NTU, December 2014



## Thinking about selection and genetic drift... in terms of trajectories

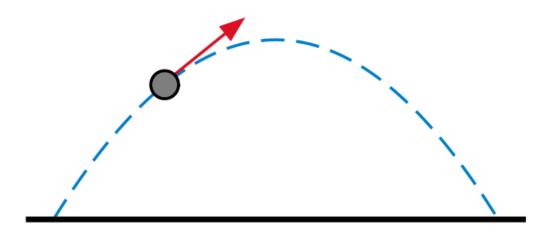
David Waxman Centre for Computational Systems Biology Fudan University, Shanghai PRC



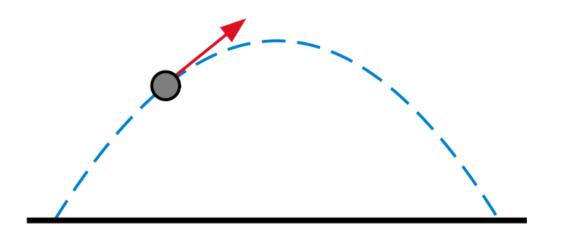
# Guanghua Tower at Fudan University

### Content

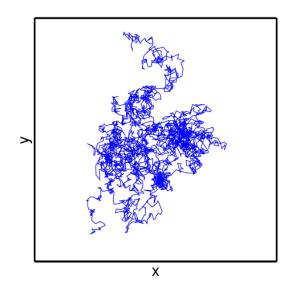
- Introduce trajectories
- Introduce selection
- Introduce random genetic drift
- Talk about conditioned trajectories and some implications



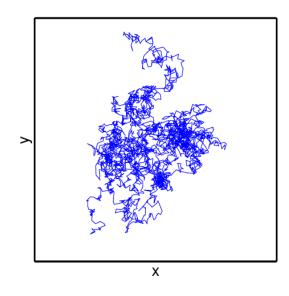
These obey well established laws (Newton,...)



These are 'deterministic' trajectories

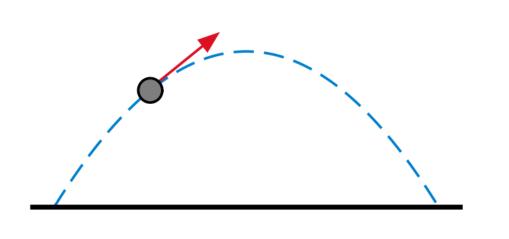


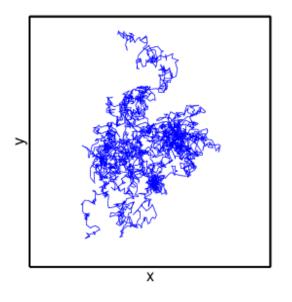
There are natural generalisations that include Brownian motion - randomness (Langevin, Einstein, Bachelier, ...)



These are 'stochastic' trajectories

In biology there are also trajectories that are analogous to





### Deterministic

Stochastic

### But ... trajectories of biology are in a different space

- Simplest case: a single genetic locus with two alternative genes i.e., two *alleles*
- The trajectory is in the space of allele frequencies

What is allele frequency - the variable in a biological trajectory?

Answer:

With the two alleles A and B, the variable is

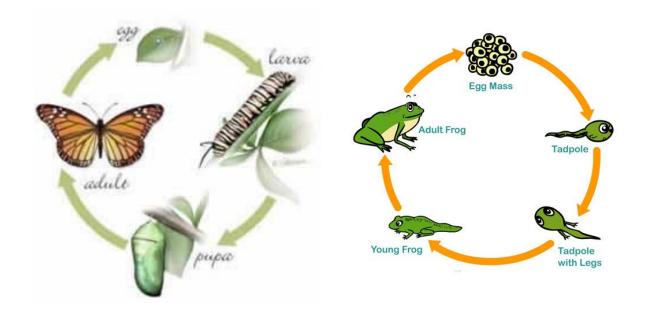
 $X_t$  = frequency (proportion) of A alleles in generation t

 $= \frac{\text{number of } A \text{ alleles in population}}{\text{number of } A \text{ alleles } + \text{ number of } B \text{ alleles}}$ 

