BNS2002: Model (and non-model) species

Your first task in this session is to look at a few of the species we have in the lab and identify an interesting evolutionary/developmental/physiological question that you could investigate with them. You could consider behavioural traits as well, but you may not have much time to watch the animals and get a good feel for their behaviour.

Some things you may like to consider could include:

Physical characteristics

- How big do they get?
- How active are they?
- Do they have distinct sexes, and are they easy to identify?
- What is the generation time? How about time to puberty/breeding?
- Are they delicate or robust?

Care

- What are their temperature or humidity requirements? Do they need seasonal changes in light or temperature?
- Can they be kept on their own, or only in groups?
- How much (and what) do they eat/drink, and how often?
- What size cage do they need?
- What cage decor do they need? Is it easily available, and can it be sterilised? Can uniform decor be provided to minimise experimental variation?
- Are they dangerous? Is it possible to develop an allergy towards them?
- How expensive are they to keep in large numbers?

Resources

- Is there much past research to build on?
- Is there a genome sequence, or genetic resources?
- Are there lab stocks available, or are they wild-caught?

Legal/ethical issues

- Are there any social, legal or ethical issues associated with their use?

Organism	**Interesting biological question** (could be evolutionary, developmental, or physiological)	**Feasibility**

BNS2002: Selection and drift simulations

Your second task will be to simulate some evolutionary processes. Natural selection driving adaptive changes is a powerful and intuitive explanation for the diversity we see in the natural world. Evolution at the molecular level however is typically governed by random genetic drift.

You will be working in groups of 4, and need to assign the following tasks:

1. Note taker
2. Dice roller
3. Token selector
4. Results summariser

Our model is based on haploid individuals competing in pairs and in non-overlapping generations, so is a quite simplistic approach, but it should demonstrate some key evolutionary processes.

Materials:

60 tokens - 20 x yellow, 40 x blue
A six-sided die

Approach:

You have received tokens that represent haploid individuals in a natural population that presents genetic variability at a given locus. The token colours mark variability for a particular character, e.g. body colour. The following exercises will explore different aspects of the interplay of selection and random drift in maintaining and eliminating genetic variation in natural populations.

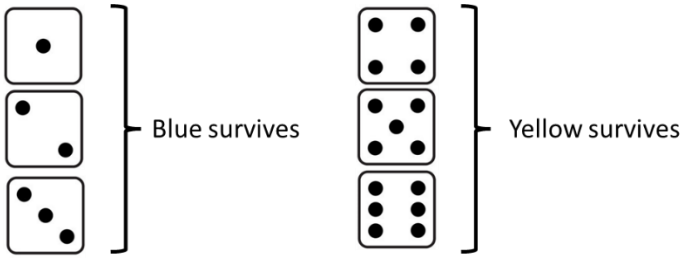
The simulations begin in the first generation after a point mutation arises in the population. The population inhabits an environment that has a **carrying capacity of ten individuals**, owing to resource limitation. At reproduction, individuals generate **two identical descendants** and die immediately (this is a very simplified model of asexual reproduction). Because the number of offspring produced at reproduction is larger than the carrying capacity of the environment, competition will occur. **Only ten individuals will survive.** You will determine the survivors to find the next generation by rolling the die according to the instructions in each exercise.

Exercise 1 – no selection

A point mutation has produced a colour change, and your starting population currently consists of 1 yellow individual and 9 blue individuals. Each individual produces two identical offspring and then dies. You therefore now have 2 yellow individuals and 18 blue ones. Place these individuals in the cup and give them a bit of a shake.

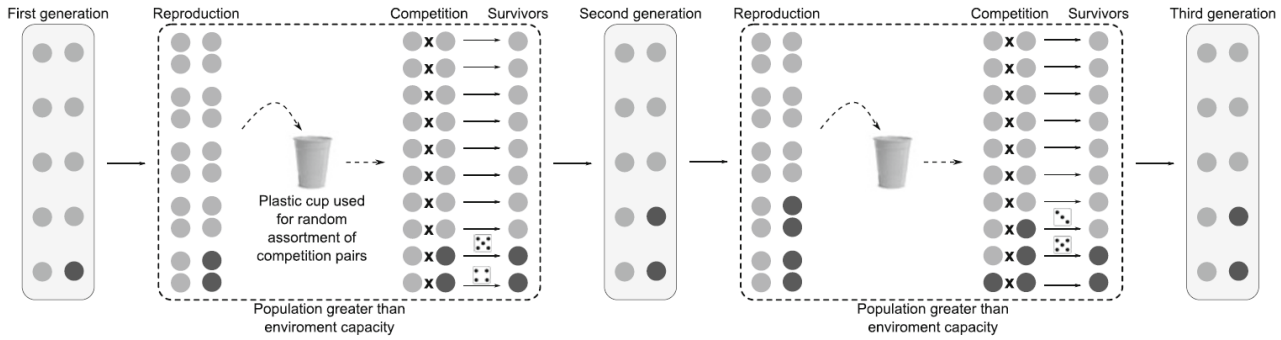
Imagine that blue and yellow are markers for body colour but the population lives in a completely dark cave so there no selective advantage to either colour. The allelic frequencies for this marker will increase and decrease purely by random genetic drift, i.e, blue and yellow are neutral characteristics that confer equal survival probabilities.

