Assignment2

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Part I

```r
set.seed(4232) # use student number to set the seed

lambda_S = 1/3 #set lambda

n = 9 #number of observations

expdist_S <- rexp(n, rate = lambda_S) #set the exponential distribution for treatment S

round(expdist_S, 3) #list the observed values
```

```
## [1] 1.106 3.465 6.241 1.791 0.694 3.743 0.872 4.589 1.885
```

```r
lambda_T = 1

expdist_T <- rexp(n, rate = lambda_T) #set the exponential distribution for treatment T

round(expdist_T, 3) #list the observed values
```

```
## [1] 0.340 0.587 0.903 0.753 1.143 1.623 0.167 2.182 0.569
```

```r
pair <- data.frame(Treatment_S = c(round(expdist_S, 3)), Treatment_T = c(round(expdist_T, 3)))

print(pair) #display the pairs of observations of treatment S and T
```

```
##   Treatment_S Treatment_T
## 1       1.106       0.340
## 2       3.465       0.587
## 3       6.241       0.903
## 4       1.791       0.753
## 5       0.694       1.143
## 6       3.743       1.623
## 7       0.872       0.167
## 8       4.589       2.182
## 9       1.885       0.569
```
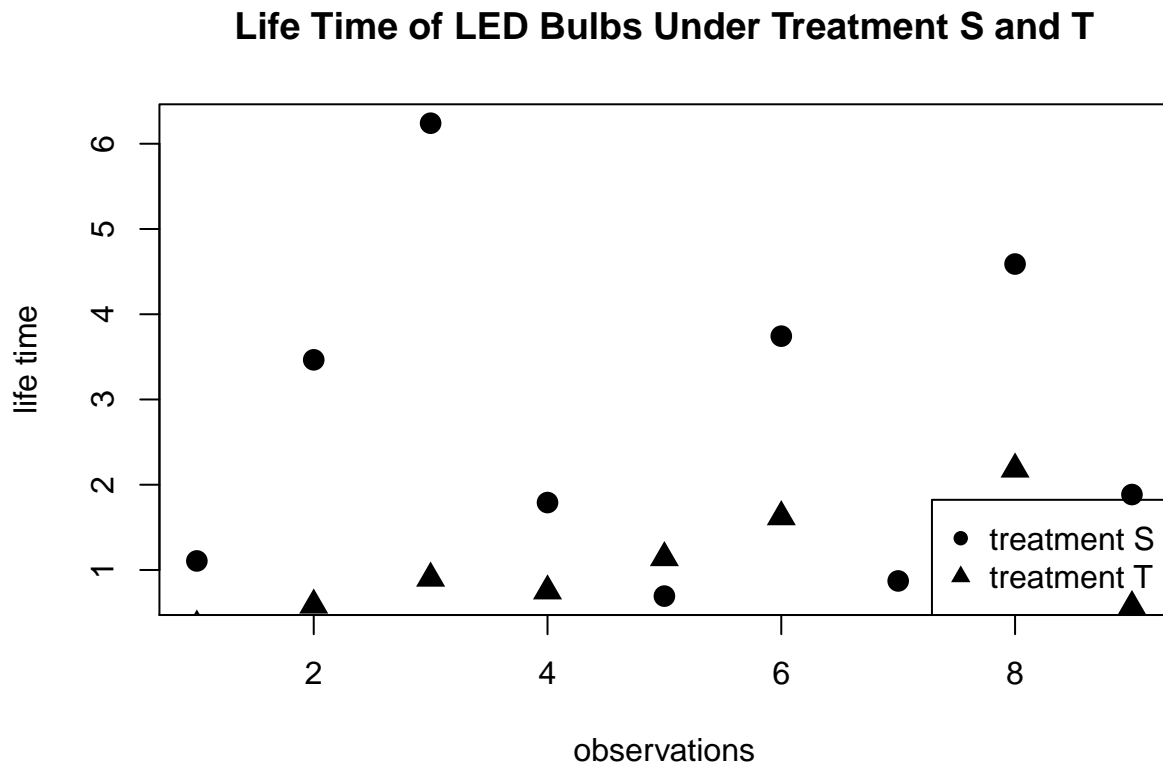
```
observations <- c(1,2,3,4,5,6,7,8,9)

plot(observations, expdist_S, xlab = "observations", ylab = "life time", main = "Life Time of LED Bulbs
points(observations, expdist_T, pch=17, cex=1.5)
legend("bottomright",legend = c("treatment S","treatment T"), pch = c(16, 17)) #display the pairs of ob
```

Life Time of LED Bulbs Under Treatment S and T

Part II

First, we use the completely randomization design. The null hypothesis is that the LED bulbs' mean life time under treatment S is equal to the LED bulbs' mean life time under treatment T and the alternative hypothesis is that the Led bulbs' mean life time under treatment T is less than the Led bulbs' mean life time under treatment S.

