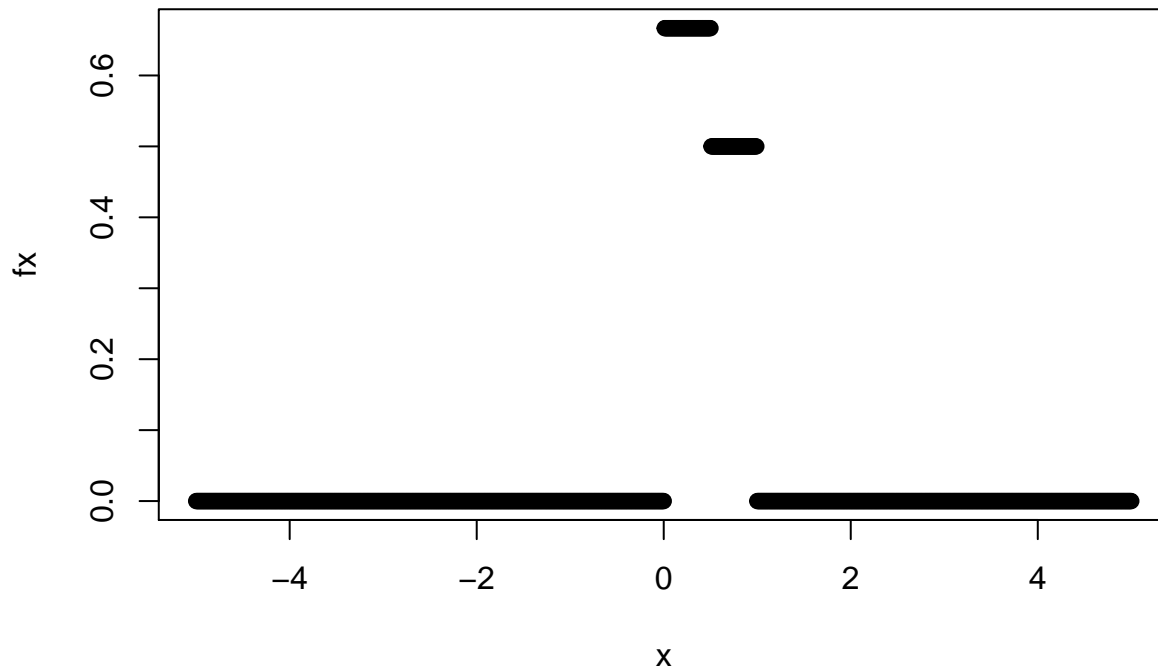# MA677HW3

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1.

```r
Df1=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(Df1$V1,Df1$V2,Df1$V3,Df1$V4,Df1$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, 2/3,
   ifelse(x > 0.5 & x < 1,  0.5, 0))
plot(x,fx)
```



```r
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
```

According to result of ks-test(P-value bigger than 0.05, fail to reject), therefore, these data is distributed as a Uniform distribution on [0,1]. Since in ks-test, the D value of fx is bigger than that of data, the model below is not better than the Uniform

