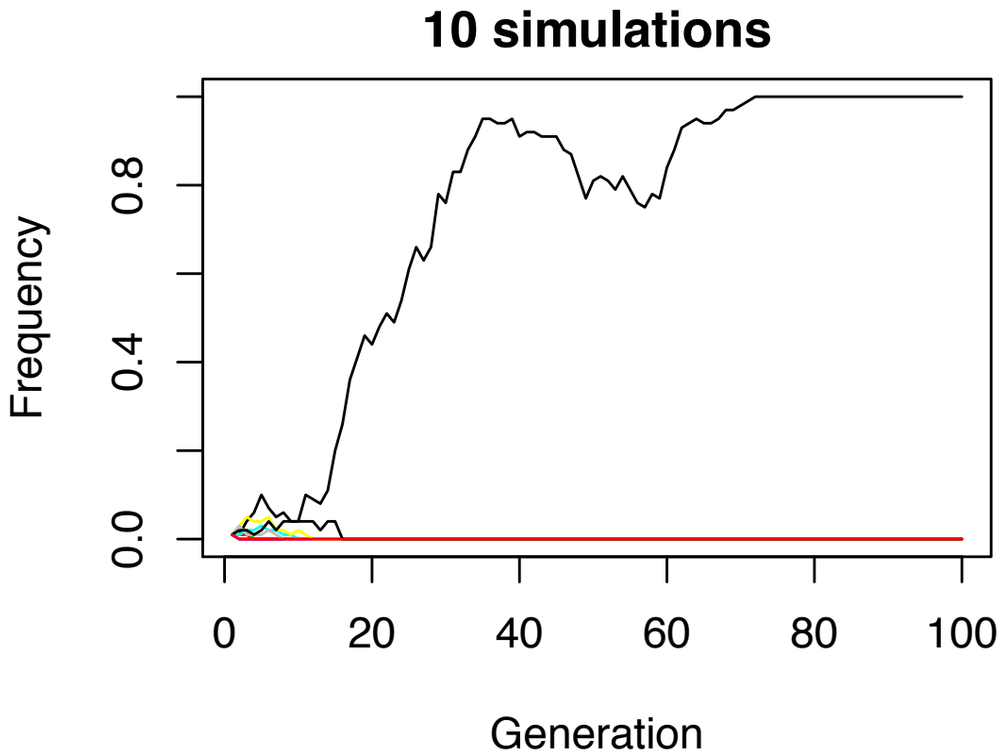
Natural Selection

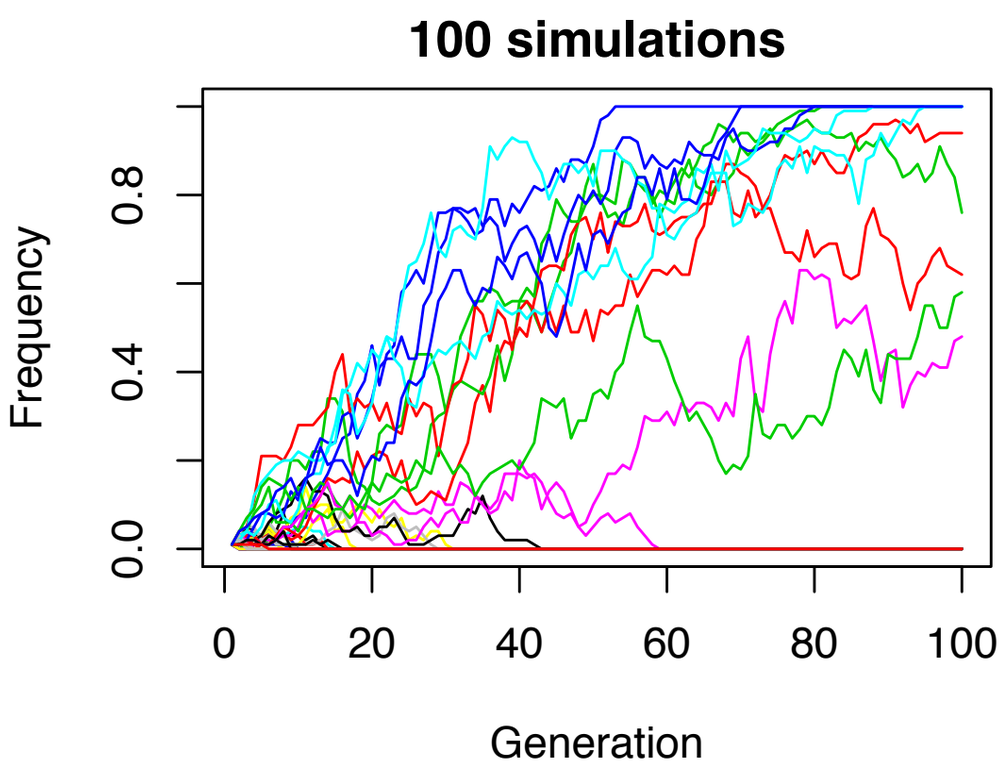
`WF.sel(100, 0.01, 0.5, 0.1, 100)`

Natural Selection

`WF.sel(100, 0.01, 0.5, 0.1, 100)`







Simulating Natural Selection

- How would you simulate both selection AND demographic effects?
- Now use this in an updated WF simulator:

pop size
initial freq
dominance
fitness
gens to simulate
Gen demographic event happens
Magnitude of size change

```
WF.demsel=function(N, q, h, s, G, Gd, v){
  t=array(,dim=G);
  t[1] = N*q;
  for(i in 2:G){
    if(i == Gd){
      N = N*v;
    }
    t[i] = rbinom(1,N,fitfreq(t[i-1], h, s))/N;
  }
  return(t);
}
```

