

Solutions for Revision Questions

Question 1

Drawing on a historic dataset, we have managed to estimate the size of an annual native grass population at 10-year time intervals (albeit with some missing census data) as follows:

Year	N
1910	629
1940	734
1960	712
1970	840
1980	864
1990	986
2000	1232
2010	1012

- (a) What is the effective size of this population in 2010? Calculate N_e/N .
- (b) We subsequently uncovered data for 1930 ($N = 450$) and 1950 ($N = 819$). Recalculate the effective population size (and N_e/N) once these data are added into the mix.

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$$N_e \sim \frac{t}{\sum(\frac{1}{N_{ei}})}$$

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- (b) We subsequently uncovered data for 1930 ($N = 450$) and 1950 ($N = 819$). Recalculate the effective population size (and N_e/N) once these data are added into the mix.

Question 1

Drawing on a historic dataset, we have managed to estimate the size of an annual native grass population at 10-year time intervals (albeit with some missing census data) as follows:

Question 1(a)			Question 1(b)		
Year	N	1/N	Year	N	1/N
1910	629	0.001590	1910	629	0.001590
1940	734	0.001362	1930	450	0.002222
1960	712	0.001404	1940	734	0.001362
1970	840	0.001190	1950	819	0.001221
1980	864	0.001157	1960	712	0.001404
1990	986	0.001014	1970	840	0.001190
2000	1232	0.000812	1980	864	0.001157
2010	1012	0.000988	1990	986	0.001014
			2000	1232	0.000812
			2010	1012	0.000988
Sum:		0.009518			0.01296
1/Sum:		840.46			771.49

(a) $N_e = 840.46$ $N_e/N = 840.46/1012 = 0.830$

(b) $N_e = 771.49$ $N_e/N = 771.49/1012 = 0.762$

Question 2

We know (full well) that the northern elephant seal experienced a bottleneck of 20 individuals in the late 19th century, and has now recovered to around 175,000. As we have worked through in lectures and tutes, assuming a population of ~175,000 individuals prior to the bottleneck gives us a projection for the current effective population of ~60 individuals.

- (a) Calculate effective population size if we knew that the seal population was 1 million prior to the bottleneck (i.e., using $N_{e(1)} = 1,000,000$).
- (b) Now say that in the bottleneck generation we knew that ten females bred with only two of the available males (i.e. with two 'harem-masters'). Adjust your estimate for N_e accordingly (still using 175,000 for the first and third censuses).

Question 2(a)

- (a) Calculate effective population size if we knew that the seal population was 1 million prior to the bottleneck (i.e., using $N_{e(1)} = 1,000,000$).

$$N_e \sim \frac{t}{\sum \left(\frac{1}{N_{ei}} \right)}$$

Question 2(a)

- (a) Calculate effective population size if we knew that the seal population was 1 million prior to the bottleneck (i.e., using $N_{e(1)} = 1,000,000$).

$$N_e \sim \frac{t}{\sum(\frac{1}{N_{ei}})}$$

Ne = 60

It is still ~ 60 . This shows how when calculated this way, effective population size is most influenced by how small the population was during a bottleneck event.

Question 2(b)

- (b) Now say that in the bottleneck generation we knew that ten females bred with only two of the available males (i.e. with two ‘harem-masters’). Adjust your estimate for N_e accordingly (still using 175,000 for the first and third censuses).

$$N_e \sim \frac{t}{\sum \left(\frac{1}{N_{ei}} \right)}$$

$$N_e \sim \frac{4N_{ef} \times N_{em}}{N_{ef} + N_{em}}$$

Question 2(b)

- (b) Now say that in the bottleneck generation we knew that ten females bred with only two of the available males (i.e. with two 'harem-masters'). Adjust your estimate for N_e accordingly (still using 175,000 for the first and third censuses).