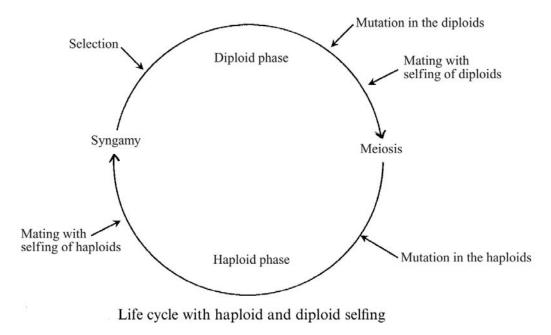
And because it is a proportion

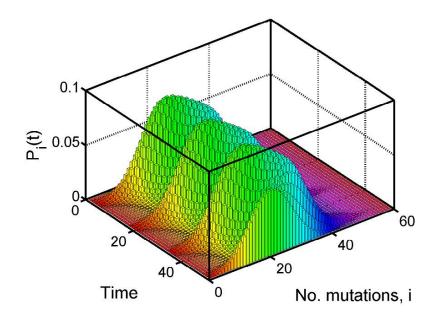
$$0 \leq X_t \leq 1.$$

## Behaviour of $X_t$ comes from the processes of a lifecycle



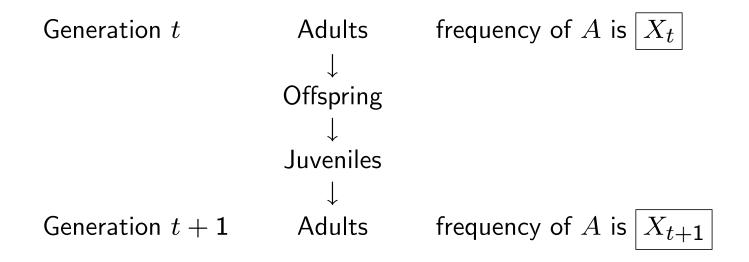
### Lifecycles can be complicated (ferns and fungi)





# Distribution of mutations in ferns and fungi - oscillates

### Lifecycle



Change of allele frequency when population size is infinite  $(N = \infty)$ 

$$X_{t+1} = X_t + M(X_t)$$

### Deterministic

M(x) comes from evolutionary forces (selection, mutation, migration,...)

#### Example: deterministic dynamics with selection

Each individual carries 2 genes (diploid).

Fitnesses of AA, AB and BB individuals are 1 + 2s, 1 + s and 1

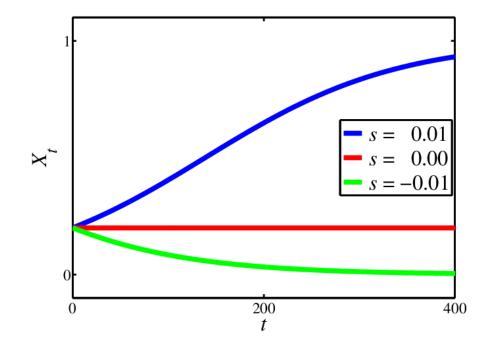
 $\frac{\text{mean number of offspring of }AA \text{ individuals}}{\text{mean number of offspring of }BB \text{ individuals}} = 1 + 2s$ 

 $\frac{\text{mean number of offspring of }AB \text{ individuals}}{\text{mean number of offspring of }BB \text{ individuals}} = 1 + s$ 

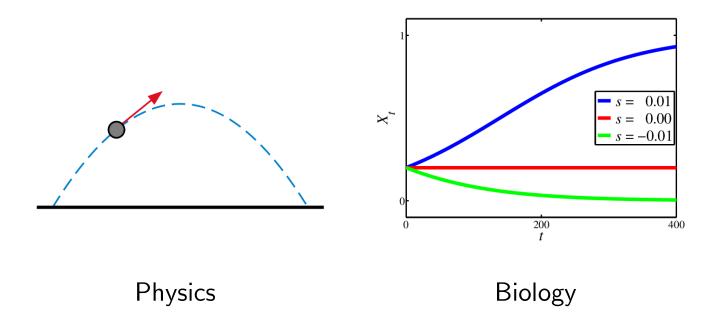
Leads to

$$X_{t+1} = X_t + sX_t(1 - X_t)$$

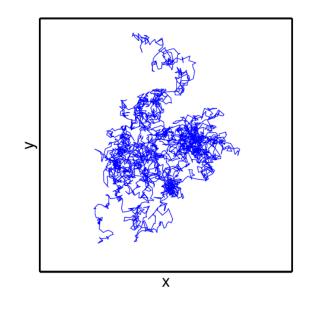
Consequences of 
$$X_{t+1} = X_t + sX_t(1 - X_t)$$

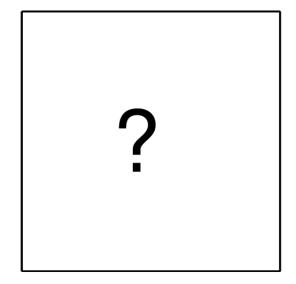


## Deterministic trajectories in physics and biology



Where do the stochastic trajectories of biology come from?



