**Answer:**  
First, I created a contingency table with the counts (based on the % and n), and I oriented it in a way that can be used for R.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Alive** | **Dead** | **Total** |
| Blue | 129 | 7 | 136 |
| Gold | 46 | 9 | 55 |
| Red | 215 | 24 | 239 |

Then I used the following R code:

In R:

> library(epitools)

Warning message:

package ‘epitools’ was built under R version 3.1.3

> RRtable<-matrix(c(129,46,215,7,9,24),nrow = 3,ncol=2)

> RRtable  
 [,1] [,2]  
 [1,]  129    7  
 [2,]   46    9  
 [3,]   215   24

> riskratio.wald(RRtable)

$data

Outcome  
 Predictor  Disease1 Disease2 Total  
 Exposed1       129        7   136  
 Exposed2        46        9    55  
 Exposed3       215       24   239  
 Total          390       40   430

$measure  
 risk ratio with 95% C.I.  
 Predictor  estimate     lower     upper  
 Exposed1 1.000000         NA       NA  
 Exposed2 3.179221 1.2459233 8.112413  
 Exposed3 1.950986 0.8634262 4.408423

$p.value  
 two-sided

Predictor  midp.exact fisher.exact chi.square  
 Exposed1          NA           NA         NA  
 Exposed2 0.01892174   0.01869132 0.01128773  
 Exposed3 0.09763517   0.11937278 0.09795593

$correction  
[1] FALSE

attr(,"method")  
[1] "Unconditional MLE & normal approximation (Wald) CI"  
Warning message:  
In chisq.test(xx, correct = correction) :  
Chi-squared approximation may be incorrect

The error message from R indicates that the expected number of counts in one of the cells was less than 5, so I need to repeat the chi-square test using chi.test (RRrtable, correct=TRUE)

> chisq.test(RRtable, correct = TRUE)

       Pearson's Chi-squared test

data:  RRtable  
X-squared = 6.1886, df = 2, p-value = 0.04531

So, the differences in mortality are statistically significant (p=0.045), but it’s actually the Gold team that that has the highest mortality rate.