



**Natural selection:** changes in alleles / genomes due to effects on reproductive success

(adaptive, responsive to environment)

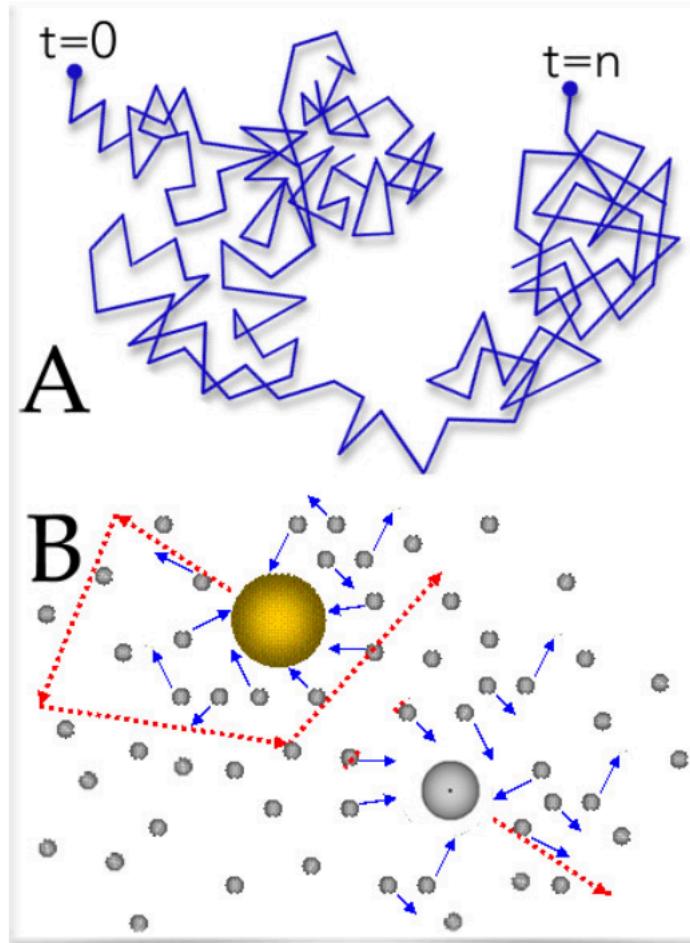
**Non-adaptive processes:** changes in alleles / genomes due to stochastic and incomplete sampling processes

gene linkage (next class)

What is a stochastic process?

What can be predicted about a single particle undergoing Brownian motion? what cannot be predicted?

Does this change when we consider a population of particles?





This is a fair die; you role it 11 times, it comes up  
1,3,1,2,1,3, 4, 5, 1, 2, 1

Which number is most likely to be come up next?



Stochastic (apparently random) processes are not always easy to understand or to accept. Hopefully these activities will be useful.

For example, suppose you roll a fair die five times and get the numbers 1, 2, 3, 4, and 5. What is likelihood that the next roll will be a 6?