Randomly select competing pairs (by taking two tokens at time) until all individuals are aligned for competition. Our habitat can only support ten individuals, so some of the offspring need to die. Roll the die for each pair, using the following rules to resolve blue vs yellow conflict:



[in the case of a blue vs blue or yellow vs yellow situation, just pick one of them to survive]

Only ten individuals should survive this process, and these will form the second generation. Each of these survivors will produce two identical offspring which will then compete to represent the third generation. Record the number of individuals of each colour that you observe in each generation until the tenth generation in the results table provided.

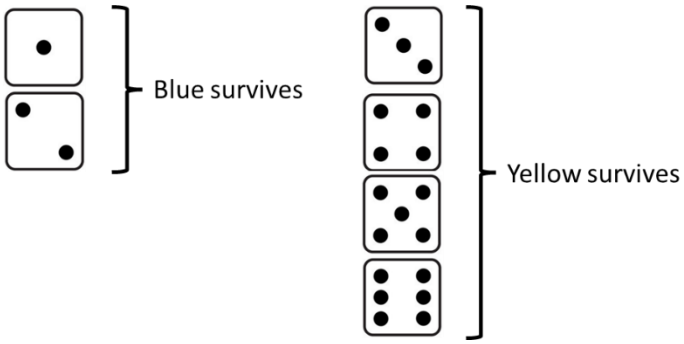


If one of the alleles is fixed (i.e., the other allele is eliminated); the die is no longer rolled. No more evolution will occur until mutation or migration creates variation at the locus again. In this case, the last results should be copied for all the subsequent generations until the tenth generation.

Exercise 2 – weak selection

In this simulation we will add the effect of natural selection, for example if there was small amount of dim light coming into the cave. Here, body colour will affect survival and competitive success.

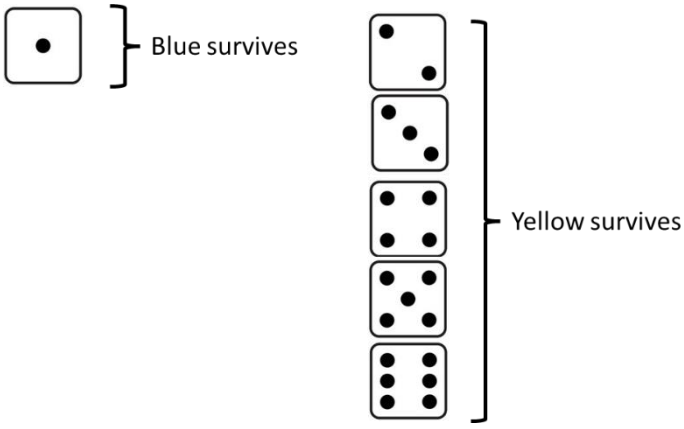
We will simulate natural selection pressure by changing the probabilities of survival of the colour variants in a competition event. In this simulation, if the die roll is 1 or 2, the blue wins the competition. If the roll is 3, 4, 5, or 6, the yellow wins



Even though the yellow variant has a selective advantage over the blue, it is possible for the blue to win several competition events. If this occurs, the evolutionary change was driven not by the directional selective pressure but by random genetic drift acting even on this adaptive scenario. Natural selection was at play, influencing but not determining the survival of variants. It is even possible that the advantageous yellow will be completely eliminated by genetic drift, although this outcome is more likely in the early generations because the frequency of the advantageous trait is initially small.

Exercise 3 – strong selection

In this third simulation, selection pressure will further increase, and body colour now determines higher chances of survival. If the die-roll result is 1, the blue wins, whereas if the result is 2, 3, 4, 5, or 6, the yellow wins the competition.



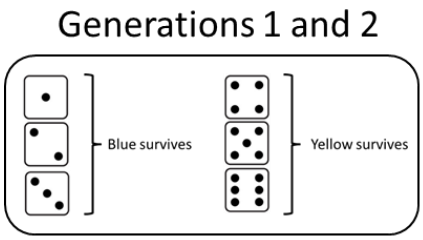
Here, the selective pressure is even stronger. Nevertheless, as before, selection does not determine the fate of the variants because random genetic drift is still at play. Notice how rapidly an advantageous allele becomes fixed. The resulting low genetic variability is expected in an adaptive scenario like this because natural selection tends to eliminate other, less adaptive alleles in only a few generations.

