

Project 2: Investigating the t-test with simulated data

Probability and statistics for modelling 1

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Testing the null hypothesis of equal means using normal and Poisson distributions (Ex. 1, 8, 9):

```
s <- rnorm(10)
t <- rnorm(10)
print(t.test(s, t))
```

```
##
## Welch Two Sample t-test
##
## data: s and t
## t = 1.1619, df = 17.995, p-value = 0.2605
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.4554517 1.5824070
## sample estimates:
## mean of x mean of y
## 0.3561214 -0.2073562
```

```
p <- rpois(10, 1)
q <- rpois(10, 1)
print(t.test(p, q))
```

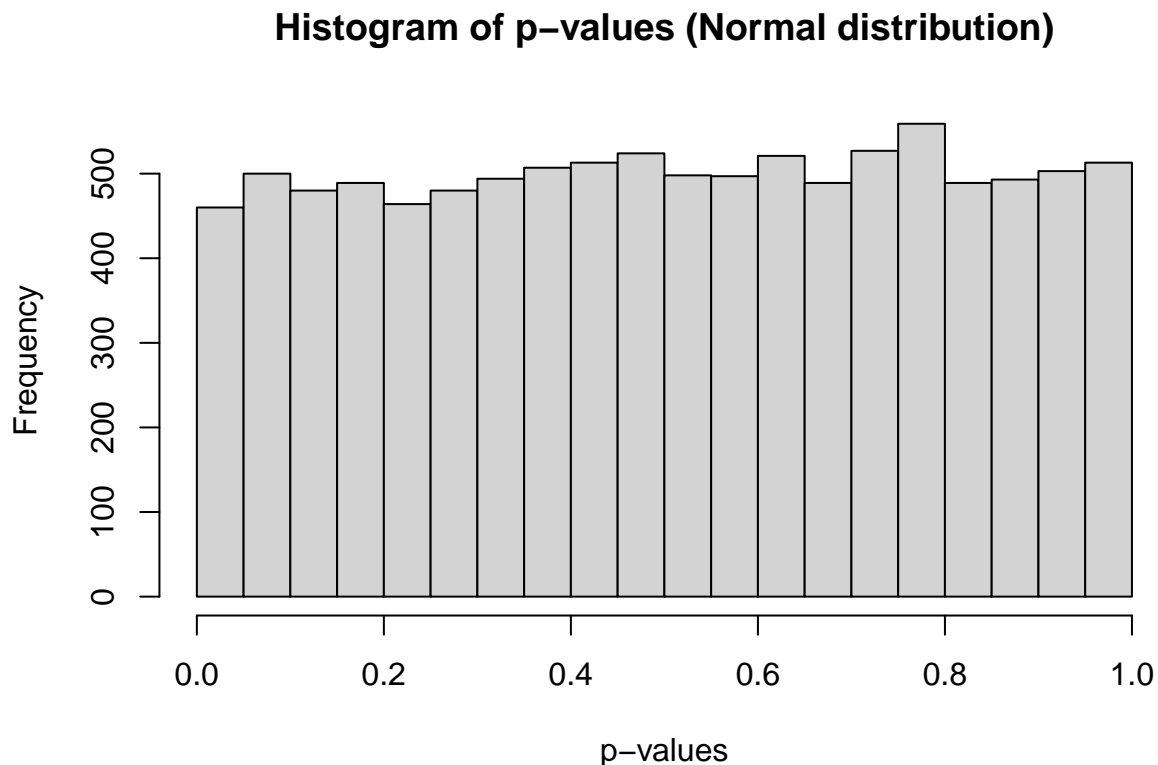
```
##
## Welch Two Sample t-test
##
## data: p and q
## t = 0.95669, df = 13.117, p-value = 0.356
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.7536798 1.9536798
## sample estimates:
## mean of x mean of y
## 1.5 0.9
```

```
p.large <- rpois(1000, 1)
q.large <- rpois(1000, 1)
print(t.test(p.large, q.large))
```

```
##
## Welch Two Sample t-test
##
## data: p.large and q.large
## t = -0.34336, df = 1996.8, p-value = 0.7314
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.10067377 0.07067377
## sample estimates:
## mean of x mean of y
## 1.027 1.042
```

