Problem 3.12

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2025-03-03

# Problem 3.12:

An experiment analyzes imperfection rates for two processes used to fabricate silicon wafers for computer chips. For treatment A applied to 10 wafers, the numbers of imperfections are 8, 7, 6, 6, 3, 4, 7, 2, 3, 4. The treatment B applied to 10 other wafers has 9, 9, 8, 14, 8, 13, 11, 5, 7, 6 imperfections. Treat the counts as independent Poisson variates having means μa and μb. Consider the model logμ = a + Bx, where x = 1 for treatment B and x = 0 for treatment A, for which B = log μb - logμa = log(μb/μa) and e^B = μb/μa.

## Part A

Here, we need to test our null hypothesis: which is μa = μb by conducting the Wald test of H0: B = 0. The alternative hypothesis would be that Ha: B != 0 which would imply that μa != μb. Our decision criteria would be Wald test statistic and p-value. If the Wald test statistic is decently large and the p-value is less than 0.05, then that would lead us to reject the null hypothesis. Otherwise, if the Wald test statistic is smaller and the p-value is large than 0.05, then we would be unable to reject H0.

## Wald Test statistic: 3.332442

## Wald Test p-value: 0.0008608747

What we find above the Wald test statistic is large (3.33) and the p-value is small (0.0086, which is less than 0.05). In conclusion, we can reject our null hypothesis (B = 0) which would lead us to our alternative hypothesis (B != 0). This would imply that there is a significant difference between the imperfections in treatment A and treatment B (μa != μb).

## Part B

For Part B, we need to construct a 95% confidence interval for μb/μa.

## 95% Confidence Interval for u\_B / u\_A: ( 1.273899 , 2.543373 )

What we find here is the 95% confidence interval for μb/μa is between 1.3 and 2.5. This means that the we are 95% confident that the ratio of imperfections between treatment B and treatment A is between 1.3 and 2.5.

## Code Appendix

#Code Appendix  
#Chad Huntebrinker  
#Problem 3.12  
  
#An experiment analyzes imperfection rates for two processes used to fabricate silicon wafers  
#for computer chips. For treatment A applied to 10 wafers, the numbers of imperfections are 8, 7,  
#6, 6, 3, 4, 7, 2, 3, 4. The treatment B applied to 10 other wafers has 9, 9, 8, 14, 8, 13, 11, 5,  
#7, 6 imperfections. Treat the counts as independent Poisson variates having means ua and ub.  
#Consider the model logu = a + Bx, where x = 1 for treatment B and x = 0 for treatment A, for which  
#B = log ub - logua = log(ub/ua) and e^B = ub/ua.  
  
#Part A  
#Setup treatment and x-value vectors  
treatment\_A <- c(8, 7, 6, 6, 3, 4, 7, 2, 3, 4)  
treatment\_B <- c(9, 9, 8, 14, 8, 13, 11, 5, 7, 6)  
  
x\_value\_A <- rep(0, length(treatment\_A))  
x\_value\_B <- rep(1, length(treatment\_B))  
both\_treatment <- c(treatment\_A, treatment\_B)  
both\_x <- c(x\_value\_A, x\_value\_B)  
  
#Fit the model using both treatments and the x-values for both treatments  
model\_1 <- glm(both\_treatment ~ both\_x, family = poisson(link = "log"))  
summary(model\_1)

##   
## Call:  
## glm(formula = both\_treatment ~ both\_x, family = poisson(link = "log"))  
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) 1.6094 0.1414 11.380 < 2e-16 \*\*\*  
## both\_x 0.5878 0.1764 3.332 0.000861 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for poisson family taken to be 1)  
##   
## Null deviance: 27.857 on 19 degrees of freedom  
## Residual deviance: 16.268 on 18 degrees of freedom  
## AIC: 94.349  
##   
## Number of Fisher Scoring iterations: 4

#Wald Test  
B\_hat <- coef(model\_1)[2]  
SE\_B\_hat <- summary(model\_1)$coefficients[2, 2]  
  
wald\_stat <- B\_hat / SE\_B\_hat  
p\_value <- 2 \* (1 - pnorm(abs(wald\_stat)))  
  
cat("Wald Test statistic: ", wald\_stat, "\n")

## Wald Test statistic: 3.332442

cat("Wald Test p-value: ", p\_value, "\n")

## Wald Test p-value: 0.0008608747

#Part B  
#Get the z-score for 0.95 (we use 0.975 because it's a two-tailed test)  
z\_score <- qnorm(0.975, mean = 0, sd = 1)  
  
#Confidence interval for B  
lower\_B <- B\_hat - z\_score \* SE\_B\_hat  
upper\_B <- B\_hat + z\_score \* SE\_B\_hat  
  
#Exponentiate to get the confidence interval for the ratio u\_B / u\_A  
lower\_ratio <- exp(lower\_B)  
upper\_ratio <- exp(upper\_B)  
  
#Print the confidence interval for u\_B / u\_A  
cat("95% Confidence Interval for u\_B / u\_A: (", lower\_ratio, ", ", upper\_ratio, ")\n")

## 95% Confidence Interval for u\_B / u\_A: ( 1.273899 , 2.543373 )