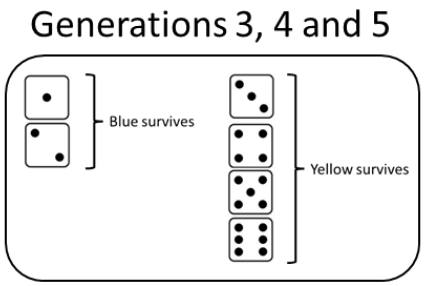
Exercise 4 – changing environment

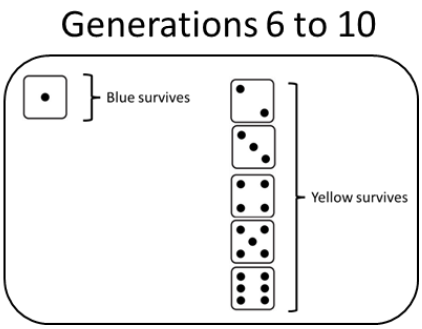
Let's imagine now that the environment is changing. At first, the population lives in a very dark cave, but light and visibility are increasing and produce an escalating advantage of one allele over another. In this simulation, a neutral yellow allele becomes more and more adaptive through the generations.

The first generation starts with nine blue individuals and one yellow mutant. At reproduction, each individual produces two identical offspring, and the carrying capacity of the environment remains at ten individuals.

In the first two generations, the cave is dark and selective pressure is absent (1-3 means blue survives and 4-6 means yellow survives). In generations. The brightness increases in the third, fourth, and fifth generations, and so does the selective advantage of the yellow (i.e., 1–2 means blue survives, 3–6 means yellow survives). From the sixth generation on, brightness increases even further, and selective pressure follows (i.e., 1 means blue survives, 2–6 means yellow survives).







Exercise 5 – difference in fertility

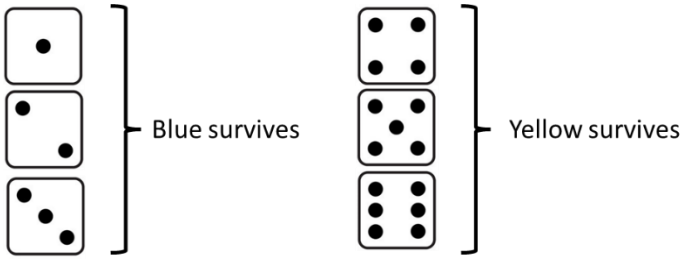
All of the previous simulations assumed that the variants produced the same number of offspring and that selective advantage was limited to competitive skills and success. But natural selection may act in different ways, such as fertility variation.

Here, the yellow individuals hold no competitive advantage over the blue variants. However:

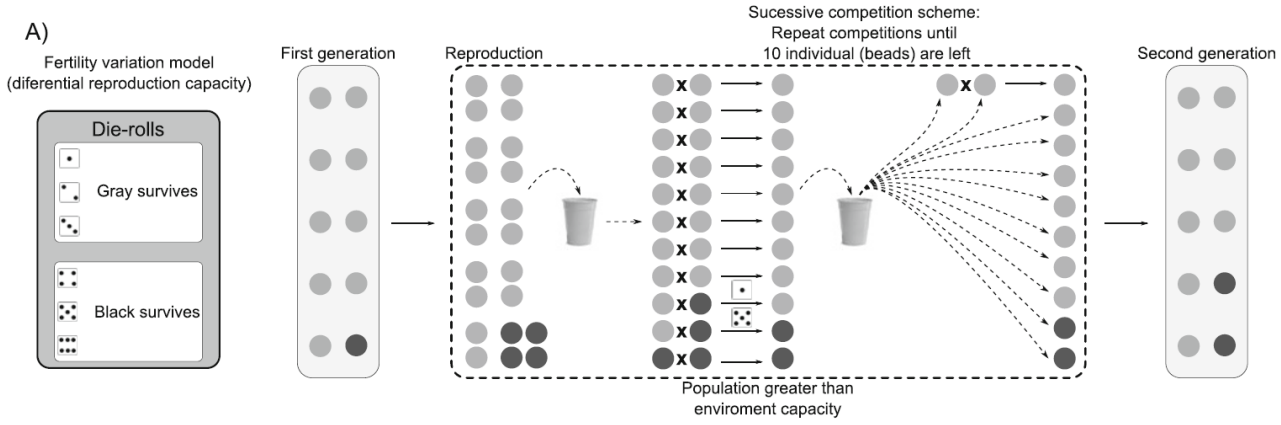
- yellow individuals **produce four descendants** during reproduction,
- blue individuals **produce two descendants**.