Wright-Fisher Model with Contraction

- Run it using: `WF.demsel(100,0.5,0.5,0.1,100,50,100)`

Wright-Fisher Model with Contraction

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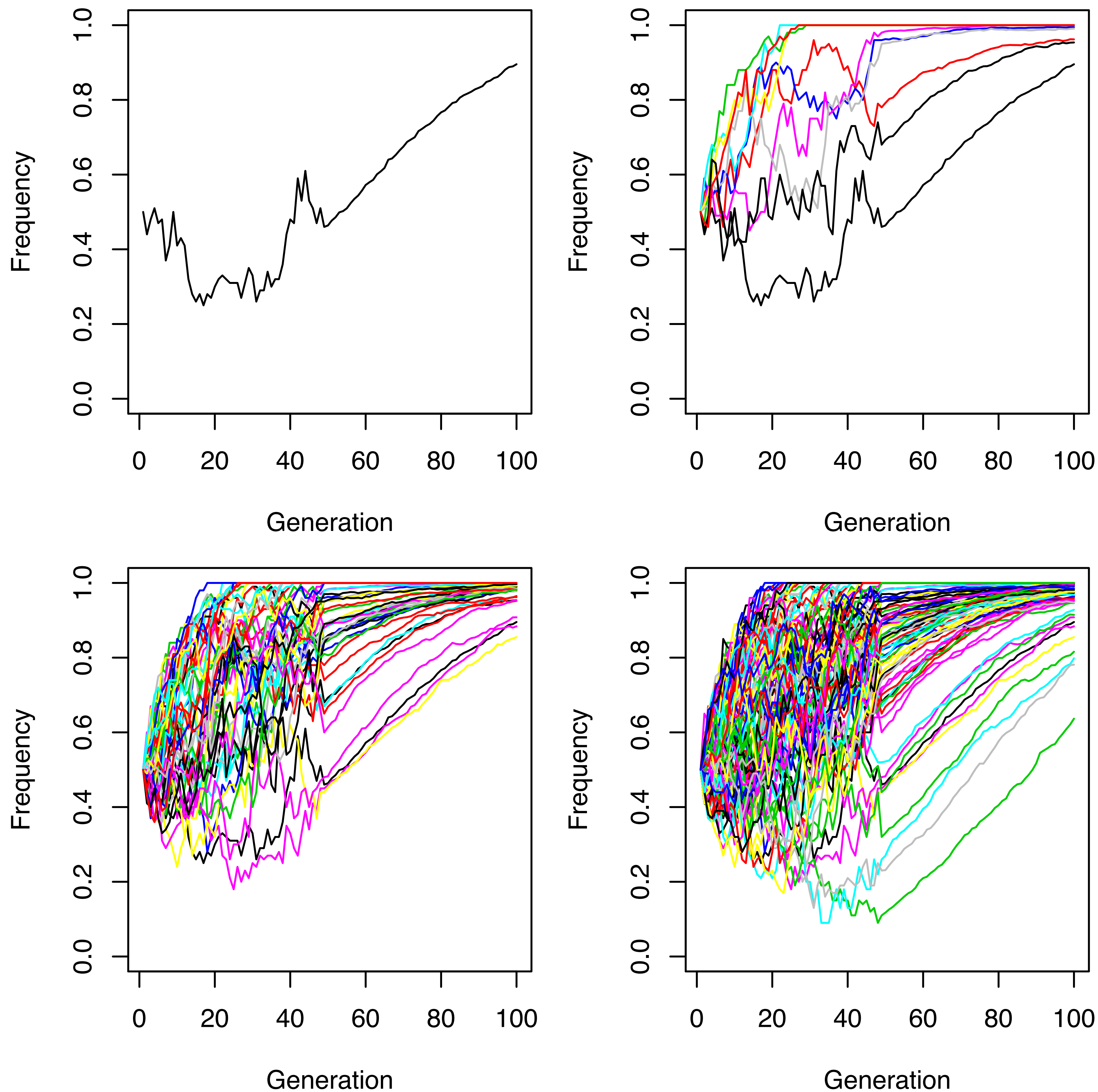
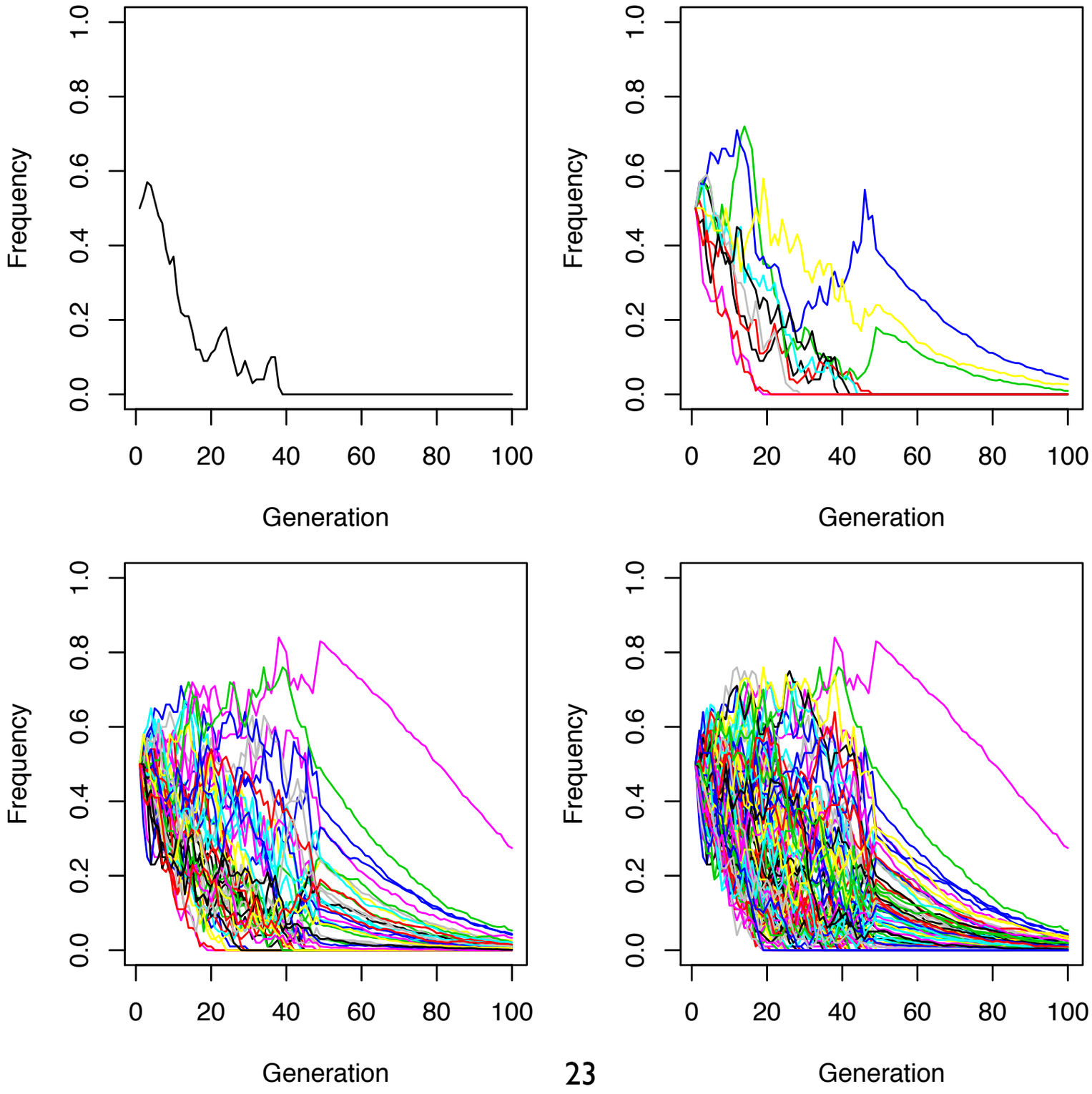