We first need to adjust our estimate of N_e for the bottleneck generation using the formula for effective number of breeders, i.e.:

$$N_e \sim \frac{4N_{ef} \times N_{em}}{N_{ef} + N_{em}} = \frac{4 \times 10 \times 2}{10 + 2} = \frac{80}{12} = 6.667$$

(Which is obviously reduced from 20). Now re-calculate N_e using the demographic formula, i.e.:

$$N_e = \frac{t}{\sum(\frac{1}{N_{ei}})} = \frac{3}{\frac{1}{175,000} + \frac{1}{6.667} + \frac{1}{175,000}} = 20$$

Question 3

Question 3.

Smurfs have become so threatened in the wild that they now only exist as a small captive population of 40 males and 40 females (i.e. $N = 80$). They are clearly not adaptively favoured in the wild by being blue...

- (a) Say we paired males with females to create 40 families. Use the formula for the effective number of breeding male and female smurfs to calculate the effective size of the breeding generation (i.e., N_e).
- (b) Now say that we didn't have control over the matings, but via later molecular work could determine all females mated with only 18 males (i.e., 22 males missed out!). Using the same approach as above, what would you then estimate for the effective population size of the breeding generation?

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- (a) Say we paired males with females to create 40 families. Use the formula for the effective number of breeding male and female smurfs to calculate the effective size of the breeding generation (i.e., N_e).

Effective population size is calculated using $N_{ef} = 40$ and $N_{em} = 40$ according to:

$$N_e \sim \frac{4N_{ef} \times N_{em}}{N_{ef} + N_{em}} = \frac{4 \times 40 \times 40}{40 + 40} = \frac{6400}{80} = 80$$

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In this case, we calculate effective population size using $N_{ef} = 40$ and $N_{em} = 18$, i.e.:

$$N_e \sim \frac{4N_{ef} \times N_{em}}{N_{ef} + N_{em}} = \frac{4 \times 40 \times 18}{40 + 18} = \frac{2880}{58} = 49.65$$

Note: It is lower in the second case because we would lose the genetic variation contained in the 22 males that didn't get to breed.

Question 4

In the smurf example (above), say that all 40 females and 40 males contributed to a generation of $N = 96$ smurfllets. We are also able to calculate the variance in smurfllet family size, which is 3.16.

- (a) What is the mean family size in this case?
- (b) What is the effective size of the breeding population?
- (c) If you had been able control the variance in offspring number among the 40 families, what value would give you maximum N_e ?
- (d) What is maximum N_e in this case?

Question 4

In the smurf example (above), say that all 40 females and 40 males contributed to a generation of $N = 96$ smurfllets. We are also able to calculate the variance in smurfllet family size, which is 3.16.

- (a) What is the mean family size in this case?

Mean family size is simply 96 offspring/40 families = **2.4** offspring

Question 4

In the smurf example (above), say that all 40 females and 40 males contributed to a generation of $N = 96$ smurfllets. We are also able to calculate the variance in smurfllet family size, which is 3.16.

- (b) Calculate the effective population size of the parental generation

Because they are monogamous, we assume that there are the same amount of males as females. Effective population size in this case would be best calculated using the formula for family size variation, according to:

$$N_e \sim \frac{4N}{Vk + 2} = \frac{4 \times 80}{3.16 + 2} = \frac{320}{5.16} = 62$$

Question 4

In the smurf example (above), say that all 40 females and 40 males contributed to a generation of $N = 96$ smurfllets. We are also able to calculate the variance in smurfllet family size, which is 3.16.

- (c) If you had been able control the variance in offspring number among the 40 families, what value would give you maximum N_e ?

$V_k = 0$, that is, equal family size. The answer to this question is always zero – because this ensures equal representation of the genes of each family in the population.

- (d) What is maximum N_e in this case?