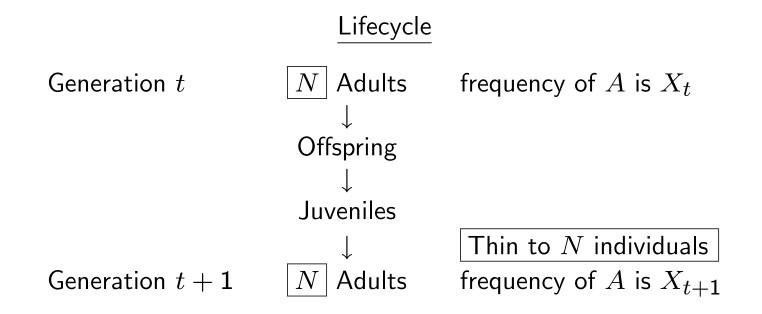


Physics

Biology

#### Where do the stochastic trajectories of biology come from?

Answer: Random genetic drift, which occurs in a finite population ( $N < \infty$ )



## **Consequence of drift**

In a finite population (  $N<\infty$  ) the deterministic equation

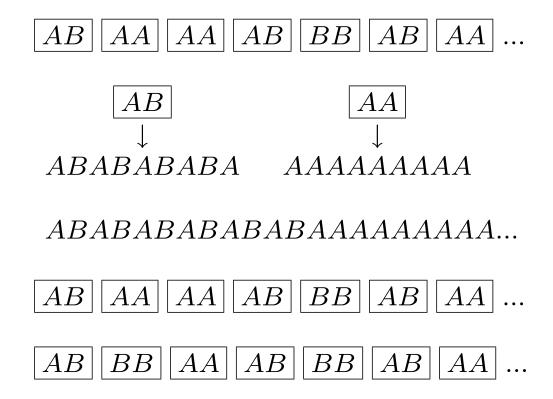
$$X_{t+1} = X_t + sX_t(1 - X_t)$$

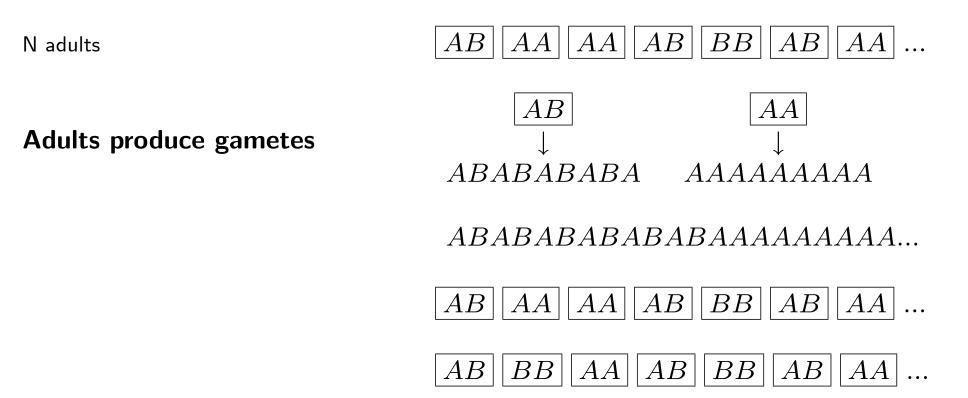
does NOT apply - because of random genetic drift.

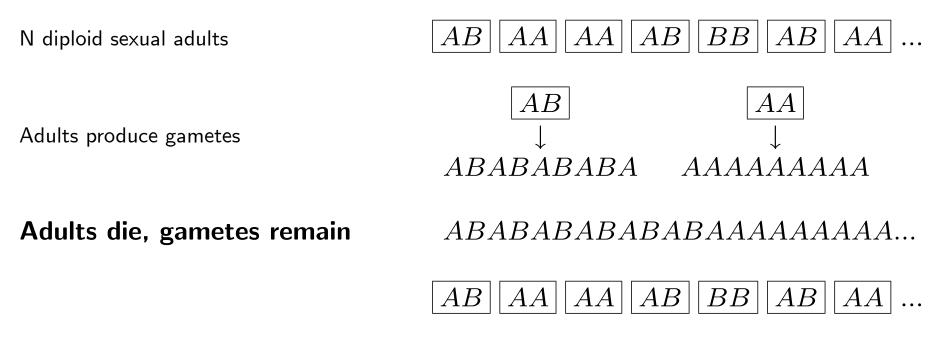
What is random genetic drift?

