### 677hw

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#### R Markdown

```
library(ACSWR)

## Warning: package 'ACSWR' was built under R version 3.5.2

library(readr)
library(sfsmisc)

## Warning: package 'sfsmisc' was built under R version 3.5.2

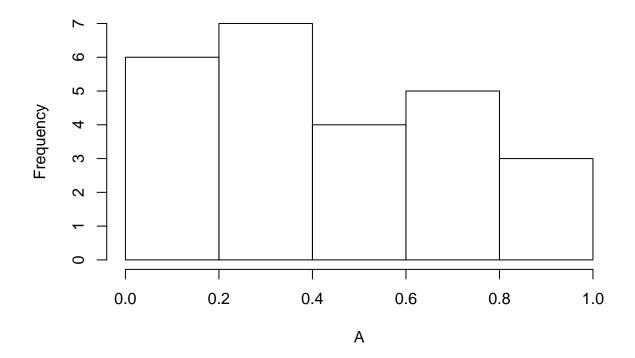
A <- read.delim("maybe_uniform.txt",header = F, sep= "",dec = " ")

## Warning in read.table(file = file, header = header, sep = sep,
## quote = quote, : incomplete final line found by readTableHeader on
## 'maybe_uniform.txt'

A <- cbind(A[1,], A[2,],A[3,],A[4,],A[5,])

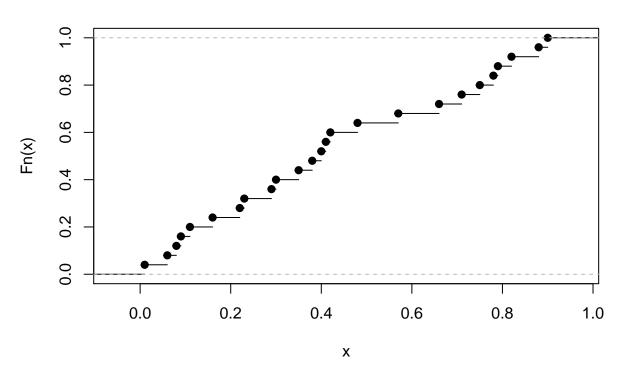
A <- as.numeric(as.vector(t(A)[,1]))
hist(A)</pre>
```

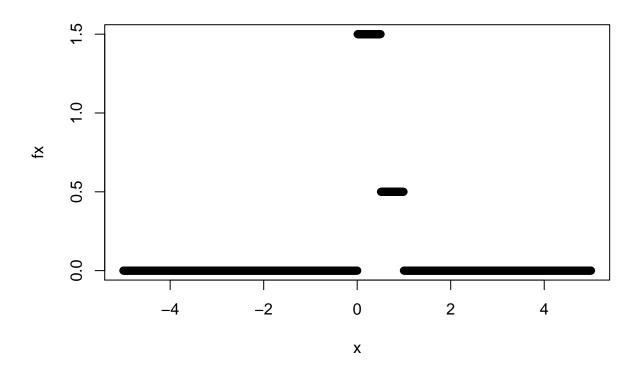
#### Histogram of A



```
dist_A <- ecdf(A)
plot(dist_A)</pre>
```

# ecdf(A)





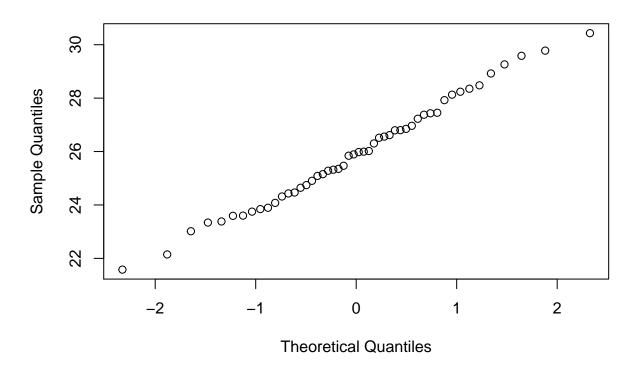
```
ks.test(fx,"punif")
```

```
## 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</pre>
```

I think the distribution of maybe\_uniform belongs to uniform distribution on [0,1]. Also, there should be better fit model.

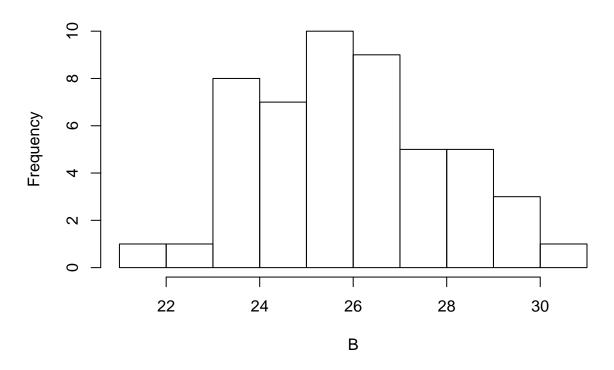
```
B <- read.table("maybe_normal.txt")
B <- cbind(B[1,], B[2,],B[3,],B[4,],B[5,],B[6,], B[7,],B[8,],B[9,],B[10,])
B <- as.numeric(as.vector(t(B)[,1]))
qqnorm(B)</pre>
```

