

**TABLE 10.5** Calculated Sample Sizes Per Treatment Group for Example 6 for Estimated Values of  $p_2$ , When the Hazard Ratio,  $h$ , Is 0.6 and  $\alpha = 0.01$  and  $\beta = 0.1$

$p_2$	$p_1 = 1 - \exp(h(\ln(1 - p_2)))$	$n = \left( \frac{4}{(p_1 + p_2)} \right) \left( \frac{(z_{1-\alpha/2} + z_{1-\beta})^2}{(\ln(h))^2} \right)$
0.3	$p_1 = 1 - \exp(0.6(\ln(1 - 0.3))) = 0.19$	$n = \left( \frac{4}{(0.3 + 0.19)} \right) \left( \frac{14.9}{(-0.511)^2} \right) = 465.81$
0.4	$p_1 = 1 - \exp(0.6(\ln(1 - 0.4))) = 0.26$	$n = \left( \frac{4}{(0.4 + 0.26)} \right) \left( \frac{14.9}{(-0.511)^2} \right) = 345.83$
0.5	$p_1 = 1 - \exp(0.6(\ln(1 - 0.5))) = 0.34$	$n = \left( \frac{4}{(0.5 + 0.34)} \right) \left( \frac{14.9}{(-0.511)^2} \right) = 271.72$
0.6	$p_1 = 1 - \exp(0.6(\ln(1 - 0.6))) = 0.42$	$n = \left( \frac{4}{(0.6 + 0.42)} \right) \left( \frac{14.9}{(-0.511)^2} \right) = 223.77$
0.7	$p_1 = 1 - \exp(0.6(\ln(1 - 0.7))) = 0.51$	$n = \left( \frac{4}{(0.7 + 0.51)} \right) \left( \frac{14.9}{(-0.511)^2} \right) = 188.63$

number of events stated in the Protocol appears reasonable based on the assumptions provided. It should be noted, however, that the number of subjects per treatment cannot be determined based on the information provided. The Protocol section only states the target hazard ratio of 0.6, but does not state the expected proportion of subjects experiencing progression-free survival occurring in either treatment group. Without this information, it is not possible to calculate the sample size per group. It is possible to estimate the required sample size by using a range of values for the expected proportion of subjects experiencing progression-free survival occurring in one of the two groups and using the relationship between the hazard ratio and the proportion of subjects experiencing progression-free survival for each of the two groups. This can be demonstrated as follows:

$$h = \frac{\ln(1 - p_1)}{\ln(1 - p_2)}$$

Solving for one of the necessary proportions, say  $p_1$ , we find that:

$$\begin{aligned} h(\ln(1 - p_2)) &= \ln(1 - p_1), \\ \exp(h(\ln(1 - p_2))) &= (1 - p_1), \\ p_1 &= 1 - \exp(h(\ln(1 - p_2))) \end{aligned}$$

Using various values of  $p_2$  and the specified value of the hazard ratio, we can estimate corresponding values of  $p_1$ , and then calculate the sample size per group. Using values of  $p_2$  ranging from 0.3 to 0.7 by 0.1, calculated sample sizes are presented in [Table 10.5](#).

Examining the values from [Table 10.5](#), it is clear that the proportion of subjects experiencing progression-free survival is an important assumption in setting the sample size for the given study. As such, this would be important information to include in the sample size section of the Protocol.

### XIII. BINARY VARIABLE: TESTING FOR EQUIVALENCE OF TWO PROPORTIONS

To this point, the sample size calculations have all corresponded to tests of superiority. By this, we want to assess whether the two treatments are different from one another. What if, however, we want to show that the two treatments are not different from one another? The objective of an equivalence trial is to provide evidence that the two treatments provide the same or nearly the same clinical