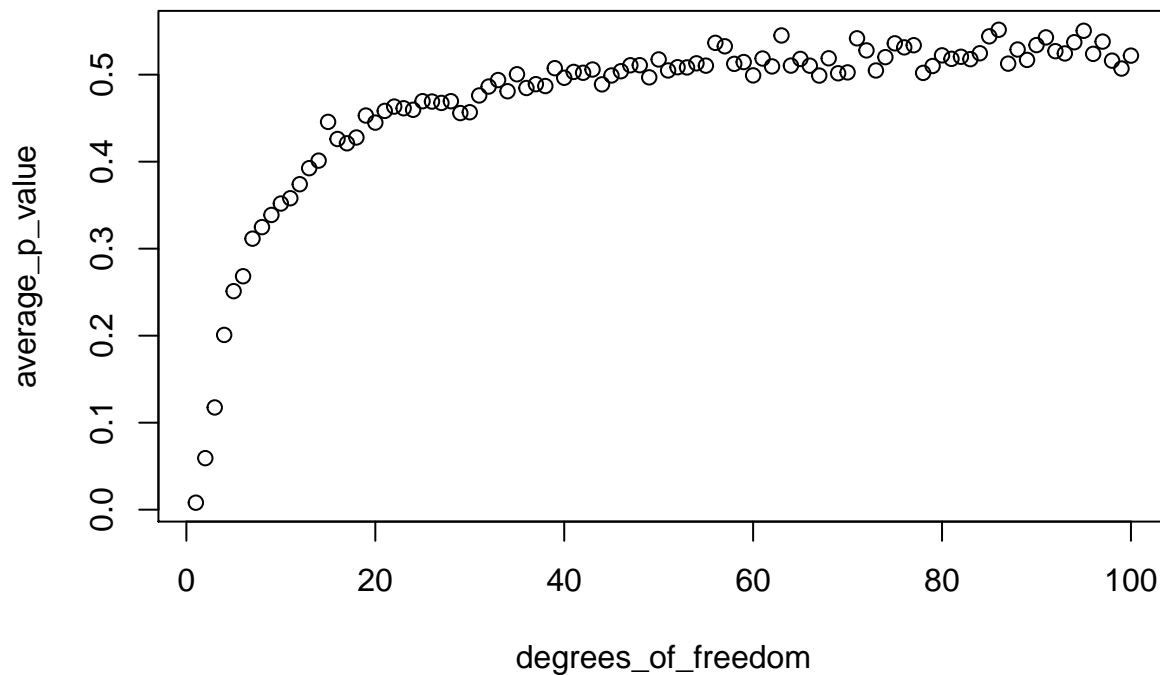


Breaking Test Assumptions

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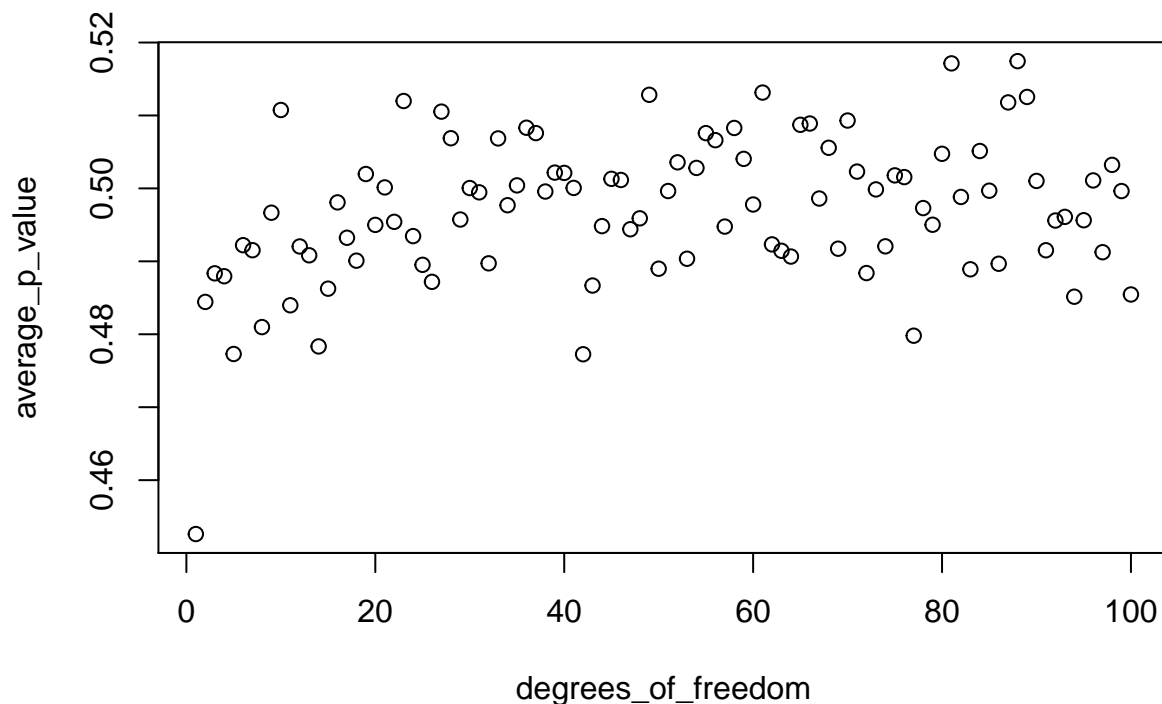
```
sign_test <- function(k) {  
  samp <- rchisq(n=100, df=k)  
  binom.test(sum(samp > k), 100, alternative="two.sided")$p.value  
}  
  
average_p_value <- sapply(1:100, function(k) {mean(replicate(1000, sign_test(k)))})  
degrees_of_freedom <- c(1:100)  
  
plot(y=average_p_value, x=degrees_of_freedom)
```



Here, I attempt to iteratively break the assumption of the sign test that the data be symmetrically distributed by starting with a sample from a chi-squared distribution with 1 degree of freedom, which is heavily skewed, and iterating up to a chi-squared distribution

with 100 degrees of freedom. I perform 1000 trials for each simulation with a different amount of degrees of freedom. Unexpectedly, the average p-values increase logarithmically as degrees of freedom increase, possibly indicating that the sign test is more robust against the skewness of the chi-squared distribution with few degrees of freedom than it is consistent under the high amounts of variance present in chi-squared distributions with many degrees of freedom. These results might be flawed because the sign test addresses a sample's median, and I use the sample's theoretical mean (the degrees of freedom, k) instead of the theoretical median, which is slightly less than a chi-squared distribution's mean.

```
average_p_value <- sapply(1:100, function(k)
  {mean(replicate(1000, t.test(rchisq(n=10, df=k), mu=k, alternative="two.sided"))$p.value)
})
plot(y=average_p_value, x=degrees_of_freedom)
```



Here, I attempt to iteratively break the assumption of the one-sample t-test that the sample data is normally distributed. This attempt was successful, with the p-values for approximately the first 5 iterations (with samples taken from skewed chi-squared distributions with few degrees of freedom) being noticeably below the expected p-value of 0.5. I use a sample size of 10 for each of the 1000 trials that I perform with each number of degrees of freedom so that the Central Limit Theorem cannot apply. Initially, I used sample sizes of 100, which caused the p-values at all degrees of freedom to be approximately 0.5 because all samples were roughly normally-distributed via the Central Limit Theorem.