# MA677 HW3

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1

```r
hw3q1 <- read.table("maybe_uniform.txt")
```

```
## Warning in read.table("maybe_uniform.txt"): incomplete final line found by
## readTableHeader on 'maybe_uniform.txt'
```

```r
test1 <- c(hw3q1$V1,hw3q1$V2,hw3q1$V3,hw3q1$V4,hw3q1$V5)
ks.test(test1,"punif")
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  test1
## D = 0.18, p-value = 0.3501
## alternative hypothesis: two-sided
```

```r
x <- seq(-5, 5, by=0.01)
fx <- ifelse(x > 0 & x <=0.5, 3/2,
   ifelse(x > 0.5 & x < 1,  0.5, 0))
plot(x,fx)
```
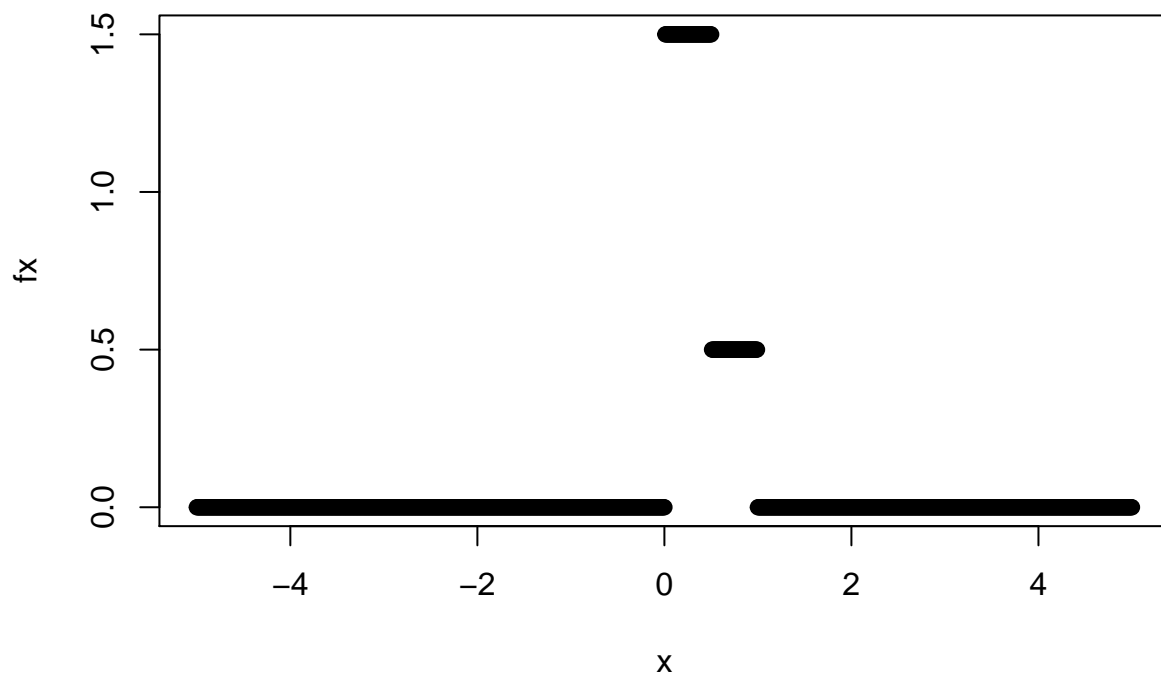
```
ks.test(fx,"punif")
```

```
