

# Permutation and Randomization Tests

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Computational Methods in Statistics and Data Science (Stats 406)

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A close analog: assume  $Y = \beta_0 + \beta_1 X + \epsilon$  and condition on  $\hat{y} = \hat{\beta}_0 + \hat{\beta}_1 x$ . The  $\hat{\epsilon} = y - \hat{y}$  is **permutation invariant** (we can shuffle them around freely).

## Permutation tests

We will consider a variety of **hypothesis tests** that exploit invariance. Suppose that  $Z$  is invariant conditional on the sample, then we need:

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Tests of this form are known as **permutation tests** when **sampling** and **randomization tests** when analyzing **randomized controlled trials**.

## Example: Developing a test for symmetry

Suppose we have some data from

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We'll develop a test in two parts: (a) a test for medians, and (b) a permutation test for symmetry

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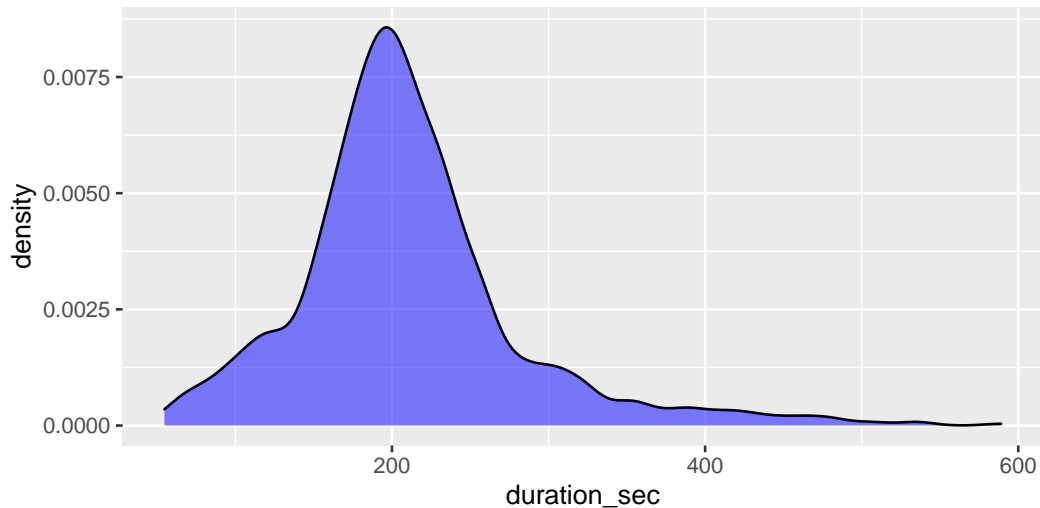
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We can use `binom.test` to test this hypothesis.



## Application: Length of songs on Spotify less than 10 minutes



## Testing $\theta = 200$

```
> testMedian <- function(median0) {  
+   y <- tracks10$duration_sec - median0 > 0  
+   binom.test(sum(y), length(y), p = 0.5)$p.value  
+ }  
> testMedian(200)  
  
[1] 0.385
```

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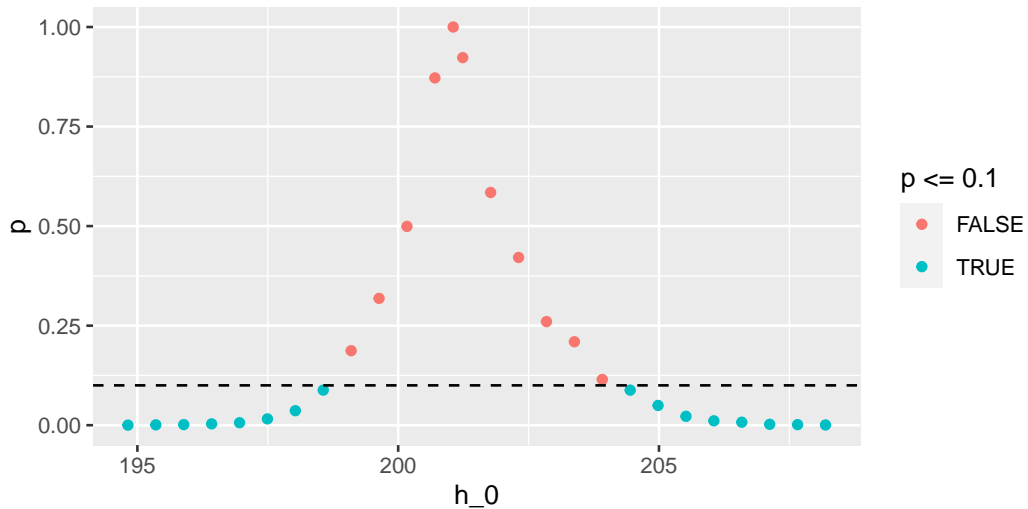
## Confidence intervals

```
> medians <- unique(sort(c(  
+           median(tracks10$duration_sec),  
+           seq(min(tracks10$duration_sec),  
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+           length.out = 1000))))  
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> pvalues <- map_dbl(medians, testMedian)  
  
> medians[which.max(pvalues)] # point estimate  
  
[1] 201.1  
  
> range(medians[0.001 <= pvalues]) # 99.9% CI  
  
[1] 195.9 207.7
```