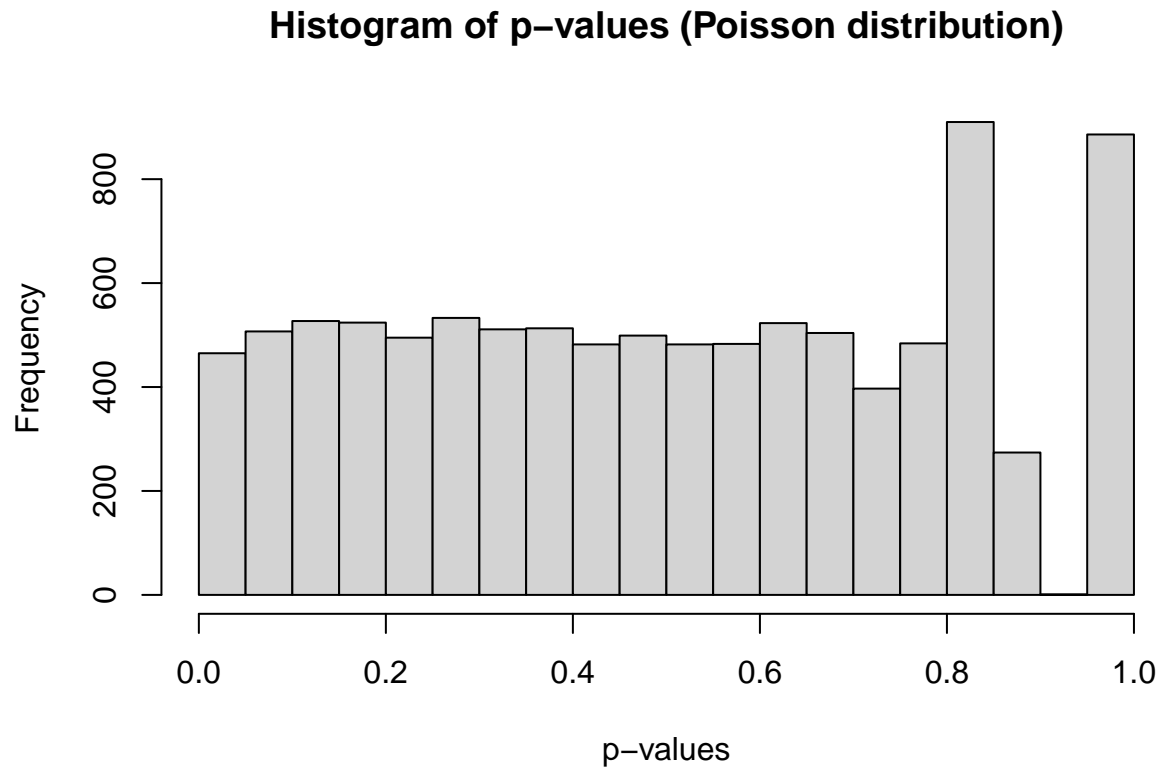
Plot resulting from multiple iterations of previous procedure (Ex. 2, 8, 9): The frequency of occurrence of p-values from the t-test of a normal distribution is uniform across all intervals.

```
results.normal <- replicate(10000, t.test(rnorm(10), rnorm(10))$p.value)
results.poisson <- replicate(10000, t.test(rpois(10, 1), rpois(10,
1))$p.value)
results.poisson.large <- replicate(10000, t.test(rpois(1000,
1), rpois(1000, 1))$p.value)
hist(results.normal, xlab = "p-values", ylab = "Frequency", main = "Histogram of p-values (Normal distr
```



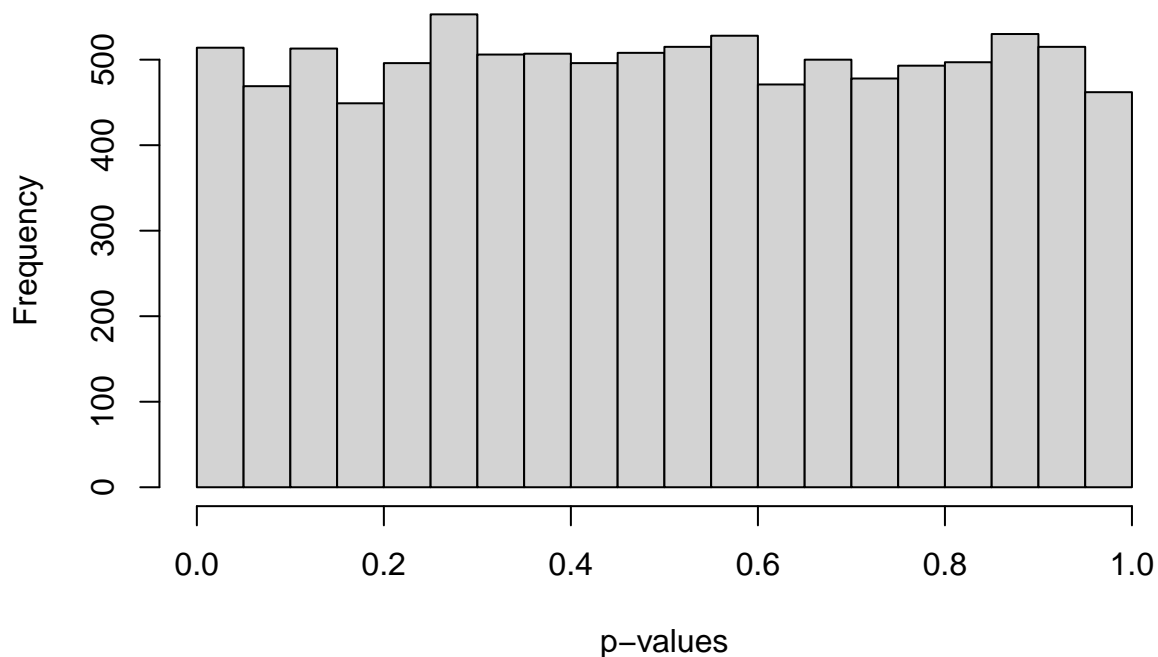
However, in the case of a Poisson distribution, testing a small sample size yields a non-uniform distribution; this non-uniformity disappears when the t-test is performed on larger samples.

```
hist(results.poisson, xlab = "p-values", ylab = "Frequency",  
      main = "Histogram of p-values (Poisson distribution)")
```



```
hist(results.poisson.large, xlab = "p-values", ylab = "Frequency",  
      main = "Histogram of p-values (Poisson distribution - large sample)")
```

