

Permutation Tests for Univariate and Multivariate Data

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1 Introduction

The idea of permutation tests was first introduced by Ronald Aylmer Fisher in 1936, but then not widely used, because available technologies back in these days could not cope with the high computational burden that these procedures generated. Discussing about how to perform a test of significance to compare the height of Frenchmen and Englishmen based on two samples of 100 units each, Fisher himself wrote:

The simplest way of understanding quite rigorously, yet without mathematics, what the calculations of the test of significance amount to, is to consider what would happen if our two hundred actual measurements were written on cards, shuffled without regard to nationality, and divided at random into two new groups of a hundred each. This division could be done in an enormous number of ways, but though the number is enormous it is a finite and a calculable number. We may suppose that for each of these ways the difference between the two average statures is calculated. Sometimes it will be less than an inch, sometimes greater. If it is very seldom greater than an inch, in only one hundredth, for example, of the ways in which the subdivision can possibly be made, the statistician will have been right in saying that the samples differed significantly. For if, in fact, the two populations were homogeneous, there would be nothing to distinguish the particular subdivision in which the Frenchmen are separated from the Englishmen from among the aggregate of the other possible separations which might have been made. Actually, the statistician does not carry out this very simple and very tedious process, but his conclusions have no justification beyond the fact that they agree with those which could have been arrived at by this elementary method.

R. A. Fisher (1936):

“The Coefficient of Racial Likeness” and the Future of Craniometry.
The Journal of the Royal Anthropological Institute of Great Britain and Ireland, Vol. 66., pp. 57–63.

This document describes the application of permutation tests to various univariate and multivariate tests. First of all, we introduce permutation tests for differences between two univariate or multivariate populations. Then, we describe tests for the mean of one population, tests for the ANOVA and for linear models. Finally, we present permutation tests for functional data. For a detailed discussion of permutation tests, please refer to Pesarin and Salmaso (2010).

2 Two-population tests

2.1 Difference between two univariate populations (independent case)

Suppose to observe two samples of sizes n_1 and n_2 from two independent random variables Y_1 and Y_2 :

$$Y_{1i} \stackrel{\text{iid}}{\sim} Y_1, \quad i = 1, \dots, n_1; \quad Y_{2i} \stackrel{\text{iid}}{\sim} Y_2, \quad i = 1, \dots, n_2.$$

Let \mathcal{Y} denote the space in which the two r.v. Y_1 and Y_2 take values. We want to develop a test for equality between the distributions of the two populations, i.e., we want to test:

$$H_0 : Y_1 \stackrel{d}{=} Y_2 \text{ vs. } H_1 : Y_1 \stackrel{d}{\neq} Y_2. \quad (1)$$

To test the hypothesis (1) in a parametric framework, we would make some assumptions on the distributions of Y_j , eliciting them in terms of a set of parameters. In a non-parametric framework, we don't want to make any assumption on the distributions of data, hence The test that will be developed will be a test conditioned on the observed data $\mathbf{Y} = [\mathbf{Y}_1, \mathbf{Y}_2]$.

Observe that, under the null hypothesis, the two populations have the same distribution ($Y_1 \stackrel{d}{=} Y_2 \stackrel{d}{=} Y$), hence:

$$Y_{ji} \stackrel{\text{iid}}{\sim} Y, \quad j = 1, 2, \quad i = 1, \dots, n_j.$$

In this case, the observations Y_{ij} are exchangeable (as they are sampled from the same population of distribution Y). In particular, every possible rearrangement of data is equally likely. Let $\mathcal{Y}_{|\mathbf{Y}}$ the set of all possible permutations of the pooled vector $\mathbf{Y} = [Y_{ij}]_{i=1, \dots, n_j, j=1, 2}$, and let $M = (n_1 + n_2)!$ be its cardinality. We have that, conditioned to the observed data, every vector in $\mathcal{Y}_{|\mathbf{Y}}$ is equally likely:

$$\mathbb{P}[\mathbf{Y} = \mathbf{y} | \mathcal{Y}_{|\mathbf{Y}}] = \mathbb{P}[\mathbf{Y}^* = \mathbf{y} | \mathcal{Y}_{|\mathbf{Y}}] = \begin{cases} 1/M & \text{if } \mathbf{y} \in \mathcal{Y}_{|\mathbf{Y}} \\ 0 & \text{if } \mathbf{y} \notin \mathcal{Y}_{|\mathbf{Y}} \end{cases}.$$

Note that, in the last equation, we conditioned on $\mathcal{Y}_{|\mathbf{Y}}$. Indeed, under the null hypothesis, the information carried by the data is the same for any permutation. Hence, conditioning on the data under H_0 can be written formally as conditioning on the set $\mathcal{Y}_{|\mathbf{Y}}$.