2.

```
Df2=read.table("maybe_normal.txt")
```

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

```
d=c(Df2$V1,Df2$V2,Df2$V3,Df2$V4,Df2$V5)
test2=(c(Df2$V1,Df2$V2,Df2$V3,Df2$V4,Df2$V5)-rep(26,4))/2
```

```
## Warning in c(Df2$V1, Df2$V2, Df2$V3, Df2$V4, Df2$V5) - rep(26, 4):
##
```

```
ks.test(test2,"pnorm")
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  test2
## D = 1, p-value = 3.331e-16
## alternative hypothesis: two-sided
```
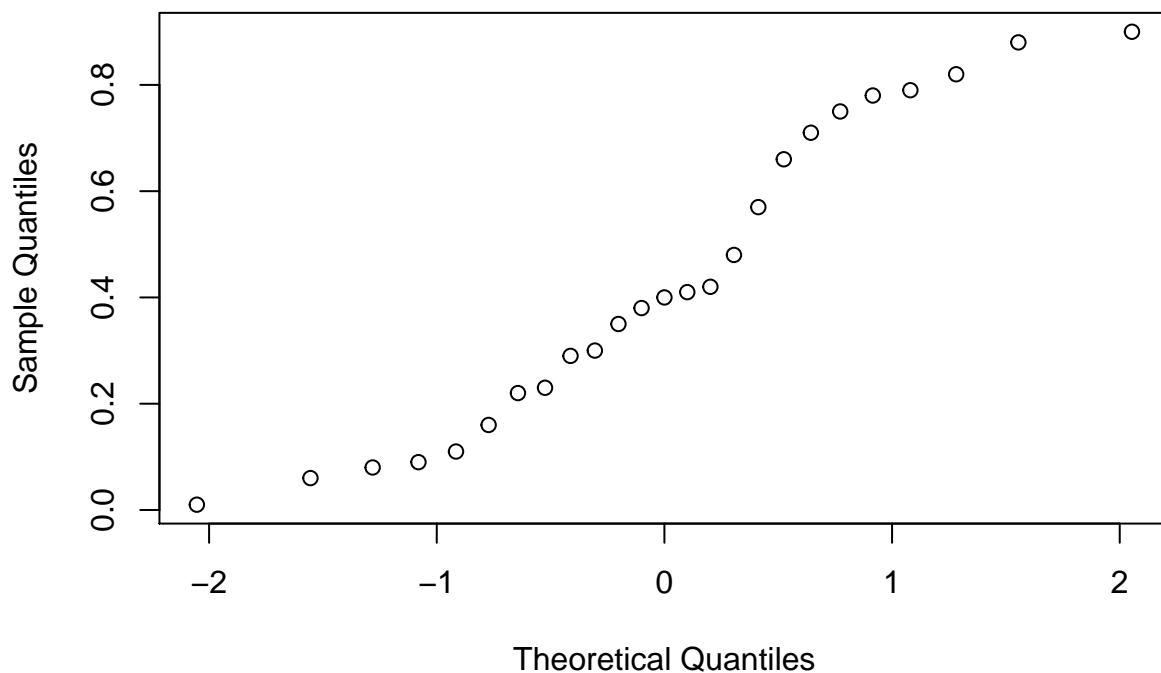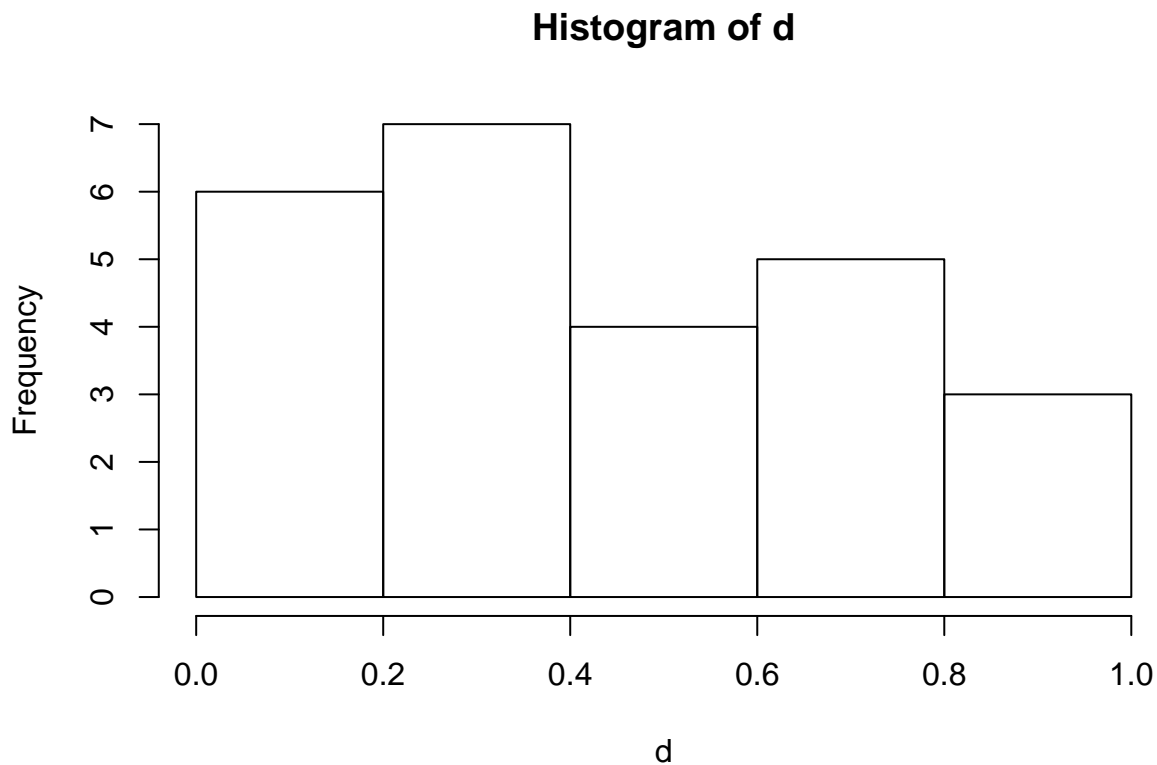
```
qqnorm(d)
```