Maximum N_e , which occurs when $V_k = 0$, is twice the observed number of individuals, that is, $2 \times 80 = 160$. You can confirm this by plugging $V_k = 0$ into the formula:

$$N_e \sim \frac{4N}{V_k + 2} = \frac{4 \times 80}{0 + 2} = \frac{320}{2} = 160$$

Note: This occurs because (by equalising family size) we retain twice the amount of genetic variance as would be retained under random processes (that is, in the idealized population). Remember that the idealized population has a variation in family size of 2 (See Frankham et al. pp247).

Question 5

As we know, the “white tiger” phenotype was originally obtained by mating a daughter with her father.

- (a) What is the inbreeding co-efficient (F) for such an individual?
- (b) Use this value to estimate the percentage of original genetic variation remaining after the father-daughter mating.

Question 5

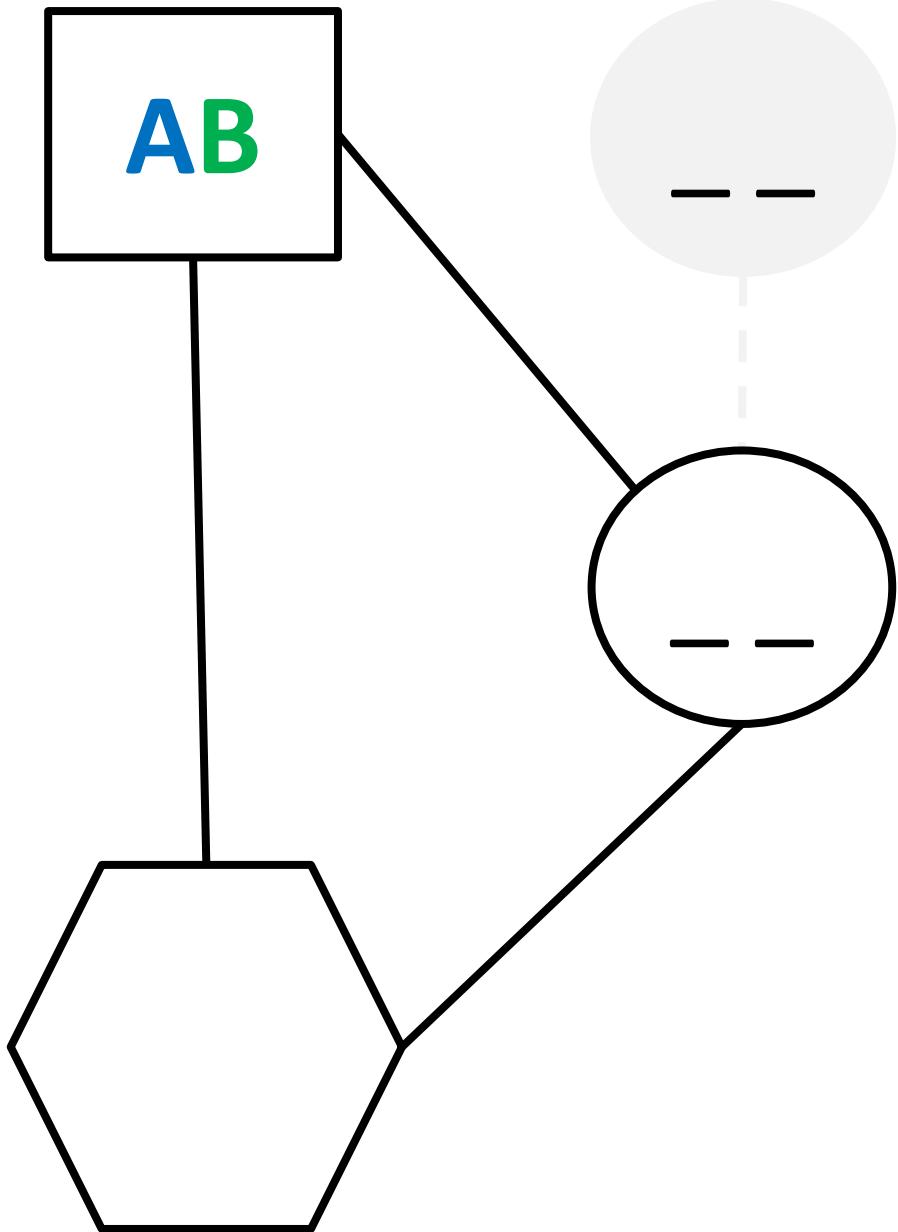
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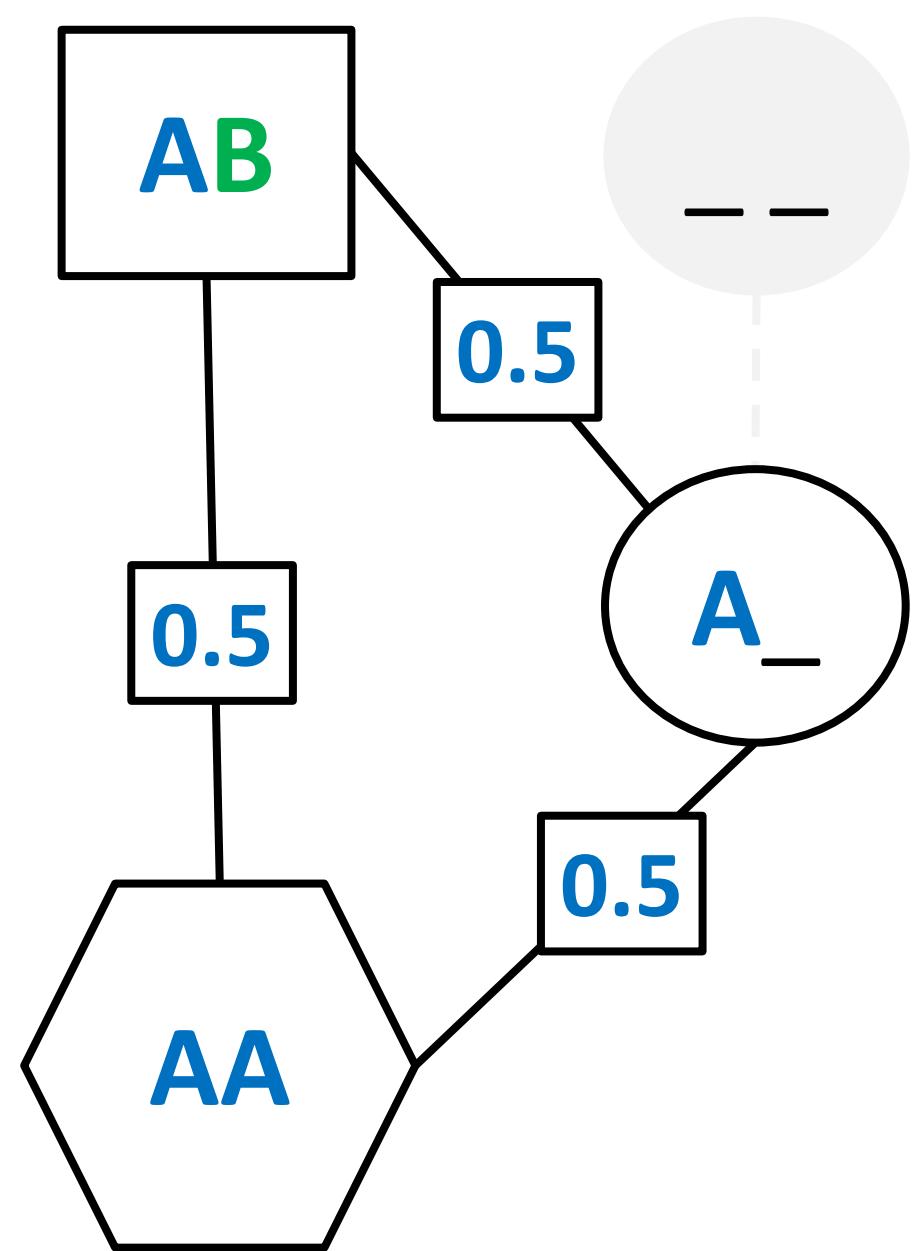
- (a) What is the inbreeding co-efficient (F) for such an individual?

