STT3030 - Labs #1

Arthur Charpentier

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Clean way to work

```
> getwd()
2 [1] "/Users/arthurcharpentier"
```

- Set up a working directory (using setwd())
- Make sure your data sets are in your working directory.
- You might want to have one directory per lab (project)

```
setwd("/Users/arthurcharpentier/stt3030")
> setwd("/Users/arthurcharpentier/stt3030/lab1")
```

R and vectors

▶ Keep in mind that R is a vector language, so I will use a lot things like

```
1 > resultat = sin(sqrt(1:10))
```

instead of

```
1 > resultat = vector(mode="numeric", length = 10L)
2 > for (i in 1:length(resultat)) {
3 + resultat[i] = sin(sqrt(i))
4 + }
```

Help function

Permutation test

A permutation test (also called re-randomization test or shuffle test) is an exact statistical hypothesis test making use of the proof by contradiction. A permutation test involves two or more samples. The null hypothesis is that all samples come from the same distribution $H_0: F = G$. Under the null hypothesis, the distribution of the test statistic is obtained by calculating all possible values of the test statistic under possible rearrangements of the observed data. Permutation tests are, therefore, a form of resampling. W

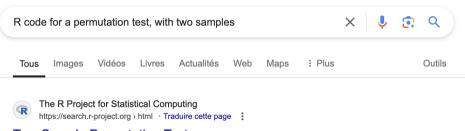
See Fisher (1936) and Pitman (1937) for statistical background

- ► Suppose we want to run a permutation test
- ▶ if you know the function to use, that's easy

```
1 > library("exactRankTests")
2 Package 'exactRankTests' is no longer under development.
3 Please consider using package 'coin' instead.
```

Help function

- ?exactRankTests::perm.test > ?perm.test
 - ► Add? after a function name to access help
 - ▶ Use google (or any web browser) to get help...



Two-Sample Permutation Test

This function carries out an hypothesis test in which the null hypothesis is that the two samples are governed by the same underlying generative probability ...

Help function



R code for a permutation test, with two samples

Q Tous

Images Vidéos Actualités

Carte

Shopping

× Aide

Chat



Canada (en) ▼

Filtre parental : modéré 🔻

Date indifférente ▼

https://search.r-project.org > CRAN > refmans > EnvStats > html > twoSamplePermutationTestLoca...

R: Two-Sample or Paired-Sample Randomization (Permutation) Test...

The two-sample permutation test works by simply enumerating all possible permutations of group assignments, and for each permutation computing the difference between the measures of location for each group (Manly, 2007, p. 113; Efron and Tibshirani, 1993, p. 202). The measure of location for a gro...

twosamples: Fast Permutation B...

Package, Fast Permutation Based Two Sample Tests. 2.0.1 Fast randomization... R: Two-Sample Permutation Test Value. A list with three components: the value of the statistic for the original tw...

R: One and Two Sample Permut...

Details. The permutation test is performed for integer valued...

> you write what you want to do in plain English and get the R code instantly



Chat

what would be the R code for a permutation test, with two samples \boldsymbol{x} and \boldsymbol{y} ?

Certainly! Below is the R code for a permutation test with two samples, x and y. This script calculates the p-value for the hypothesis that the two samples come from the same distribution by comparing the observed difference in means to the distribution of differences obtained by randomly permuting the combined data.

```
# Sample data
2 x <- c(1, 2, 3, 4, 5)
3 y <- c(6, 7, 8, 9, 10)

# Function to perform permutation test
6 permutation_test <- function(x, y, num_permutations = 10000) {
    # Combine the data
    combined <- c(x, y)
    n_x <- length(x)</pre>
```

```
n_y <- length(y)</pre>
10
11
    # Calculate the observed difference in means
12
    observed_diff <- mean(x) - mean(y)</pre>
13
14
    # Initialize a vector to store the permutation differences
15
    perm_diffs <- numeric(num_permutations)</pre>
16
17
18
    # Perform the permutations
    for (i in 1:num_permutations) {
19
       # Permute the combined data
20
       permuted <- sample(combined)</pre>
21
22
       # Split the permuted data into two new samples
23
       perm_x <- permuted[1:n_x]</pre>
24
       perm_y \leftarrow permuted[(n_x + 1):(n_x + n_y)]
25
26
       # Calculate the difference in means for the permuted samples
27
```

```
perm_diffs[i] <- mean(perm_x) - mean(perm_y)</pre>
28
29
30
    # Calculate the p-value
31
    p_value <- mean(abs(perm_diffs) >= abs(observed_diff))
32
33
34
    # Return the observed difference and p-value
    list(observed_diff = observed_diff, p_value = p_value)
35
36 }
37
  # Run the permutation test
result <- permutation test(x, y)</pre>
40 print (result)
```

