Computational Statistics and Data Analysis 55 (2011) 3244–3256

Contents lists available at ScienceDirect

Computational Statistics and Data Analysis

journal homepage: www.elsevier.com/locate/csda

Repeated measures analysis for functional data

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ARTICLE INFO

Article history:
Received 22 June 2010
Received in revised form 7 June 2011
Accepted 7 June 2011
Available online 15 June 2011

Keywords:
Repeated measure
Functional data analysis
Paired design
Bootstrap method

ABSTRACT

Most of the traditional statistical methods are being adapted to the Functional Data Analysis (FDA) context. The repeated measures analysis which deals with the *k*-sample problem when the data are from the same subjects is investigated. Both the parametric and the nonparametric approaches are considered. Asymptotic, permutation and bootstrap approximations for the statistic distribution are developed. In order to explore the statistical power of the proposed methods in different scenarios, a Monte Carlo simulation study is carried out. The results suggest that the studied methodology can detect small differences between curves even with small sample sizes.

1. Introduction

The great advances of computational and analytical techniques have allowed many processes to be continuously monitored. The increase in the number of the data to be analyzed is its direct consequence and, as usual, new statistical methods must be developed. Functional data analysis (FDA) deals with the statistical study of samples of random functions. The books by Ramsay and Silverman (1997, 2002, 2005) have contributed to popularize the FDA techniques. They offer a broad perspective of the available methods and a number of appealing case studies and practical methodologies. The book of Ferraty and Vieu (2006) offers a nonparametric perspective on FDA. As usual, a lot of standard statistical methods are being adapted for functional data. For example, principal component analysis (see, for example, Boente and Fraiman, 2000 and references therein or Berrendero et al., 2011 for a recent issue), discriminant analysis (Ferraty and Vieu, 2003), regression (see, for example, Cuevas et al., 2002 among other). Of course, techniques for testing the homogeneity in high dimensional and functional frameworks have also been considered. Mas (2007) proposed a test for the regression operator in a linear model with functional inputs and Jiofack and Nkiet (2009) studied the equality of functional means. These two last papers considered random variables defined on an abstract probability space with values in a infinite, real and separable Hilbert space. The traditional *k*-sample problems as the parametric ANOVA (see, Cuevas et al., 2004, Cuesta and Febrero, 2010 and references therein) and the non-parametric one (Delicado, 2007) have also been considered.

FDA is strongly linked with the better known area of longitudinal data analysis (LDA). Both fields even shared a special issue of the journal Statistica Sinica. Although both methodologies are devoted to analyze data collected over time on the same subjects, FDA and LDA are also intrinsically different (Davidian et al., 2004).

Longitudinal data are involved in follow up studies (common on biomedical sciences) which, usually, require several (few) measurements of the variables of interest for each individual along the period of study. They are often treated by multivariate parametric techniques which study the variation among the means along the time controlled by a number of covariates. In contrast, functional data are frequently recorded by mechanical instruments (more common

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doi:10.1016/j.csda.2011.06.007

in engineering and physical sciences although also in a increasing number of biomedical problems) which collect many repeated measurements per subject. Its basic *units of study* are complex objects such as curves (commonly), images or shapes (information along the time of the same individual is jointly considered). Conceptually, functional data can be considered sample paths of a continuous stochastic process (Valderrama, 2007) and to study the covariance structure is the usual focus on FDA. In addition, the infinite dimensional structure of the functional data makes that the links with standard nonparametric statistics (in particular with smoothing techniques) were specially strong (González-Manteiga and Vieu, 2007).

Despite these differences, which involve, mainly, the viewpoints and ways of thinking about the data of both fields, Zhao et al. (2004) connected them and, illustrating the ideas in the context of a gene expression study example, introduced LDA to the FDA viewpoint.