F is the prob of getting two copies of the same gene through descent...

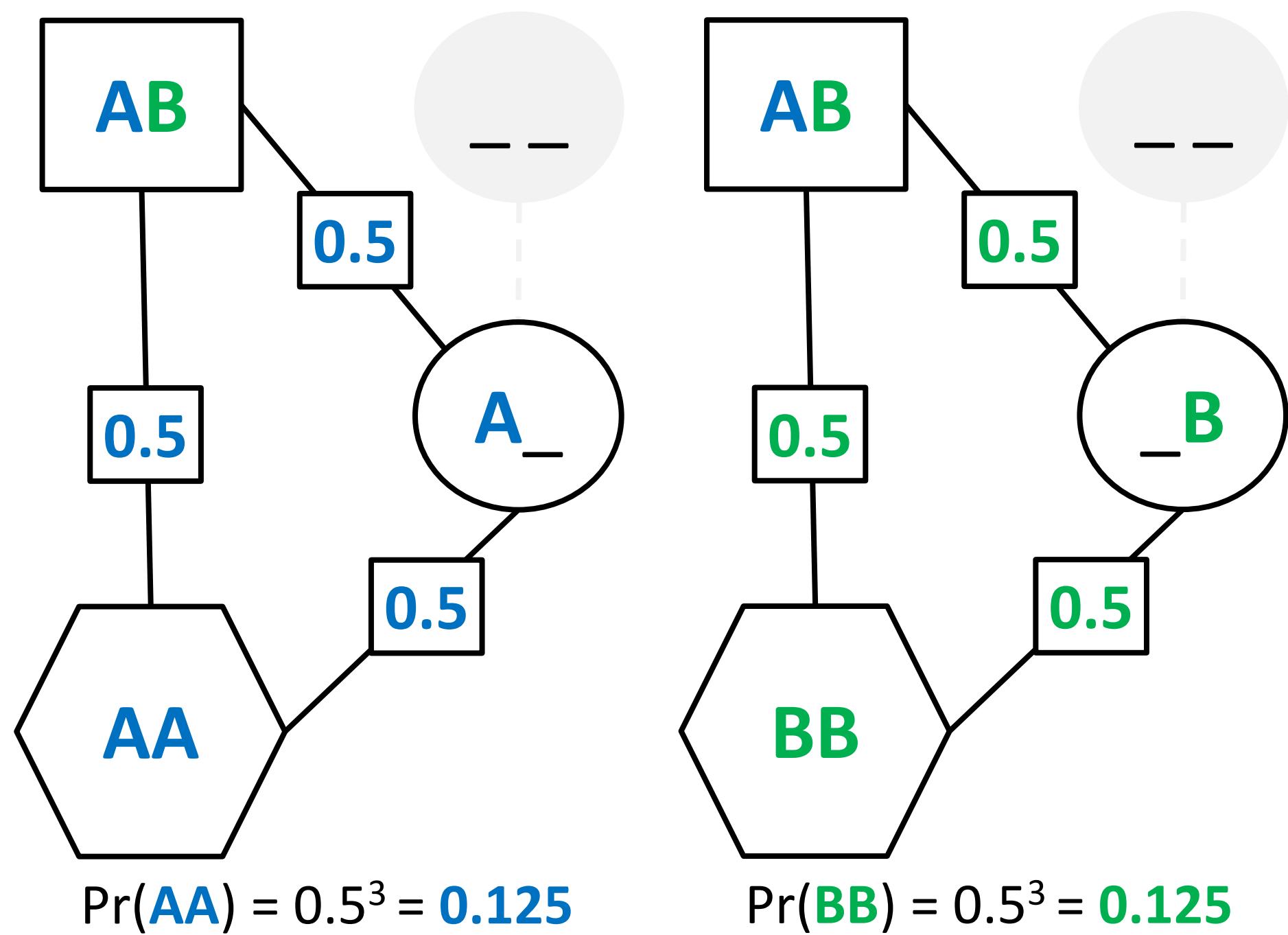
F is the prob of
getting two copies
of the same gene
through descent...