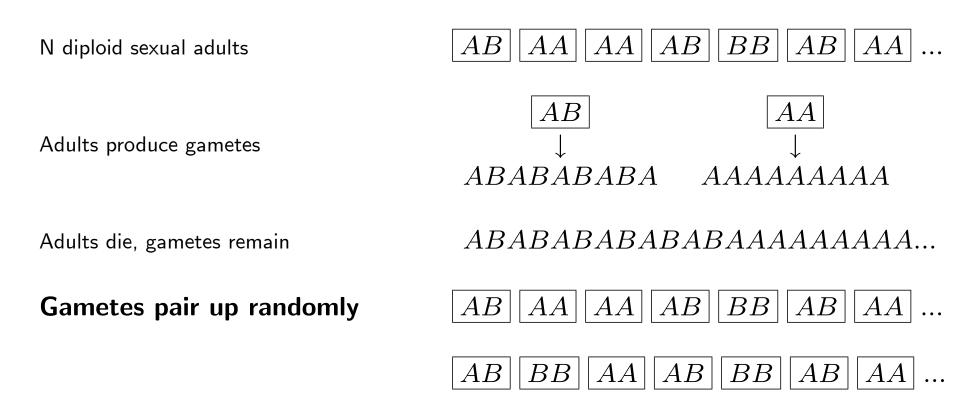


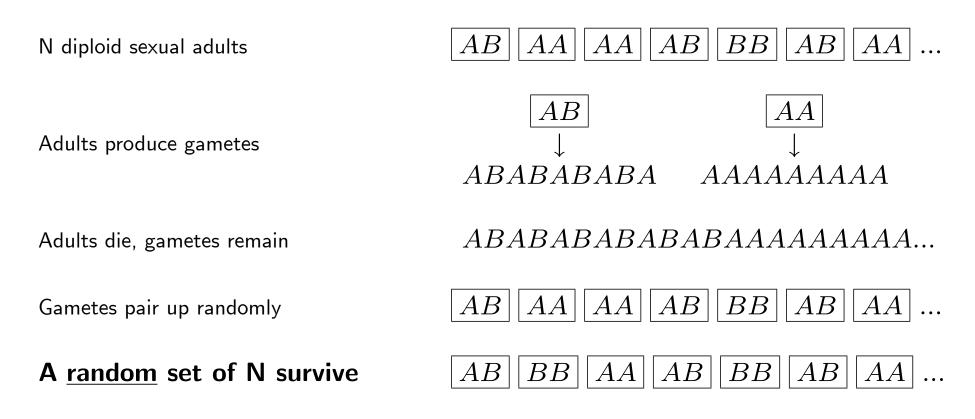
N diploid sexual adults

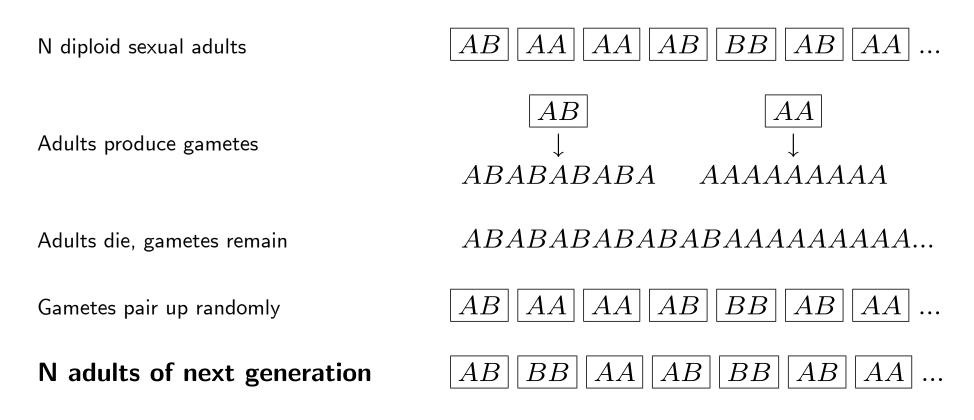




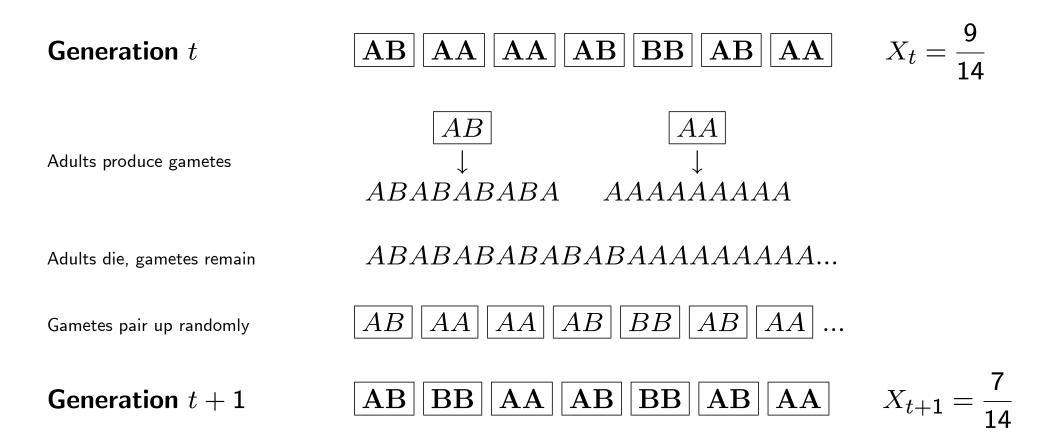








#### Random genetic drift - causes trajectory to be stochastic



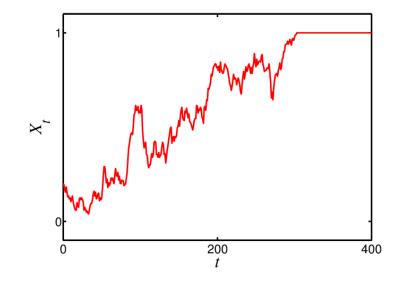
### Random genetic drift - leads to stochastic trajectories

$$X_t = \frac{\text{Number of } A \text{ alleles}}{\text{Total Number of alleles}}$$