Now, we introduce a test statistic T as a function mapping the sample space \mathcal{Y} into \mathbb{R} :

$$T : \mathcal{Y} \mapsto \mathbb{R}.$$

In permutation tests, the test statistic is always supposed to assume larger values under the alternative hypothesis. In particular, we suppose that the distribution of T under H_1 is stochastically greater than its distribution under H_0 . For instance, in the case of the test for differences between two populations means, the statistic can be the absolute mean difference:

$$T(\mathbf{Y}) = |\bar{Y}_1 - \bar{Y}_2|,$$

where $\bar{Y}_j = \sum_{i=1}^{n_j} Y_{ji}/n_j$.

Instead of trying to elicit the distribution of T (which requires to make assumptions on the data distribution), we will compute the distribution of T conditioned to the data, i.e., the distribution of $T(\mathbf{Y}^*)$, for any $\mathbf{Y}^* \in \mathcal{Y}_{|\mathbf{Y}}$. This distribution can easily be computed, since every point of $\mathcal{Y}_{|\mathbf{Y}}$ has the same probability:

$$\mathbb{P}[T(\mathbf{Y}^*) \leq t | \mathcal{Y}_{|\mathbf{Y}}] = \frac{\#\{T(\mathbf{Y}^*) \leq t\}}{M}.$$

Note that the statistic can assume $\binom{n_1+n_2}{n_1} < (n_1 + n_2)!$ different values. The conditional distribution of T can thus be calculated exactly, by evaluating the values $T(\mathbf{Y}^*)$, for any permutation \mathbf{Y}^* . In the following, we will denote by T^* the conditional distribution of T .

The permutation test is then performed by using the conditional distribution of the test statistic. Let $T_0 = T(\mathbf{Y})$ indicate the value of the test statistic on the observed unpermuted data.

Critical Region The α -level critical region of the test, for any $\alpha \in [0, 1]$ is the following:

$$\{T_0 \geq T_\alpha\},$$

where T_α is the α -th quantile of the discrete distribution of T^* .

p -value The p -value p of the test is calculated as the proportion of $T(\mathbf{Y}^*)$ exceeding the value T_0 :

$$p = \mathbb{P}[T^* \geq T_0 | \mathcal{Y}_{|\mathbf{Y}}] = \frac{\#\{T^* \geq T_0\}}{M}.$$

Note that, since the distribution of T^* is discrete, the p -value of the test can only assume a finite number of values in the interval $[0, 1]$. In detail the p -value takes values in the set $\Lambda = \{k / \binom{n_1+n_2}{n_1}\}_{k=1, \dots, \binom{n_1+n_2}{n_1}}$.

If we choose an attainable level $\alpha \in \Lambda$, the permutation test is exact:

$$\mathbb{P}[p \leq \alpha | H_0] = \mathbb{P}[p \leq \alpha | \mathcal{Y}_{|\mathbf{Y}}] = \mathbb{P}\left[\frac{\#\{T^* \geq T_0\}}{M} \leq \alpha | \mathcal{Y}_{|\mathbf{Y}}\right] = \alpha, \forall \alpha \in \Lambda. \quad (2)$$

If, on the other hand, $\alpha \notin \Lambda$, we have that:

$$\mathbb{P}[p \leq \alpha | H_0] = \mathbb{P}[p \leq \alpha | \mathcal{Y}_{|\mathbf{Y}})] \leq \alpha, \forall \alpha \notin \Lambda. \quad (3)$$

Hence, we say that a permutation test is exact if both (2) and (3) hold.

In the general case, a permutation test for testing a null hypothesis H_0 against the alternative H_1 , is based on the following:

- a set of transformations of the data set equally likely under H_0 ;
- a test statistic stochastically greater under H_1 than under H_0 .

If we provide this two elements, we can always construct an exact permutation test.