This paper deals with the issue of comparing two (or more) functions from paired design (classical repeated measures analysis). This situation occurs in a variety of problems. Most direct application is the comparison of biomedical parameter measured during a period of time on the same patients in different situations. For instance, in pharmacokinetic (or the absorption, distribution, and elimination of drugs), the comparison of the concentration versus time curves for different drugs is studied on the same individuals. Formally, we have $X_{i,j}(t),\ i \in 1, \ldots, n,\ j \in 1, \ldots, k,\ t \in [a, b]$, $n \times k$ trajectories, from n (random) subjects, drawn from L^2-processes $X_{j,\bullet}$ $(1 \leq j \leq k)$ such that $\mathbb{E}[X_{j,\bullet}(t)] = m_j(t)$, and we want to test the null hypothesis

$$H_0 : m_1(t) = \cdots = m_k(t) \quad (=m(t)) \forall t \in [a, b]. \tag{1}$$

Although in FDA the data are considered as curves, in practice, they are invariably in a discrete fashion and, really, only certain (finites) values for the trajectories are known. From these values, the trajectories are often estimated from some interpolation or smoothing method (usually based on local-polynomial or spline methods) in order to obtain the smooth curves to which the functional data analysis methods are applied. Hall and Van Keilegom (2007) suggested ways of pre-processing the data, so as to minimize the effects of smoothing, for two-sample tests. We assume that the values of the trajectories are known for a huge number of arbitrary points t_l $(1 \leq l \leq H)$, besides these points are not necessarily the same for the different curves. It is worth mentioning that the interpolation method effect (also the fact that the known points are different) is negligible from adequately large H. The rest of the paper is organized as follows: In Section 2, additivity is assumed and the usual parametric repeated measures test (for two-sample problems) for functional data is developed. In the Theorem 1 a not fully asymptotic distribution for the considered statistic is developed (based on the L_2-norm). This result can be used in practice arguing as in Cuevas et al. (2004) and approximating the P-value from the Monte Carlo method. Section 3 is devoted to the nonparametric approach and a bootstrap and a permutation tests are explored (also for the two-sample case). The bootstrap procedure uses an *auxiliary statistic* and has a similar distribution (asymptotically equal) to the original statistic under the null whether the data verifies the null hypothesis or not. Its main particularity is that the null is involved in order to compute the bootstrap value instead of in order to obtain the bootstrap samples. A Monte Carlo simulation study is carried out in Section 4. Finally, in Section 5, some indications for the k-sample case are considered.

2. Two-sample case: Methodology

For independent and homoscedastic samples, it is assume that each trajectory (we can assume, without lost of generality that [0, 1] is the considered interval) is in the way

$$X_{i,j}(t) = m_j(t) + e_{i,j}(t) \quad t \in [0, 1]$$

where $e_{i,j}(t)$ with $t \in [0, 1]$ $(1 \leq i \leq n, 1 \leq j \leq k)$ are random functions centered in the mean. Cuevas et al. (2004) computed the ratio of variability between samples and intra-sample and proposed the following functional version for the classical F-ratio of the ANOVA model,

$$F_N = \frac{\sum_{j=1}^{k} n_j \int \left(X_{j,\bullet}(t) - X_{\bullet,\bullet}(t)\right)^2 \mathrm{d}t/(k-1)}{\sum_{j=1}^{k}\sum_{i=1}^{n_j} \int (X_{i,j}(t) - X_{j,\bullet}(t))^2 \mathrm{d}t/(n-k)}, \tag{2}$$

where $X_{j,\bullet}(t) = n_j^{-1} \sum_{i=1}^{n_j} X_{i,j}(t)$ $(1 \leq j \leq k)$ and $X_{\bullet,\bullet}(t) = N^{-1} \sum_{j=1}^{k} n_j X_{j,\bullet}(t)$ $(N = \sum_{j=1}^{k} n_j)$. Due to homoscedasticity not being an essential assumption, Cuevas et al. (2004) proposed to use a test based on the numerator of the above statistic, i.e.,

$$V_N = \sum_{j=1}^{k} n_j \int \left(X_{j,\bullet}(t) - X_{\bullet,\bullet}(t)\right)^2 \mathrm{d}t. \tag{3}$$

This paper is concerned with the paired sample setting. In the studied case, both curves are from the same subject (probably submitted to different conditions) and we are interested in comparing whether they are equal or not. Note that, really, we