Normal Q–Q Plot

```
hist(d)
```

Histogram of d

d

According to Ks-test(p smaller than 0.05 fail to reject) and qqnorm, the data generally follow normal disatribution.

3.

```
Df31=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'
```

```
x=c(Df31$V1,Df31$V2,Df31$V3,Df31$V4,Df31$V5)
Df32=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'
```

```
y=c(Df32$V1,Df32$V2,Df32$V3,Df32$V4,Df32$V5)
ks.test(x,y)
```

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

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  x and y
## D = 0.15, p-value = 0.9639
## alternative hypothesis: two-sided
```

```
ks.test(x+2,y)
```

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

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  x + 2 and y
## D = 0.85, p-value = 2.129e-07
## alternative hypothesis: two-sided
```

Since p-value of of ks.test(X,Y) is much larger than 0.05. Then we fail to reject the null hypotheses, thus X and Y are from the same distribution. Since p-value of of ks.test(X+2,Y) is much smaller than 0.05.Then we reject the null hypotheses, therefore X+2 and Y are not from the same distribution

   4.

```
Df4=readRDS("norm_sample.Rdata")
Df4_ecdf=ecdf(Df4)
summary(Df4_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
```

```
plot.ecdf(Df4)
```

ecdf(x)
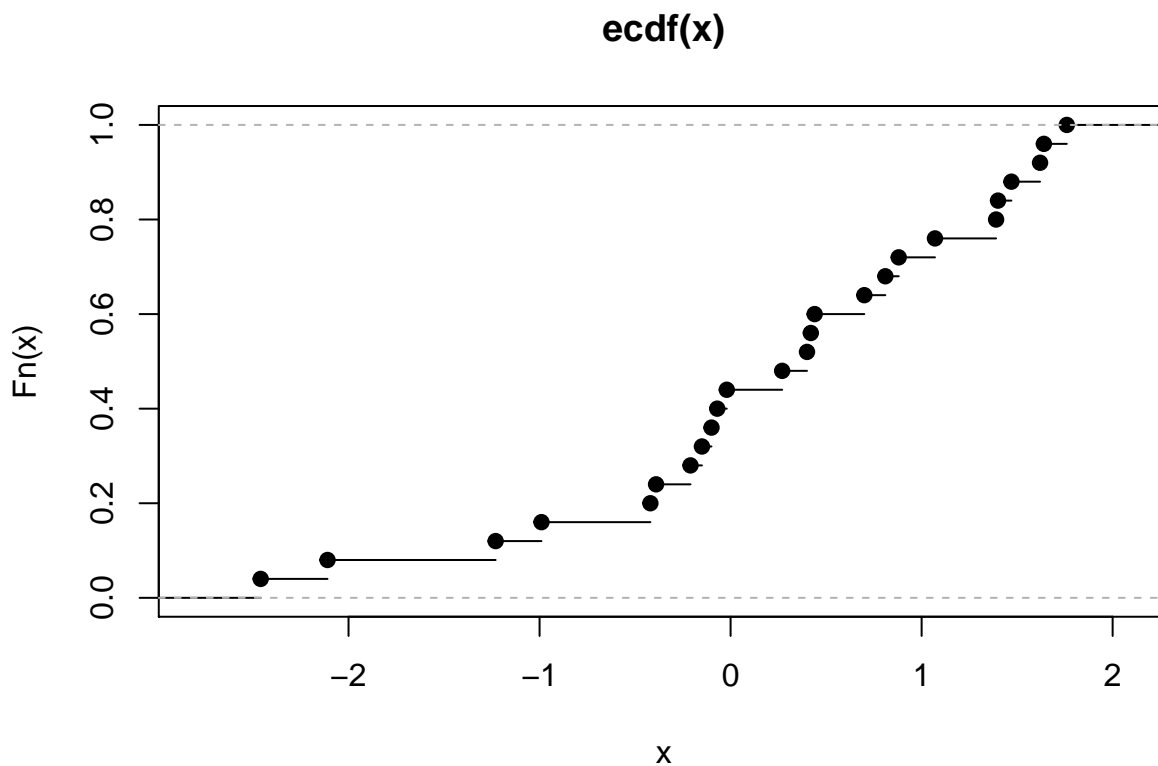

```
us=rnorm(25)
ks.test(Df4,us)
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Df4 and us
## D = 0.24, p-value = 0.4755
## alternative hypothesis: two-sided
```