Either AA or BB





$$\Pr(\text{AA}) = 0.5^3 = 0.125$$



AB

AB

$$\begin{aligned}F &= \Pr(\text{AA}) \text{ or } \Pr(\text{BB}) \\&= 0.125 + 0.125 \\&= 0.25\end{aligned}$$

AA

BB

$$\Pr(\text{AA}) = 0.5^3 = 0.125$$

$$\Pr(\text{BB}) = 0.5^3 = 0.125$$

Question 5(b)

As we know, the “white tiger” phenotype was originally obtained by mating a daughter with her father.

- (b) Use this value to estimate the percentage of original genetic variation remaining after the father-daughter mating.

What proportion of the original genetic variation remains in the white tiger genome? Here, given that you know F and that there is one generation, you can calculate H_1/H_0 , according to:

$$F = 1 - \frac{H_t}{H_0}$$

Which re-arranges to:

$$\frac{H_t}{H_0} = 1 - F$$

So, $H_1/H_0 = 1 - 0.25 = 0.75$. So, 75 % of the original genetic variance remains.

Question 6

Having graduated as a conservation biologist, you are called in to a wildlife sanctuary to manage a captive population of 376 F1 bilbies (188 males & 188 females). They are derived from an initial sample of 216 presumably un-related individuals (of unknown gender and sex ratio) sampled from the wild.

- (a) Using the demographic information provided here, estimate the effective size of your F1 population.
- (b) Given this value for N_e for the F1s, what would you predict as the inbreeding co-efficient for your captive population following 6-generations of random mating?
- (c) What proportion of the F1 genetic variation would then remain?

Question 6(a)

Having graduated as a conservation biologist, you are called in to a wildlife sanctuary to manage a captive population of 376 F1 bilbies (188 males & 188 females). They are derived from an initial sample of 216 presumably un-related individuals (of unknown gender and sex ratio) sampled from the wild.

- (a) Using the demographic information provided here, estimate the effective size of your F1 population.

All we know here is N in the original sample (216) and N now (376). Our best and only way to estimate N_e in the F1s is to use the demographic formula for change in N over time:

$$N_e \sim \frac{t}{\sum(\frac{1}{N_{ei}})} = \frac{2}{\frac{1}{216} + \frac{1}{376}} = 274.4$$

Question 6(b)

Having graduated as a conservation biologist, you are called in to a wildlife sanctuary to manage a captive population of 376 F1 bilbies (188 males & 188 females). They are derived from an initial sample of 216 presumably un-related individuals (of unknown gender and sex ratio) sampled from the wild.

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To calculate the inbreeding co-efficient after $t = 6$, we use:

$$F = 1 - \left(1 - \frac{1}{2N_e}\right)^t = 1 - \left(1 - \frac{1}{2 \times 274.4}\right)^6 = 1 - (0.99818)^6 = 0.0109$$

Question 6(c)

Having graduated as a conservation biologist, you are called in to a wildlife sanctuary to manage a captive population of 376 F1 bilbies (188 males & 188 females). They are derived from an initial sample of 216 presumably un-related individuals (of unknown gender and sex ratio) sampled from the wild.

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- (c) What proportion of the F1 genetic variation would then remain?

