(a) The usual Mendelian ratio for four phenotypes controlled by two independent genes after crosses of individuals heterozygous for both genes is 9:3:3:1. Interactions between genes can cause phenotypic ratios to be different. This sort of interaction is called epistasis.

Consider the following example with two genes. The genotype $A−$ is a short-hand notation for either $AA$ or $Aa$. Suppose that presence of an allele $A$ results in a black phenotype while presence of an allele $B$ in the absence of $A$ produces a gray phenotype. When both $A$ and $B$ are absent, the observed color is white.

The following table describes the probability distribution of genotypes and phenotypes for offspring from an $AaBb \times AaBb$ cross if the previous genetic description is true.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Phenotype</th>
<th>Probability</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A−B−$</td>
<td>black</td>
<td>9/16</td>
</tr>
<tr>
<td>$A−bb$</td>
<td>black</td>
<td>3/16</td>
</tr>
<tr>
<td>$aaB−$</td>
<td>gray</td>
<td>3/16</td>
</tr>
<tr>
<td>$aabb$</td>
<td>white</td>
<td>1/16</td>
</tr>
</tbody>
</table>

In an observed cross of two individuals believed to be of genotype $AaBb$, there are 200 offspring with the following observed counts: 160 black, 34 gray, and 6 white.

Test the hypothesis that the offspring probabilities for black, gray, and white are in a 12:3:1 ratio as predicted by the previous theory versus the alternative that they are different using a chi-square test for goodness-of-fit. State hypotheses, compute a test statistic, and use the chi-square table to find a range for the $p$-value. Interpret the results in the context of the problem.

Solution:

The null hypothesis is that the genetic model is accurate and that the probabilities of black, gray, and white are 12/16, 3/16, and 1/16, respectively. The alternative hypothesis is that the probabilities of these phenotypes are different.

With 200 offspring, the expected counts are 150, 37.5, and 12.5 respectively. The $\chi^2$ test statistic is 4.37 and there are two degrees of freedom. Using R, the $p$-value is 0.11. Using the tables, $0.10 < p < 0.20$.

There is little evidence that the probabilities of the colors of offspring differ from those predicted by the genetic 12:3:1 theory ($p > 0.10$, chi-square goodness-of-fit test).

It would be wrong to conclude that there is evidence that the genetic hypothesis is true. Statistical hypothesis testing can only measure evidence against a null hypothesis.

(b) In a different genetic experiment, offspring are either short or tall and green or yellow. Observed counts of 250 individuals are tabulated here.

<table>
<thead>
<tr>
<th>Height</th>
<th>Color</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Green</td>
</tr>
<tr>
<td>Tall</td>
<td>165</td>
</tr>
<tr>
<td>Short</td>
<td>50</td>
</tr>
</tbody>
</table>

Use a chi-square test to test if these two traits are independent of one another. State hypotheses, compute a test statistic, and use the chi-square table to find a range for the $p$-value. Interpret the results in the context of the problem.

Solution:

The null hypothesis is that the color is independent of height. The alternative hypothesis is that these traits are dependent.

The observed counts are 165, 50, 25, and 10 and the corresponding expected counts are 163.4, 51.6, 26.6, and 8.4. The $\chi^2$ test statistic is 0.47. There is one degree of freedom.

Using R, we can find the exact $p$-value to be 0.49. With the table, the $p$-value is greater than 0.2.

The data is consistent with the hypothesis that height and color are independent.
It is wrong to conclude that there is strong evidence in favor of independence. We just observe consistency with the hypothesis of independence.

It is interesting to note that the data is not consistent with an expected 9:3:3:1 ratio as would be expected with a simple two gene Mendelian model. The observed counts for the second and third categories are rather different from one another. One possible explanation is some sort of selection against individuals with the yellow phenotype. The observed ratio of 215:35 is far from the expected 3:1 ratio. However, this says nothing about the possible independence between the height and color.

(c) Let \( p_1 \) be the proportion of green individuals among tall plants and \( p_2 \) be the proportion of green individuals among short plants in the relevant populations for which these individuals are a representative sample. For the hypothesis test \( H_0 : p_1 = p_2 \) versus the alternative \( p_1 > p_2 \), the p-value from Fisher’s Exact Test is equal to the following probability. (Fill in the blanks with numbers and circle one option from each set.)

\[
\text{The probability of drawing 165 red balls \[ \text{OR MORE} \mid \text{OR FEWER} \mid \text{EXACTLY} \] from a bucket with }
\]
\[
\text{\[ \text{red balls and \[ \text{white balls when \[ \text{balls are drawn from the } \]
\]
\text{bucket at random \[ \text{WITH} \mid \text{WITHOUT} \] replacement.}}}
\]

Solution: There are two possible solutions depending on whether or not you treat the height or color as “color”. The solutions are either

The probability of drawing 165 red balls \textbf{or more} from a bucket with 215 red balls and 35 white balls when 190 balls are drawn from the bucket at random \textbf{without} replacement.

or

The probability of drawing 165 red balls \textbf{or more} from a bucket with 190 red balls and 60 white balls when 215 balls are drawn from the bucket at random \textbf{without} replacement.

Using R, the p-value is 0.312, by the way.