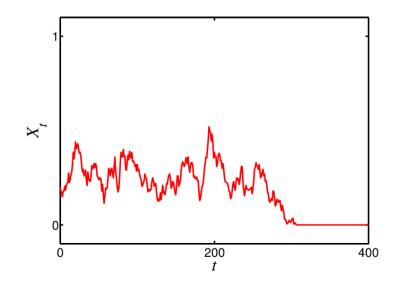
randomly takes values on

$$\left[rac{0}{2N},rac{1}{2N},rac{2}{2N},...,rac{2N}{2N}
ight]$$

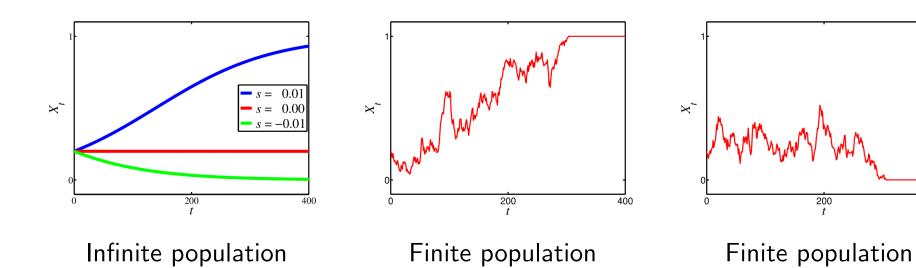
### **Drift dynamics**





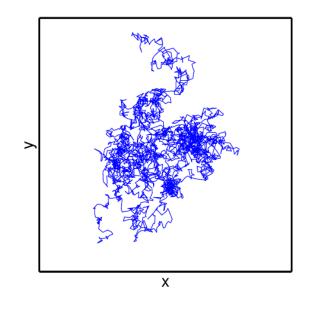


# Comparison

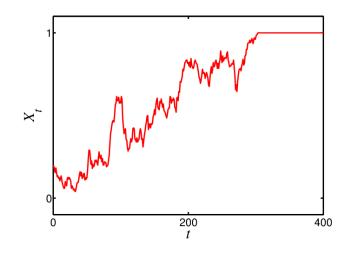


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Stochastic trajectories in physics and biology

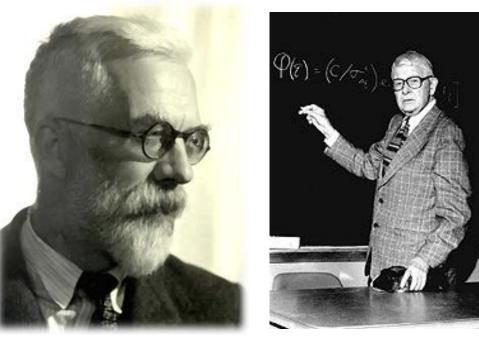


Physics



Biology (finite population)

### Two scientists mathematically formulated the problem of genetic drift



R. A. Fisher

Sewall Wright

Statistical formulation of genetic drift

 $\{N\}$  = a population with N individuals

#### Statistical formulation of genetic drift of Wright and Fisher

## 

Imagine many copies of a population, each with N individuals

Wright and Fisher followed the fates of these copies of a population.

All initially *identical* 

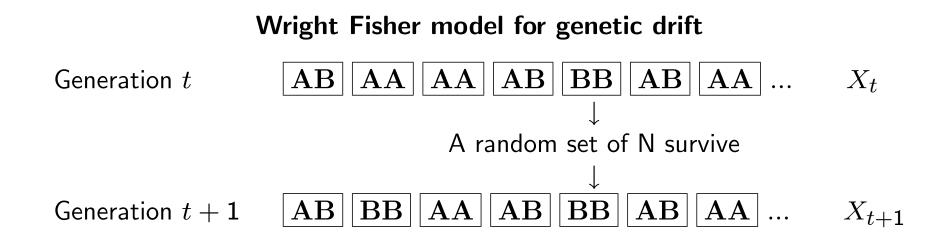
#### Yields statistical information

For example, with just selection, <u>all</u> populations eventually fix A or B

$$\begin{cases} N \\ A \text{ fixed} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \end{cases} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \end{cases} \begin{cases} N \\ B \text{ fixed} \end{cases} \end{cases} \end{cases} \end{cases} \end{cases} \end{cases}$$