This distribution contains $\binom{18}{9}$ which is 48620 values and the probability of the observed treatment is $1/\binom{18}{9}$ which is 1/48620.

```
treatment <- c(expdist_S,expdist_T) #pool data
index <- combn(18,9)
N = ncol(index)
res <-numeric(N)# store the results
for(i in 1:N)
  {res[i] <-mean(treatment[index[,i]])-mean(treatment[-index[,i]])} #Generate N treatment assignments

hist(res,xlab="ybarT-ybarS",  main="Randomization Distribution of difference in means") #histogram of c
```

```
observed <- mean(expdist_T) - mean(expdist_S) #store observed mean difference
abline(v=observed, col="blue") #add line at observed mean diff
```

Randomization Distribution of difference in means
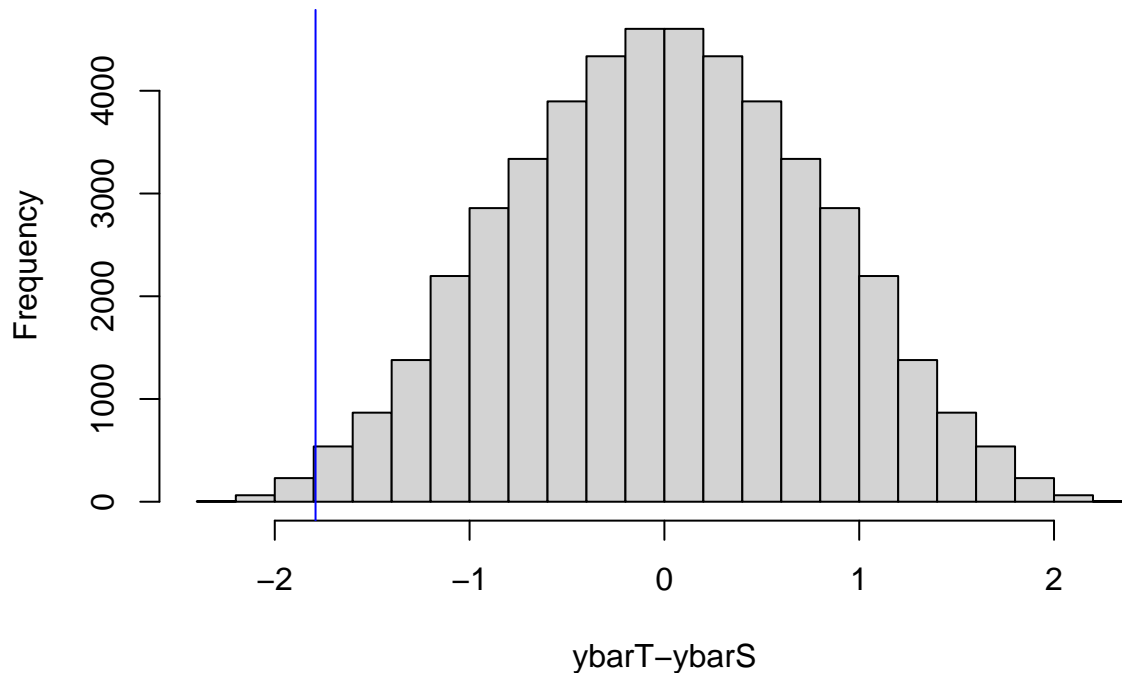

```
pval <- sum(res<=observed)/N# Randomization p value
round(pval,2)
```

```
## [1] 0.01
```