Finally, note that evaluate every possible permutation of $\mathcal{Y}_{|\mathbf{Y}}$ may be computationally intensive. Hence, in applications, the p -value of the test is usually evaluated through a Monte Carlo algorithm, by sampling from the set $\mathcal{Y}_{|\mathbf{Y}}$. The general algorithm may be written as follows:

1. evaluate the test statistic under the observed data $T_0 = T(\mathbf{Y})$;
2. repeat the following B times:
 - (a) choose a random permutation $\mathbf{Y}_b^* \in \mathcal{Y}_{|\mathbf{Y}}$;
 - (b) evaluate the test statistic on the permuted data $T_b^* = T(\mathbf{Y}_b^*)$;
 - (c) save the value of T_b^* ;
3. evaluate the p -value of the test as the proportion of permuted scenarios in which the test statistic exceed the value T_0 :

$$p = \frac{\#\{T_b^* \geq T_0\}}{B}.$$

2.2 Difference between two univariate populations (paired case)

We now assume a paired dependence between the units of the first group and the ones of the second group. In particular, $n_1 = n_2 = n$ and units are paired across groups, i.e., $(Y_{i1}, Y_{i2}) \stackrel{\text{iid}}{\sim} (Y_1, Y_2)$, $i = 1, \dots, n$. We still want to test for differences between the two distributions, i.e., we want to test:

$$H_0 : Y_1 \stackrel{d}{=} Y_2 \text{ vs. } H_1 : Y_1 \stackrel{d}{\neq} Y_2.$$

In this case, observations of the two variables Y_1 and Y_2 are paired. Thus the simple permutations of the data do not have the same likelihood. This problem can be solved by restricting the set of permutations. Indeed, under $H_0^{(k)}$ exchangeability is just between and within pairs (e.g., if we want to preserve likelihood, pairs cannot be splitted up). The family of transformations is thus composed by between and within-couple permutations of the observed values.

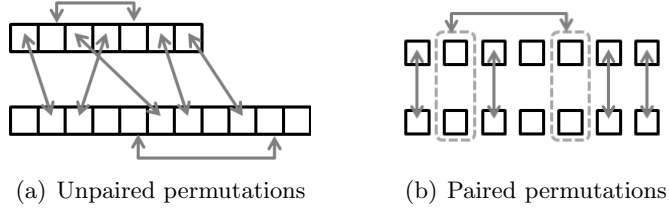


Figure 1: Examples of some possible likelihood-invariant transformations of the original data set in the paired and unpaired scenarios.

Examples of possible likelihood-invariant transformations of the original data set in the unpaired and paired scenario are presented in Figure 1.

The test statistic can be the contrast between the two sample means, as used in the unpaired test, i.e.:

$$T(\mathbf{Y}) = |\bar{\mathbf{Y}}_1 - \bar{\mathbf{Y}}_2|$$

Note that in the paired scenario, the total number of permutations leading to different values of the test statistic is 2^n .

2.3 Difference between two multivariate populations

Suppose now that we are testing for the difference in mean between two p -variate populations, in the independent case. We have now $\mathbf{Y}_{i1} \stackrel{\text{iid}}{\sim} \mathbf{Y}_1 \in \mathbb{R}^p$, and $\mathbf{Y}_{i2} \stackrel{\text{iid}}{\sim} \mathbf{Y}_2 \in \mathbb{R}^p$. We want to test for equality between the two distributions \mathbf{Y}_1 and \mathbf{Y}_2 :

$$H_0 : \mathbf{Y}_1 \stackrel{d}{=} \mathbf{Y}_2 \text{ vs. } H_1 : \mathbf{Y}_1 \stackrel{d}{\neq} \mathbf{Y}_2.$$

Under the null hypothesis, data are exchangeable with respect to units, as in the one-dimensional case. Hence, we can apply the $(n_1 + n_2)!$ unit permutations.

We only have to provide a test statistic stochastically greater under H_1 than under H_0 . If we are testing for the mean difference between the two populations, any distance between the sample means can here be used. A natural choice is the Hotelling T -square (Johnson et al., 1992):

$$T^2 = \frac{n_1 n_2}{n_1 + n_2} (\bar{\mathbf{Y}}_1 - \bar{\mathbf{Y}}_2)' S_p^{-1} (\bar{\mathbf{Y}}_1 - \bar{\mathbf{Y}}_2),$$

where $\bar{\mathbf{Y}}_j \in \mathbb{R}^p$ is the sample mean of the data \mathbf{Y}_{ij} , $j = 1, 2$, and S_p is the pooled variance-covariance matrix estimate. Note that, under H_0 , \mathbf{Y}_1 and \mathbf{Y}_2 have the same distribution, in particular they also have the same variance-covariance matrix.