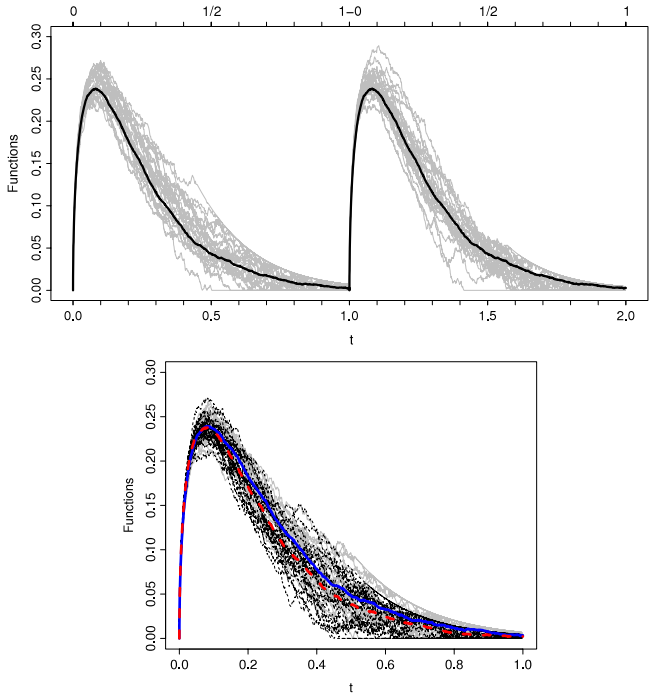

Fig. 1. Artificial example from Model 1 (see Section 4) with $\rho = 0$, normal errors and $n = 25$. The upper plot depicts the trajectories (gray lines) and the average curve under the null (wide black curve) for $t \in [0, 2]$). The lower plot shows $m_i(t)$ (gray lines) and $m_i(1 + t)$ (dashed black lines) with $t \in [0, 1]$ $(1 \leq i \leq n)$, and the respective average curves (wide lines).

only have n (sample size) independent trajectories and (ignoring the (possible) period in which the patient is not monitored) above the additivity assumption, it is

$$X_i(t) = m(t) + e_i(t) \quad t \in [0, 2],$$

where $e_i(t)$ with $t \in [0, 2]$ $(1 \leq i \leq n)$ are random functions centered in the mean. Hence, the null is

$$H_0 : m(t) = m(1 + t) \quad \forall t \in [0, 1]. \tag{4}$$

In order to avoid the homoscedasticity assumption, we propose to use the statistic

$$\mathcal{C}_n = n \int_0^1 (X_\bullet(t) - X_\bullet(1 + t))^2 \, \mathrm{d}t, \tag{5}$$

where $X_\bullet(t) = n^{-1} \sum_{i=1}^n X_i(t)$ with $t \in [0, 2]$. The main difference between the classical ANOVA adapted to FDA for Cuevas et al. (2004) and the problem which is the focus of the current study is that while, in the first case, only the covariance structure must be estimated within each curve, we also must estimate the covariance between different curves for the same subject. Although, in practice, without homoscedasticity assumption, this problem is equivalent to computing the covariance function, $\mathbb{C}(s, t)$, along the complete curve (the union of the two involved curves), i.e., for $s, t \in [0, 2]$. Of course, the homoscedasticity assumption could be easily incorporated in order to estimate $\mathbb{C}(s, t)$.

Fig. 1 depicts a simulated example (corresponding with the Model 1, with $\rho = 0$ and normal residuals, see Section 4) with 25 independent curves. The upper plot shows the whole individual (gray) curves ($t \in [0, 2]$) and the average curve (black) under the null ($m(t) = m(1 + t)$). The lower plot depicts the different trajectories $m_i(t)$ (gray lines) and $m_i(1 + t)$ (dashed black lines) with $t \in [0, 1](1 \leq i \leq 25)$. Respective average curves $m(t)$ (wide continuous line) and $m(1+t)$ (wide dashed line) are also shown.

Usually, the theoretical results related with functional data analysis are written in very technical functional terminology which involves Hilbert spaces (with particular conditions, usually, real and separable) and to define general norms. Obviously, this approach can be applied to the FDA repeated measures problem. The reader is referred to Mas (2007), Jiofack and Nkiet (2009) and references therein for complete guidelines of the technical details. In practice, both the considered space and the used norm are really friendly and they often satisfy all (and more) the common required theoretical properties. In the following result, which guarantees the asymptotic convergence for $\mathcal{C}_n$ under useful (and usual) conditions, we argue similarly to the Theorem 1 of Cuevas et al. (2004).