is there a R package to do the same?

Yes, there are R packages that can perform permutation tests. One commonly used package is coin. The coin package provides a comprehensive framework for conditional inference procedures, including permutation tests. Below is an example of how to perform a permutation test using the coin package.

First, you'll need to install the **coin** package if you haven't already:

```
install.packages("coin")
```

Then, you can use the following code to perform a permutation test on two samples x and y:

```
1 # Load the coin package
2 library(coin)
3
4 # Sample data
5 \times (-c(1, 2, 3, 4, 5))
6 \text{ v} \leftarrow c(6, 7, 8, 9, 10)
8 # Combine the data into a data frame
g data <- data frame(</pre>
values = c(x, y),
  group = factor(rep(c("x", "y"), times = c(length(x), length(y))))
12 )
13
14 # Perform the permutation test
result <- oneway_test(values ~ group, data = data, distribution = "</pre>
      approximate")
16
17 # Print the result
```

18 print(result)

In this code:

- The coin package is used to perform the permutation test.
- The data from the two samples x and y are combined into a single data frame with a grouping factor.
- The oneway_test function from the coin package is used to perform the permutation test.
- The result of the test is printed.

can you explain the maths of that test?

Certainly! The permutation test, also known as a randomization test, is a non-parametric statistical test used to determine if there is a significant difference between two groups. Unlike traditional parametric tests (like the t-test), permutation tests do not make assumptions about the distribution of the data, making them robust and versatile

Permutation Test: Mathematical Explanation

- ▶ Null Hypothesis (H0): The two samples come from the same distribution.
- Alternative Hypothesis (H1): The two samples come from different distributions

Procedure:

1. Compute the test statistic for the observed data:

$$T_{\text{obs}} = \bar{x} - \bar{y}$$

- 2. Combine and permute the data.
- 3. Compute the test statistic for each permutation:

$$T_i = \bar{x}_i - \bar{y}_i$$

- Generate the permutation distribution.
- 5. Calculate the p-value:

$$p = \frac{\sum_{i=1}^{B} I(|T_i| \ge |T_{\text{obs}}|)}{B}$$

Example: Difference in Means Consider two samples:

$$x = \{1, 2, 3, 4, 5\}, y = \{6, 7, 8, 9, 10\}$$

1. Observed Test Statistic:

$$T_{\text{obs}} = \bar{x} - \bar{y} = 3 - 8 = -5$$

2. Permutation Process:

• Combine x and v:

$$combined = 1, 2, 3, 4, 5, 6, 7, 8, 9, 10$$

- Shuffle and split into two new groups (of sizes 5 each):
 - Permutation 1: {1,2,3,4,6} and {5,7,8,9,10}
 - Permutation 2: {2,3,4,5,7} and {1,6,8,9,10}
 - ... and so on.