Finally, note that if we are in a paired scenario, we can still use the same test statistic, and the $2^{n_1} = 2^{n_2}$ paired data permutation, as described in Section 2.2.

3 One-population tests

3.1 Test for the mean of a univariate population

Suppose that we are testing the mean of one univariate population Y , based on the sample $Y_1, \dots, Y_n \stackrel{\text{iid}}{\sim} Y \in \mathbb{R}$. The test that we want to construct is the following:

$$H_0 : \mathbb{E}[Y] = \mu_0 \text{ vs. } H_1 : \mathbb{E}[Y] \neq \mu_0.$$

Again, we need to define a family of likelihood-invariant data transformation and a test statistic.

Data are exchangeable with respect to units both under H_0 and H_1 , hence, in this case data permutations cannot be applied (a test based of data permutations is correct, but cannot be a solution, as the test statistic will be the same under all permutations). To solve this problem, one have to introduce the additional hypothesis that data distribution f is symmetric (with respect to its mean μ): $f(y) = f(2\mu - y)$. By adding this assumption, under the null hypothesis the reflections of data with respect to μ_0 are likelihood-invariant: $f(y_i) = f(2\mu_0 - y_i)$. Hence, the transformations to apply in this case are all possible 2^n reflections of the data Y_i across the mean under H_0 .

The test statistic can be simply chosen as a contrast between the sample mean \bar{Y} and μ_0 : $T(Y_1, \dots, Y_n) = |\bar{Y} - \mu_0|$.

Note that, within this framework, testing for differences between two paired populations and testing if the mean of the population of differences is equal to zero leads to the exact same test. Indeed, the paired permutations introduced in Section 2.2 corresponds to a change of the sign (i.e., a reflection across zero) of the difference between the two paired observations, and the test statistic is the same.

3.2 Test for the mean of a multivariate population

Suppose now that we are testing the mean of a p -variate population \mathbf{Y} , based on the sample $\mathbf{Y}_1, \dots, \mathbf{Y}_n \stackrel{\text{iid}}{\sim} \mathbf{Y} \in \mathbb{R}^p$. We want to test:

$$H_0 : \mathbb{E}[\mathbf{Y}] = \boldsymbol{\mu}_0 \text{ vs. } H_1 : \mathbb{E}[\mathbf{Y}] \neq \boldsymbol{\mu}_0.$$

Also in this case, to test for the mean of the population \mathbf{Y} we have to suppose that the p -variate data distribution $f(y_1, \dots, y_p)$ is symmetric with respect to the mean $\boldsymbol{\mu} = (\mu_1, \dots, \mu_p)$, i.e., that $f(y_1, \dots, y_p) = f(2\mu_1 - y_1, \dots, 2\mu_p - y_p)$, or with a vectorial notation, $f(\mathbf{y}) = f(2\boldsymbol{\mu} - \mathbf{y})$. Under this assumption, under the null hypothesis the reflections of data with respect to $\boldsymbol{\mu}_0$ are likelihood-invariant: $f(\mathbf{y}_i) = f(2\boldsymbol{\mu}_0 - \mathbf{y}_i)$. Hence, the transformations to apply in this case are all possible 2^n reflections of the data \mathbf{Y}_i across the mean under H_0 . Note that the reflection has to be applied jointly to all the p features of the data.

As test statistic for the multivariate case we can choose, again, the Hotelling's T-square statistic:

$$T^2 = n(\bar{\mathbf{Y}} - \boldsymbol{\mu})' S^{-1} (\bar{\mathbf{Y}} - \boldsymbol{\mu}),$$

where S is the estimate of the variance-covariance matrix.

Again, testing for differences between two multivariate paired populations and testing if the mean of the multivariate population of differences is equal to zero for all features leads to the exact same test.

4 ANOVA

Suppose to observe $g > 2$ samples of sizes n_j from g independent random variables Y_j , $j = 1, \dots, g$:

$$Y_{ij} \stackrel{\text{iid}}{\sim} Y_j, \quad i = 1, \dots, n_j; \quad j = 1, \dots, g.$$

We want to test for equality between the distributions of the g populations, i.e., we want to test:

$$H_0 : Y_1 \stackrel{d}{=} Y_2 \stackrel{d}{=} \dots \stackrel{d}{=} Y_g \text{ vs. } H_1 : \exists j_1, j_2 \in \{1, \dots, g\}, \text{ s.t. } Y_{j_1} \stackrel{d}{\neq} Y_{j_2}.$$

Under the null hypothesis, all data come from the same population. Hence, exactly as in the two-populations case, the family of likelihood-invariant transformations of the data set is constituted by all possible $(n_1 + n_2 + \dots + n_g)!$ permutations of the data indexes.