Theorem 1. *Assume that $X_i(t) = m(t) + e_i(t)$ with $1 \leq i \leq n$, are n independent trajectories from a L^2-processes (defined on $[0, 2]$), with $\mathbb{E}[e_i(t)] = 0$ (for $t \in [0, 2]$) and covariance function $\mathbb{C}(s, t)$. Then, if $m(t) = m(1+t)$ $\forall t \in [0, 1]$ (null hypothesis),*

it holds

$$\mathcal{C}_n \xrightarrow{\mathcal{L}}_n \sum_{l\in\mathbb{N}} \lambda_l \mathcal{N}_l^2, \tag{6}$$

where $\{\lambda_l\}_{l\in\mathbb{N}}$ *is a non-negative sequence satisfying* $\lambda_1 \geq \lambda_2 \geq \cdots \geq \lambda_s \geq \cdots \geq 0$ *and* $\sum_{l\in\mathbb{N}} \lambda_l^2 < \infty$ *and* $\{\mathcal{N}_l\}_{l\in\mathbb{N}}$ *is a sequence of independent random variables following a standard normal distribution.*

Proof. According with the Central Limit Theorem for random variables taking values in a Hilbert space (see, for example, Laha and Rohatgi, 1979), in the space of probability measure on $L^2[0, 2]$, it had the weak convergence

$$\sqrt{n}(X_\bullet(t) - m(t)) \xrightarrow{\mathcal{L}}_n \mathcal{Z}(t) \quad \forall t \in [0, 2],$$

where $\mathcal{Z}$ is a Gaussian process with zero mean and covariance function $\mathbb{C}(s, t)$. Under the null, and directly from the continuous mapping theorem (see, for example, Billinsley, 1968) we have

$$\mathcal{C}_n = n \int_0^1 (X_\bullet(t) - X_\bullet(1+t))^2 \, \mathrm{d}t \xrightarrow{\mathcal{L}}_n \int_0^1 (\mathcal{Z}(t) - \mathcal{Z}(1+t))^2 \, \mathrm{d}t. \tag{7}$$

Obviously, the process $\xi(t) = \mathcal{Z}(t) - \mathcal{Z}(1+t)$ $(t \in [0, 1])$ is also Gaussian with mean zero. Its covariance, $\mathbb{K}(s, t)$, is a $L^2[0, 1]$ function (note that $\mathbb{K}(s, t) = \mathbb{C}(s, t) - \mathbb{C}(s, 1+t) - \mathbb{C}(1+s, t) + \mathbb{C}(1+s, 1+t)$). Therefore, the Karhunen–Loève decomposition (see, for example, Adler, 1990) can be applied in order to obtain the equality

$$\int_0^1 \xi(t)^2 \mathrm{d}t = \sum_{l\in\mathbb{N}} \lambda_l \mathcal{N}_l^2, \tag{8}$$

where $\{\lambda_l\}_{l\in\mathbb{N}}$ is a non-negative sequence satisfying $\lambda_1 \geq \lambda_2 \geq \cdots \geq \lambda_s \geq \cdots \geq 0$ and $\sum_{l\in\mathbb{N}} \lambda_l^2 < \infty$ and $\{\mathcal{N}_l\}_{l\in\mathbb{N}}$ is a sequence of independent random variables following a standard normal distribution.