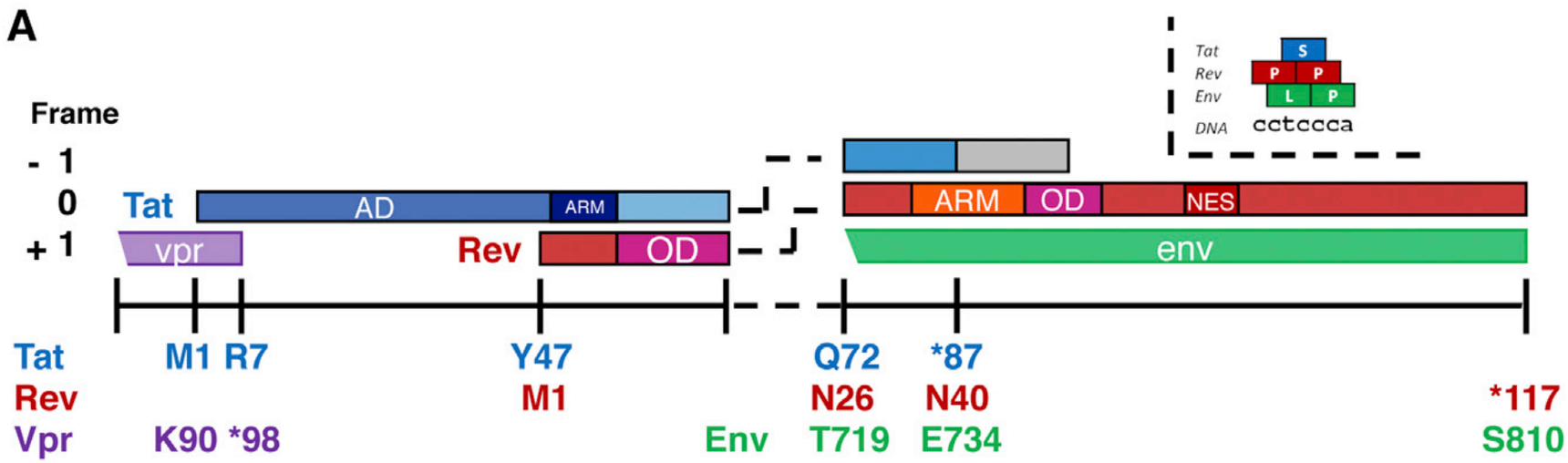
What parameters generated these?