## Warning in ks.test(fx, "punif"): ties should not be present for the
## Kolmogorov-Smirnov test
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  fx
## D = 0.9011, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```
#Based on the result in ks test, the model below is better than the Uniform
```
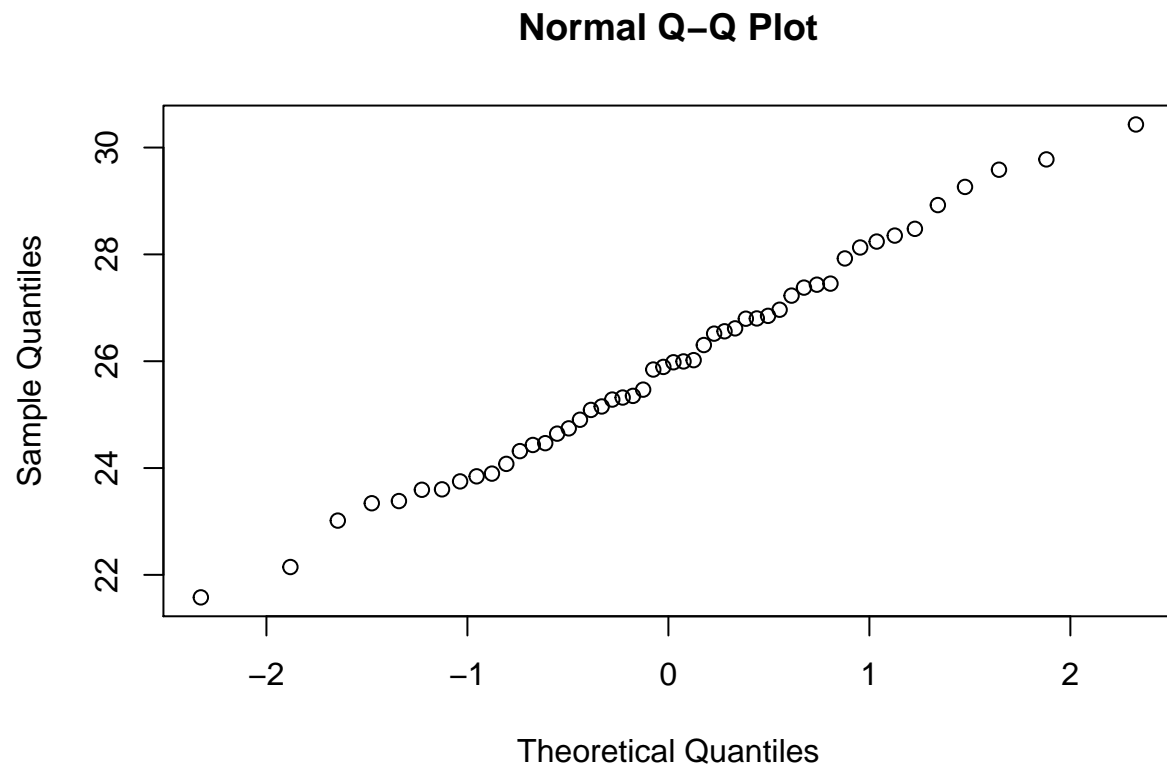
2

```
hw3q2 <- read.table("maybe_normal.txt")
a <- c(hw3q2$V1,hw3q2$V2,hw3q2$V3,hw3q2$V4,hw3q2$V5)
test2 <- (c(hw3q2$V1,hw3q2$V2,hw3q2$V3,hw3q2$V4,hw3q2$V5)-rep(26,50))/2
ks.test(test2,"pnorm")
```
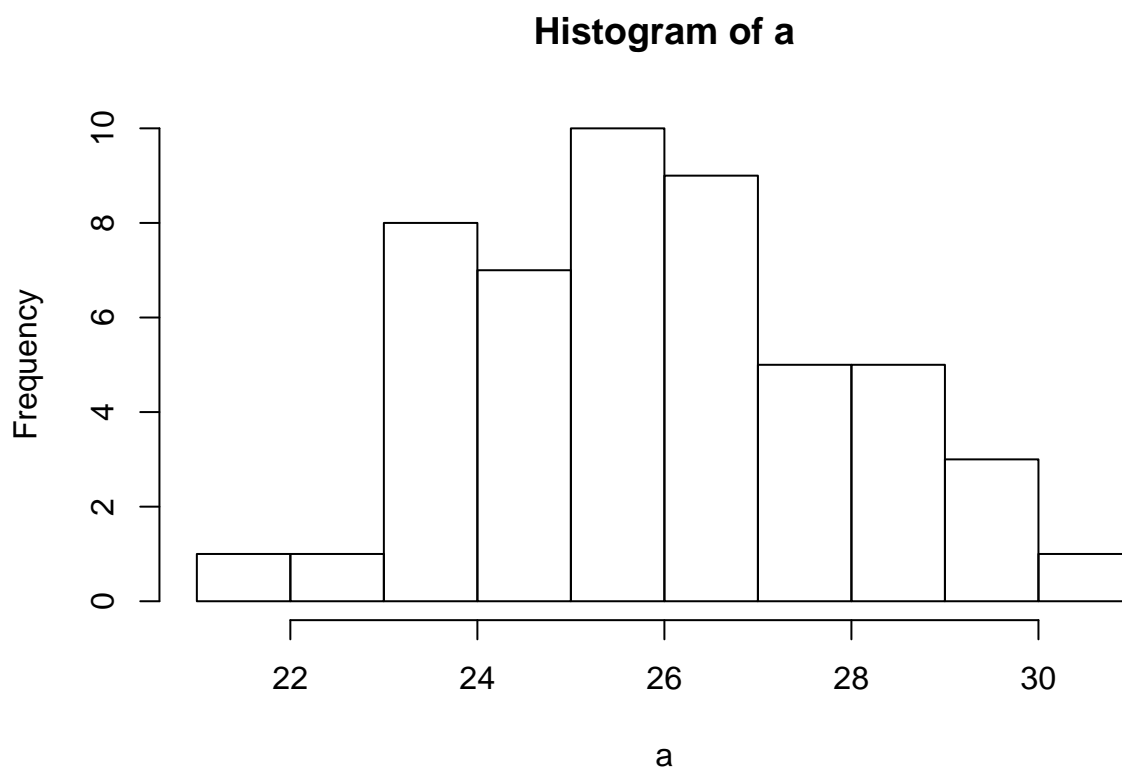
```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  test2
```

```
## D = 0.06722, p-value = 0.9663
## alternative hypothesis: two-sided
```

```
qqnorm(a)
```