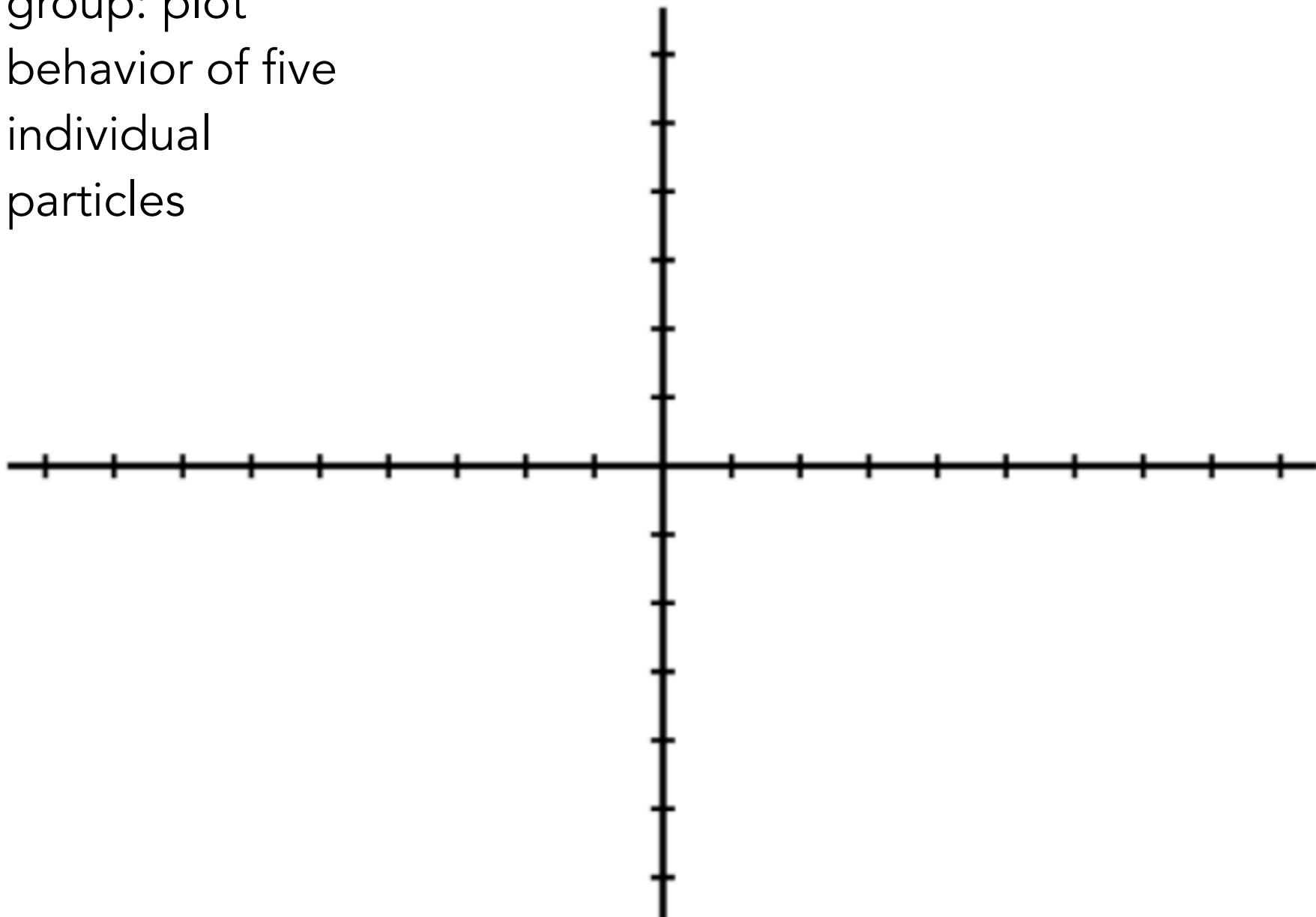
1

1/6

impossible to predict

explain the logic  
of your choice

group: plot  
behavior of five  
individual  
particles



Draw

Adjust

Erase

Check

Reset

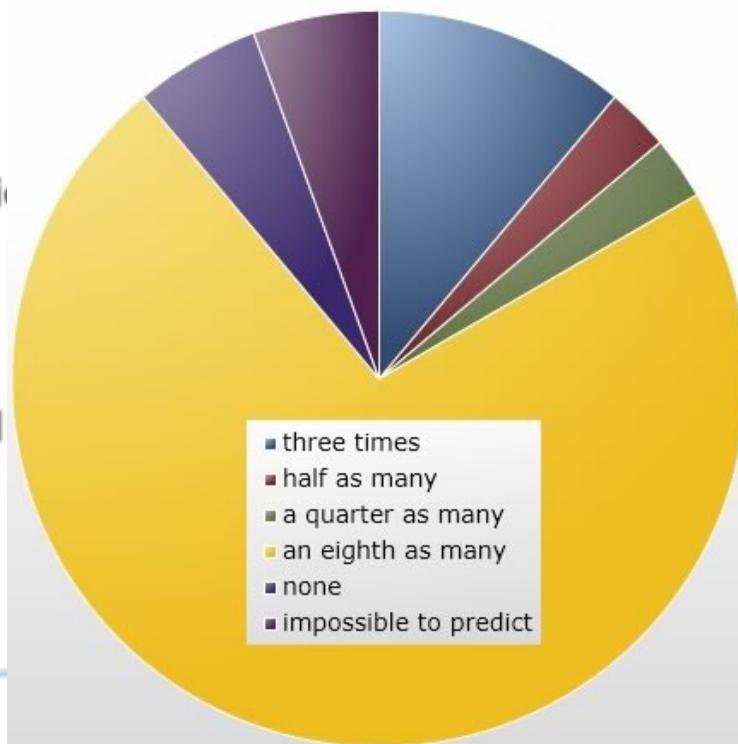
Average distance of population's traveled

Science has to do with predictable processes, even stochastic processes can be predictable at the macroscopic level, the world that we can directly experience.

Predictable processes can be described mathematically as a function of one variable (such as time) with respect to another (a particular event). Consider an example from physics: the radioactive decay of an unstable isotope atom.

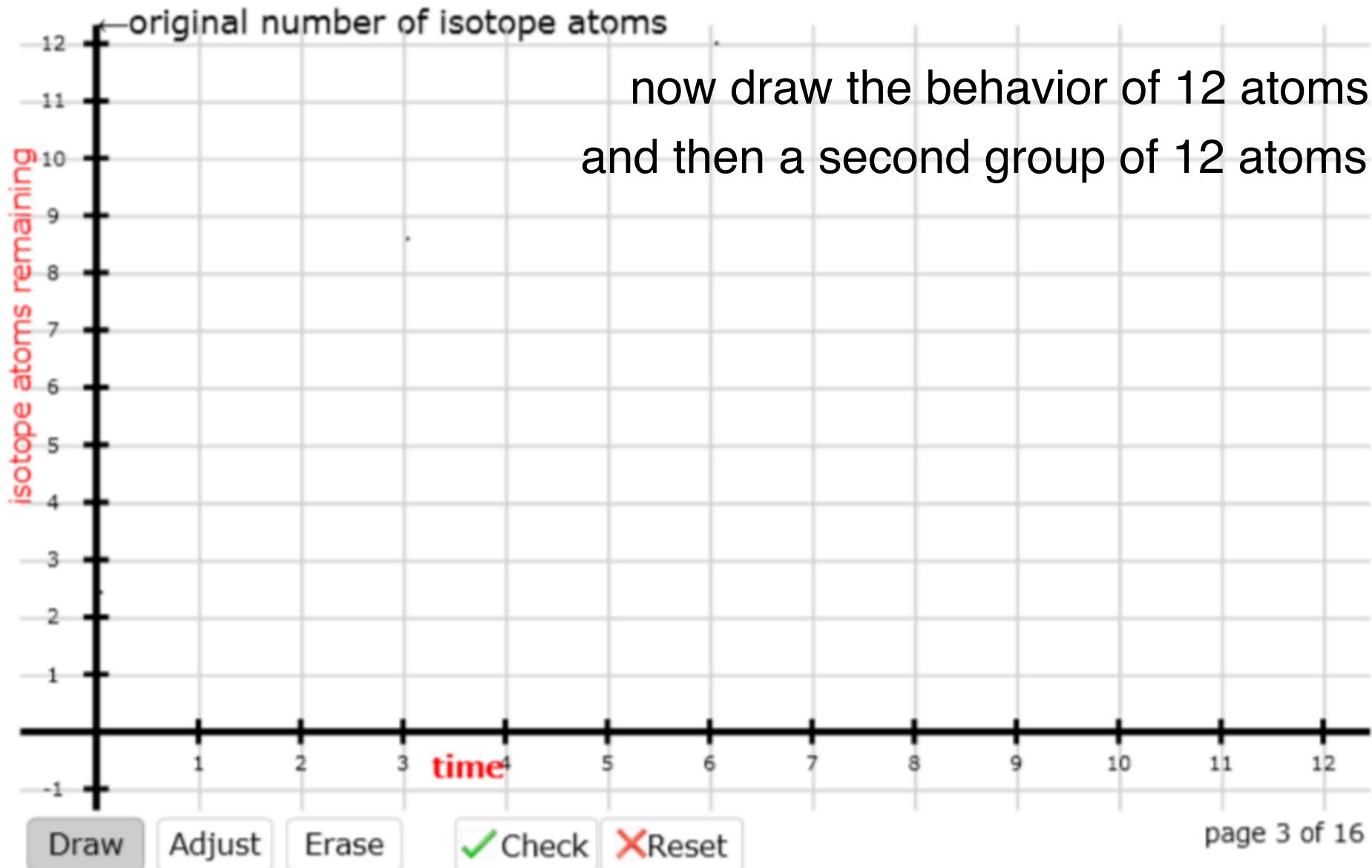
Such an isotope is characterized by its half-life ( $t_{1/2}$ ), which is the time it takes for half of the original population to decay.

If we look at a population of isotopic atoms after three half-lives ( $3 \times t_{1/2}$ ) we will find how many of the original isotope will be left (**pick**) ...



explain the logic  
of your choice

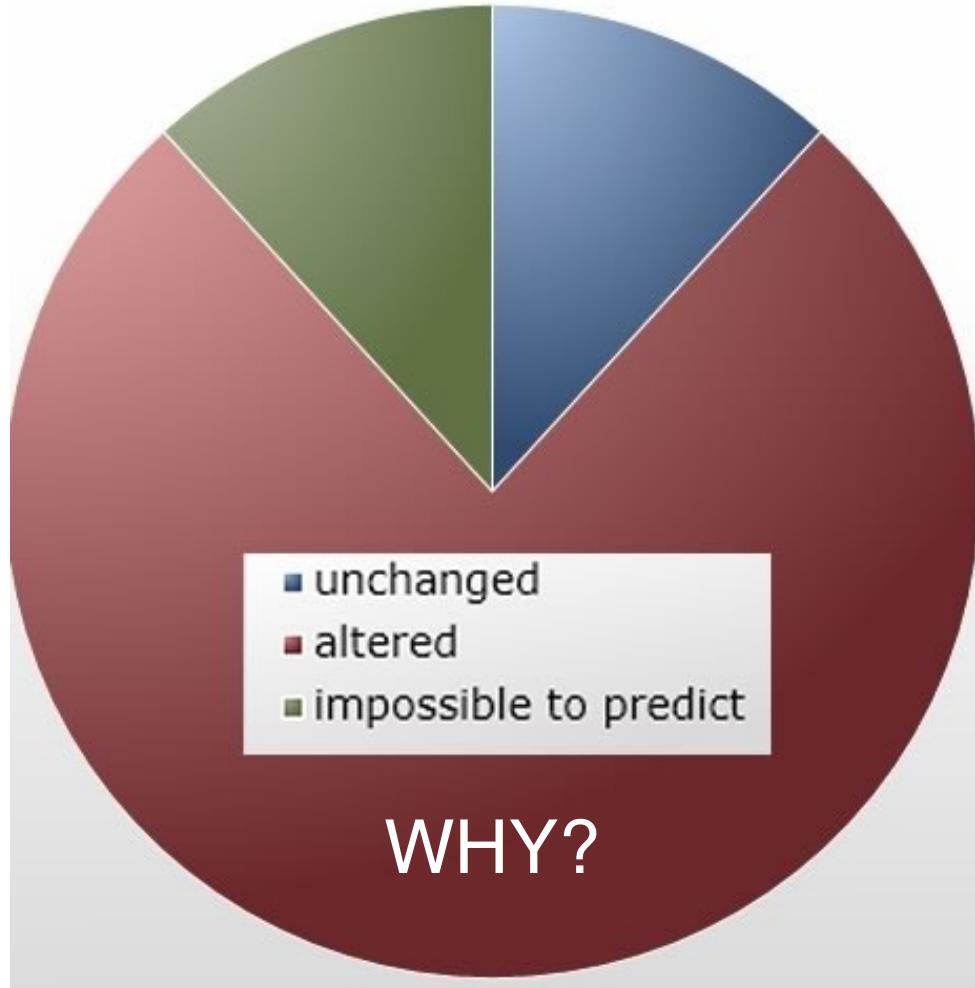
You start with a population of 12 billion isotope atoms - this particular isotope has a half-life of 4 time units. **Draw** the half life relationship as a function of time.