The p-value for the test is 0.01 and is smaller than the significance level which is smaller than 0.05. Thus, the null hypothesis will be rejected which means the Led bulbs' mean life time under treatment T is less than the Led bulbs' mean life time under treatment S.
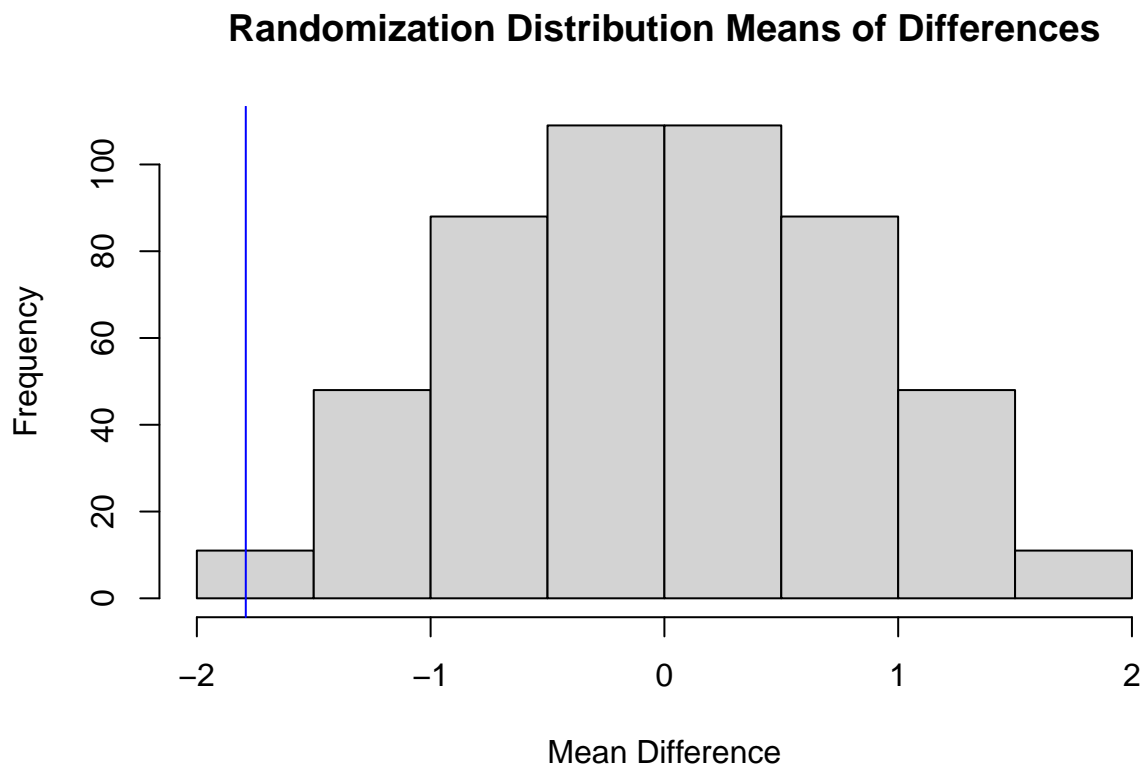
Then, we use the randomized paired design. The null hypothesis is that there's no difference between the LED bulbs' mean life time under treatment S and the LED bulbs' mean life time under treatment T and the alternative hypothesis is that the difference between the LED bulbs' mean life time under treatment S and the LED bulbs' mean life time under treatment T is less than 0.

This distribution contains 2^9 which is 512 values and the probability of the observed treatment is $1/2^9$ which is 1/512.

```
diff <- expdist_T - expdist_S
meandiff <- mean(expdist_T) - mean(expdist_S)
N <- 2^(9)# number of treatment assignments
res <-numeric(N) #store results
LR <-list(c(-1,1))# difference is multiplied by -1 or 1
```

```
trtassign <-expand.grid(rep(LR, 9))
for(i in 1:N){
  res[i] <- mean(as.numeric(trtassign[i,])*diff)}

hist(res, xlab="Mean Difference",main="Randomization Distribution Means of Differences")
abline(v = meandiff,col="blue")#add line at observed mean diff
```

Randomization Distribution Means of Differences


```
pval <- sum(res<=meandiff)/N# p-value
round(pval,2)
```

```
## [1] 0
```

The p-value for the test almost equal to 0 and is smaller than the significance level which is smaller than 0.05. Thus, the null hypothesis will be rejected which means the difference between the LED bulbs' mean life time under treatment S and the LED bulbs' mean life time under treatment T is less than 0.