3. Compute Test Statistic for Each Permutation:

For Permutation 1:

$$T_1 = (\overline{x} - \overline{y}) = \frac{16}{5} - \frac{39}{5} = -4.6$$

- Repeat this process for all permutations.
- **4. P-value Calculation:** Suppose after 10,000 permutations, 200 permutations resulted in a test statistic as extreme or more extreme than |-5|:

$$p = \frac{200}{10000} = 0.02$$

If the p-value is less than the chosen significance level (e.g., 0.05), you reject the null hypothesis, suggesting that there is a significant difference between the two samples. The permutation test involves calculating the observed test statistic, repeatedly shuffling and splitting the combined data to form new samples, calculating the test statistic for each permutation, and then comparing the observed statistic to the distribution of permuted statistics to determine the p-value. This method is powerful

because it relies on the data itself rather than assumptions about the underlying distributions.

```
1 > result
2
3    Approximative Two-Sample Fisher-Pitman
4    Permutation Test
5
6    data: values by group (x, y)
7    Z = -2.6112, p-value = 0.0094
8    alternative hypothesis: true mu is not equal to 0
```

why T_{-} obs is not the same as Z=-2.6112 returned by the R function ?

Great question! The difference between $T_{\rm obs}$ and the Z-value returned by the coin package can be attributed to the different test statistics used by each method. Let me explain in detail.

T_{obs} in Manual Permutation Test

In the manual permutation test example provided, $T_{\rm obs}$ is the observed difference in means between the two samples. This is a straightforward calculation:

$$T_{\text{obs}} = \bar{x} - \bar{y}$$

where \bar{x} and \bar{y} are the sample means of the two groups x and y, respectively. Z-value in the coin Package

The coin package in R, when performing permutation tests, often standardizes the test statistic. Specifically, the oneway_test function computes a standardized statistic under the null hypothesis, which is typically a Z-value in the context of asymptotic approximations.

Example Calculation:

Here's the detailed step-by-step process:

Observed Test Statistic:

In the manual method, the observed test statistic T_{obs} is calculated as the difference in means:

$$T_{\text{obs}} = \bar{x} - \bar{y} = 3 - 8 = -5$$

Standardization in the coin Package:

The coin package uses a different approach to calculate the test statistic. It computes a standardized version of the test statistic, which is often akin to the Z-score. This standardization takes into account the variance and sample sizes.

The *Z*-score is typically calculated as:

$$Z = \frac{(\bar{x} - \bar{y}) - \text{ Expected Difference under } H_0}{\text{Standard Error}}$$

However, the coin package's oneway_test function may use a different form of the statistic that is robust and appropriate for the permutation context. This involves more complex adjustments and standardizations that reflect the permutation distribution.

- Include details in your query to get more relevant answers e.g. "Comment the code liberally to explain what each piece does and why it's written that way"
- Specify the steps required to complete a task e.g.

► See more on prompt engineering, prompts for data science, or prompt engineering guide

using osmdata R library, write R codes to find locations of all Jean Coutu stores in Montréal, Qc. Then use mapview to visualize those stores on a map

Certainly! Below is an R script that uses the osmdata and mapview packages to find and visualize all Jean Coutu stores in Montréal, Quebec.

```
# Install and load necessary packages
if (!requireNamespace("osmdata", quietly = TRUE)) {
   install.packages("osmdata")
}
if (!requireNamespace("sf", quietly = TRUE)) {
   install.packages("sf")
}
```

```
8 if (!requireNamespace("mapview", quietly = TRUE)) {
    install.packages("mapview")
10 }
12 library (osmdata)
13 library(sf)
14 library(mapview)
16 # Define the bounding box for Montr al, QC
montr al_bbox <- getbb("Montr al , Qu bec")</pre>
18
19 # Query OSM for all Jean Coutu locations in Montr al
 iean coutu query <- opg(bbox = montr al bbox) %>%
    add_osm_feature(key = "name", value = "Jean Coutu")
21
  # Extract data
24 jean_coutu_data <- osmdata_sf(jean_coutu_query)</pre>
25
```

```
# Check the structure of the returned data
print(names(jean_coutu_data))

# Extract the points data (store locations)
jean_coutu_locations <- jean_coutu_data$osm_points

# Visualize the locations on a map using mapview
mapview(jean_coutu_locations)
```

Explanation:

Install and load packages: The script checks if the required packages (osmdata, sf, and mapview) are installed. If not, it installs them. Then, it loads these packages into the R session.