As test statistic, we can use the Fisher's F (Johnson et al., 1992):

$$T_F = \frac{\sum_{j=1}^g (\bar{Y}_j - \bar{Y})^2 / (g - 1)}{\sum_{j=1}^g \sum_{i=1}^{n_j} (Y_{ij} - \bar{Y})^2 / (n_j - g)},$$

where $\bar{Y} = \sum_{j=1}^g \sum_{i=1}^{n_j} Y_{ij} / (n_1 + \dots + n_g)$ is the common sample mean and $\bar{Y}_j = \sum_{i=1}^{n_j} Y_{ij} / n_j$ is the sample mean of group j .

5 Linear models

We now want to develop tests for the coefficients of a linear model, in a semi-parametric framework. We suppose that data can be expressed in terms of some covariates x_{il} by the model:

$$Y_i = \beta_0 + \sum_{l=1}^L \beta_l x_{il} + \epsilon_i, \quad i = 1, \dots, n. \quad (4)$$

The model is semi-parametric in the sense that it is expressed in terms of the parameters β_l , but the distribution of the errors ϵ is not expressed. The only

hypothesis that we make is that the errors are independent and identically distributed from a zero-mean r.v.

The inference for the linear model consists in different tests. First of all, we may want to develop a global test for the model (the analog of the F-test of the linear regression model). In this case the test is:

$$H_{0,model} : \beta_1 = \beta_2 = \dots = \beta_L = 0 \text{ vs. } H_{1,model} : \exists l \in \{1, \dots, L\}, \text{ s.t. } \beta_l \neq 0.$$

Under the null hypothesis the model (4) becomes:

$$Y_i = \beta_0 + \epsilon_i, \quad i = 1, \dots, n.$$

And in this case, the data Y_i are exchangeable under H_0 . Hence, we can build the test using the $n!$ permutations of the data Y_i .

As test statistic, we can use the F test statistic (Johnson et al., 1992):

$$T_F = \frac{\sum_{i=1}^n (\hat{y}_i - \bar{Y})^2 / (L - 1)}{\sum_{i=1}^n (\hat{y}_i - Y_i)^2 / (n - L)}.$$

More importantly, we also want to test for the significance of each regression coefficient. In particular, for each $\tilde{l} = 1, \dots, L$ we want to test:

$$H_{0,\tilde{l}} : \beta_{\tilde{l}} = 0 \text{ vs. } H_{1,\tilde{l}} : \beta_{\tilde{l}} \neq 0. \quad (5)$$

The test statistic for (5) can, again, be chosen as the absolute value of the t-test statistic of the parametric case.

Under the null hypothesis, the model (4) becomes:

$$Y_i = \beta_0 + \sum_{l=1, l \neq \tilde{l}}^L \beta_l x_{il} + \epsilon_i, \quad i = 1, \dots, n. \quad (6)$$

Here, under the null hypothesis, data are no longer exchangeable, due to the effect of all other covariates x_{il} , with $l \neq \tilde{l}$. The errors ϵ_i of the reduced regression model (6) are the only exchangeable quantities. The only issue is that the ϵ_i are not known. The solution most proposed in literature is based on exchanging the residuals e_i estimated from the model (6) instead of the errors. This solution lead to an asymptotically correct permutation test, as the residuals are asymptotically exchangeable quantities. The permutation test of (5) works as follows:

1. estimate the full model (4);
2. calculate the t-test statistic for the effect of the covariate $x_{i\tilde{l}}$, and save its value T_0 ;
3. estimate the reduced model (6), and save the residuals e_i ;
4. repeat the following B times:

- (a) permute the residuals of the reduced model (6);
 - (b) calculate the permuted responses, by adding the permuted residuals e_i^* to the fitted values of model (6): $Y_i^* = \hat{\beta}_0 + \sum_{l=1, l \neq \tilde{l}}^L \hat{\beta}_l x_{il} + e_i^*$;
 - (c) estimate the full model (4) with the permuted responses Y_i^* ;
 - (d) evaluate the t-test statistic for the effect of the covariate $x_{i\tilde{l}}$, and save its value;
5. evaluate the p -value of the test as the proportion of permuted scenarios in which the test statistic exceed T_0 .