Explain your reasoning: did you draw the two  $^{12}$  isotope atoms experiments identically or differently?

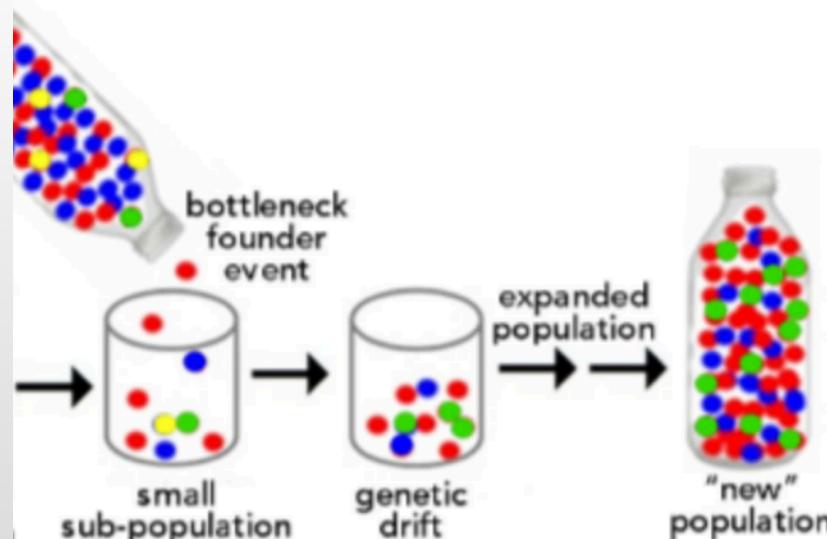
- they should be the same
- they should be different
- it is impossible to predict
- no idea what I did

discuss and respond (~2 minutes)



populations of organisms and their isolation bottlenecks, and genetic drift.

In effect, a small subset of the original founder effect) or survives an event such as a loss of genetic diversity in the population; a (yellow, green, blue or red) represents a

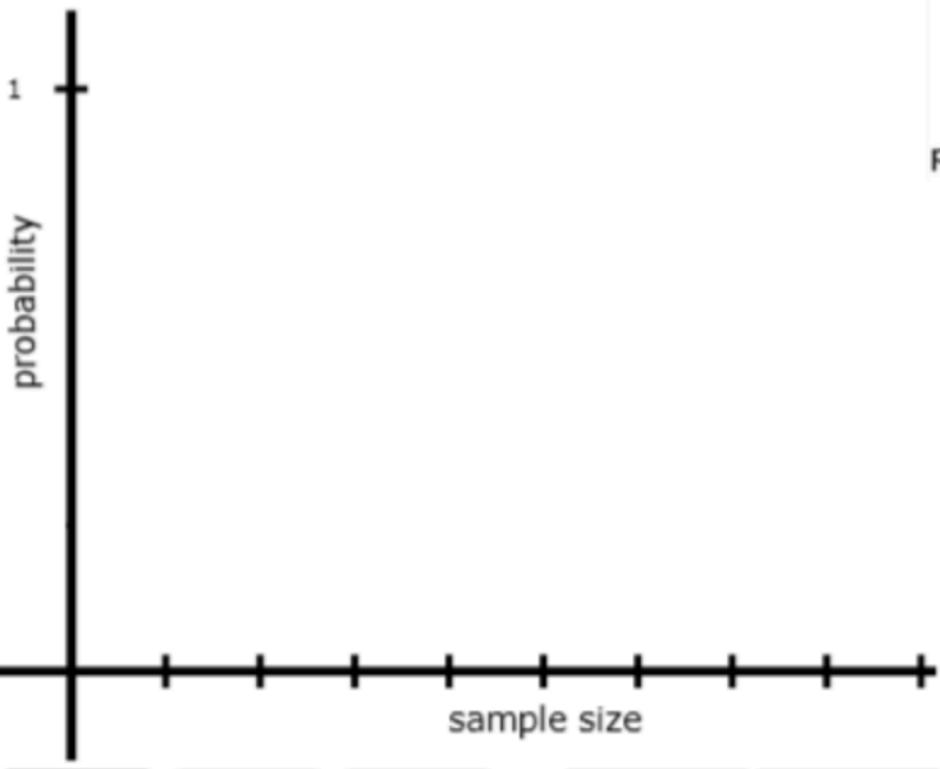
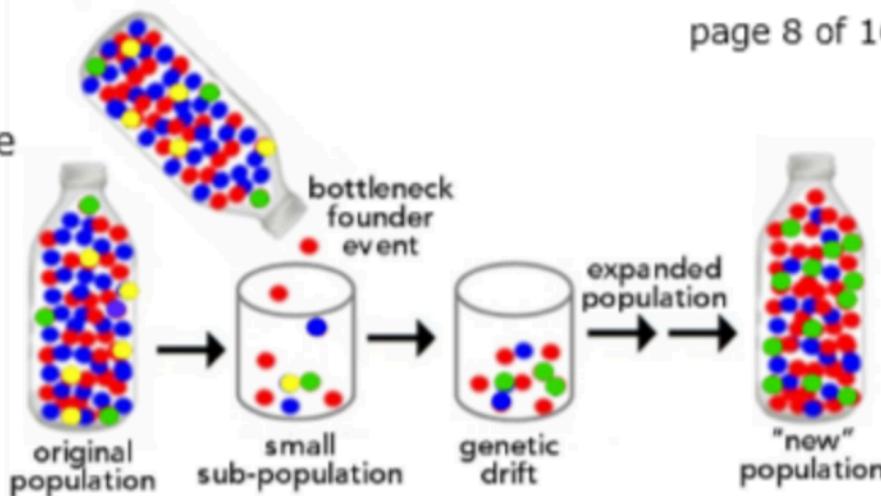


The combination of a bottleneck/founder event and genetic drift is likely to leave the original population's genetic diversity...

- unchanged
- altered
- impossible to predict
- no idea

Now let us get a little more quantitative. **Draw a graph** that predicts the probability that a bottleneck/founder event will lead to a change in the genetic complexity of the resulting "new" population. The axes are probability (Y) vs sub-population (sample) size (X). This is the same problem faced by pollsters, who want to examine the smallest number of people, while accurately reflecting the total population.

