

# Assignment 3

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Reaction times were recorded for 13 individuals under the influence of either drug A or drug B, giving the following data:

- Drug A: 2.07 1.71 2.24 1.62 2.11
- Drug B: 2.41 1.96 1.93 2.71 2.50 2.84 2.88 2.43

a) Use **R** to carry out a Mann-Whitney U-test on these data.

```
rm(list = ls())
drug.a <- c(2.07, 1.71, 2.24, 1.62, 2.11)
drug.b <- c(2.41, 1.96, 1.93, 2.71, 2.50, 2.84, 2.88, 2.43)

wilcox.test(drug.a, drug.b, alternative='two.sided', exact=TRUE)
```

```
##
## Wilcoxon rank sum test
##
## data: drug.a and drug.b
## W = 6, p-value = 0.04507
## alternative hypothesis: true location shift is not equal to 0
```

Suppose *drug.a* is a random sample from the random variable  $X$ , while *drug.b* is a random sample from the random variable  $Y$ .

$H_0 : X, Y$  have the same distribution

$H_1 : X, Y$  don't have the same distribution

The assumptions for this test are:

1.  $X$  and  $Y$  are independent -which is true since they are different patients.
2. The observations are at least ordinal -which is true since the data are times, and therefore continuous ratio data.

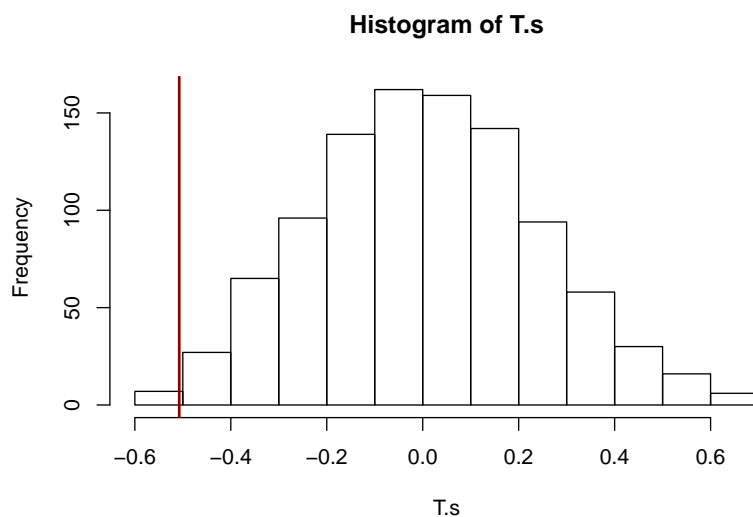
Our data have no ties in them, therefore the *p-value* calculated is exact and does not rely on a Normal approximation. Since the *p-value* of the test is 0.04507, that means that we **reject** the null hypothesis on  $\alpha = 5\%$  significance level. Therefore, the random variables **do not have** the same distribution.

b) Use **R** to carry out a two-sample randomisation test, based on sample means, to assess whether the effects of the two drugs differ, and state your conclusions.

```
set.seed(1903)
n <- length(drug.a)
m <- length(drug.b)
z <- c(drug.a, drug.b)
T.obs <- mean(drug.a) - mean(drug.b)
B <- 1e3
T.s <- NULL

for(b in 1:B){
  s <- sample(1:(n+m), n, replace=FALSE)
  T.sample <- mean(z[s]) - mean(z[-s])
  T.s <- c(T.s, T.sample)
}

T.s <- c(T.s, T.obs)
hist(T.s)
abline(v=mean(T.obs), col='red4', lwd=2)
```



```
pvalue.right <- mean(T.s >= T.obs)
pvalue.left <- mean(T.s <= T.obs)

pvalue.twosided <- 2*min(pvalue.right, pvalue.left)
print('Randomization test approximate p-value:', pvalue.twosided)

## [1] "Randomization test approximate p-value:"
```

According to the two-sample randomization test based on the sample means, the *p-value* is 0.009, and it was calculated for 1000 iterations. This is significant on the  $\alpha = 5\%$  significance level, which means that we **reject** the null hypothesis. Therefore the two random variables **do not have** the same mean.

**c) Will the *p-value* calculated in part (b) differ to one calculated by enumerating all permutations at least as extreme as the observed one? Explain your answer**

The *p-value* of the randomization test will be different from the one calculated by enumerating all the permutations. This is because all the permutations are `choose(n+m,n) = choose(13,8) = 1287` which is bigger than our  $B=1000$ . Therefore, some permutations are not checked on the randomization test. The final result though wouldn't be that different and since our *p-value* is much less than 5%, it makes sense to not explore the full permutation test.