 $\{N\}_{A \text{ fixed}} = a \text{ population with } A \text{ allele fixed}$ estimate of fixation probability of A = 5/15 = 1/3

 $\{N\}_{B \text{ fixed}} = a \text{ population with } B \text{ allele fixed}$ estimate of fixation probability of B = 10/15 = 2/3



Wright-Fisher model gives the rule

$$X_{t+1} = \frac{\mathsf{Binom}(2N, X_t + sX_t(1 - X_t))}{2N}$$

Binom(n, p) = binomial random <u>number</u> = No. successes on n trials, each with probability p of success

### Wright Fisher model for genetic drift

#### Define

 $f_{t,n}$  = probability of n copies of the A allele in generation t

= probability that 
$$X_t$$
 has the value  $\frac{n}{2N}$   $n = 0, 1, 2, ..., 2N.$ 

 $f_{t,n}$  obeys

$$f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m}$$
 Markov chain

#### Wright Fisher model

Probability distribution obeys  $f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m}$ 

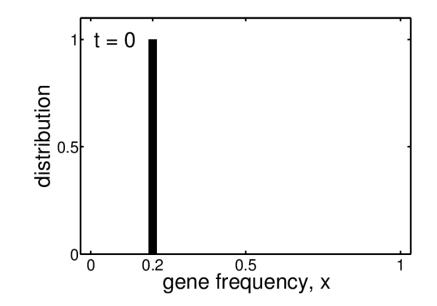
 $W_{n,m}$  = transition probabilities, contains information about probabilities of trajectories. A trajectory with

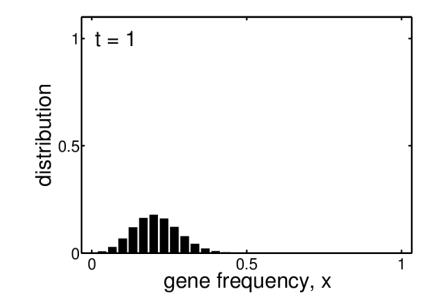
Number of $A$ alleles	time
a	0
b	1
C	2
:	:

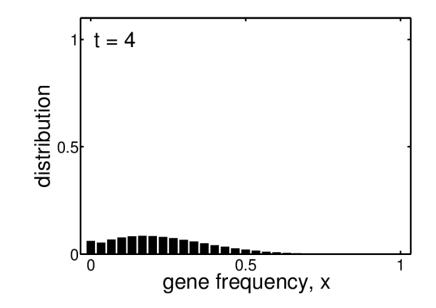
has

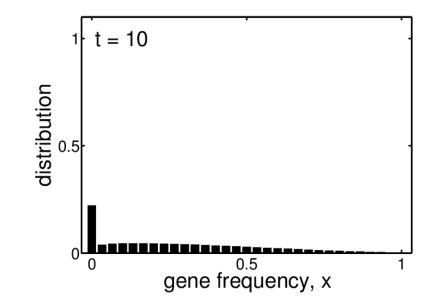
probability = 
$$\cdots W_{d,c} W_{c,b} W_{b,a}$$

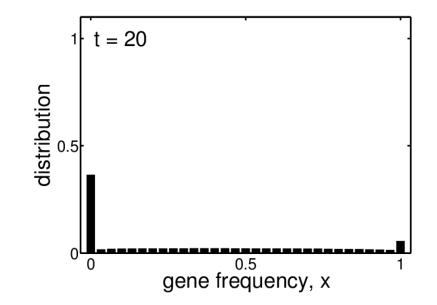
Can look at where trajectories have reached, after time t

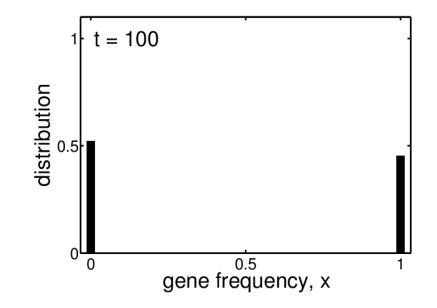




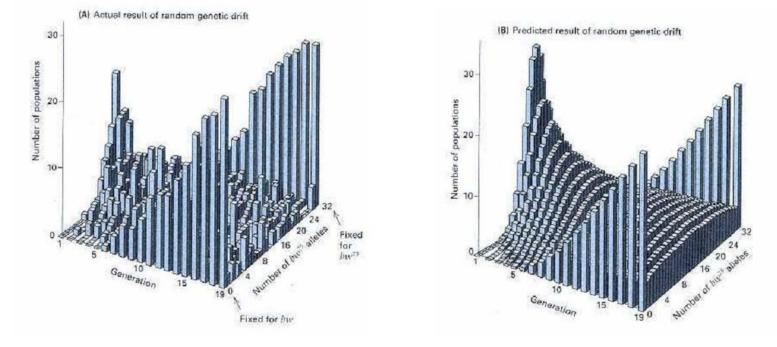








### **Experimental basis**



From experiments on fly populations

From theory

### The above behaviour suggests a sort of diffusion

To make analytical progress, use the

"diffusion approximation"

- replaces  $f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m}$  by a diffusion equation which can sometimes be solved.