6 Permutation tests for functional data

We here present a way to apply permutation tests to functional data in the case of testing for differences between two functional populations. Extensions to other cases are possible, following what is done in the previous sections.

Suppose to observe two populations of curves $Y_{ij}(t) \stackrel{\text{iid}}{\sim} Y_j$ $i = 1, \dots, n_j$, $j = 1, 2$.

$$H_0 : Y_1 \stackrel{d}{=} Y_2 \text{ vs. } H_1 : Y_1 \neq Y_2.$$

Suppose that the curves are observed exactly, or that an appropriate smoothing of the data has been already done, with some of the techniques presented in Ramsay and Silverman (2005, 2002).

As before, we just need to introduce a proper set of data transformations and a test statistic.

The data transformations can be the permutations of unit labels across the two groups, exactly as in the univariate and multivariate cases.

The test statistic can be chosen as a suitable distance between the two sample means. In FDA, different choices of distance are available (some of them are test statistics proposed in a parametric or asymptotic framework for testing functional data, as in Horváth and Kokoszka (2012)):

- the L^2 distance:

$$T_{L^2} = \left(\int_T (\bar{Y}_1(t) - \bar{Y}_2(t))^2 dt \right)^{1/2}.$$

This statistic does not take into account the covariance structure in any way, and gives the same weight to each interval of the domain of the same length. If data are unstationary (i.e., the dispersion of the curves is not constant through the domain), this may not be the most appropriate choice, as the dispersion of data will not be considered at all by the test.

- the standardised L^2 distance (i.e., the L^2 distance between standardised data):

$$T_{L_t^2} = \left(\int_T \frac{(\bar{Y}_1(t) - \bar{Y}_2(t))^2}{S(t, t)} dt \right)^{1/2}.$$

This statistic makes use of the point-wise estimate of the variance $S(t, t)$. In the case of unstationary data, it is preferable to the L^2 distance, as the weight given to each point is proportional to the inverse of the variability on that point.

All the presented are global tests, in the sense that they focus on answering the question of testing for differences between two groups of curves considering the whole curve. If we reject the null hypothesis, we know that the two groups are significantly different. The answer, anyway, does not provide the information of how the groups are different. For instance, the difference can be in a part of the domain, or only on some frequencies. The following procedure is a test for functional data focusing in selecting the differences between the two groups, i.e., understanding how data are different.

The procedure is the Interval Testing Procedure (ITP), presented in Pini and Vantini (2013b). The starting point is the expansion of data on a suitable high-dimensional basis (e.g., Fourier, B-splines, (Ramsay and Silverman, 2005)):

$$y_{ij}(t) = \sum_{k=1}^p c_{ij}^{(k)} \phi^{(k)}(t). \quad (7)$$

Then, each coefficient of the basis expansion is tested $H_0^{(k)} : C_1^{(k)} \stackrel{d}{=} C_2^{(k)}$, and the associated p -values are corrected in order to take into account multiplicity. The final result is a set of corrected p -values $p_{ITP}^{(k)}$, one for each basis function, that provide a selection of the significantly different basis components.

The corrected p -values provide an interval-wise control of the Family Wise Error Rate:

Definition 6.1 *An inferential procedure is provided with an interval-wise control of the FWER at level α if, for any interval of ordered null hypotheses, the probability of rejecting at least one of those hypotheses is less than α when all the hypotheses of the interval are true.*

In simple words, interval-wise control of the FWER means that, given any interval of components associated to true null hypotheses, the probability that at least one of the null hypotheses associated to the interval is wrongly detected as false is always less than α .

This type of control provides a way to select the statistically significant intervals of basis components. If applied to a local basis (e.g., B-splines), this selection becomes a selection of the intervals of the domain which present statistically significant differences between the two populations. If it is applied to the Fourier basis, on the contrary, it provides a selection of the significantly different bands of frequencies.

An R-package (`fdatest`) implementing the ITP is available on CRAN (Pini and Vantini, 2013a). The current version of the package requires functional data

evaluated on a uniform grid; it projects each function on a chosen functional basis; it performs the entire family of multivariate tests; and, finally, it provides the matrix of the p -values of the previous tests and the vector of the corrected p -values. The functional basis, the paired or unpaired scenario, and the kind of test can be chosen by the user. The package provides also a plotting function creating a graphical output of the ITP: the p -value heat-map, the plot of the corrected p -values, and the plot of functional data.

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