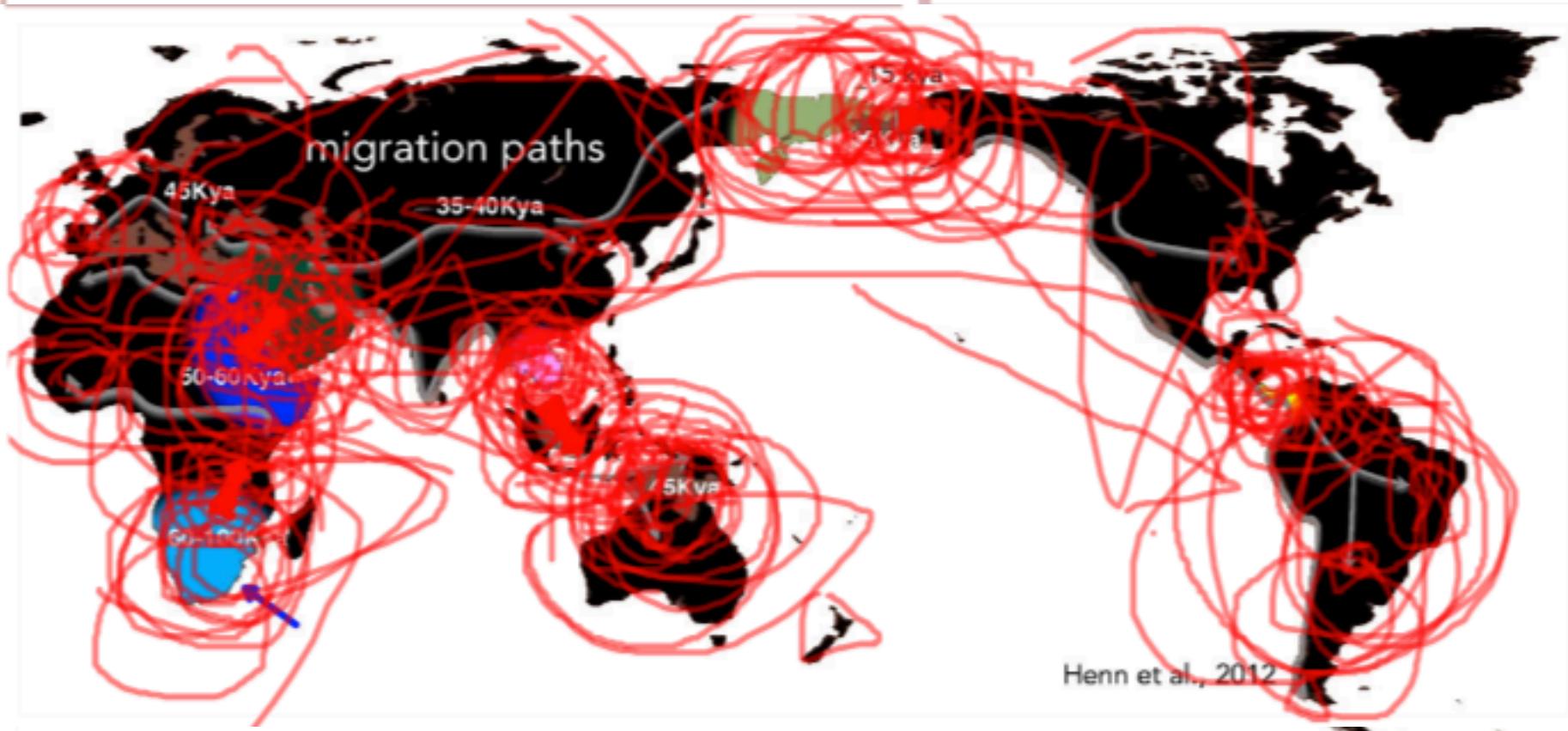
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How might a bottleneck/founder effect the future evolution of a population.

draw and explain why

Here is a map of the history of human migrations out of Africa. Circle the various places where you think bottlenecks/founder effects might have occurred. There are likely to have been number of such events. Explain, where would you expect to find the greatest amount of genetic diversity and why



Draw

Erase

Reset

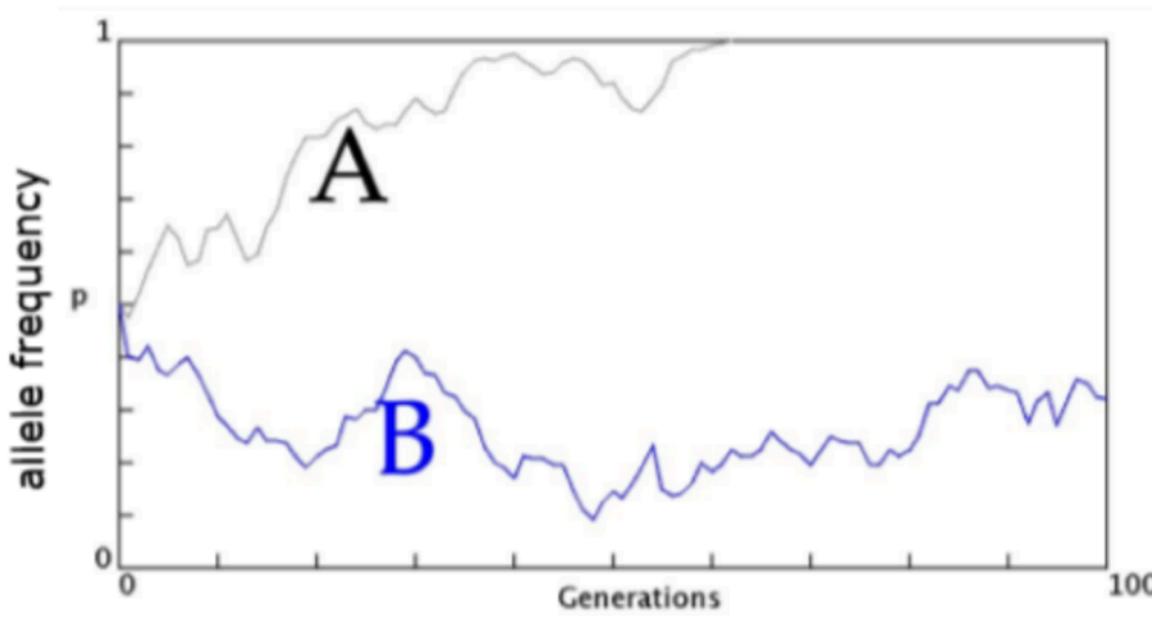
**Getting a feel for genetic drift:** You are considering various populations of an organism. Population size (**N**) varies from 10 to 250 individuals.

There are two alleles for the specific gene we are considering; both are present in equal numbers in each population at the start of the experiment. The frequency of one of these alleles is plotted along the Y-axis. Each experiment runs for 100 generations (plotted along the X-axis).

One or the other allele is lost when allele frequency reaches either 1 or 0; once this occurs, frequency no longer changes.

This graph shows how allele frequency changes in two populations (A and B) ( $N=100$ ) over 100 generations.

In which population has an allele been lost?