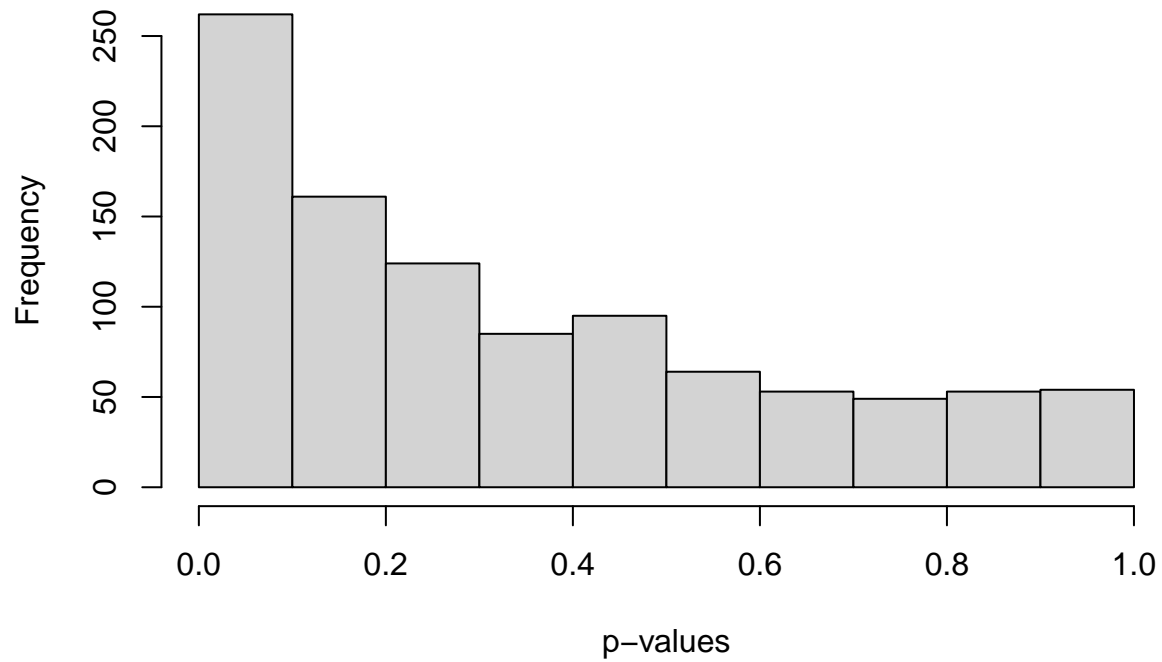
Histogram of p-values (Poisson distribution – large sample)



Similar plot for results of a t-test on a sample with different means (Ex. 3, 8, 9):

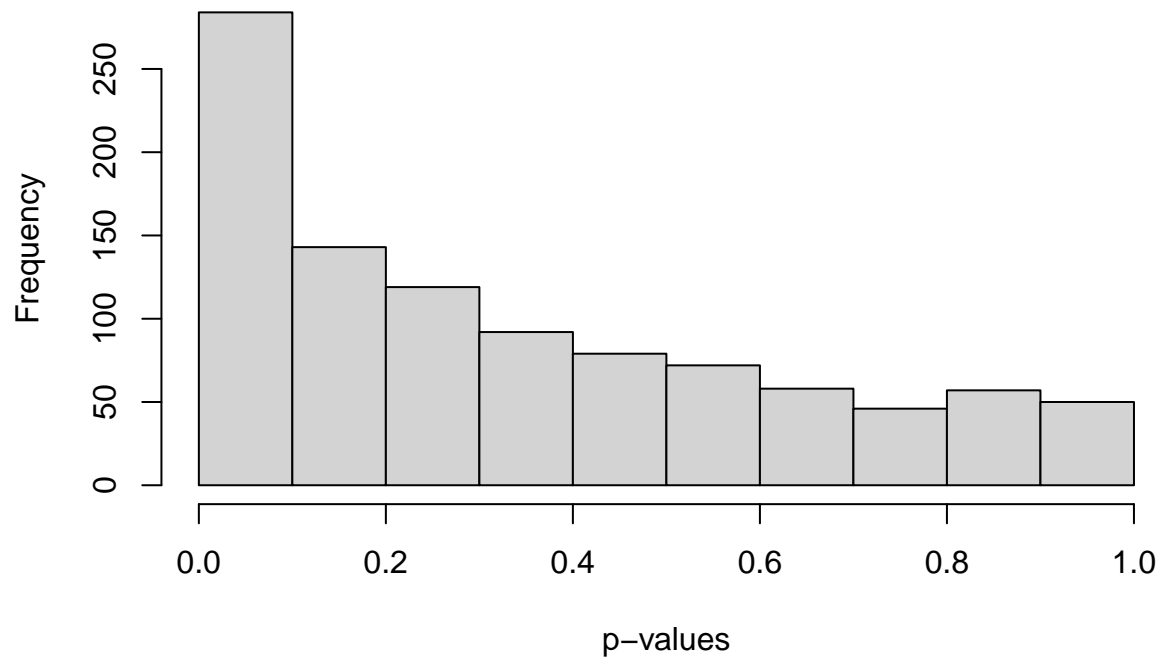
```
test.custom.means <- function(n, x, v, f) {  
  pvalues <- c()  
  for (i in 1:1000) {  
    if (f == 0) {  
      s <- rnorm(n, -x, v)  
      t <- rnorm(n, x, v)  
    } else {  
      s <- rpois(n, 1) - x  
      t <- rpois(n, 1) + x  
    }  
    pvalues <- append(pvalues, t.test(s, t)$p.value)  
  }  
  return(pvalues)  
}  
hist(test.custom.means(10, 0.25, 1, 0), xlab = "p-values", ylab = "Frequency",  
     main = "Histogram of p-values (Normal dist - diff means)")
```