Part III

Since the population distributions and parameters are unknown, we don't know if the two samples have equal variances. Thus, we are going to use the Welch two sample t-test. The null hypothesis is that the LED bulbs' mean life time under treatment S is equal to the LED bulbs' mean life time under treatment T and the alternative hypothesis is that the Led bulbs' mean life time under treatment T is less than the Led bulbs' mean life time under treatment S.

```r
t.test(expdist_T,expdist_S,alternative = "less") #Welch Two Sample t-test
```

```
##
##  Welch Two Sample t-test
##
## data:  expdist_T and expdist_S
## t = -2.6661, df = 9.7884, p-value = 0.01203
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.5706533
## sample estimates:
## mean of x mean of y
## 0.9187204 2.7093738
```

The p-value of the two sample t-test is 0.01 and is smaller than the significance level which is smaller than 0.05. Thus, the null hypothesis will be rejected which means the Led bulbs' mean life time under treatment T is less than the Led bulbs' mean life time under treatment S.

Then, we are going to use the qq-plot to check the normality assumption.

```r
qqnorm(expdist_S, main = "QQ-plot for Treatment S")
qqline(expdist_S) #QQ-plot for Treatment S
```

QQ–plot for Treatment S
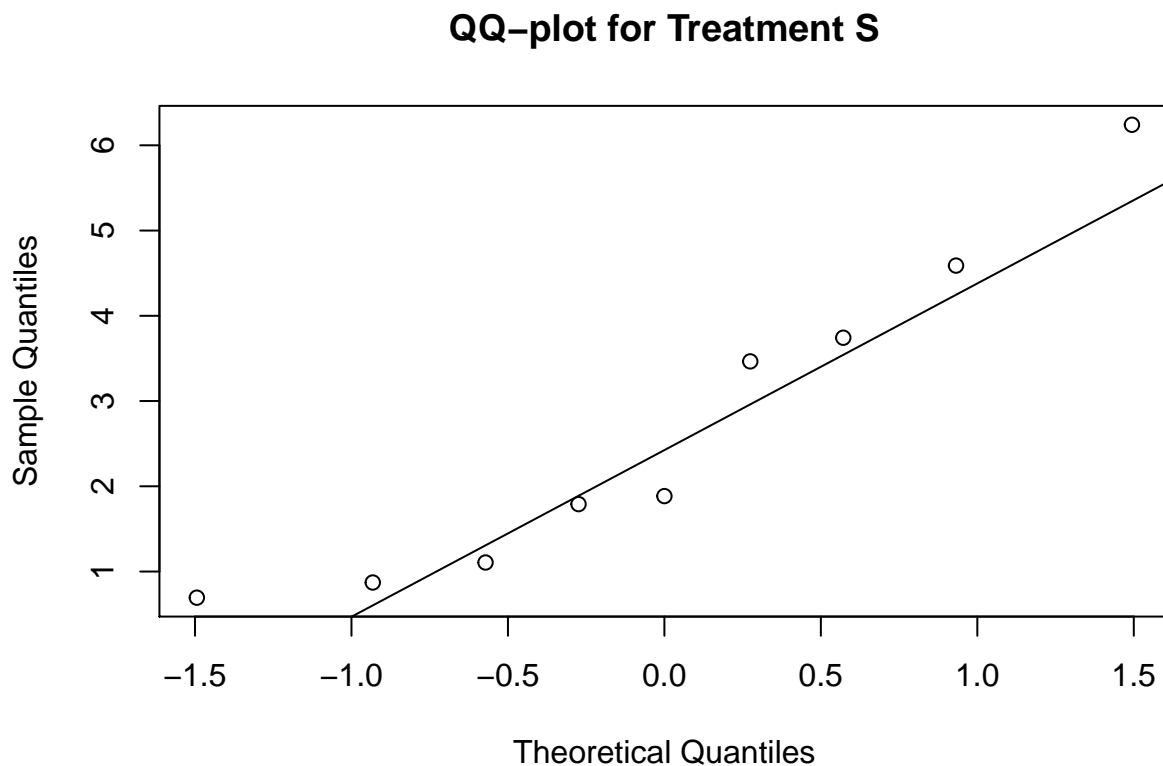
```r
qqnorm(expdist_T, main = "QQ-plot for Treatment T")
qqline(expdist_T) #QQ-plot for Treatment T
```