Normal Q–Q Plot


```
hist(a)
```

Histogram of a


```
#We fail to reject the null hypothesis.
```

3

```
hw3q3 <- read.table("maybe_same_1.txt")
```

```
## Warning in read.table("maybe_same_1.txt"): incomplete final line found by
## readTableHeader on 'maybe_same_1.txt'
b <- c(hw3q3$V1,hw3q3$V2,hw3q3$V3,hw3q3$V4,hw3q3$V5)
hw3q3.2 <- read.table("maybe_same_2.txt")
```

```
## Warning in read.table("maybe_same_2.txt"): incomplete final line found by
## readTableHeader on 'maybe_same_2.txt'
c <- c(hw3q3.2$V1,hw3q3.2$V2,hw3q3.2$V3,hw3q3.2$V4,hw3q3.2$V5)
ks.test(b,c)
```

```
## Warning in ks.test(b, c): cannot compute exact p-value with ties
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  b and c
## D = 0.25, p-value = 0.491
## alternative hypothesis: two-sided
```

```r
ks.test(b+2,c)
```

```
## Warning in ks.test(b + 2, c): cannot compute exact p-value with ties
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  b + 2 and c
## D = 0.65, p-value = 0.0001673
## alternative hypothesis: two-sided
```

```
#Since the p value from the first test is larger than 0.05, we fail to reject the null hypothesis. Thos
```

4

```r
hw3q4 <- readRDS("norm_sample.Rdata")
q4_ecdf=ecdf(hw3q4)
summary(q4_ecdf)
```
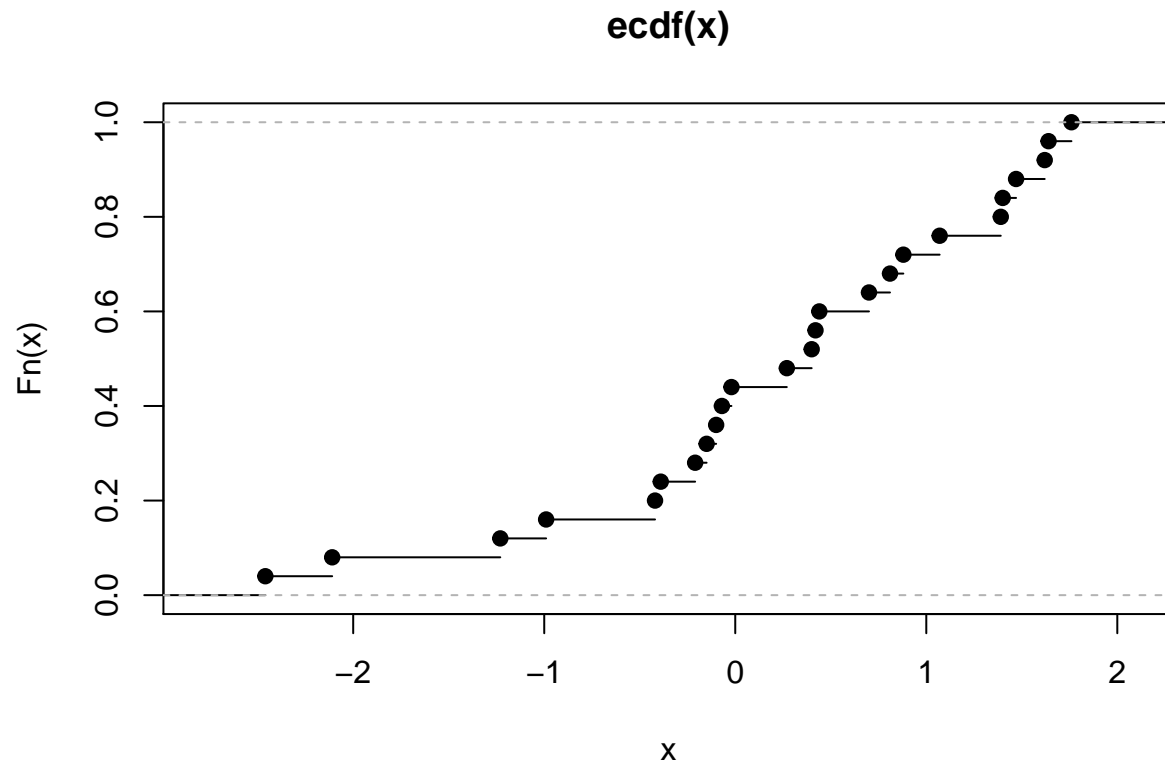
```
## Empirical CDF:      25 unique values with summary
##     Min. 1st Qu.  Median     Mean 3rd Qu.     Max.
## -2.4600 -0.2100  0.4000   0.2448  1.0700   1.7600
```

```r
plot.ecdf(hw3q4)
```

ecdf(x)

```
us=rnorm(25)
ks.test(hw3q4,us)
```

```
## 
##  Two-sample Kolmogorov-Smirnov test
## 
## data:  hw3q4 and us
## D = 0.2, p-value = 0.7102
## alternative hypothesis: two-sided
```