Define bounding box: The getbb function is used to get the bounding box for Montréal, Quebec, which serves as the spatial extent for our query.

Query OSM data: We use the opq function to initiate an Overpass API query with the defined bounding box. We then add a feature using add_osm_feature to filter for locations with the name "Jean Coutu".

Extract data: The osmdata_sf function is used to retrieve the data as an sf object (simple features). This object contains multiple layers, including points, lines, polygons, etc.

Extract store locations: We specifically extract the point data from the retrieved OSM data, which represents the locations of the stores.

Visualize: Finally, we use mapview to visualize these store locations on an interactive map.

Running the Script:

Make sure you have an active internet connection since the script relies on querying the OpenStreetMap database through the Overpass API.

When you run this script, a map will appear in the RStudio Viewer or your default browser, showing the locations of Jean Coutu stores across Montréal.

If the map doesn't display any stores, it might be due to a lack of precise tagging in OSM. You can try refining the query by including different filters or tags.



```
> str(result)
2 Formal class 'ScalarIndependenceTest' [package "coin"] with 7 slots
    .. @ parameter : chr "mu"
4 ... @ nullvalue : num 0
5 .. @ distribution:Formal class 'ApproxNullDistribution' [package "
    coin" | with 12 slots
    .. .. ..@ seed : int [1:626] 10403 202 1544423891
     -753397414 -138716415 524441244 1725742425 -816412468 1172112304
     -939627685 ...
    .. .. .. @ nresample : int 10000
8
    .. @ statistic :Formal class 'ScalarIndependenceTestStatistic' [
    package "coin"] with 15 slots
    .. .. ..@ alternative
                                  : chr "two.sided"
10
    .. .. ..@ paired
                                : logi FALSE
11
    ..... 0 teststatistic : num -0.839
12
    .. .. .. @ standardizedlinearstatistic: num -0.839
13
    .. .. ..@ linearstatistic : num [1, 1] -5.54
14
```

▶ We can get only the numerical value of the test statistic Z

```
> result@statistic@teststatistic
[1] -0.8391545
```

- ► S3 class, call elements using \$
- ► S4 class, call elements (slots) using @

► S3 class

```
1 > regression = lm(dist ~ speed, data = cars)
2 > str(regression)
3 List of 12
$ coefficients : Named num [1:2] -17.58 3.93
5 ..- attr(*, "names") = chr [1:2] "(Intercept)" "speed"
6 $ residuals : Named num [1:50] 3.85 11.85 -5.95 12.05 2.12 ...
7 ..- attr(*, "names") = chr [1:50] "1" "2" "3" "4" ...
8 $ effects : Named num [1:50] -303.914 145.552 -8.115 9.885 0.194
9 ..- attr(*, "names") = chr [1:50] "(Intercept)" "speed" "" "" ...
10 $ rank : int 2
$ fitted.values: Named num [1:50] -1.85 -1.85 9.95 9.95 13.88 ...
..- attr(*, "names") = chr [1:50] "1" "2" "3" "4" ...
13 $ assign : int [1:2] 0 1
14 $ qr :List of 5
15 .. $ gr : num [1:50, 1:2] -7.071 0.141 0.141 0.141 0.141 ...
```

If we want σ , standard deviation of residuals $\hat{\varepsilon}$, in a regression

```
> summary(regression)$sigma
2 [1] 15.37959
3 > sqrt(sum(regression$residuals^2)/regression$df.residual)
4 [1] 15.37959
```

Reports

► To produce a nice report, use R-Markdown documents

```
title: "Regression Analysis Report"
3 author: "Your Name"
4 date: "'r Sys.Date()'"
5 output: html_document
8 '''(fr}
9 regression = lm(dist ~ speed, data = cars)
sigma = summary(regression)$sigma
  ""
11
 Standard deviation is '{r} round(sigma, 2)'.
```

Reports

► The outcome will be

Regression Analysis Report

Your Name

```
regression = lm(dist ~ speed, data = cars)
sigma = summary(regression)$sigma
```

Standard deviation is 15.38.

you write ask to get simple functions

Import a CSV file called "data.csv" into a data frame called

To import a CSV file called "data.csv" into a data frame called "df" in R, you can use the read.csv() function from base R. Here is how you can do it:

```
df <- read.csv("data.csv")</pre>
```

Filter the rows in the data frame "df" where the variable "gender" is equal to "female".

