CHI-SQUARE PRACTICE PROBLEMS

First, <u>write out</u> the H_O & H_A hypotheses for each problem. Then use X^2 to test if you reject the H_O or not. <u>SHOW ALL STEPS & ALL CALCULATION WORK</u>! Finally, <u>describe</u> what the results mean in words. Is there support for H_O or do you reject H_O in favor of supporting H_A?

(Two answers, just to see if you are doing it right, are at found at the end.)

1. A genetics engineer was attempting to cross a tiger and a cheetah. She predicted phenotypic outcome of the traits she was observing to be in the following ratio 4 stripes only : 3 spots only : 9 both stripes and spots. When the cross was performed and she counted the individuals she found 50 with stripes only, 41 with spots only and 85 with both. According to the Chi-square test, did she get the predicted outcome?

2. In the garden pea, yellow cotyledon color is dominant to green, and inflated pod shape is dominant to the constricted form. Considering both of these traits jointly in self-fertilized dihybrids, the progeny appeared in the following numbers:

> 193 green, inflated
> 184 yellow constricted
> 556 yellow, inflated
> 61 green, constricted

Do these genes assort independently? Support the answer using X^2 analysis.

3. A newly identified fruit fly mutant, cyclops eye (large and single in the middle of the head), is hypothesized to be autosomal dominant. The experimenter started with homozygous wild type females and homozygous cyclops males. The data from the F2 generation was 44 wild type males, 60 wild type females, 110 cyclops males and 150 cyclops females. Does this data support or reject the hypothesis? Use chi square to prove your position.

4. Another fictitious mutant, bloodshot eyes, is hypothesized to be autosomal recessive. Again the experimenter used homozygous wild type females but this time the males had homozygous blood shot eyes. The F2 data was 75 wild type males, 60 wild type females, 31 bloodshot males and 45 bloodshot females. Does this data support or reject the hypothesis? Use chi square to prove your position.

5. Still another imaginary trait, bristles-with-split-ends, is hypothesized to be X-linked dominant. As before, the P1 females were homozygous wild type however this time the males had bristles-with-split-ends. The F1 84 males were all wild type while the 90 females all had split-ends. In addition, the data for the F2 generation revealed 26 wild type males, 35 wild type females, 29 split-end males and 40 split-end females. Does this data support or reject the hypothesis? Use chi square to prove your position.

6. Finally, bow-legs is hypothesized to be X-linked recessive in Drosophila melanogaster. The P1 females were, once again, homozygous wild type but the males were bow-legged. There were 52 wild type males and 67 wild type females in the F1 generation. The F2 generation contained 30 wild type males, 75 wild type females, 40 bow-legged males and no bow-legged females. Does this data support or reject the hypothesis? Use chi square to prove your position.

SAMPLE SOLUTIONS

1. A genetics engineer was attempting to cross a tiger and a cheetah. She predicted phenotypic outcome of the traits she was observing to be in the following ratio 4 stripes only: 3 spots only: 9 both stripes and spots. When the cross was performed and she counted the individuals she found 50 with stripes only, 41 with spots only and 85 with both. According to the Chi-square test, did she get the predicted outcome?

H_0 = The phenotypic outcome of a cross between a tiger and a cheetah follows an expected ratio of 4 with stripes : 3 with spots : 9 with stripes and spots (The observed versus expected values are not significantly different)

H_A = The phenotypic outcome of a cross between a tiger and a cheetah does not follow the expected ratio of 4 with stripes : 3 with spots : 9 with stripes and spots (The observed versus expected values are significantly different)

Observed # = 50 w. stripes, 41 w. spots, 85 w. spots and stripes

The total number of offspring = 50 + 41 + 85 = 176

Expected # = (176 x 3/16 or 4/16 or 6/16) = 44 w. stripes, 33 w. spots, and 99 w.stripes & spots

$$X^2 = \sum (O-E)^2 / E$$

$$X^2 = ((50-44)^2 / 44) + ((41-33)^2 / 33) + ((85-99)^2 / 99)$$

$$X^2 = 0.82 + 1.94 + 1.98$$

$$X^2 = 4.74$$

DF = 3 (3 different characteristics spots, stripes, spots & stripes) – 1 = 2

Critical Value X^2 at p-value 0.05 (that the H_0 is correct and there is a 5% of seeing the deviation or an even greater deviation from the expected observed by chance) = 5.99

If your calculated X^2 is larger than the X^2 at p-value 0.05, reject the H_0 and accept the H_A. *(This means there is a less than 5% chance of seeing the deviation from expected you see by chance alone)*

If your calculated X^2 is smaller than the X^2 at p-value 0.05, fail to reject H_0. *(The deviation from expected could have occurred by chance).*

The calculated X^2 of 4.74 is smaller than 5.99 so we fail to reject H_0

The phenotypic outcome of a cross between a tiger and a cheetah follows the expected ratio of 4 stripes : 3 spots : 9 stripes and spots.

2. In the garden pea, yellow cotyledon color is dominant to green, and inflated pod shape is dominant to the constricted form. Considering both of these traits jointly in self-fertilized dihybrids, the progeny appeared in the following numbers:

<div align="center">
193 green, inflated
184 yellow constricted
556 yellow, inflated
61 green, constricted
</div>

Do these genes assort independently? Support the answer using X^2 analysis.

H_0 = The gene for cotyledon color and the gene for inflated pod shape assort independently. (The observed versus expected values are not significantly different)

H_A = The gene for cotyledon color and the gene for inflated pod shape do not assort independently. (The observed versus expected values are significantly different)

<u>Observed #</u> = 193 green - inflated, 184 yellow - constricted, 556 yellow - inflated, 61 green - constricted

The total number of offspring = 193 + 184 + 556 + 61 = 994

Two heterozygotes for two genes with two alleles and sorting independently should result in a 9:3:3:1 phenotypic ratio.

<u>Expected #</u> = [9 yellow – inflated (994 x 9/16) : 3 yellow – constricted (994 x 3/16) : 3 green – inflated (994 x 3/16) : 1 green – constricted (994 x 1/16] = 186.4 green - inflated, 186.4 yellow - constricted, 559.13 yellow - inflated, 62.1 green - constricted

$$X^2 = \sum (O-E)^2 / E$$

$$X^2 = ((193-186.38)^2 / 186.38) + ((184-186.38)^2 / 186.38) + ((556-559.13)^2 / 559.13) + ((61-62.13)^2 / 62.13)$$

$$X^2 = 0.234 + 0.030 + 0.017 + 0.021$$

$$X2 = 0.31$$

DF = 4 (4 different possibilities) – 1 = 3

Critical Value X^2 at p-value 0.05 (that the H_0 is correct and there is a 5% of seeing the deviation or an even greater deviation from the expected observed by chance) = 7.82

If your calculated X^2 is larger than the X^2 at p-value 0.05, reject the H_0 and accept the H_A. *(This means there is a less than 5% chance of seeing the deviation from expected you see by chance alone)*

If your calculated X^2 is smaller than the X^2 at p-value 0.05, fail to reject H_0. *(The deviation from expected could have occurred by chance).*

The calculated X^2 of 0.31 is smaller than 7.82 so we fail to reject H_0

The genes for cotyledon color and the gene for pod shape assort independently according to a 9:3:3:1 ratio.