5.

```
#Find a 95for F(4.9) - F(4.3).
Df51=read.table("faithful.dat",header=TRUE,skip=25,sep="")
Df52=read.table("fijiquakes.dat",header=T,sep="")
 mag<-Df52$mag
par(mfrow=c(2,1))
hist( mag,main="Earthquake Fiji data")
u<-ecdf(mag)
plot(u)
```

Earthquake Fiji data

ecdf(mag)
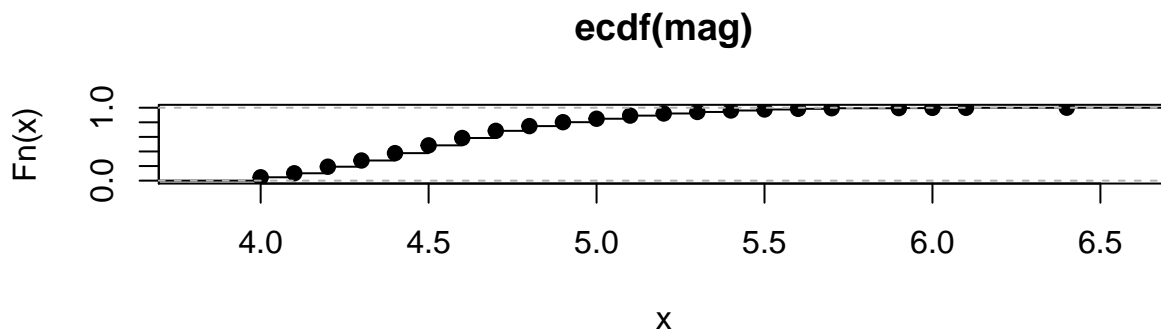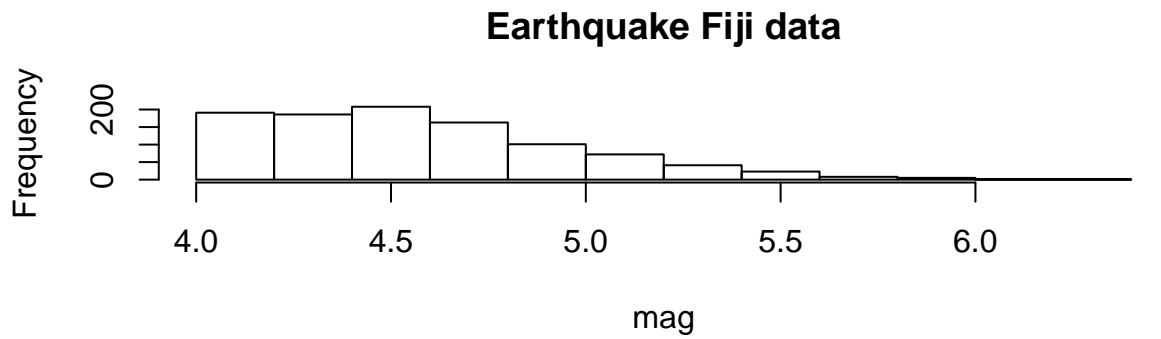
```
print(th<-u(4.9)-u(4.3))
```

```
## [1] 0.526
```

```
# Estimate a 90 percent confidence interval for the mean waiting time
ecdf.ksCI(Df51$waiting)
```

ecdf(Df51$waiting) + 95% K.S. bands