To filter the rows in the data frame df where the variable gender is equal to "female". you can use the subset() function or the dplyr package for a more tidyverse-friendly approach.

Here are both methods:

Using Base R

```
df_female <- subset(df, gender == "female")</pre>
```

Using dplyr Package

First, install and load the dplyr package if you haven't already. Then, filter the data frame::

```
install.packages("dplyr")
2 library(dplyr)
3 df_female <- df %>% filter(gender == "female")
```

• generate $X \sim \sum_{i=1}^{N} Y_i$ (compound Poisson)

can you write a R function that generate compound poisson variables, with gamma jumps ?

Certainly! In R, you can generate compound Poisson variables with gamma-distributed jumps using the following function. The function will take the parameters for the Poisson distribution (lambda) and the gamma distribution (shape and scale) as inputs. Here's a sample implementation:

```
1 # Load necessary library
2 install.packages("MASS")
3
4 generate compound poisson <- function(n, lambda, shape, scale) {
    # n: number of compound Poisson variables to generate
    # lambda: rate parameter for the Poisson distribution
6
    # shape: shape parameter for the gamma distribution
8
    # scale: scale parameter for the gamma distribution
Q
    # Generate Poisson random variables
10
    num jumps <- rpois(n, lambda)</pre>
11
12
    # Initialize vector to store compound Poisson variables
13
    compound_poisson_vars <- numeric(n)</pre>
14
15
    # Generate compound Poisson variables
16
    for (i in 1:n) {
17
      if (num_jumps[i] > 0) {
18
```

```
# Generate gamma jumps
19
        jumps <- rgamma(num_jumps[i], shape, scale)</pre>
20
        # Sum the jumps to get the compound Poisson variable
21
        compound_poisson_vars[i] <- sum(jumps)</pre>
      } else {
23
        # If there are no jumps, the value is 0
24
        compound_poisson_vars[i] <- 0</pre>
25
26
27
28
    return(compound_poisson_vars)
29
30 }
31
  # Example usage
33 n <- 1000
            # Number of variables to generate
34 lambda <- 2 # Poisson rate parameter
35 shape <- 2 # Gamma shape parameter
36 scale <- 1
                  # Gamma scale parameter
```

```
37
  compound_poisson_samples <- generate_compound_poisson(n, lambda, shape
      . scale)
```

The function generate_compound_poisson generates n compound Poisson random variables.

It first generates the number of jumps from a Poisson distribution with parameter lambda.

For each generated Poisson variable, if the number of jumps is greater than zero, it generates gamma-distributed jumps using the rgamma function and sums them up to get the compound Poisson variable.

If there are no jumps, the value is set to zero.

Replication

► Replication of random samples ?

```
1 > ?set.seed

2 > set.seed(12345)

3 > (x=rnorm(1))

4 [1] 0.5855288

5 > (x=rnorm(1))

6 [1] 0.709466

7 > (x=rnorm(1))

8 [1] -0.1093033

9 > set.seed(12345)

10 > (x=rnorm(1))

11 [1] 0.5855288
```

References

Fisher, R. (1936). The use of multiple measurements in taxonomic problems. Annals of eugenics, 7(2):179–188.

Gallic, E. (2020). Notes de cours de R. https://egallic.fr/Enseignement/R/Book/.

Pitman, E. J. (1937). Significance tests which may be applied to samples from any populations. Journal of the Royal Statistical Society, 4(1):119–130.