Diffusion approximation of 
$$f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m}$$

- Approximate time t as continuous
- Approximate frequency  $X_t$  as continuous: X(t)
- $f_{t,n} \rightarrow f(x,t) = \text{probability density of } X(t)$
- $f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m} \rightarrow \text{diffusion equation.}$

$$\frac{\partial}{\partial t}K(x,t|y,u) = \frac{1}{4N}\frac{\partial^2}{\partial x^2}\left[x(1-x)K(x,t|y,u)\right] - \frac{\partial}{\partial x}\left[sx(1-x)K(x,t|y,u)\right]$$

# Diffusion approximation

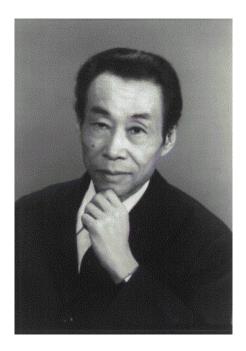
$$f_{t+1,n} = \sum_{m=0}^{2N} W_{n,m} f_{t,m} \quad \text{is approximated by}$$
$$\frac{\partial}{\partial t} K(x,t|y,u) = \frac{1}{4N} \frac{\partial^2}{\partial x^2} \left[ x(1-x) K(x,t|y,u) \right] - \frac{\partial}{\partial x} \left[ sx(1-x) K(x,t|y,u) \right]$$

or equivalently

$$X_{t+1} = \frac{\mathsf{Binom}(2N, X_t + sX_t(1 - X_t))}{2N}$$
 is approximated by

$$dX_t = sX_t(1 - X_t)dt + \sqrt{\frac{X_t(1 - X_t)}{2N}}dB_t$$

# Motoo Kimura - famous population geneticist



Extensively developed and applied the diffusion approximation

### Conditioning

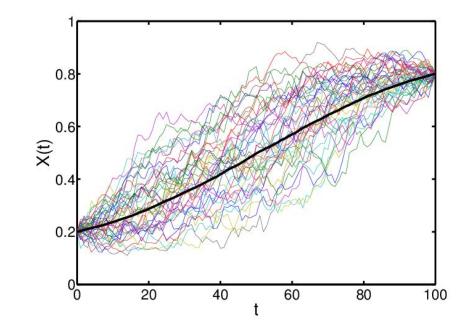
It is very natural to have observational data in the form of

an initial frequency, y, at an initial time, 0

an final frequency, z, at a final time, T

In this case we look only at trajectories going through these points.

For example from ancient DNA that is  $\sim$  100,000 years old and DNA in modern humans.



Trajectories starting at frequency 0.2 at t = 0and reaching frequency 0.8 at t = 100

#### What can we say about the conditioned problem?

Conditioning:

```
initial frequency is y at time t = 0
```

final frequency is z at time t = T

From a diffusion analysis: a conditioned problem has an identical description of an unconditioned one except selection gets modified:

selection strength  $s \rightarrow s_{fict}(x, t)$  (depends on y, z and T)

#### How does this come about?

The unconditioned problem, has fundamental solution (probability density of X(t) at value x)

$$K(x,t|y,u) = E\left[\delta(x - X(t))|X(u) = y\right]$$

The conditioned problem has a fundamental solution, that achieves z at final time T, given by

$$K^{[z,T]}(x,t|y,u) = \frac{K(z,T|x,t)K(x,t|y,u)}{K(z,T|y,u)}$$

### What can we say about the conditioned problem?

Unconditioned

$$\frac{\partial}{\partial t}K(x,t|y,u) = \frac{1}{4N_e}\frac{\partial^2}{\partial x^2}\left[x(1-x)K(x,t|y,u)\right] - \frac{\partial}{\partial x}\left[sx(1-x)K(x,t|y,u)\right]$$

Conditioned

$$\frac{\partial}{\partial t}K(x,t|y,u) = \frac{1}{4N_e}\frac{\partial^2}{\partial x^2}\left[x(1-x)K(x,t|y,u)\right] - \underbrace{\frac{\partial}{\partial x}\left[s_{\mathsf{fict}}(x,t)x(1-x)K(x,t|y,u)\right]}_{\underbrace{\partial x}}$$

What is the form of  $s_{fict}(x, t)$ ?