Histogram of p-values (Normal dist – diff means)



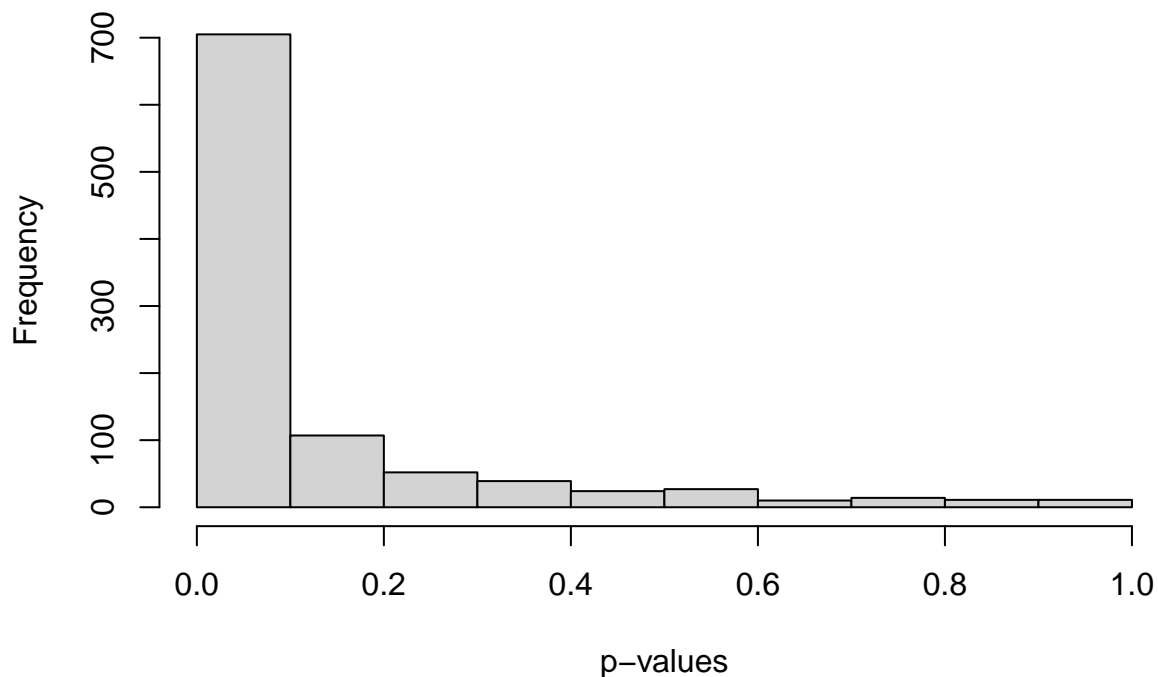
```
hist(test.custom.means(10, 0.25, 1, 1), xlab = "p-values", ylab = "Frequency",  
     main = "Histogram of p-values (Poisson dist - diff means)")
```

Histogram of p-values (Poisson dist – diff means)



```
hist(test.custom.means(1000, 0.05, 1, 1), xlab = "p-values",  
     ylab = "Frequency", main = "Histogram of p-values (Poisson dist - diff means & larger sample)")
```

