

# KJPipho\_PS\_5

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*September 30, 2018*

Question 1.

Are Ts in common and uncommon words equally perceptible? We will test this by assessing T finding while reading a passage.

a.  $H_0 : p(\text{Finding Ts in common words}) = p(\text{Finding Ts in uncommon words})$

If common words contain 28 out of the 94 Ts in the passage we would expect mistakes in common words to comprise 28/94ths of the total mistakes.

b. My results are as follows:

Ts found in common words: 15 Ts missed in common words: 13 Ts found in uncommon words: 53 Ts missed in uncommon words: 13

```
# Input my results into 'results'
results <- c(15,53,13,13)
# Format 'results' to have 2 rows and 2 columns
dim(results) = c(2,2)
results
```

```
##      [,1] [,2]
## [1,]   15   13
## [2,]   53   13
```

```
# Naming columns in 'results'
colnames(results) <- c("Correct", "Incorrect")
# Naming rows in 'results'
rownames(results) <- c("Common", "Uncommon")
# Making 'results' be of the type 'table'
results <- as.table(results)

# Performing chi square analysis on results and 'parking it' as results.chi
results.chi <- chisq.test(results)
# Print results of chi sq
results.chi
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data:  results
## X-squared = 5.7486, df = 1, p-value = 0.0165
```

```
print ("Observed")
```

```
## [1] "Observed"
```

```
results.chi$observed
```

```
##           Correct Incorrect
## Common      15          13
## Uncommon    53          13
```

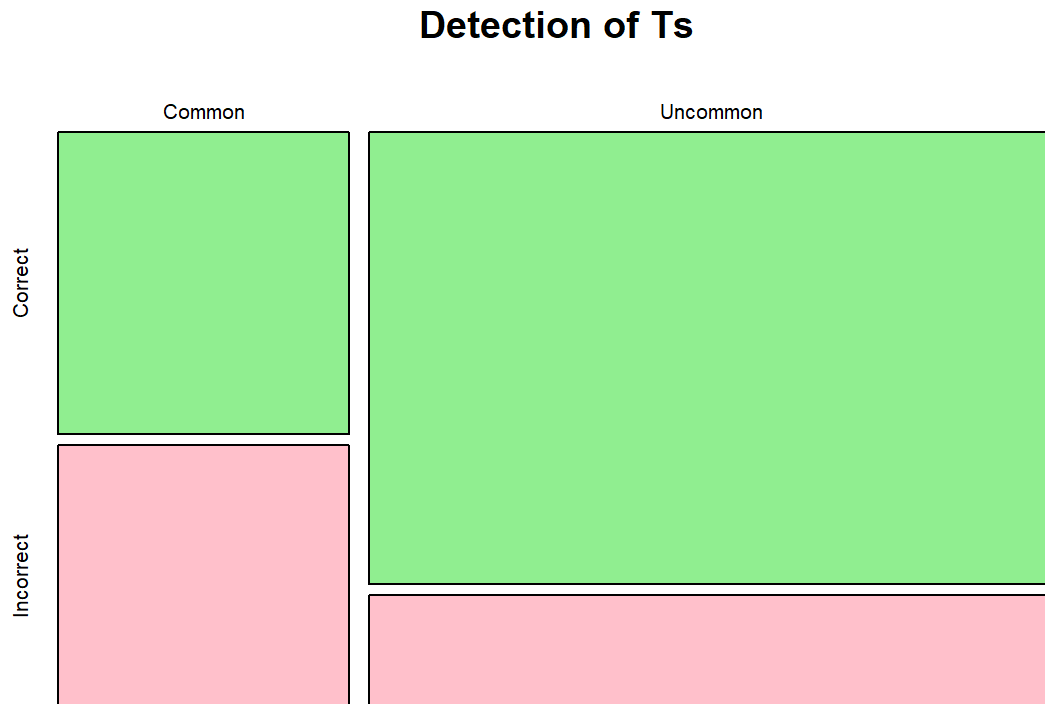
```
print ("Expected")
```

```
## [1] "Expected"
```

```
results.chi$expected
```

```
##           Correct Incorrect
## Common  20.25532  7.744681
## Uncommon 47.74468 18.255319
```

```
# Make mosaic plot to visualize relationship
mosaicplot(results, main = "Detection of Ts", col = c("Light Green", "Pink"))
```



It appears that

we must reject  $H_0$  and accept that Ts are more likely to go unnoticed when situated in common words.

Question 2.