As in the last question, we can use:

$$\frac{H_t}{H_0} = 1 - F = 1 - 0.0109 = \textcolor{red}{0.9891}$$

Question 7

The managers at this sanctuary then decided to establish another captive colony of bilbies, and sampled 62 pregnant females from a large outbred population.

- (a) If you only have the resources to handle an F1 population of 186 individuals, what average family size would you ideally aim for?
- (b) If you could perfectly equalize family size, use the family size-based demographic formula to estimate N_e in the F0 generation.

Question 7

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- (a) If you only have the resources to handle an F1 population of 186 individuals, what average family size would you ideally aim for?

We should aim for equal family size:

$$186 \text{ individuals} / 62 \text{ females} = 3 \text{ offspring from each female}$$

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- (a) If you only have the resources to handle an F1 population of 186 individuals, what average family size would you ideally aim for?
- (b) If you could perfectly equalize family size, use the family size-based demographic formula to estimate N_e

N.B. For the variance if family size formula, we use the parental population size as N

$$N_e = 4N / (V_k + 2)$$

$$= (4 \times (62 \times 2)) / 2$$

$$= 496 / 2$$

$$= \mathbf{248}$$

Question 8

If you randomly sampled 864 individuals from a large idealized population of hermaphroditic turbellarians, can you estimate the value of N_e for this sample?

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If you randomly sampled 864 individuals from a large idealized population of hermaphroditic turbellarians, can you estimate the value of N_e for this sample?

In a large idealized population $N = N_e$

Mean family size = 2
....and variance (V_k) = 2

$$N_e \sim \frac{4N}{V_k + 2} = \frac{4 \times 864}{4} = 864$$

Question 8

If you randomly sampled 864 individuals from a large idealized population of hermaphroditic turbellarians, can you estimate the value of N_e for this sample?

Or...

In a hermaphroditic population:

No of males = No of females = $\frac{1}{2} N$

$$N_e \sim \frac{4N_{ef} \times N_{em}}{N_{ef} + N_{em}}$$

$$\begin{aligned} N_e &= (4 \times 432 \times 432) / (432 + 432) \\ &= 746\,496 / 864 \\ &= 864 \end{aligned}$$

Question 9

Question 9.

Next year (2017) you're called in to manage an isolated population of Banksias. By analysing microsatellite variation you determine the heterozygosity of this population as 0.690. Everything is going well, but a devastating bushfire causes the population to completely regenerate in 2018, and then again in 2019 (the incidence of fire is on the rise...).

- (a) A molecular census of the population in 2019 using the same microsatellite loci indicates a heterozygosity value of 0.683. Use these data to calculate N_e .
- (b) In the process, you find two completely differentiated haplotypes and conclude that there are actually two different Banksia species (i.e., "cryptic species"). You now divide your 2019 Banksia population into **Species A** ($H = 0.231$) and **Species B** ($H = 0.432$). Going back to your 2017 data allows you to estimate H for each species as 0.243 and 0.437, respectively. Calculate N_e for each species.
- (c) Use the change in H over these generations to estimate the inbreeding coefficient for each haplotype.

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- (a) A molecular census of the population in 2019 using the same microsatellite loci indicates a heterozygosity value of 0.683. Use these data to calculate N_e .

N.B. See appendix at end of slides to see how to rearrange formulae.

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- (a) A molecular census of the population in 2019 using the same microsatellite loci indicates a heterozygosity value of 0.683. Use these data to calculate N_e .

Here we use $t = 2$ (for 2 generations), $H_0 = 0.690$ and $H_t = 0.683$.