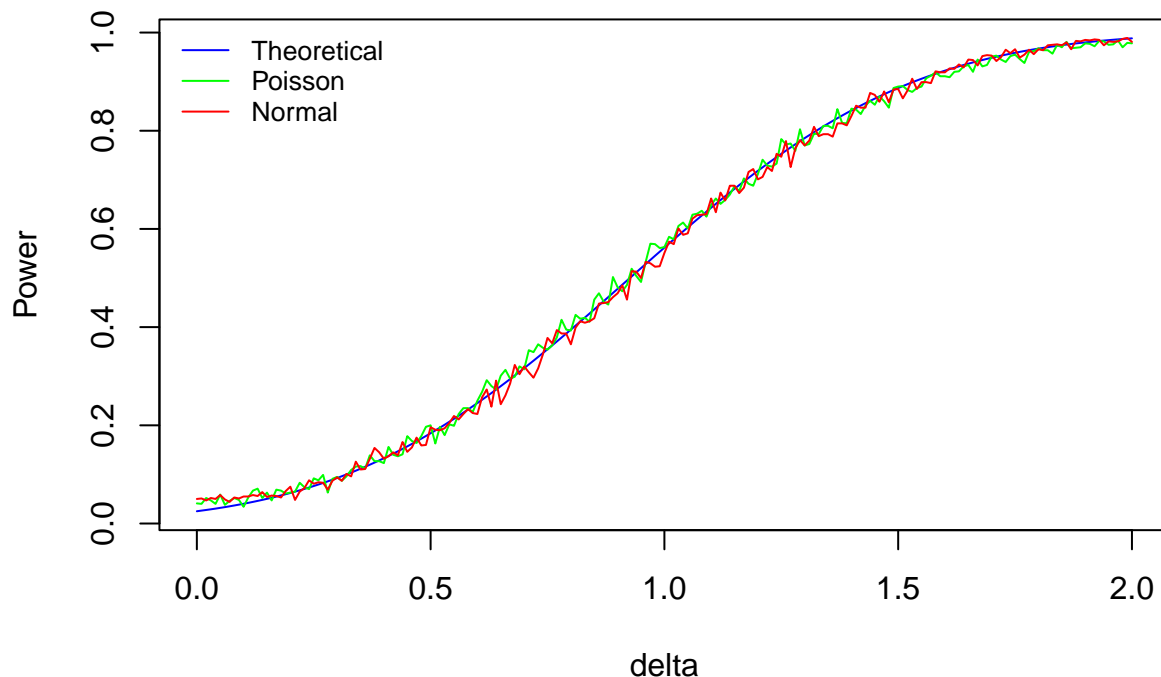
Histogram of p-values (Poisson dist – diff means & larger sample)



Comparison of the power of a t-test on different distributions (Ex. 4, 8): The power of t-tests on both a normal and a Poisson distribution closely follows the path of a theoretical power curve when plotted against the absolute difference in means (delta).

```
rpowers.normal <- c()
rpowers.poisson <- c()
tpowers <- c()
delta.list <- seq(0, 2, 0.01)
for (d in delta.list) {
  pvalues.normal <- replicate(1000, t.test(rnorm(10, -d/2),
    rnorm(10, d/2))$p.value)
  pvalues.poisson <- replicate(1000, t.test(rpois(10, 1) -
    d/2, rpois(10, 1) + d/2)$p.value)
  tpowers <- append(tpowers, power.t.test(10, delta = d)$power)
  rpowers.normal <- append(rpowers.normal, sum(pvalues.normal <
    0.05)/1000)
  rpowers.poisson <- append(rpowers.poisson, sum(pvalues.poisson <
    0.05)/1000)
}
plot(delta.list, tpowers, type = "l", col = "blue", xlab = "delta",
  ylab = "Power", main = "Power comparison between t-tests on different distributions")
lines(delta.list, rpowers.poisson, col = "green")
lines(delta.list, rpowers.normal, col = "red")
legend(x = "topleft", legend = c("Theoretical", "Poisson", "Normal"),
  cex = 0.8, lty = c(1, 1, 1), col = c("blue", "green", "red"),
  bty = "n")
```

Power comparison between t-tests on different distributions



Comparison of power between two different versions of a t-test (Ex. 5, 9): Initially, the powers of the two different versions of a t-test on a normally-distributed sample seem to vary slightly from each other (when sample size = 10). However, sample size = 100, 1000, the power curves overlap, thereby suggesting that the difference between the powers of the two different versions of the t-test decreases as sample size increases.

```
for (sample.size in c(10, 100, 1000)) {  
  v.equal.power <- c()  
  v.unequal.power <- c()  
  for (d in delta.list) {  
    pvalues.equal <- c()  
    pvalues.unequal <- c()  
    for (i in 1:1000) {  
      s <- rnorm(sample.size, -d/2)  
      t <- rnorm(sample.size, d/2)  
      pvalues.equal <- append(pvalues.equal, t.test(s,  
        t, var.equal = TRUE)$p.value)  
      pvalues.unequal <- append(pvalues.unequal, t.test(s,  
        t)$p.value)  
    }  
    v.equal.power <- append(v.equal.power, sum(pvalues.equal <  
      0.05)/1000)  
    v.unequal.power <- append(v.unequal.power, sum(pvalues.unequal <  
      0.05)/1000)  
  }  
  plot(delta.list, v.equal.power, type = "l", col = "blue",  
    xlab = "delta", ylab = "Power", main = paste0("Plot with sample size ",  
      sample.size))  
}
```