This difference illustrates another mode of selective advantage. One important aspect of the simulation is that the carrying capacity of the environment does not change, so that more than one round of competition will take place between generations. The fixed carrying capacity ensures that only ten individuals will survive and constitute the subsequent generation.

The die must be rolled if different-coloured individuals form a pair for competition. Neither variant enjoys a competitive advantage and if the result of the die roll is 1–3, the blue survives, whereas if it is 4–6, the yellow survives.



For example, if the single yellow individual in the first generation produced four yellow individuals and the nine blue individuals produced 18 blue offspring the total offspring count is 22. The first round of competition will reduce these 22 individuals to 11 individuals. From these 11 individuals, one pair must be randomly chosen from the cup to compete again. The second round of competition will produce ten survivors. These survivors will establish the second generation, and the process will continue until the tenth generation.



BNS2002: Selection and drift simulation results table:

	Exercise 1		Exercise 2		Exercise 3		Exercise 4		Exercise 5	
	No selection		**Weak selection**		**Strong selection**		**Changing environment**		**Difference in fertility**	
Generation	Blue	Yellow	Blue	Yellow	Blue	Yellow	Blue	Yellow	Blue	Yellow
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										

BNS2002: Sensory genetics

Perception of odours relies on olfactory sensory neurons, which detect and recognise chemicals on the basis of their shape. Presence or absence of these olfactory receptors therefore determines whether we can perceive a particular chemical or not. Humans have many hundreds of olfactory receptor genes, each of which encodes a different receptor that detects one or a few related chemicals and therefore mutations and natural variation mean that it is very likely that we all perceive our environment in slightly different ways. For those mammals which rely on pheromones for intraspecific communication, an inability to detect these chemicals can have important implications for their ability to find a mate or to defend a territory. For a nice overview of the genetic basis of variation in olfactory perception see Logan (2014).

The loss of an olfactory receptor via a mutation or genomic deletion can result in "anosmia", an inability to detect a particular odour. We will investigate the prevalence of two such anosmias in the latter part of this practical and in both cases the exact olfactory receptors and mutations responsible have been characterised. You will be provided with a small strip of filter paper dipped in the chemicals below, and asked to provide an assessment of whether you can smell anything. If you can, you'll then be asked to rate it as 'pleasant' or 'unpleasant'.

Androstenone

Around half the human population cannot detect androstenone, and the other half tend to be split between describing it as pleasant or sweet and urinous and musky. Androstenone is detected by olfactory receptor 7D4 (OR7D4) and there are two mutations known to affect function. Both of these mutations change only a single nucleotide (and are therefore single nucleotide polymorphisms, or SNPs) and cause a change in the resulting amino acid sequence:

R88W the 88th amino acid is changed from arginine (R) to tryptophan (W)
T133M the 133rd amino acid is changed from threonine (T) to methionine (M)

Humans with RT/WM or WM/WM genotypes are less sensitive to androstenone and find the odour less unpleasant than those with the RT/RT genotype (Keller et al. 2007).

β-Ionone

Ability to detect β-Ionone is bimodally distributed in human populations. Whilst the genetic basis underlying an ability to detect androstenone is slightly complicated, a single mutation in a single olfactory receptor (OR5A1) is sufficient to explain 96% of observed phenotypic variation in humans (Jaeger et al. 2013):

N183D the 183rd amino acid is changed from asparagine (N) to aspartic acid (D)

Let's assume that only individuals with a DD genotype can't detect β-Ionone, whilst homozygous NN and heterozygous ND individuals can (and do not differ in their sensitivity).

If in our class of around 300 students, we get the following result:

Detect β-Ionone (NN or ND)	240
Can't detect β-Ionone (DD)	60

Then we know that the frequency of DD is 60/300 = 0.2
If DD is taken to be q^2, then we know that the frequency of q (D) in the population = 0.45

Since p + q = 1, then we now also known that p (N) = 0.55

If the class were in Hardy-Weinberg equilibrium and were allowed to mate (please don't do this), then we'd expect your offspring to have the following allele frequencies:

NN, detector	(p^2)	= 0.30
ND, detector	(2pq)	= 0.50
DD, non-detector	(q^2)	= 0.20

***

If RT/RT and RT/WM individuals are less sensitive to androstenone than WM/WM individuals, then we can do the same again.

If the class data are:

Detectors	150
Non-detectors	150

Then the frequency of p^2 (detector, WM/WM) is 150/300 = 0.5 and the value of p = 0.71

The value for q must therefore be 0.29 and the frequencies of the next generation would be:

WM/WM, detector	(p^2)	= 0.50
RT/WM, detector	(2pq)	= 0.41
RT/RT, non-detector	(q^2)	= 0.08

There are tubes containing B-ionone and androstenone on your bench. Gently smell each tube.

You need to score intensity and pleasantness of each on the class date sheet. We'll work through some data calculations from previous years in the session.