A

B

while you can run the (flash) genetic drift applet yourself, we have generated a data set for you. We examined 24 populations at each of various population sizes (N) over the course of 100 generations.

flash genetic drift applet

[http://www.radford.edu/~rsheehy/Gen\\_flash/popgen/](http://www.radford.edu/~rsheehy/Gen_flash/popgen/)

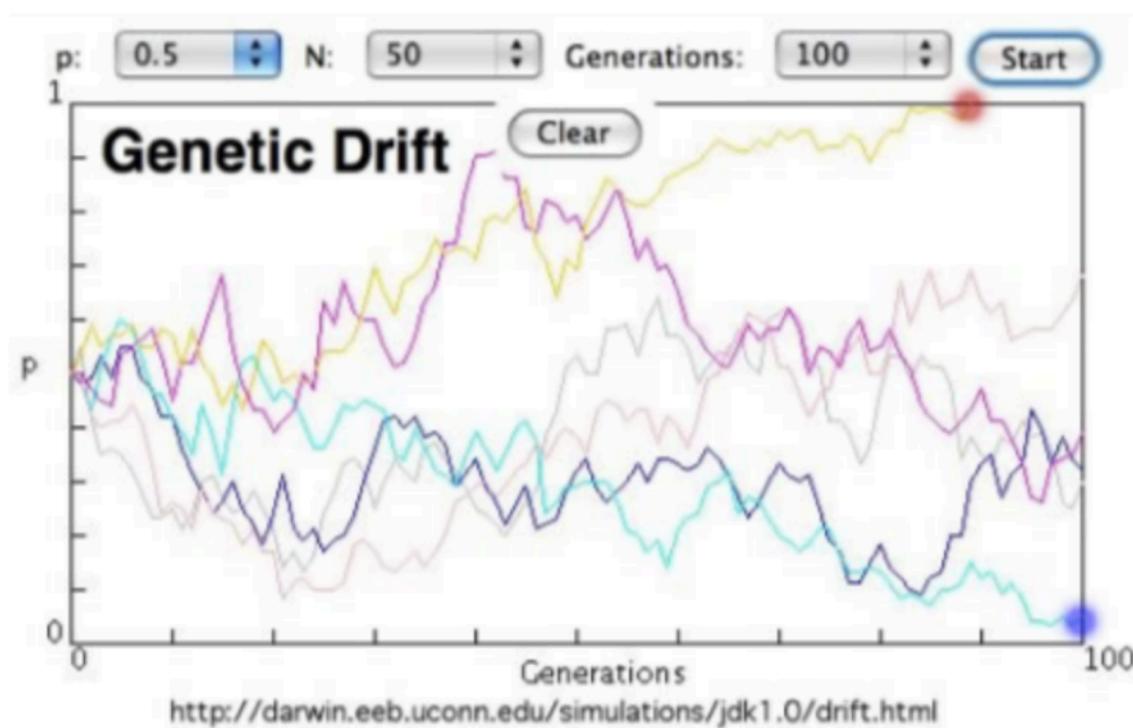
The number of times one or the other allele is lost is given

L.	Pop. Size	L
	N=10	24
	N=25	21
	N=50	10
	N=100	4
	N=250	1

From this data, you can calculate the frequency of allele loss ( $f_L$ ), which is equal to  $L/24$ .

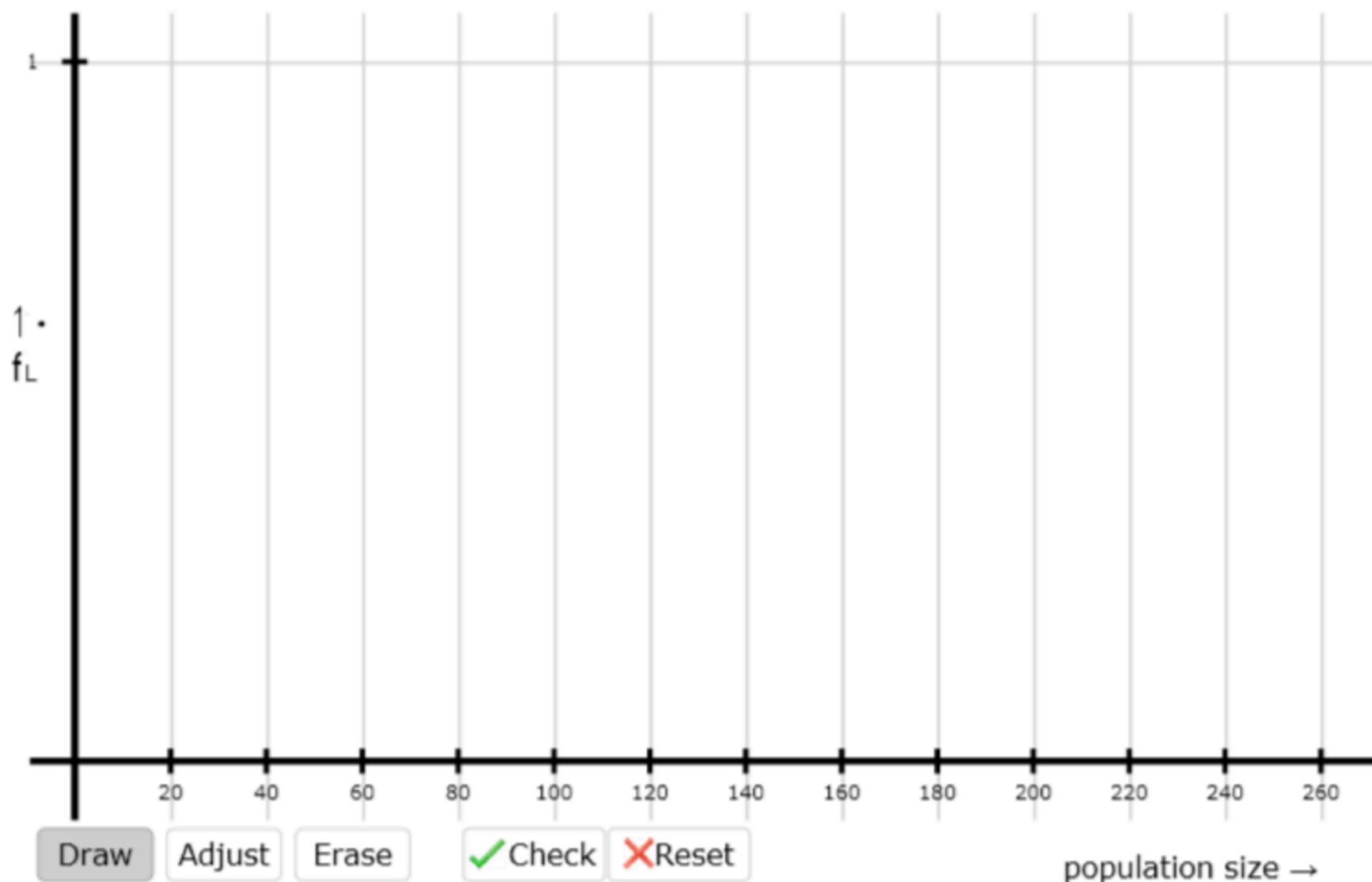
Calculate the value of  $f_L$  for each population (and write it down).

On the next page make a graph of  $f_L$  as a function of population size.