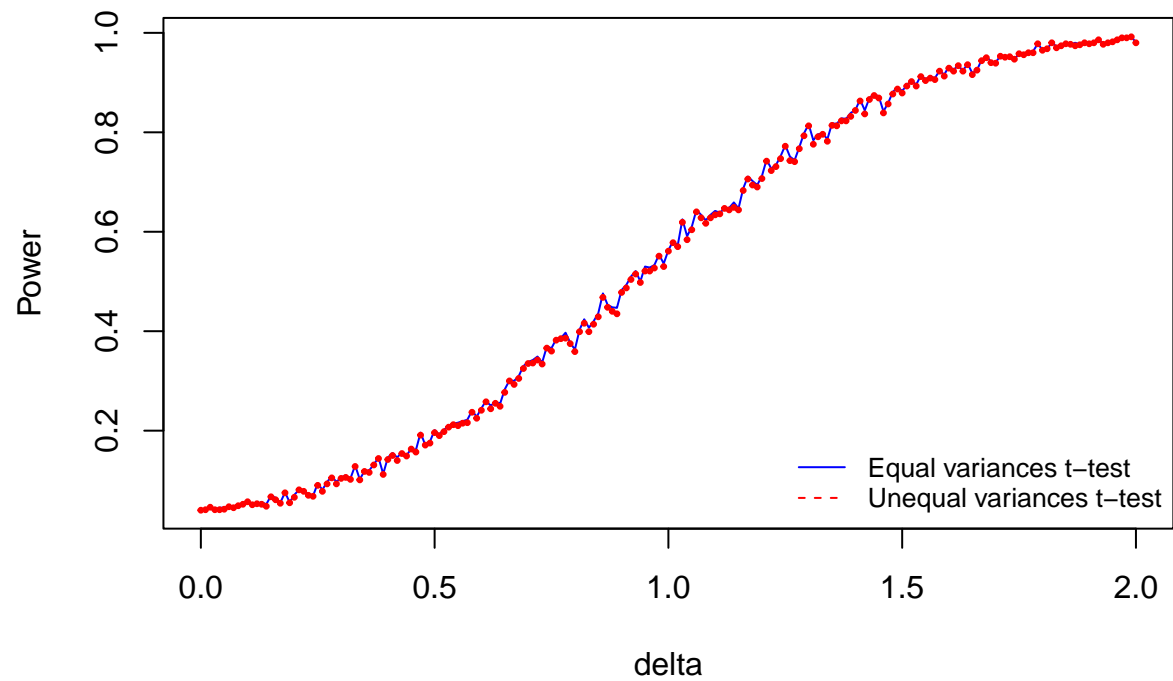


```

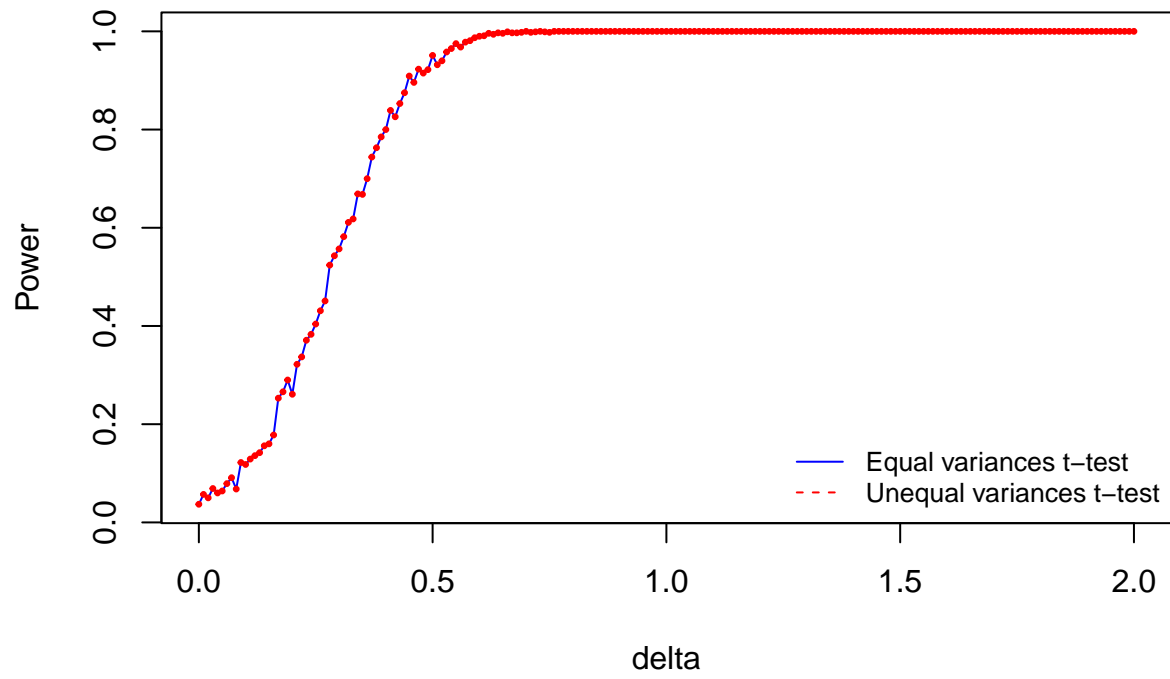
points(delta.list, v.unequal.power, col = "red", pch = 20,
       cex = 0.5)
legend(x = "bottomright", legend = c("Equal variances t-test",
    "Unequal variances t-test"), cex = 0.8, lty = c(1, 2),
       col = c("blue", "red"), bty = "n")
}