## Graphing $p$ -values (90% CI)



# Symmetry

Recall the **decomposition of Laplace/Double Exponential** random variables that were **symmetric about  $\theta$** :

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## Monte Carlo

It will be difficult to enumerate all  $2^n$  possible values, but we can use **Monte Carlo sampling**:

```
> testSymmetry <- function(x, theta, k = 1000) {  
+   n <- length(x)  
+   s_0 <- sum(x - theta)  
+   y <- abs(x - theta)  
+   dist <- map_dbl(rerun(k, 2 * rbinom(n, size = 1, p = 0.5) - 1),  
+     ~ sum(y * .x))  
+   2 * min(dist >= s_0, dist <= s_0) / k  
+ }  
> testSymmetry(tracks10$duration_sec, 201)  
[1] 0
```

## Example: Two Sample Problems

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We conceptualized this problem as **two samples**

$$X_1, \dots, X_n \sim F, \quad \text{iid,} \quad (\text{Phonenix})$$

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Previously, we found a confidence interval for  $\theta = E(X) - E(Y)$ , but we could also ask a more general question:

$$H_0 : F = G \quad \text{vs} \quad H_1 : F \neq G$$

## Combined Sample Notation

It's often convenient to think about a combined sample of the form:

$$(W_i, Z_i), \quad i = 1, \dots, n + m$$

Where

$$W_i = \begin{cases} X_i & i \leq n \\ Y_i & i > n \end{cases}$$

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The permutation approach then just requires shuffling the  $Z_i$  values.

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A permutation test will permute the  $Z_i$  to get a conditional distribution for  $T$ .

## Some Example Statistics

- Difference of means:  $T(\mathbf{Z}) = \frac{1}{n} \sum_{i=1}^n Z_i w_i - \frac{1}{n} \sum_{i=1}^n (1 - Z_i) w_i$  (Welch's permutational t-test)



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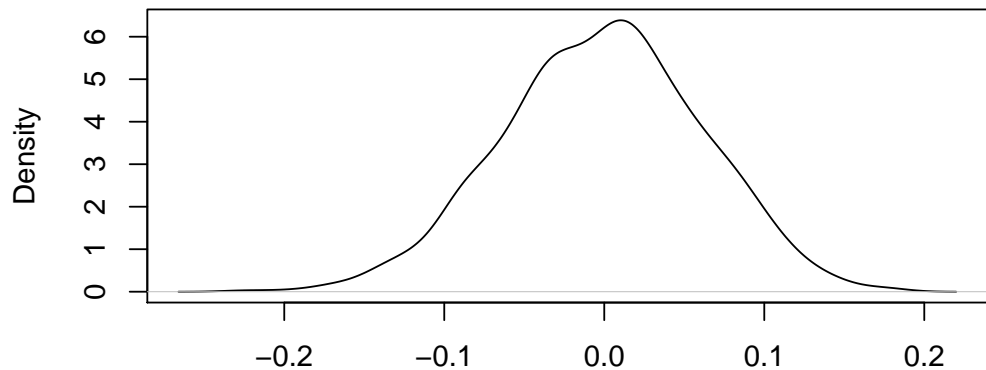
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- Comparisons of ECDFs (Kolmogorov-Smirnov, Anderson-Darling, Cramer-von Mises)

```
> mean_diff <- function(w, z) {mean(w[z], na.rm = TRUE) -  
+                               mean(w[!z], na.rm = TRUE)}
```

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> mean_diff <- function(w, z) {mean(w[z], na.rm = TRUE) -  
+                               mean(w[!z], na.rm = TRUE)}  
  