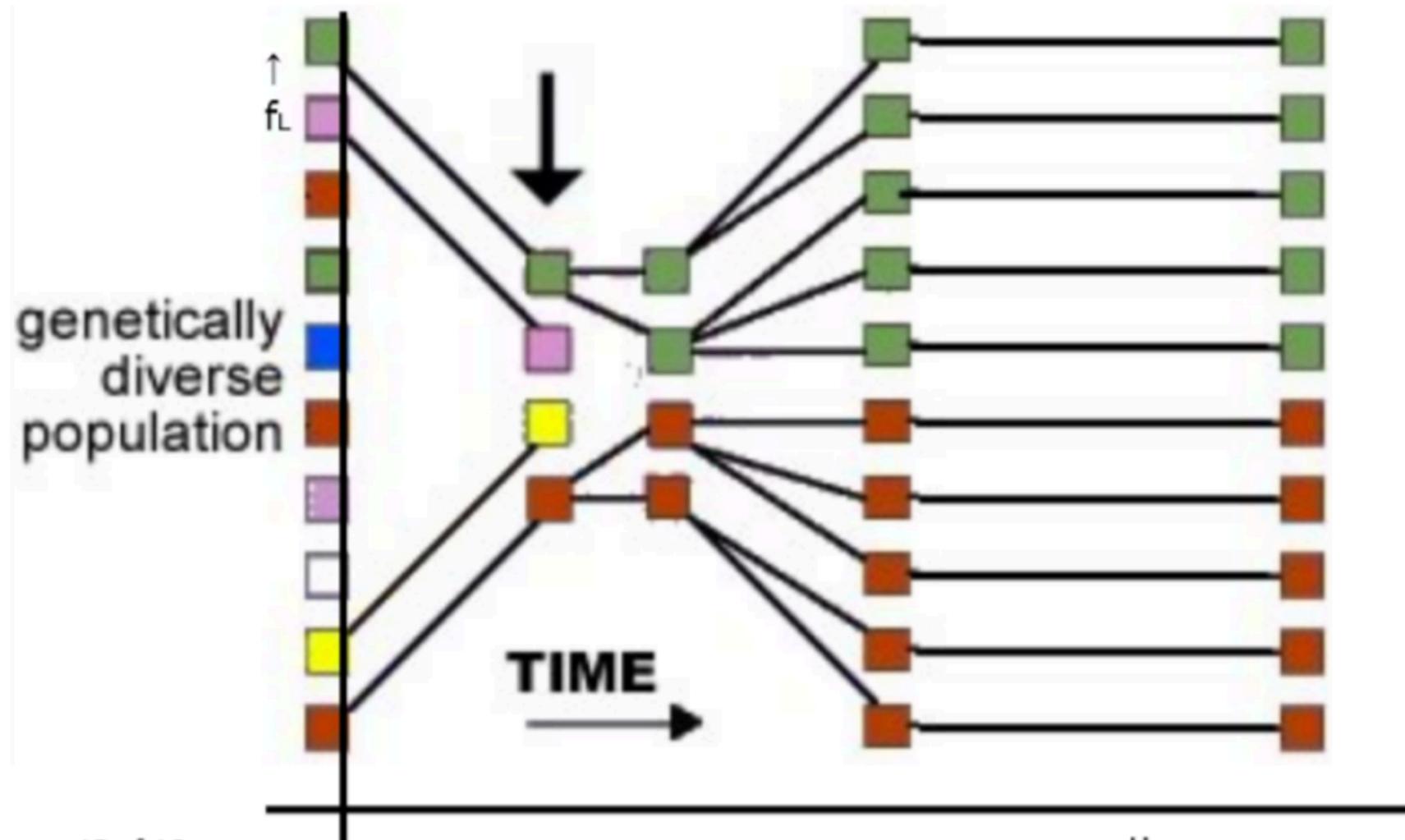
Take your data from the previous page and draw a graph of the relationship between population size and  $f_L$

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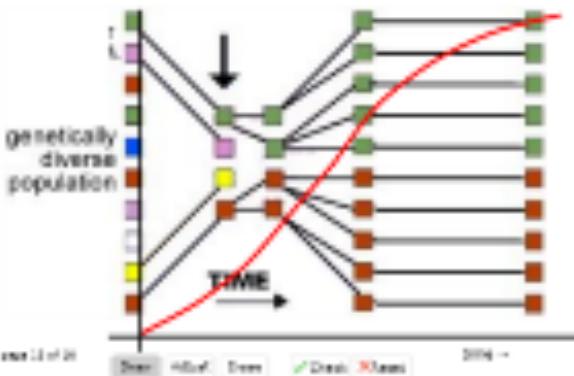
You begin with a genetically diverse population at t=0. A population bottleneck occurs (down arrow) after which the population rapidly increases in size.

**Draw a curve** that represents the impact of genetic drift ( $f_L$ ) as a function of time.

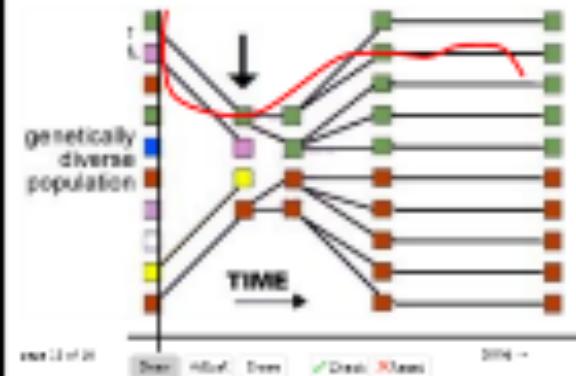


# impact of genetic drift

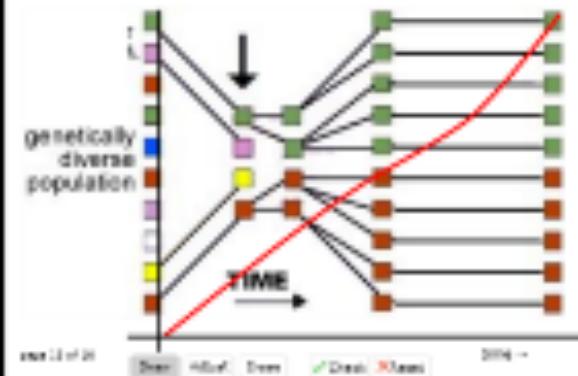
You begin with a genetically diverse population of 100. A population bottleneck occurs when you select after which the population rapidly increases in size.  
A red arrow bar represents the impact of genetic drift on your population over time.