```

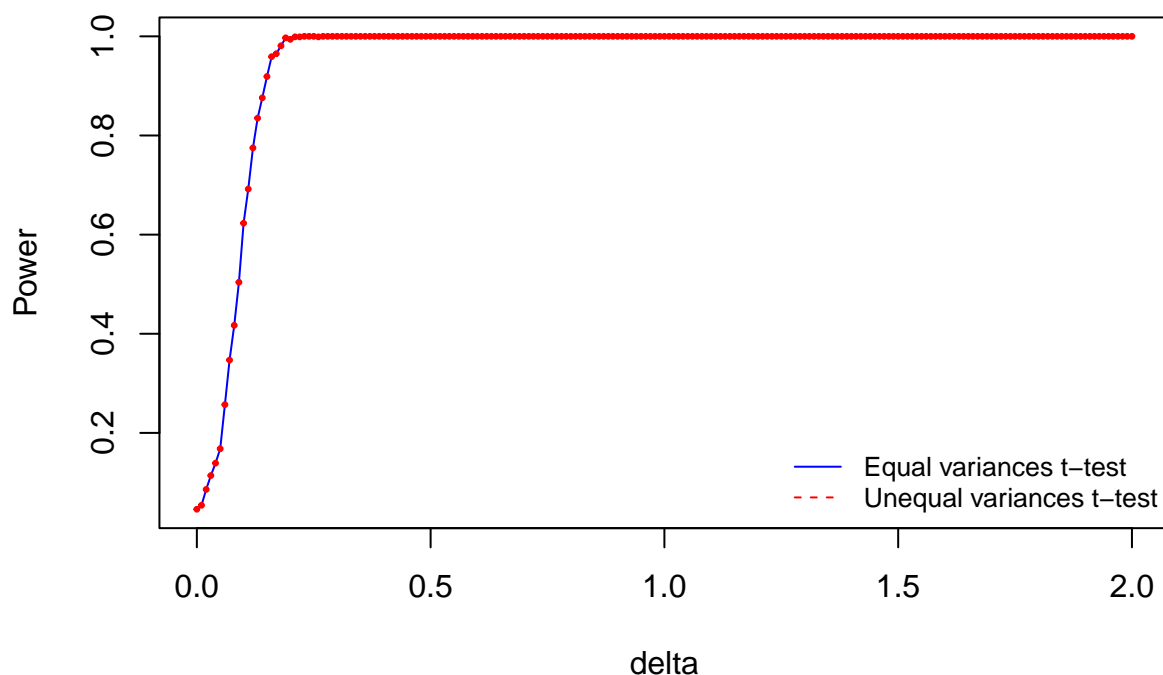
Plot with sample size 10



Plot with sample size 100



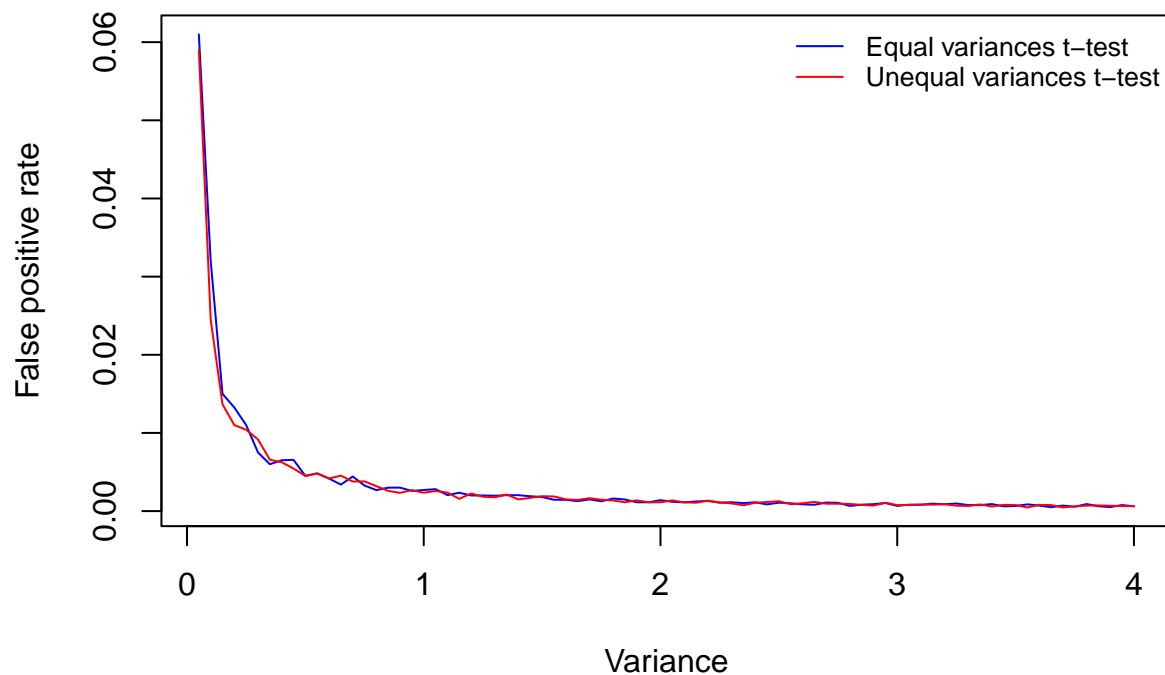
Plot with sample size 1000



Comparison of the false-positive rates of the two versions of a t-test (Ex. 6): False-positive rates plotted against varying variance in the normal distribution follow a rectangular hyperbolic curve similar to other another.

```
v.seq <- seq(0.05, 4, 0.05)
f.pos.eq.list <- c()
f.pos.uneq.list <- c()
for (v in v.seq) {
  f.pos.equal <- replicate(1000, t.test(rnorm(100, 0, 0.5),
    rnorm(100, 0, v), var.equal = TRUE)$p.value) < 0.05
  f.pos.unequal <- replicate(1000, t.test(rnorm(100, 0, 0.5),
    rnorm(100, 0, v))$p.value) < 0.05
  f.pos.eq.list <- append(f.pos.eq.list, mean(f.pos.equal))
  f.pos.uneq.list <- append(f.pos.uneq.list, mean(f.pos.unequal))
}
f.pos.eq.rate <- f.pos.eq.list/seq_along(v.seq)
f.pos.uneq.rate <- f.pos.uneq.list/seq_along(v.seq)
plot(v.seq, f.pos.eq.rate, type = "l", col = "blue", xlab = "Variance",
  ylab = "False positive rate", main = "Evolution of false positive rate for a normally-distributed s
lines(v.seq, f.pos.uneq.rate, col = "red")
legend(x = "topright", c("Equal variances t-test", "Unequal variances t-test"),
  cex = 0.8, lty = c(1, 1), col = c("blue", "red"), bty = "n")
```

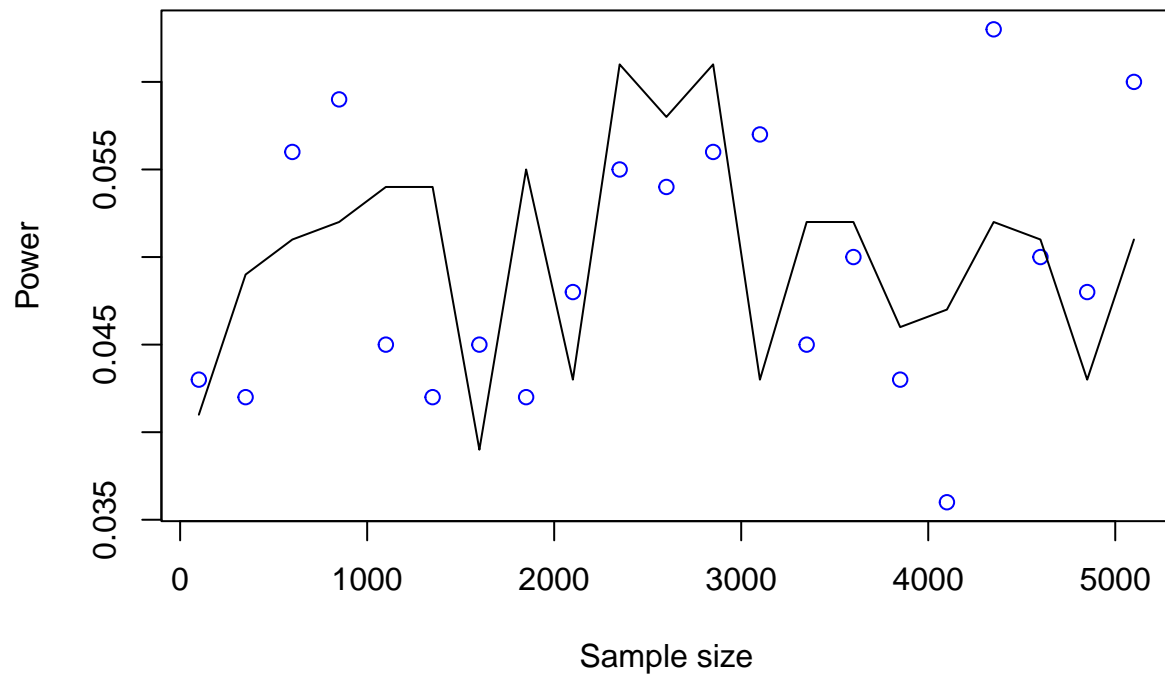