For trajectories that fix by a specific time  ${\cal T}$ 

$$s_{\text{fict}}(x,t) = s + \frac{1}{2N_e} \frac{\partial}{\partial x} P_{fix}(T|x,t)$$

$$= s \coth(2N_e sx) \text{ for } T \to \infty$$

where generally

$$P_{fix}(T|x,t) = \begin{cases} \text{probability of fixing by time } T, \text{ given} \\ \text{an initial frequency of } x \text{ at time } t \end{cases}$$

What is the form of  $s_{fict}(x, t)$ ?

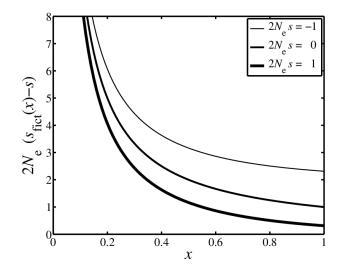
For trajectories that achieve frequency z by a specific time T

$$s_{\mathsf{fict}}(x,t) = s + \frac{1}{2N_e} \frac{\partial}{\partial x} K(z,T|x,t)$$

where

 $K(z,T|x,t) = \begin{array}{l} \text{probability density of the frequency at time } T, \\ \text{frequency } z, \text{ given a frequency of } x \text{ at time } t \end{array}$ 

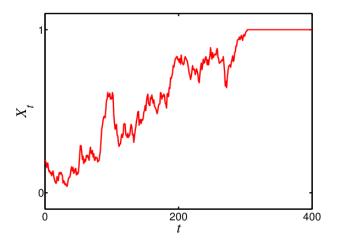
Conditioning leads to: selection strength  $s \rightarrow s_{fict}(x, t)$ 



Much of the selection in a conditioned problem is fictitious:  $|s| \ll s_{\text{fict}}(x,t)$ 

### Example

Suppose we are given a single trajectory, where the A allele fixes



### Example

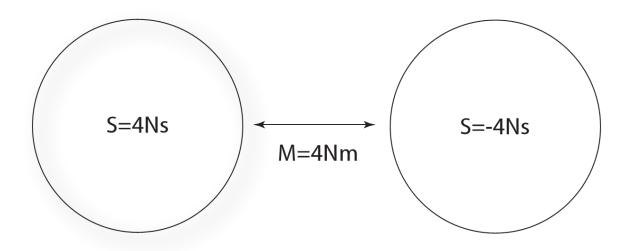
There are two alternatives

- 1. Assume this is a consequence of deterministic dynamics of a very large population, so  $X_{t+1} = X_t + sX_t(1 - X_t)$
- 2. Assume this just is a chance fixation in a finite population then it is a conditioned trajectory that arises from a problem with  $s \rightarrow s_{\text{fict}}(x, t)$ .

If (2) is correct, then (1) can drastically overestimate the true value of s (can be off by more than 1000% or even of the wrong sign).

- Strong evolutionary forces may be invoked in problems where effectively, conditioning has been carried out
- These strong forces may largely be an outcome of the conditioning
- They do not have a real existence and can strongly distort estimates of selection strength and other parameters

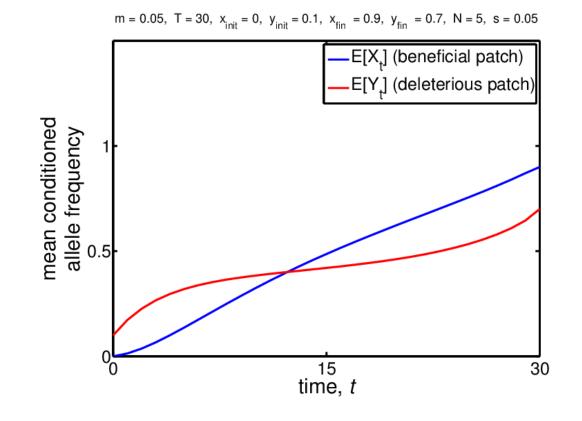
# Other problems



Problems of drift, involving spatial structure

$$X(t+1) = \frac{\text{Bin}(2N, X(t) + D_1(X(t), Y(t)))}{2N}$$
$$Y(t+1) = \frac{\text{Bin}(2N, Y(t) + D_2(X(t), Y(t)))}{2N}$$

Problems with spatial structure involve coupled diffusion equations...



Mean trajectories in a diffusion problem involving spatial structure

### Summary

- Problems in genetics and evolution can usefully be looked at in terms of trajectories
- Random genetic drift can lead to very different trajectories compared with deterministic dynamics of an infinite population
- The act of conditioning restricting trajectories because of observations, can lead to fictitious forces in the problem which can greatly distort parameter estimates

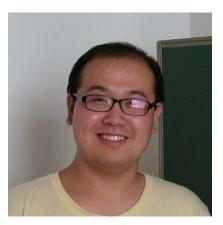
# Acknowledgements



Martin Lascoux



Andy Overall



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Thank you for listening