QQ–plot for Treatment T
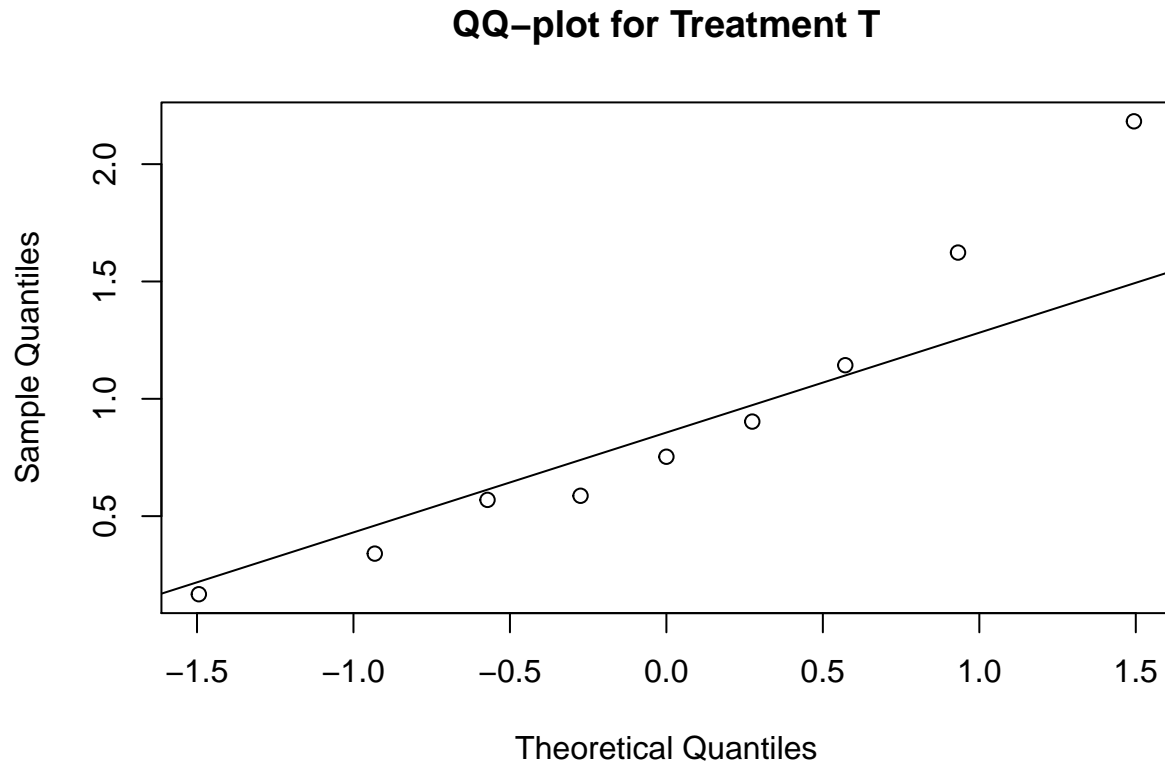
From the qq-plot for treatment S, we can see it's left tailed and some of the points do not fit the normal distribution well, especially the points on the both ends. From the qq-plot for treatment T, we can see it's right skewed and some of the points do not fit the normal distribution well, especially the points on the right end. Therefore the t-test might not fully follow a normal distribution.

Since the p-value of two sample t-test is closed to the p-value of completely randomization design and both of them are small than the significance level, we can say the results of the t-test agree with the results of the randomization test.

In a paired t-test, the variance is not assumend to be equal so we can use the paired t-test to compare our two sample. The null hypothesis is that the true mean which is the mean of difference is equal to zero and the alternative hypothesis is that the true mean is less than 0 which is the mean of difference is less than 0.

```r
t.test(diff, alternative = "less") #paired t-test
```

```
##
##  One Sample t-test
##
## data:  diff
## t = -3.218, df = 8, p-value = 0.006138
## alternative hypothesis: true mean is less than 0
## 95 percent confidence interval:
##        -Inf -0.7559005
## sample estimates:
```

```
## mean of x
## -1.790653
```

The p-value of the paired t-test is 0.006 and is smaller than the significance level which is smaller than 0.05. Thus, the null hypothesis will be rejected which means the mean of difference is less than 0 and not equal to 0.