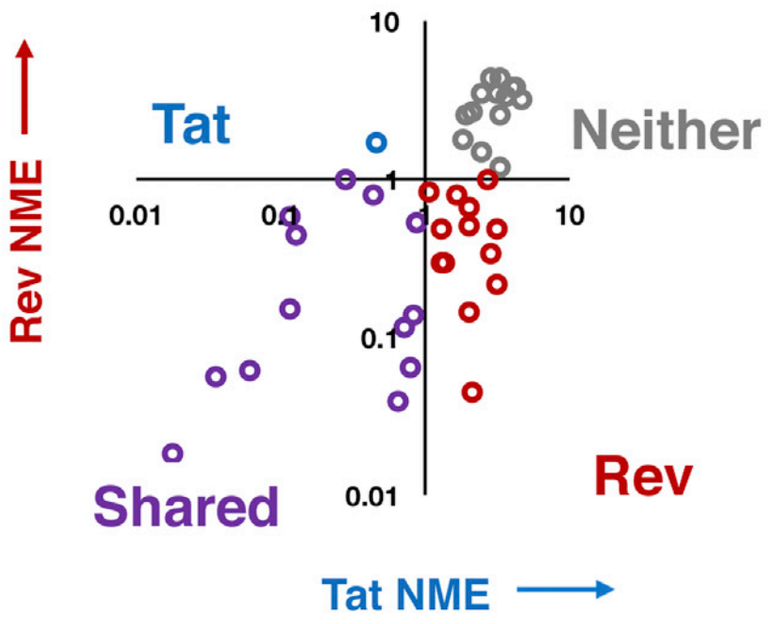


Cell

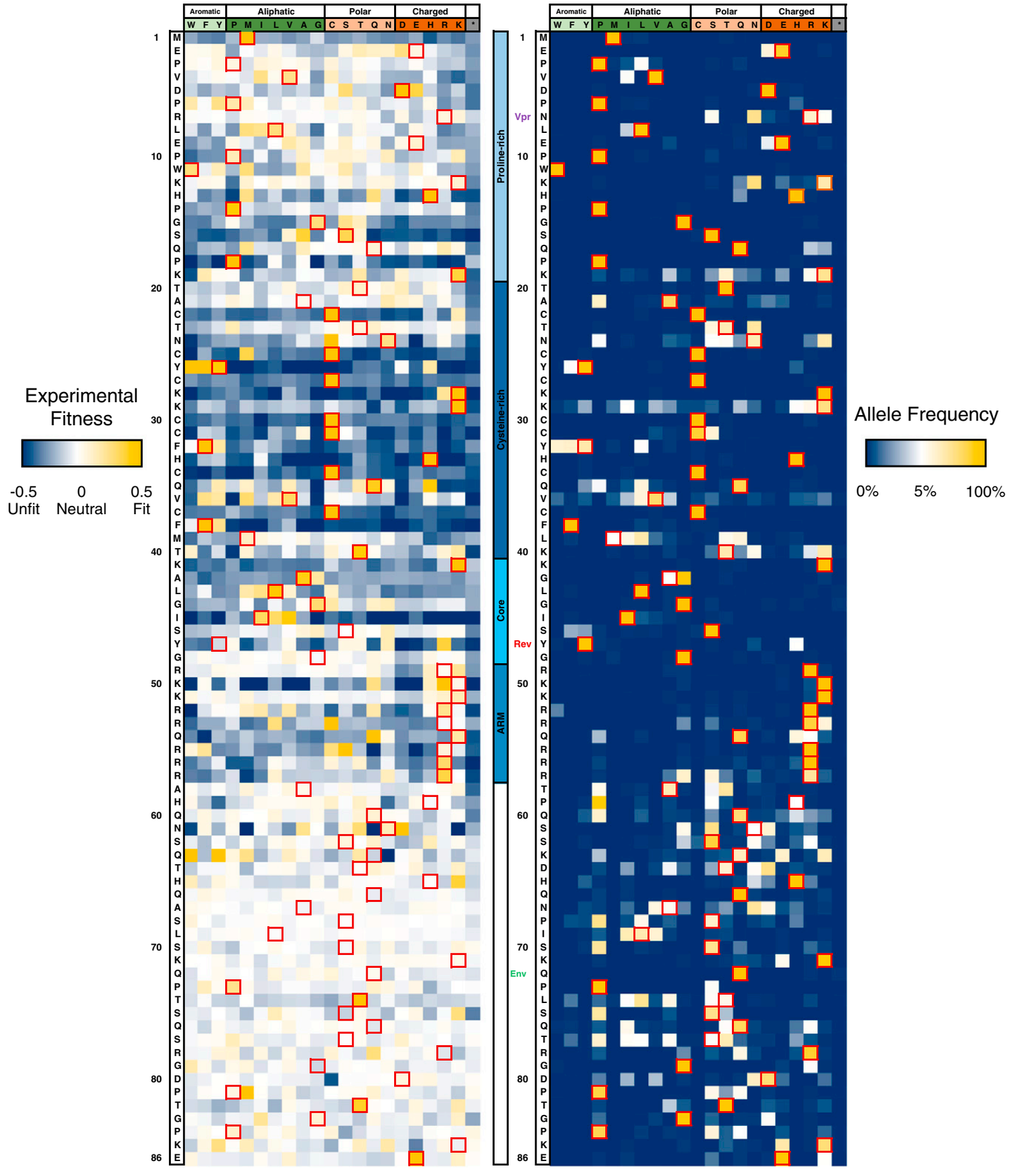
Functional Segregation of Overlapping Genes in HIV