Evolution of false positive rate for a normally-distributed sample



Comparison of the power and false-positive rates of the t-test and the Mann-Whitney U test (Ex. 7, 8, 9):

```
n.list <- seq(100, 5100, 250)
t.powers.normal <- c()
w.powers.normal <- c()
t.powers.poisson <- c()
w.powers.poisson <- c()
for (n in n.list) {
  t.powers.normal <- append(t.powers.normal, mean(replicate(1000,
    t.test(rnorm(n), rnorm(n), var.equal = TRUE)$p.value) <
    0.05))
  w.powers.normal <- append(w.powers.normal, mean(replicate(1000,
    wilcox.test(rnorm(n), rnorm(n))$p.value) < 0.05))
  t.powers.poisson <- append(t.powers.poisson, mean(replicate(1000,
    t.test(rpois(n, 1), rpois(n, 1))$p.value) < 0.05))
  w.powers.poisson <- append(w.powers.poisson, mean(replicate(1000,
    wilcox.test(rpois(n, 1), rpois(n, 1))$p.value) < 0.05))
}
plot(n.list, t.powers.normal, main = "Comparison of t-test and Mann-Whitney U test - normal distribution",
     xlab = "Sample size", ylab = "Power", col = "blue")
lines(n.list, w.powers.normal)
```

Comparison of t-test and Mann-Whitney U test – normal distributio



```
plot(n.list, t.powers.poisson, main = "Comparison of t-test and Mann-Whitney U test - Poisson distribut.  
      xlab = "Sample size", ylab = "Power", col = "blue")  
lines(n.list, w.powers.poisson)
```

Comparison of t-test and Mann-Whitney U test – Poisson distributic