> n <- nrow(gamoran)  
> dist.t <- replicate(1000, {  
+   ## shuffle the "Z_i" values  
+   permuted_label <- sample(gamoran$PH.AZ)  
+   ## compute the test statistic  
+   mean_diff(gamoran$READ_PCTZ, permuted_label)  
+ })
```

## Distribution under the null



$N = 1000$  Bandwidth = 0.014

## Computing a $p$ -value

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$$H_1 : F \neq G$$

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In other words, we can use created “two tailed”  $p$ -value:

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```
> (t_observed <- mean_diff(gamoran$READ_PCTZ, gamoran$PH.AZ))
```

```
[1] 0.2568
```

```
> 2 * min(mean(dist.t <= t_observed), mean(dist.t >= t_observed))
```

```
[1] 0
```

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- Select a test statistic  $T$  that compares two samples
- Compute the observed value  $\hat{T}$
- Randomly generate  $B$  permutations of the  $n + m$  group labels and compute  $T_b$
- Depending on the alternative, compute the  $p$ -value as

$$p^+ = \frac{1}{B} \sum_{b=1}^B I(T_b \geq \hat{T}), \quad p^- = \frac{1}{B} \sum_{b=1}^B I(T_b \leq \hat{T}), \quad p = 2 \times \min(p^+, p^-)$$

(Note: some sources add one to both numerator and denominator. For large  $B$  both approaches are about the same.)

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But the power can be poor if we don't pick **good test statistics**.



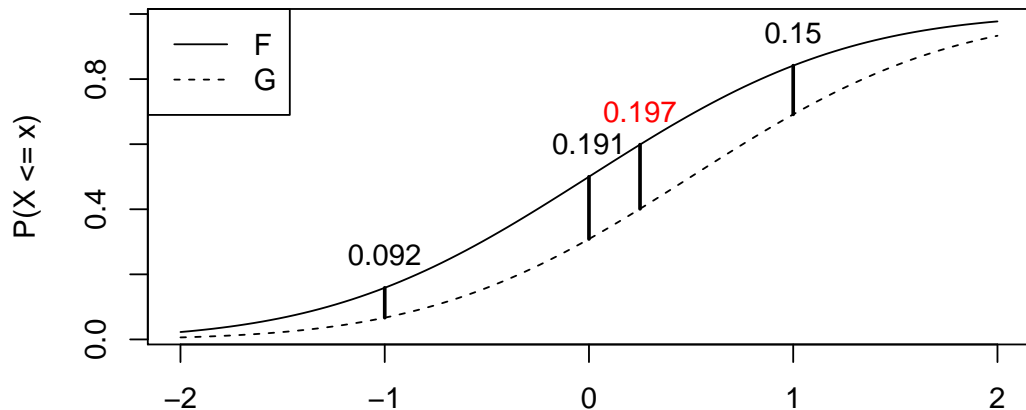
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Next we'll look at a class of test statistics that have proved useful for many problems.

## Kolmogorov-Smirnov



$$T(W, Z) = \max_{1 \leq i \leq n+m} \left| \hat{F}_Z(W_i) - \hat{G}_Z(W_i) \right|$$

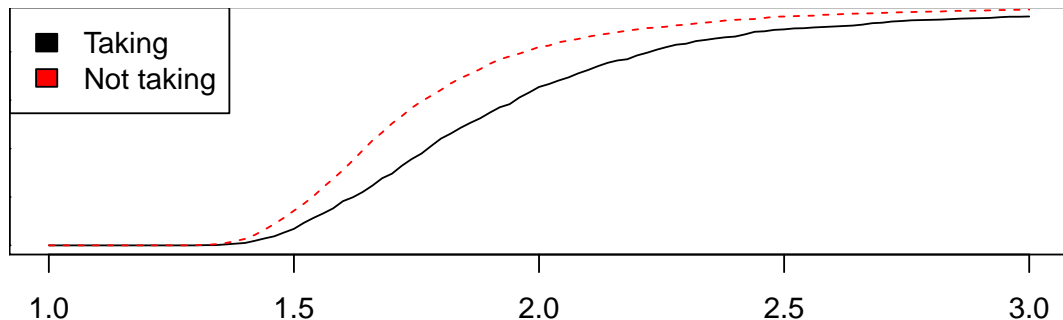
## Blood pressure for subjects taking aspirin vs. not

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One way to summarize the BP measurements was to take the **ratio of systolic to diastolic** pressure:

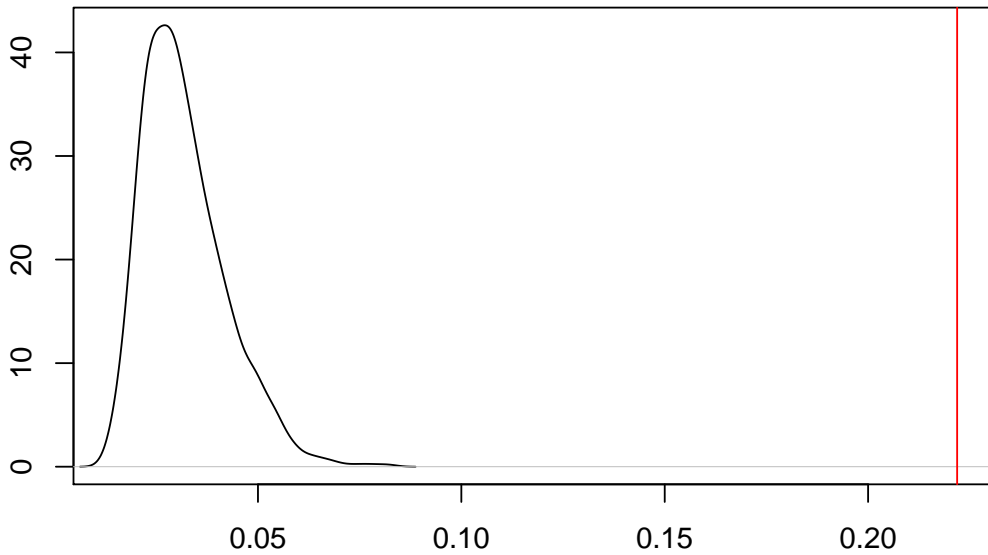


## Implementing KS

```
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+ }  
  
> perms <- replicate(1000, sample(nhanes$taking_aspirin))  
> ts <- apply(perms, 2, function(zstar) {  
+   ks(nhanes$ratio, zstar)  
+ })  
  
> observed_ks <- ks(nhanes$ratio, nhanes$taking_aspirin)  
> (ksp <- 2 * min(mean(ts >= observed_ks), mean(ts <= observed_ks)))  
  
[1] 0
```



Interesting fact: when  $H_0 : F = G$  is true, we can figure out the distribution of  $D$  **without even seeing the data**  $(W, Z)$ , provided we know  $n$  and  $m$ .



## Distribution Free Statistics

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This is because we can express the test statistic with respect to the **ranks** of the  $W_i$ .  
E.g.,

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E.g.,

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Claim: Let

$$D^+ = \max_i \hat{F}(W_i) - \hat{G}(W_i), \quad D^- = \max_i \hat{G}(W_i) - \hat{F}(W_i)$$

Then the statistic  $\max(D^+, D^-)$  is **distribution free**.

## Proof

For all  $i = 1, \dots, n + m$ , let  $R_i$  be the **rank** of  $W_i$  in the combined sample. We'll show that  $D^+$  only depends on the ranks, and the rest of the claim follows similarly.

## Proof

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This is precisely what we call **distribution free**. (Technically, we have parameters  $n$  and  $m$ , but nothing that depends on the data.)

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As with the KS test, it doesn't matter what the actual  $W$  values are, we can get the distribution of  $T(Z, R)$  **without observing any data**.

This test is known as the **Wilcoxon-Mann-Whitney** test.

## Distribution Free Tests in R

- Kolmogorov-Smirnov: `ks.test`
- Wilcoxon-Mann-Whitney: `wilcox.test`
- Normal Scores: for  $H_i = \Phi^{-1}(R_i/(n + m + 1))$ :

$$T(Z, H) = \frac{1}{n} \sum_{i=1}^{n+m} Z_i H_i - \frac{1}{m} \sum_{i=1}^{n+m} (1 - Z_i) H_i$$

is implemented in the `SuppDist` package.

And we can always estimate any other test statistic distribution using a Monte Carlo approach.

```
> with(nhanes, ## creates variables ratio, taking_apsirin  
+      ks.test(x = ratio[taking_aspirin],  
+             y = ratio[!taking_aspirin]))
```

Two-sample Kolmogorov-Smirnov test

data: ratio[taking\_aspirin] and ratio[!taking\_aspirin]

D = 0.22, p-value <2e-16

alternative hypothesis: two-sided

```
> with(nhanes,  
+      wilcox.test(x = ratio[taking_aspirin],  
+                  y = ratio[!taking_aspirin]))
```

Wilcoxon rank sum test with continuity correction

data: ratio[taking\_aspirin] and ratio[!taking\_aspirin]

W = 1645455, p-value <2e-16

alternative hypothesis: true location shift is not equal to 0

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Very common setting is the **two sample problem** where we are testing that groups have the same distribution:  $H_0 : F = G$ .

**Distribution free tests** replace data with ranks (or similar) to make test statistics not depend on the underlying distribution of the data.