Jason D. Fernandes,[1,2] Tyler B. Faust,[1,3] Nicolas B. Strauli,[4,5] Cynthia Smith,[1] David C. Crosby,[1] Robert L. Nakamura,[1] Ryan D. Hernandez,[4] and Alan D. Frankel[1,6,*]





- HIV genes Tat and Rev overlap.
- At protein level, many overlapping sites are conserved in both, but some sites only conserved in Rev.
- Is joint conservation due to dual function or genetic code?



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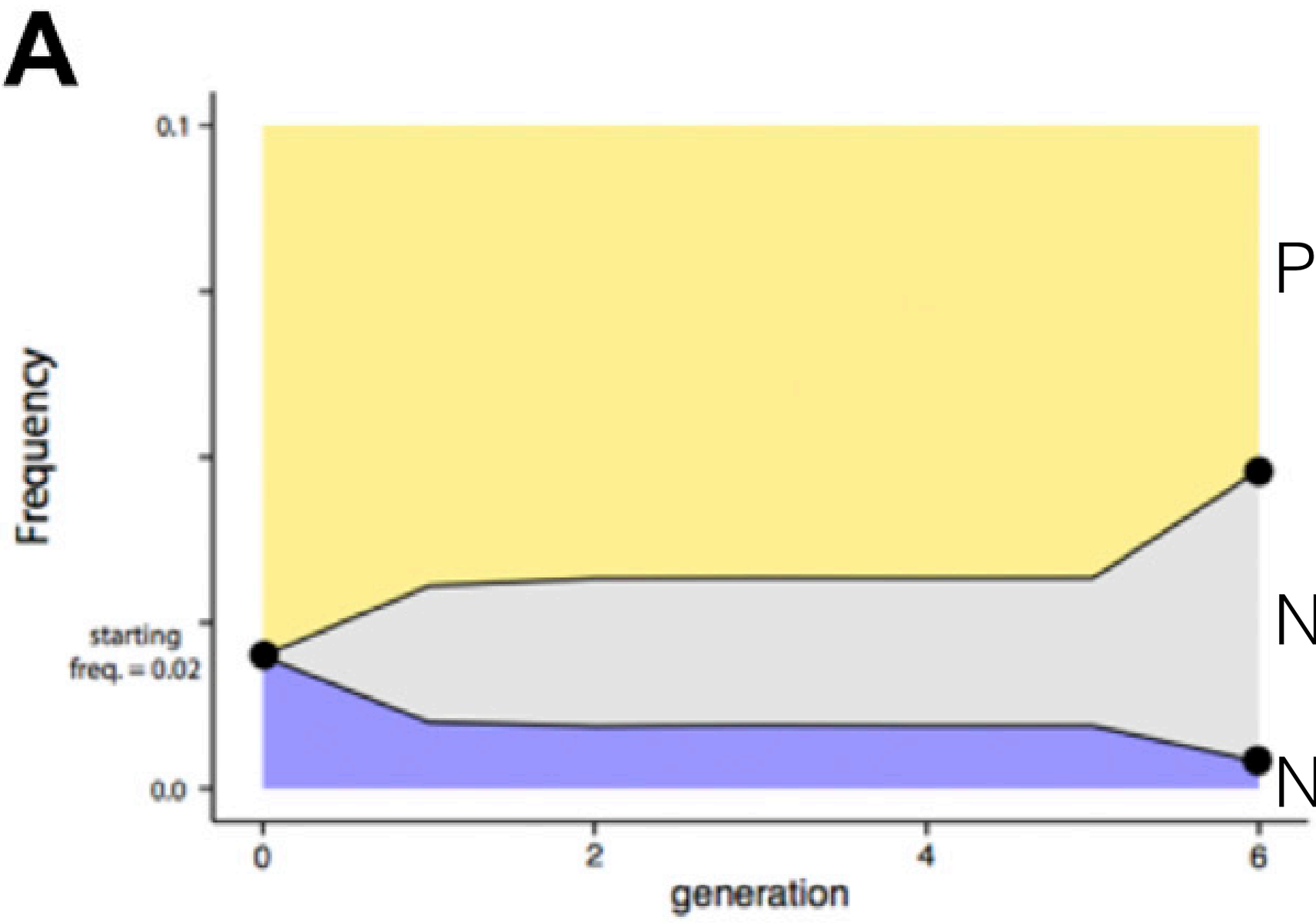
- In patient data, Tat sites that overlap with Rev are highly conserved.
- HIV can be engineered so that Tat and Rev do not overlap
- Deep mutational scanning in non-overlap context (all possible codons at each position) shows that many sites lack conservation in cell lines.
- Is this due to drift (neutral) or selection?