Then, we are going to use the qq-plot to check the normality assumption.

```
qqnorm(diff, main = "QQ-plot for difference")
qqline(diff) #QQ-plot for difference
```

QQ−plot for difference
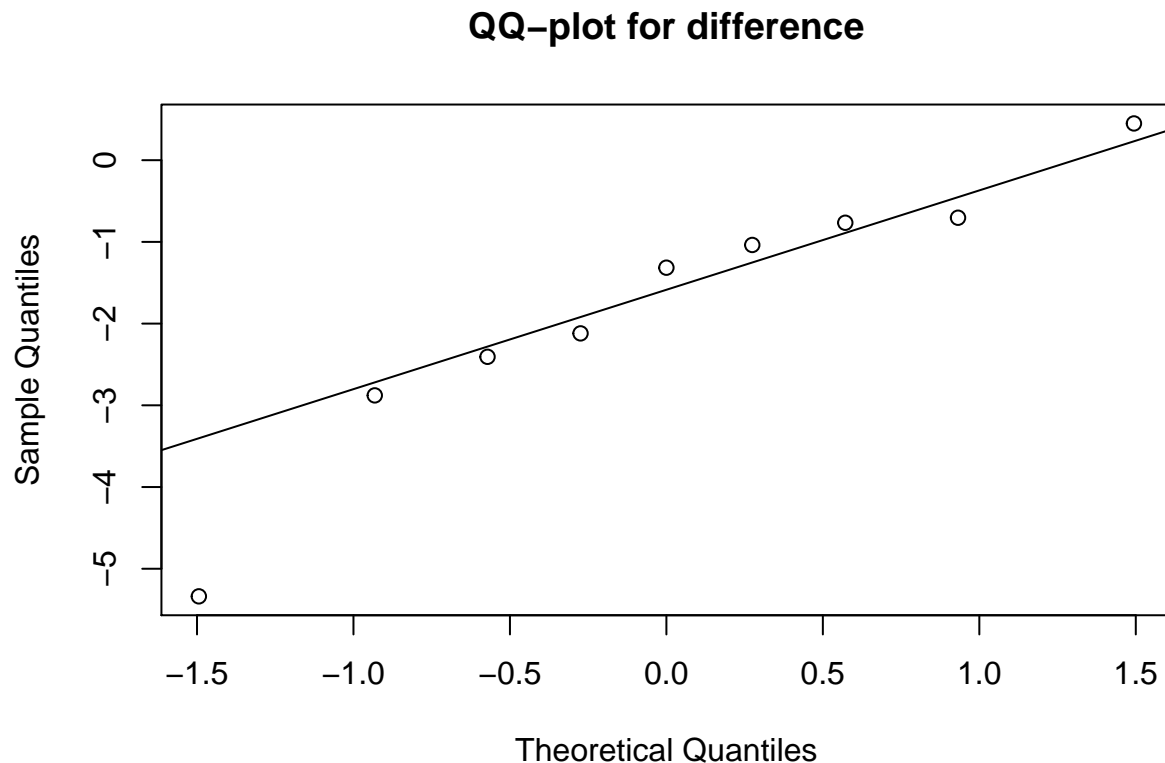
From the qq-plot for the difference between treatment S and treatment T, we can see almost all the points fit the normal distribution except the point on the left tail. Therefore the t-test might basically follow a normal distribution.

Since the p-value of paired t-test is closed to the p-value of randomized paired design and both of them are small than the significance level, we can say the results of the t-test agree with the results of the randomization test.

Part IV

```
set.seed(4232) # use student number to set the seed
```

```r
pvals <- replicate(1000, t.test(rexp(20,rate = 1),
                               rexp(20,rate = 1/3))$p.value) #completely randomized design and t-test

sum(pvals<=0.05)/1000
```

```
## [1] 0.883
```

```r
pvals <- replicate(1000, t.test(rexp(20,rate = 1),
                               rexp(20,rate = 1/3),
                               paired = TRUE)$p.value) #Randomized paired design and t test

sum(pvals<=0.05)/1000
```

```
## [1] 0.878
```

```r
pvals <- replicate(1000, wilcox.test(rexp(20,rate = 1),
                                    rexp(20,rate = 1/3))$p.value) #completely randomized design and Wi

sum(pvals <= 0.05)/1000
```

```
## [1] 0.803
```

```r
pvals <- replicate(1000, wilcox.test(rexp(20,rate = 1),
                                    rexp(20,rate = 1/3),
                                    paired = TRUE)$p.value) #Randomized paired design and Wilconxon te
sum(pvals <= 0.05)/1000
```

```
## [1] 0.848
```

The power is the proportion of times that the test correctly rejects the null hypothesis in repeated sampling so that we prefer to use the statistical test have better power.

For the completely randomization design, I would recommend t-test since t-test have better power than Wilconxon test.

For the randomized paired design, I would also recommend t-test since t-test have better power than Wilconxon test.