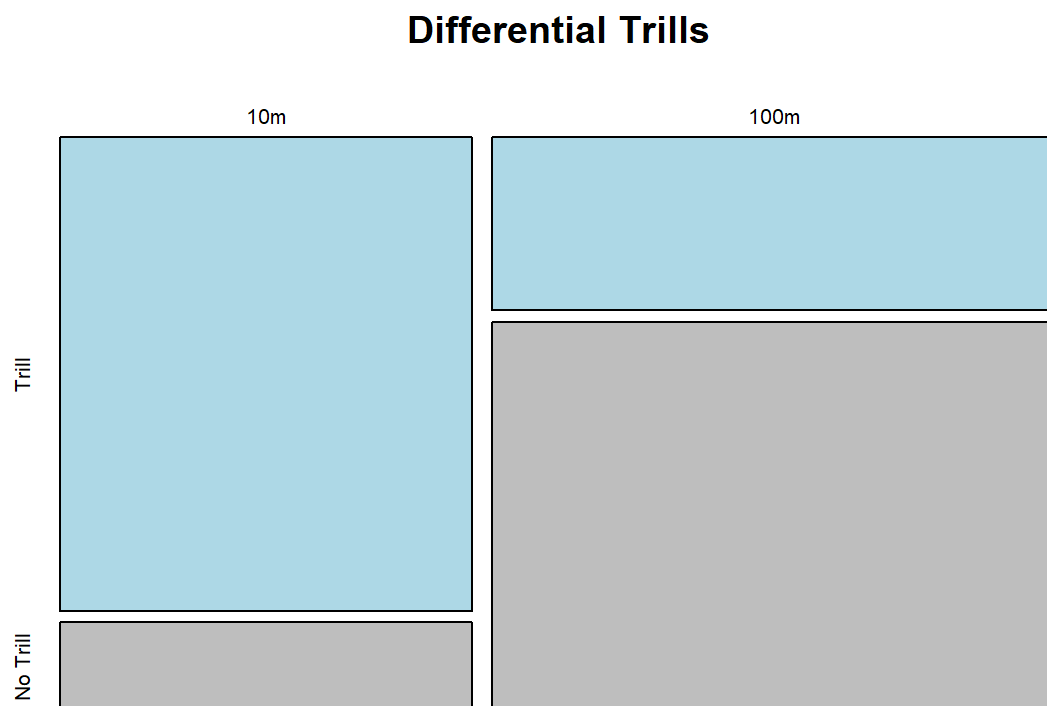
Do chipmunks trill differently under different circumstances?

$H_0 : p(\text{trill}, \text{near}) = p(\text{trill}, \text{far})$   $H_a : p(\text{trill}, \text{near}) \neq p(\text{trill}, \text{far})$

```
# Placing data in Chipmunk_Trill
Chipmunk_Trill <- c(16,8,3,18)
# Setting dimensions
dim(Chipmunk_Trill) <- c(2,2)
# Making Chipmunk_Trill a 'table' type
Chipmunk_Trill <- as.table(Chipmunk_Trill)
# Naming columns
colnames(Chipmunk_Trill) <- c("Trill", "No Trill")
# Naming rows
rownames(Chipmunk_Trill) <- c("10m", "100m")
# Printing the table
Chipmunk_Trill
```

```
##      Trill No Trill
## 10m      16       3
## 100m     8       18
```

```
# Making a mosaic plot of the table
mosaicplot(Chipmunk_Trill, main = "Differential Trills", color = c("light blue", "gray"))
```



```
# Performing Fisher test
Chipmunk_Trill.Fisher <- fisher.test(Chipmunk_Trill)
# Printing test results
Chipmunk_Trill.Fisher
```

```
##
## Fisher's Exact Test for Count Data
##
## data: Chipmunk_Trill
## p-value = 0.0006862
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  2.32073 77.46500
## sample estimates:
## odds ratio
##  11.23249
```

Conclusion : We reject the null hypothesis and conclude that chipmunks are more likely to trill when close to their burrow

Question 3.

Does nesting site affect penguin survival?

Ho :  $p(\text{alive,lower}) = p(\text{alive,middle}) = p(\text{alive,upper})$  Ha :  $p(\text{alive,lower}) \neq p(\text{alive,middle})$ , or  $p(\text{alive,lower}) \neq p(\text{alive,upper})$  or  $p(\text{alive,middle}) \neq p(\text{alive,upper})$

```
# Placing data in Penguin_Survival
Penguin_Survival <- c(43,44,49,7,6,1)
# Setting dimensions for the data matrix
dim(Penguin_Survival) <- c(3,2)
# Naming the columns
colnames(Penguin_Survival) <- c("Alive", "Dead")
# Naming the rows
rownames(Penguin_Survival) <- c("Lower", "Middle", "Upper")
# Printing the matrix
Penguin_Survival
```

```
##           Alive Dead
## Lower      43     7
## Middle     44     6
## Upper      49     1
```

```
# Making a mosaicplot of the data
mosaicplot(Penguin_Survival, main = "Penguin Survival", color = c("light green", "red"))
```

# Penguin Survival



```
# Performing fisher test
Penguin_Survival.Fisher <- fisher.test(Penguin_Survival)
# Printing test results
Penguin_Survival.Fisher
```

```
##
## Fisher's Exact Test for Count Data
##
## data: Penguin_Survival
## p-value = 0.08963
## alternative hypothesis: two.sided
```