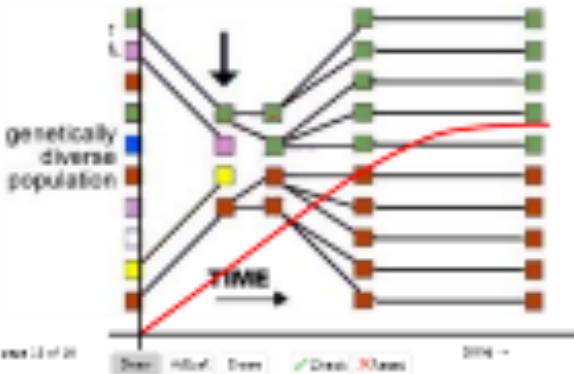
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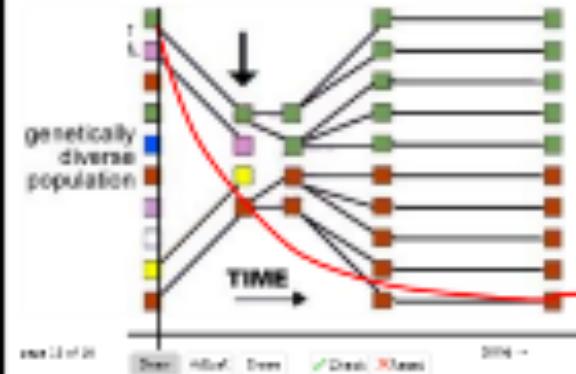
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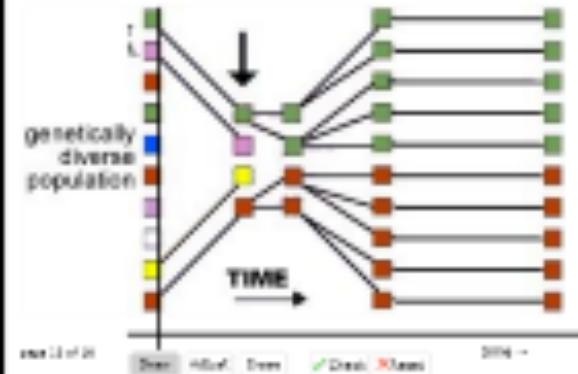
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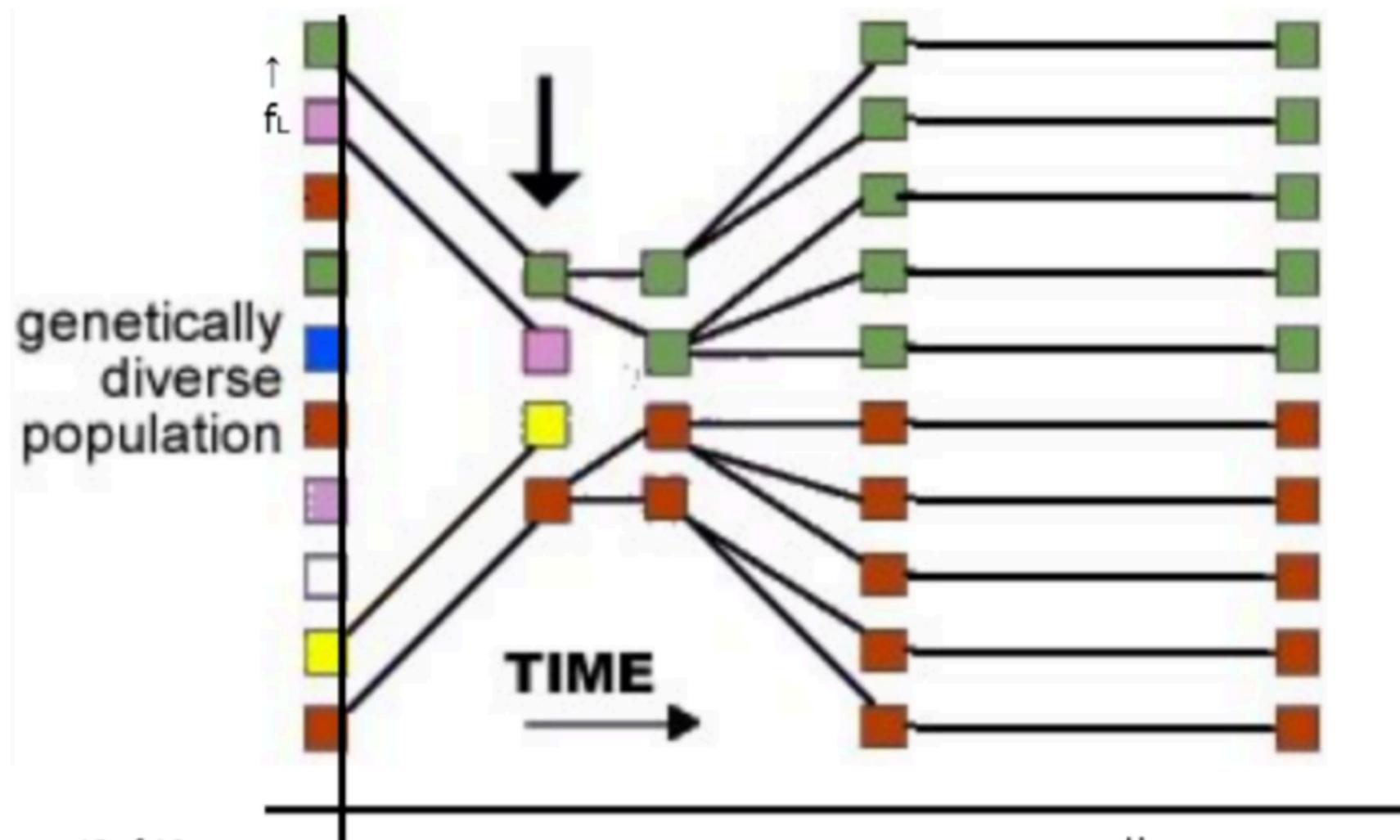


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You begin with a genetically diverse population at t=0. A population bottleneck occurs (down arrow) after which the population rapidly increases in size.

**Draw a curve** that represents the impact of genetic drift ( $f_L$ ) as a function of time.



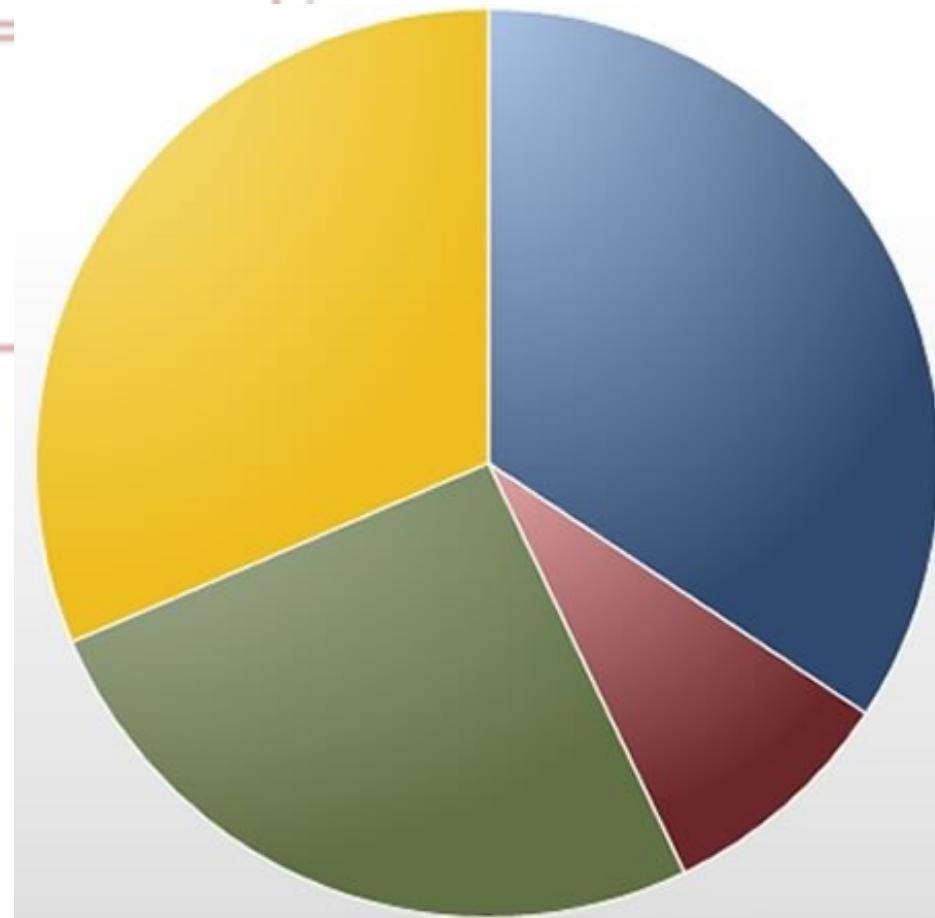
Immediately after a genetic bottleneck we predict that the effects of genetic drift will ....