Fernandez, et al., Cell (2016)

Functional Segregation of Overlapping Genes in HIV

- **Deep mutational scanning:**
  - Create exhaustive libraries with all possible codons at all overlapping positions
  - Allow population mixture to evolve for *G* generations, then sequence to measure final frequencies of all amino acids
  - Simulate to evaluate significance of allele frequency change
- **Factors you might want to include in your simulation:**
  - the overall population growth function
  - the number of generations
  - the starting allele frequency
  - the ending read depth for the experiment
  - and the amino acid identity of the allele

Fernandez, et al., Cell (2016)



Fernandez, et al., Cell (2016)

Natural Selection

Time-course data from artificial selection/ancient DNA

- Let's estimate some selection coefficients!
- Given 2 alleles at a locus with frequencies p_0 and q_0, and fitnesses w_1 and w_2 (with w the population-wide fitness).
- Expected freq. in next generation is: $p_1 = p' = p_0 w_1 / w$.
- We can then write:

$$\frac{p_1}{q_1} = \frac{p_0 w_1 / w}{q_0 w_2 / w} = \left(\frac{p_0}{q_0}\right)\left(\frac{w_1}{w_2}\right)$$

- Using induction, you could prove for any generation t:

$$\frac{p_t}{q_t} = \frac{p_0 w_1 / w}{q_0 w_2 / w} = \left(\frac{p_0}{q_0}\right)\left(\frac{w_1}{w_2}\right)^t$$

Natural Selection

- Taking the natural log of this equation:

$$\log\left(\frac{p_t}{q_t}\right) = \log\left(\frac{w_1}{w_2}\right)t + \log\left(\frac{p_0}{q_0}\right)$$

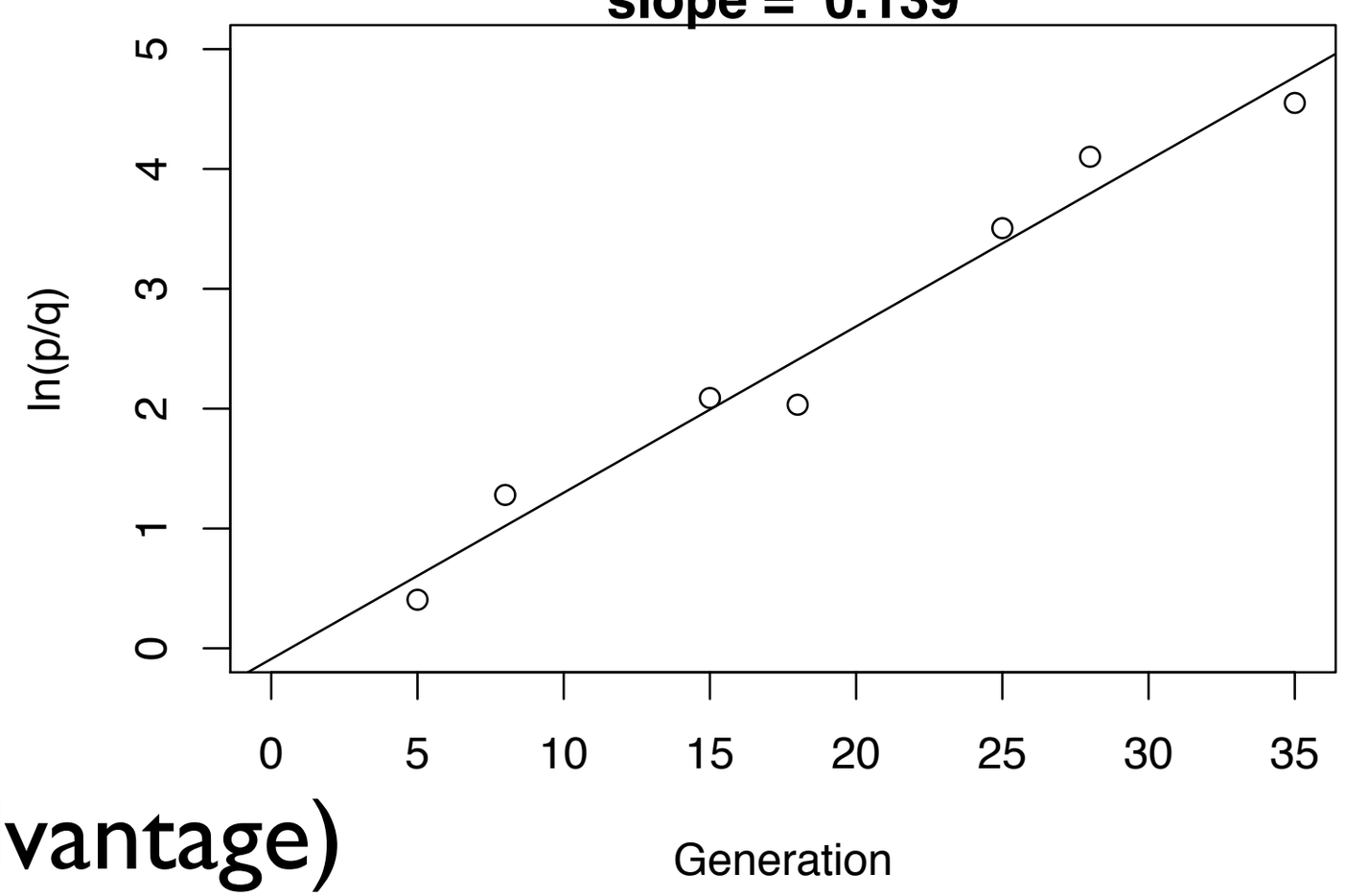
- Which is now a linear function of t, the number of generations.
- Therefore, the ratio of the fitnesses w_1/w_2 = e^{slope}

