

Assignment 6

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Carry out a test for independence between testing positive and participation in the Stanford study, using significance level 0.05. To do so, state the Null and alternative hypotheses and report the p-value. Do you find sufficient evidence to conclude that the Stanford study shows a higher chance of testing positive than the manufacturer's test did? Interpret this result briefly in your own words. Is your result consistent with or in contradiction to the Stanford study's stated results?

The null hypothesis states that the events of testing positive and participating in the Stanford study or the Manufacturer's study are independent of each other. Another hypothesis is that the proportion of positives are the same in both the Manufacturers' and Stanford study.

	Manufacturer	Stanford
Negative	369	3280
Positive	2	50

```
##
## Fisher's Exact Test for Count Data
##
## data: SeroprevalenceTable
## p-value = 0.1647
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.7334765 23.9538125
## sample estimates:
## odds ratio
##  2.811973

## [1] 0.1647436
```

From the above results we can see that the p-value of this test is 0.1647436. The significance level was $\alpha=0.1$, thus the p-value is greater than the significance level. Due to the p-value being greater than α we fail to reject the null hypothesis. This means that the proportions of positive test results were the same in the manufacturers' as in the Stanford study. In other words being positive or negative is independent with participating in the Manufacturer or Stanford study.

Discussion of Results

We cannot find evidence that the chances of testing positive are higher for the Stanford study as compared to the Manufacturer's study. From the null hypothesis it also seems that the event of testing positive is independent of having participated in the Stanford study.

Appendix: R Script

```
knitr::opts_chunk$set(echo = FALSE)
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library(knitr)
SeroprevalenceTable <- matrix(c(369,2,3280,50),2,2)
rownames(SeroprevalenceTable) <- c("Negative","Positive")
colnames(SeroprevalenceTable) <- c("Manufacturer", "Stanford")
kable(SeroprevalenceTable)

fisher.test(SeroprevalenceTable)
pVal <- fisher.test(SeroprevalenceTable)$p.val
pVal
```