- be unaffected
- increase

explain your logic behind your choice

If genetic drift leads to the fixation of a deleterious allele, we can expect ...

explain your logic behind your choice



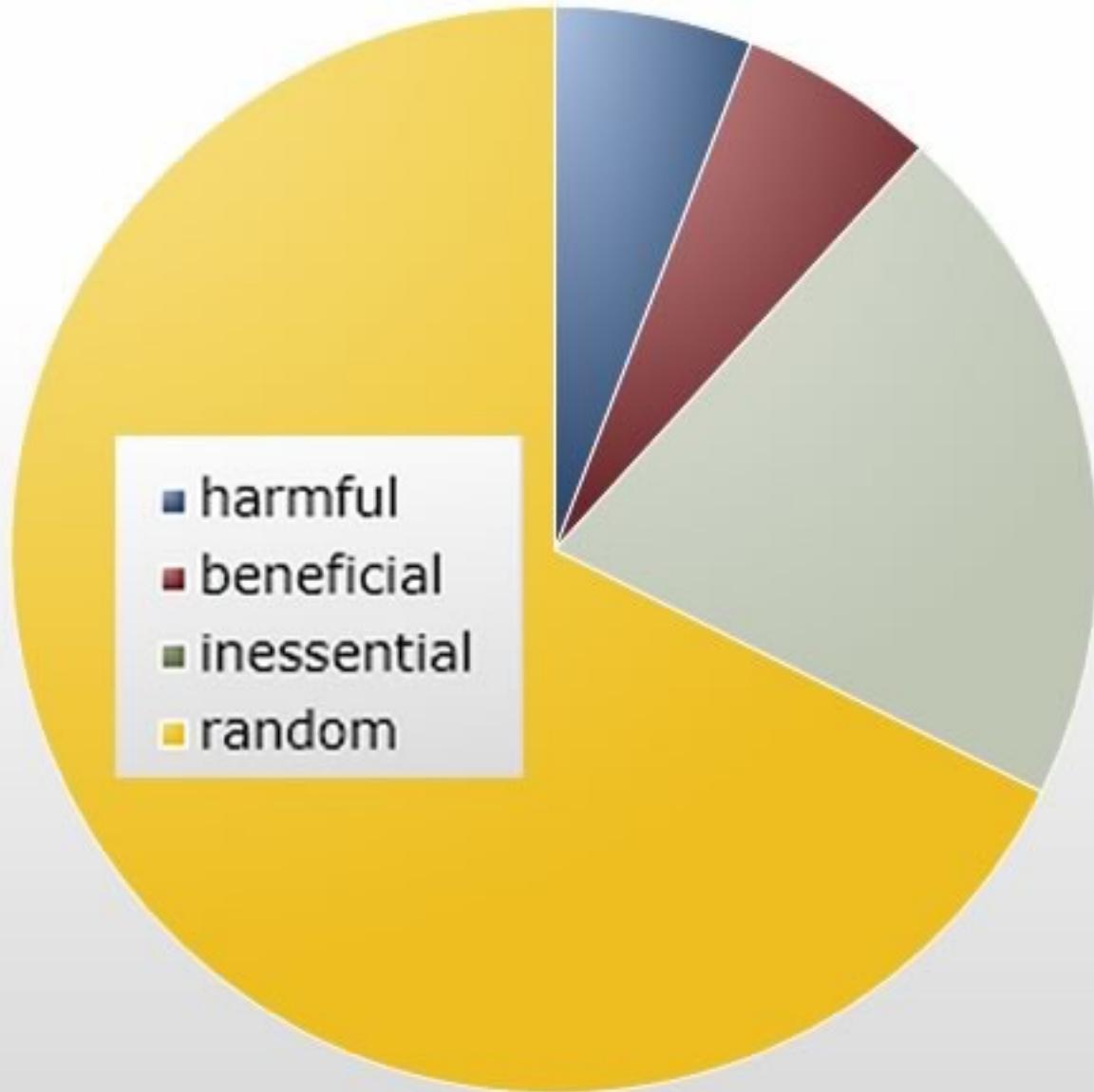
- subsequent evolutionary events to reduce these negative effects
- the species to go extinct
- the gene with the deleterious allele to be deleted
- the negative trait will be maintained

Explain (in the box below) what is genetic drift and how can it influence the evolution of a population.

The allele lost due to genetic drift will be ...

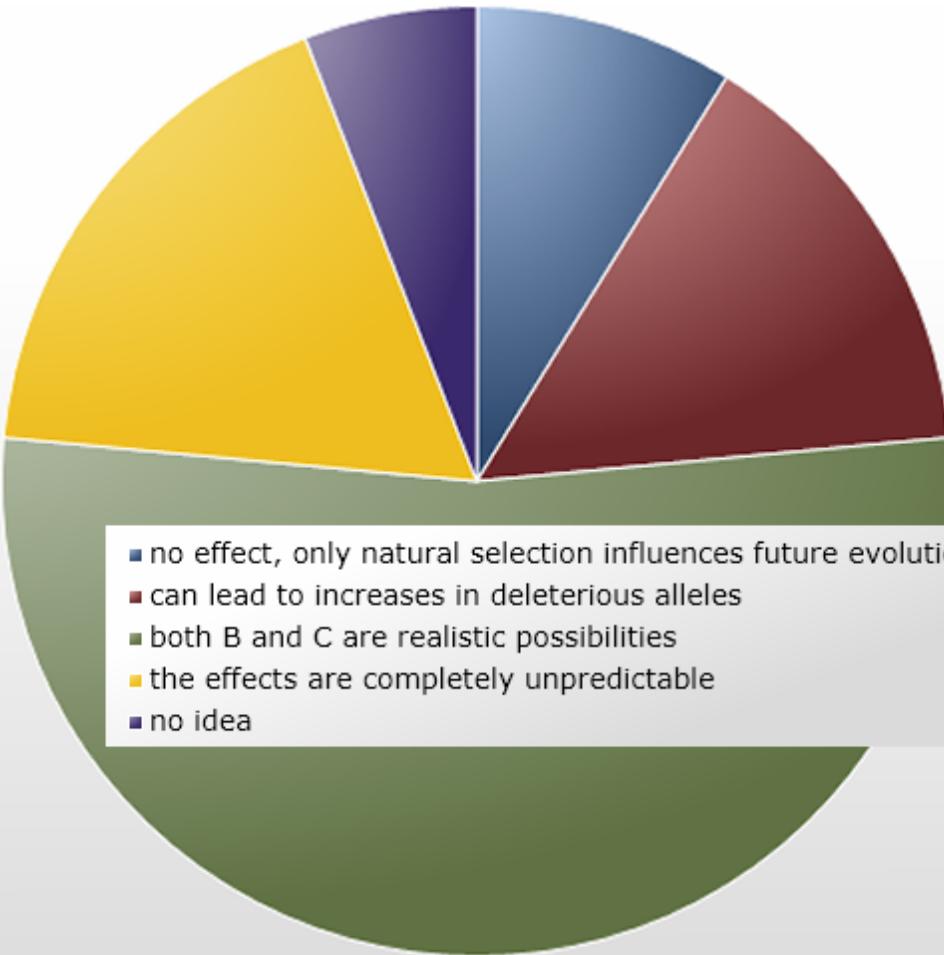
- harmful
- beneficial
- essential
- inessential
- random
- always the same

exp



Which ones are wrong and why?

How can the size of a population influence a population's future evolution?



**Explain** the logic of your answer

What types of behaviors define a stochastic event?

Is the outcome of all stochastic events  
theoretically unknowable?

## **Questions to answer:**

32. What happens if a sample of a population is not random, how does that influence one's conclusions about the behavior of the larger population?
33. How does the extinction of one type of organism influence the evolution of others?
34. What factors make a bottleneck different from a founder effect?
35. How can a founder effect/bottleneck lead to deleterious alleles becoming more frequent in a population? How does that impact future evolution?

## **Questions to answer:**

36. How does natural selection influence the effects of genetic drift and vice versa?
37. Describe the relative effects of selection and drift following a bottleneck.
38. How is it that drift (the probability of allele loss) can be accurately quantified, but is unpredictable in any particular population?

## **Questions to ponder:**

Does passing through a bottleneck improve or hamper a population's chances for evolutionary success?