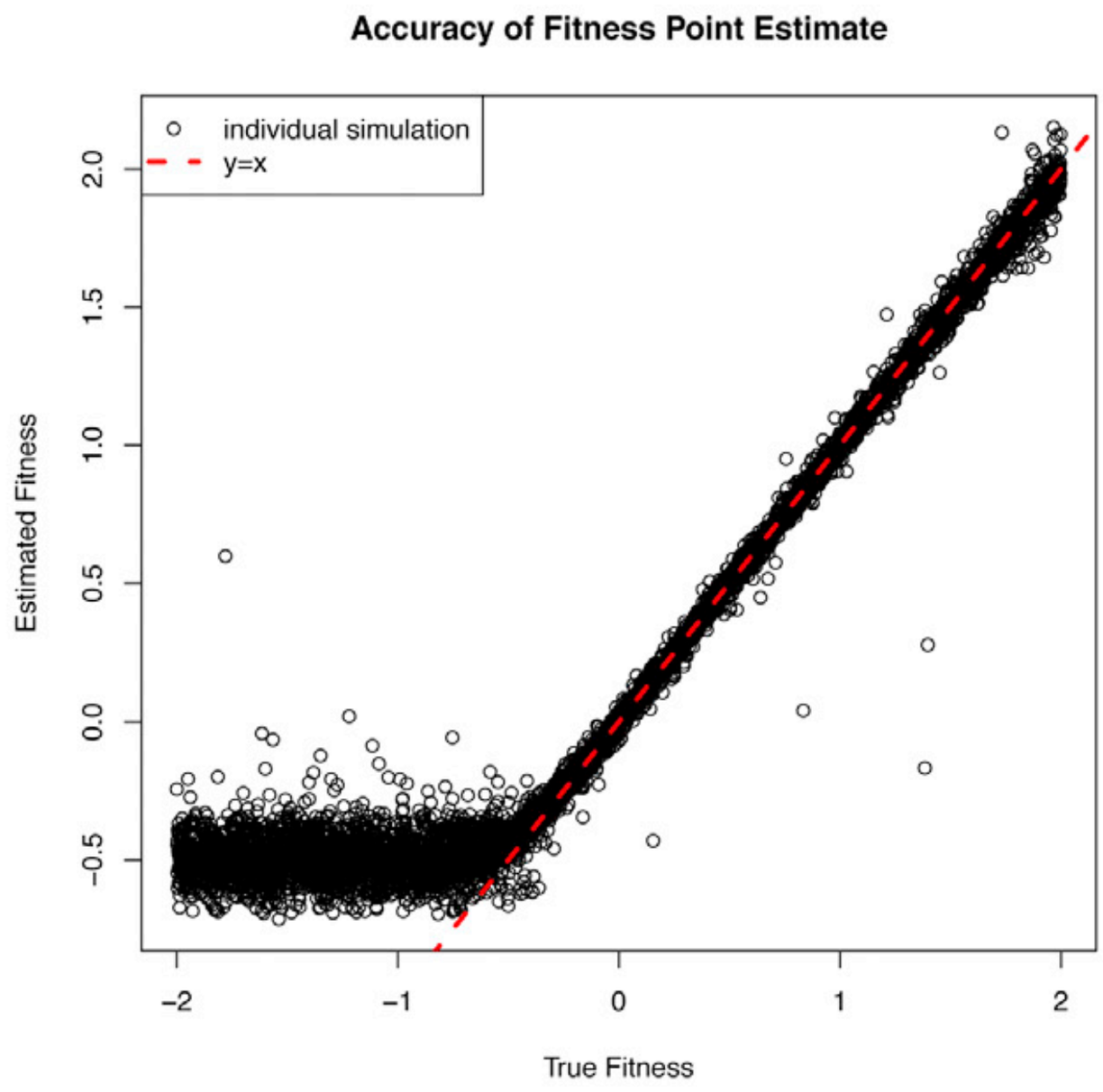
Natural Selection

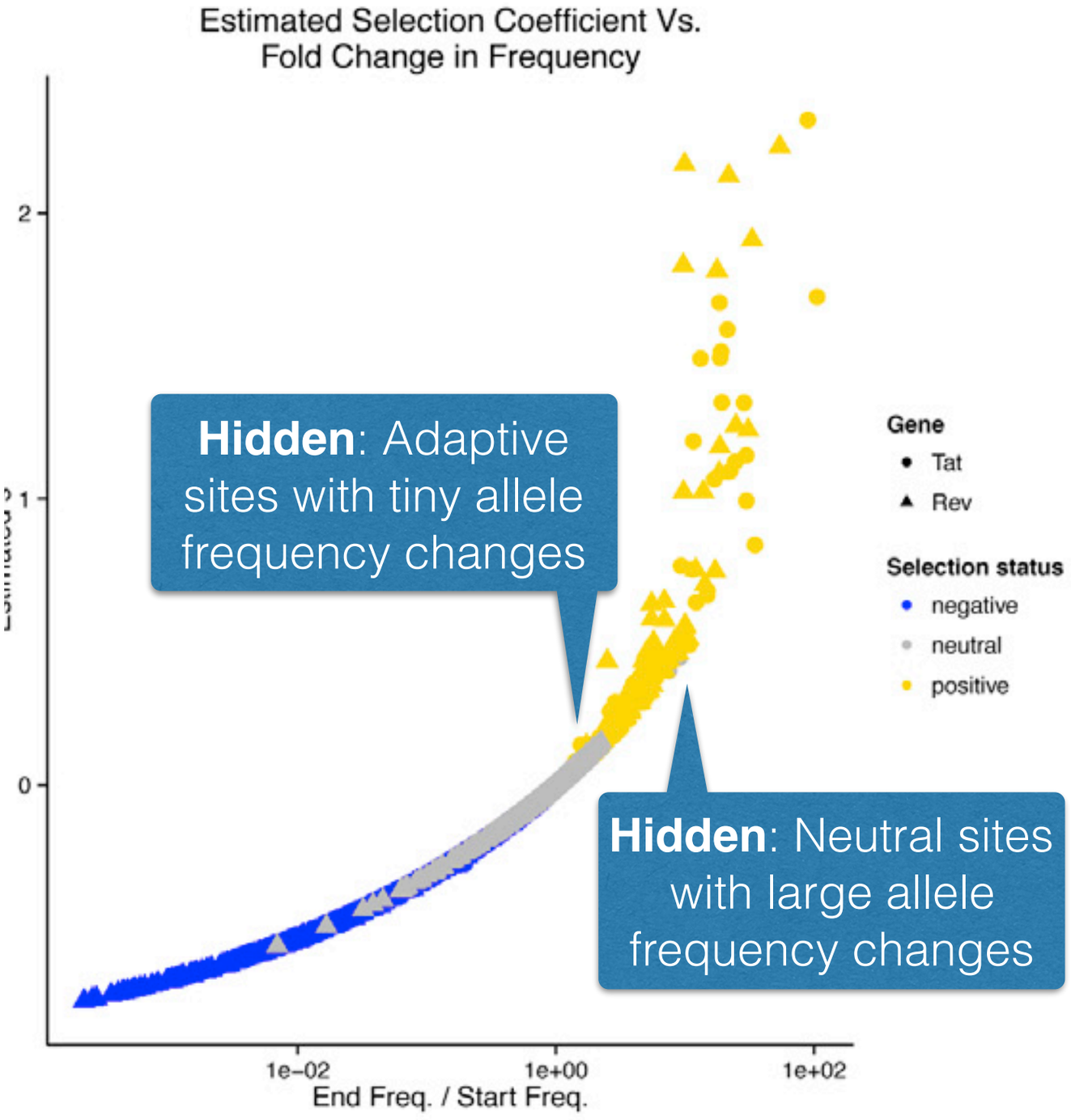
- Experiment: Set up a population of bacteria in a chemostat, and let them reproduce.
- Sample roughly every 5 generations.
- A slope of 0.139 implies:

  $w_1 = e^{0.139} = 1.15$

- Assume $w_2 = 1$.
- Thus, allele p has a 15% fitness advantage over allele q!
- (simulated with 20% advantage)







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Existing forward simulators

- **SFS_CODE: Hernandez (2008)**
  - Command-line flexibility… shameless plug!
- **SLIM 2: Haller & Messer (2017)**
  - R-like scripting environment that provides control over most aspects of the simulated evolutionary scenarios
- **FWDPP: Thornton (2014)**
  - C++ library of routines intended to facilitate the development of forward-time simulations under arbitrary mutation and fitness models