We use 2 generations because the Banksia population has regenerated completely twice, which basically means there have been 2 discrete generations since what we started with. The full working is:

$$N_e = \frac{1}{2 \left(1 - \sqrt[t]{\frac{H_t}{H_0}} \right)}$$

$$N_e = \frac{1}{2 \left(1 - \sqrt[2]{\frac{0.683}{0.690}} \right)} = 98.32$$

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	Species A	Species B
H_0	0.243	0.437
H_2	0.231	0.432
	$N_e = \frac{1}{2(1 - \sqrt[2]{\frac{0.231}{0.243}})} = 19.996$	$N_e = \frac{1}{2(1 - \sqrt[2]{\frac{0.432}{0.437}})} = 87.149$

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Next year (2017) you're called in to manage an isolated population of Banksias. By analysing microsatellite variation you determine the heterozygosity of this population as 0.690. Everything is going well, but a devastating bushfire causes the population to completely regenerate in 2018, and then again in 2019 (the incidence of fire is on the rise...).

- (c) Use the change in H over these three generations to estimate the inbreeding coefficient for each.

$$F = 1 - \frac{H_t}{H_0}$$

	Species A	Species B
H_0	0.243	0.437
H_2	0.231	0.432
	$F = 1 - \frac{0.231}{0.243} = 0.04938$	$F = 1 - \frac{0.432}{0.437} = 0.01144$

Question 10

In the future, a small population of humans – let's hypothetically call them the Kardashians – are shipped off to live on another habitable planet in a very distant galaxy. The small effective population of 8 Kardashians has a low heterozygosity value of 0.232 to start with, perhaps due to a bottleneck in the past...

- (a) What would you estimate heterozygosity to be in 6 generations, should they survive that long?
- (b) What percentage of original H would therefore remain at this point?

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- (a) What would you estimate heterozygosity to be in 6 generations, should they survive that long?

Use $H_0 = 0.232$, $t = 6$ and $N_e = 8$.

$$\frac{H_t}{H_0} = \left(1 - \frac{1}{2N_e}\right)^t$$

$$\frac{H_t}{0.232} = \left(1 - \frac{1}{16}\right)^6$$

$$\frac{H_t}{0.232} = (1 - 0.0625)^6 = (0.9375)^6 = 0.6789$$

$$H_t = 0.6789 \times 0.232 = 0.1575$$

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- (a) What would you estimate heterozygosity to be in 6 generations, should they survive that long?
- (b) What percentage of original H would therefore remain at this point?

Heterozygosity has reduced from 0.232 to 0.1575.

This is $0.1575/0.232 = \textcolor{red}{0.6789}$ or **67.89 %** of the starting value.

Appendix

How to re-arrange formulae

(...just in case you ever wondered – Don't worry,
this won't be necessary for the problem test!)

Appendix

(a) If you have the formula $y = mx + c$, re-arranging to get x as a function of y is as follows:

$$y = 2x + 5$$

Step 1: subtract c from both sides of the equation:

$$2x = y - 5$$

Step 2: divide both sides of the equation by m :

$$x = \frac{y - 5}{2}$$

(b) If we have the formula $y = x^2$, what is x as a function of y ?

Rearranging to get x is simply: $x = \sqrt{y}$

Appendix

(c) Rearranging this formula $y = 1 + \frac{2}{x}$ to get x on one side:

The long way:

Step 1: subtract 1 from both sides of the equation:

$$y - 1 = \frac{2}{x}$$

Step 2: multiply both sides by x:

$$(y - 1)x = 2$$

Step 3: divide both sides by (y-1):

$$x = \frac{2}{y - 1}$$

Appendix

(d) To get from this $\left(1 - \frac{1}{2N_e}\right)^t = \frac{H_t}{H_0}$ to this: $N_e = \frac{1}{2\left(1 - \sqrt[t]{\frac{H_t}{H_0}}\right)}$

$$\left(1 - \frac{1}{2N_e}\right)^t = \frac{H_t}{H_0}$$

$$1 - \frac{1}{2N_e} = \sqrt[t]{\frac{H_t}{H_0}}$$

$$\frac{1}{2N_e} = 1 - \sqrt[t]{\frac{H_t}{H_0}}$$

$$N_e = \frac{1}{2\left(1 - \sqrt[t]{\frac{H_t}{H_0}}\right)}$$