### Normal Q-Q Plot



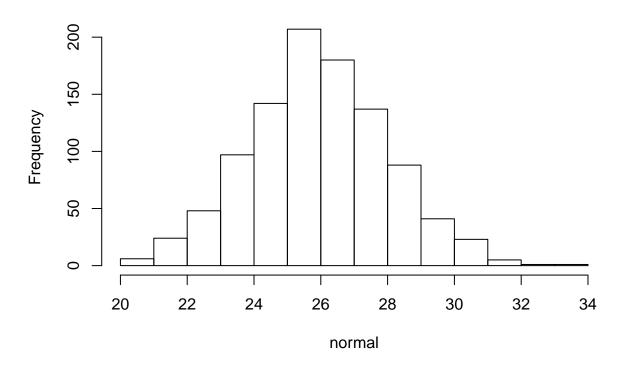
hist(B)

# Histogram of B



normal <- rnorm(1000,26,2)
hist(normal)</pre>

#### **Histogram of normal**



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

##

## One-sample Kolmogorov-Smirnov test

##

## data: B

## D = 1, p-value = 8.882e-16
```

According to the ks-test result, the maybe\_normal belongs to normal distribution.

## alternative hypothesis: two-sided

```
C1=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(C1$V1,C1$V2,C1$V3,C1$V4,C1$V5)

C2=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(C2$V1,C2$V2,C2$V3,C2$V4,C2$V5)
ks.test(x,y)
```

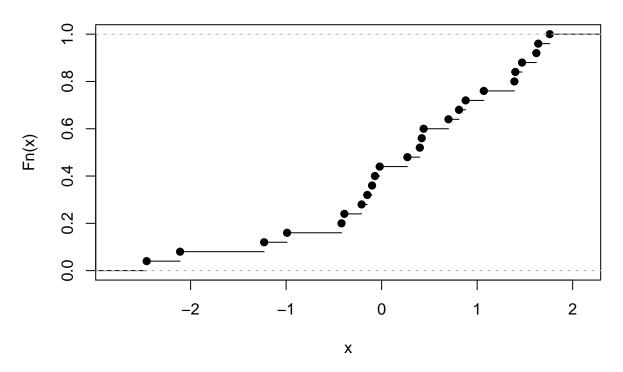
## Warning in ks.test(x, y): cannot compute exact p-value with ties

```
##
##
   Two-sample Kolmogorov-Smirnov test
##
## data: x and y
## D = 0.25, p-value = 0.491
## 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 = 0.65, p-value = 0.0001673
## alternative hypothesis: two-sided
```

For the first question. Since p-value of of ks.test is much larger than 0.05, we cannot to reject the null hypotheses, C1,C2 are from the same distribution. Also, for the second question. Since p-value of ks-test is much smaller than 0.05. Then we reject the null hypotheses, therefore C1+2 and C2 are not from the same distribution

```
D <- readRDS("norm_sample.Rdata")</pre>
ks.test(D,"pnorm")
##
##
    One-sample Kolmogorov-Smirnov test
##
## data: D
## D = 0.17724, p-value = 0.3683
## alternative hypothesis: two-sided
D_ecdf <- ecdf(D)</pre>
summary(D_ecdf)
## Empirical CDF:
                      25 unique values with summary
     Min. 1st Qu. Median
                               Mean 3rd Qu.
## -2.4600 -0.2100 0.4000 0.2448 1.0700 1.7600
plot.ecdf(D)
```

# ecdf(x)



```
D_norm <- rnorm(1000)
ks.test(D,D_norm)

##

## Two-sample Kolmogorov-Smirnov test
##

## data: D and D_norm

## D = 0.194, p-value = 0.3177

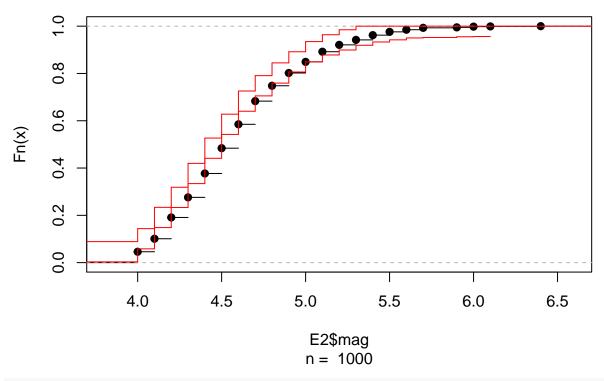
## alternative hypothesis: two-sided

E1 <- read.table("faithful(1).dat",header = T,skip = 25)

E2 <- read.table("fijiquakes(1).dat",header = T)

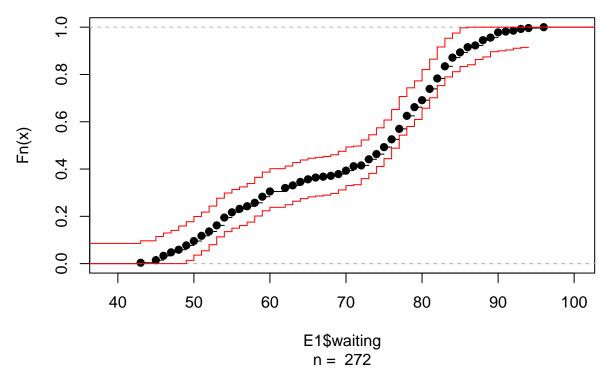
ecdf.ksCI(E2$mag)</pre>
```

ecdf(E2\$mag) + 95% K.S. bands



ecdf.ksCI(E1\$waiting)

# ecdf(E1\$waiting) + 95% K.S. bands



```
mag <- ecdf(E2$mag)
mag(4.9) - mag(4.3)
```

```
## [1] 0.526

s = sd(E2$mag)
n = length(E2$mag)
error <- qt(0.95,df=n-1)*s/sqrt(n)

up <- mean(E1$waiting)+error
low <- mean(E1$waiting) -error

sprintf("The CI is %e - %e",low,up)</pre>
```

## [1] "The CI is 7.087609e+01 - 7.091803e+01"