

Cougar in Class Example (Type I Problem)

Pop 1

What is the frequency of the "L" allele in this population?
 (Imagine dropping all these letters into the same bucket!
 What is the frequency of the "l" allele in this population?
 What are the genotype frequencies?
 Actual freq of LL individuals =
 Actual freq of Ll individuals =
 Actual freq of ll individuals =

Next we will ask..Is this population in Hardy Weinberg Equilibrium? (Notice how I use the calculations below to answer this question.)

You answer this by calculating what you would **expect** the genotype frequencies to be. Imagine mixing around all those alleles that you just put in the bucket and pulling alleles out.

What is the chance of pulling out an L allele? = .5

What is the chance of pulling out another L allele? = .5

(imagine the population size is really large so you don't have to worry about replacement)

Go back to your middle school math class on probability...if you are interested in the chance of pulling out two "L" alleles, what do you do to calculate probability? You multiply!

You multiply the chance of pulling out one with the chance of pulling out the other!

So your chance of getting an "LL" individual is $.5 \times .5$ right? = $.25$ (p^2)

Lets do the same for your ll individual.

What is the chance of an "ll" individual?

It will also be $.5 \times .5$ right? = $.25$ (q^2)

Now lets work on those heterozygotes! (I have filled in some of this)

The chance of getting an "L" is .5, the chance of an "l" is .5 too.

So this would =.25 again for an "Ll" individual

BUT there are actually TWO ways of getting a heterozygote!

Biologists do not care about the ORDER of the two alleles. Both Ll and lL are in the category heterozygote so in addition to the Ll way we need to add the other way which is lL.

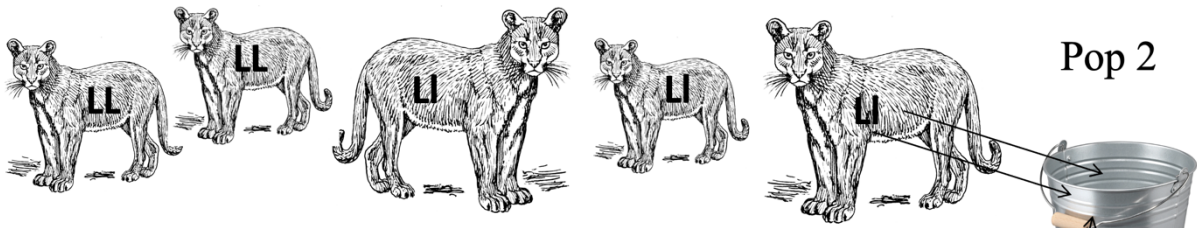
When we do this we find the chance of getting an lL individual is also .25

So we add these two ways ($.25 + .25$) to get $.5 = (2pq)$

⇒ So how do the actual and expected genotype frequencies compare? Is this population in HW? How close are the actual and expected frequencies? **THEY are the same so yes it is in HW!**

Now look at the population below and repeat the procedure from the following page!

Our question is the same-Is THIS population in HW????

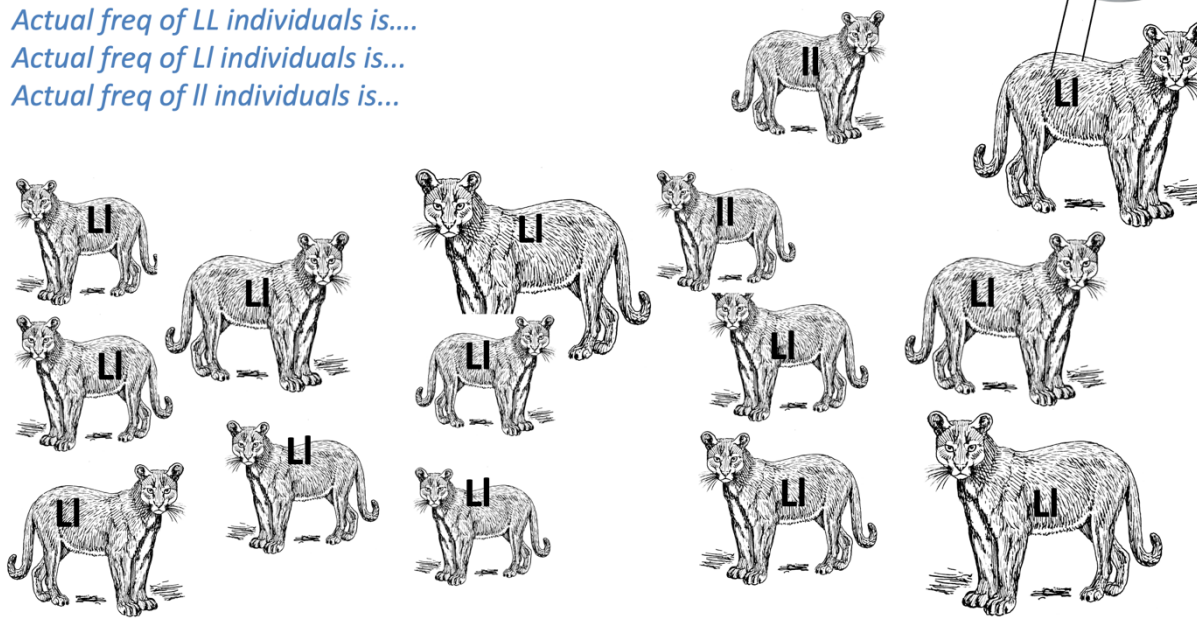


What are the actual genotype frequencies in this population?

Actual freq of LL individuals is...

Actual freq of LI individuals is...

Actual freq of II individuals is...



I counted LL genotype $2/20=.10$ LI= $16/20=.6$ II= $2/20=.10$ WOW INTERESTING!

16 L alleles from the heterozygotes + 4 L alleles from the homozygous LL individuals= $20/40$ (remember when there are 20 individuals there are 40 alleles)

Once a gain we have 16 "l" alleles from the heterozygote individuals and 4 from the II homozygotes for a total of 20 "l" alleles out of 40 in the population.

So Freq of L=.5

Freq of l=.5

It's the same!!

Now you calculate the **expected genotype** frequencies. (Remember to do that you need to throw all those alleles in a bucket first.)

Since the allele frequencies are the same as the previous problem, the expected genotype frequencies are also the same!! Now compare the actual with the expected!

I counted LL genotype $2/20=.10$ LI= $16/20=.6$ II= $2/20=.10$ WOW INTERESTING!

Expected LL= $(.5)^2=.25$ Expected LI= $2(.5)(.5)=.5$ Expected II= $(.5)^2=.25$

They seem pretty darn different. (In reality you would do a statistical test.)