The result (6) is immediately derived from (7) and (8). □

Theorem 1 guarantees the consistence and gives us the convergence ratio for the studied statistic. However, strictly speaking, it does not provide its distribution in full and, in order to build asymptotic critical regions, the explicit values for the $\{\lambda_l\}_{l\in\mathbb{N}}$ coefficients must been computed. Unfortunately, they strongly depend on the covariance structure hence there is no universal solution. However, Eq. (7) allows developing a simple Monte Carlo algorithm in order to approximate a final P-value. From a fixed (by the researcher) grid of points within $[0, 1]$, $\mathcal{T} = \{t_1, \ldots, t_l\}$ (I is an arbitrary large number), estimate the covariance function $\mathbb{C}$ from the data ($\mathbb{S}$ denotes this estimation) and compute $\mathbb{S}(t_u, t_v)$ $(1 \leq u, v \leq I)$. Then simulate B (B is a large number also fixed by the investigator) discretized artificial trajectories based on $\{\mathcal{Z}^b(t_v)\}_{v=1}^I$ $(1 \leq b \leq B)$ from $\mathcal{Z}$, where $\mathcal{Z}$ is the Gaussian process which appears in (7) and whose covariance matrix is $\mathbb{S}$. From these trajectories $\tilde{\mathcal{C}}_n^b = \int_0^1 \left(\mathcal{Z}^b(t) - \mathcal{Z}^b(1+t)\right)^2 \mathrm{d}t$ is computed and the final P-value is $P = B^{-1} \sum_{b=1}^B I\{\mathcal{C}_n \leq \tilde{\mathcal{C}}_n^b\}$ ($I\{A\}$ stands for the usual indicator function on the set A). This procedure is similar to the one described by Cuevas et al. (2004).

3. Non-parametric approach

Additivity assumption is not adequate for a number of functions. For instance, when working with densities. Density functions must verify some particular conditions (being non negative and integrating 1 on $\mathbb{R}$) which make inappropriate fixed structures. In this section, from a nonparametric approach, we propose two different resample plans which do not require any previous assumptions.

Although the use of the bootstrap on the paired-sample problem is straightforward (even in FDA context) in order to build confidence intervals and related estimates, its use on hypothesis testing is not clear. It is not trivial how to involve the null hypothesis in the resample plan. Martínez-Camblor et al. (unpublished manuscript) proposed a resample plan, useful for the Cramér–von Mises criterion, whose main particularity is that the null is involved at the moment to compute the value of the statistic instead of at the moment to draw the bootstrap sample. Taking into account that, under the null, we have the equality,

$$\mathcal{C}_n = n \int_0^1 (X_\bullet(t) - m(t) + m(1+t) - X_\bullet(1+t))^2 \, \mathrm{d}t. \tag{9}$$

The direct adaptation of the above mentioned bootstrap procedure to the functional context, in particular, on the $\mathcal{C}_n$ statistic is as follows

B$_1$ From a fixed partition of $[0, 1]$, $\mathcal{T}$, compute $\mathcal{C}_n$.

B$_2$ Select B independent bootstrap samples, $\boldsymbol{X}_1^*, \ldots, \boldsymbol{X}_B^*$. Each consisting of n curves, $\boldsymbol{X}_b^* = \{X_1^{*,b}(t), \ldots, X_n^{*,b}(t)\}$ with $t \in [0, 2]$ $(1 \leq b \leq B)$ drawn with replacement from the n original curves.

B_3 By using (9), compute the values of $\mathcal{C}_n^{*,b}$ with $b \in 1, \ldots, B$ ($\mathcal{C}_n$ on the bootstrap samples). Note that, in the bootstrap setting, $X_\bullet = X_\bullet^{*,b}$ $(1 \leq b \leq B)$ and $m = X_\bullet$.

B_4 The distribution of $\mathcal{C}_n$ is approximated from $\mathcal{C}_n^{*,1}, \ldots, \mathcal{C}_n^{*,B}$. The final P-value is

$$P_B = \frac{1}{B}\sum_{b=1}^{B} I\{\mathcal{C}_n > \mathcal{C}_n^{*,b}\}.$$

Note that, on one hand, the step B_1 is more related with the integral computation than with the bootstrap algorithm. We want to make note that, the known points of the curves, are not necessarily the same (for each different curve, even within a same subject), and the integral computation cannot be directly made on them. On the other hand, if $\mathcal{C}_n^*$ is the statistic computed by using the above algorithm (B_1–B_4), from (7) we have

$$\mathcal{C}_n^* = n\int_0^1 \left(X_\bullet^*(t) - X_\bullet(t) + X_\bullet(1+t) - X_\bullet^*(1+t)\right)^2 \mathrm{d}t \xrightarrow{\mathcal{L}}_n \int_0^1 \left(\mathbb{Z}^*(t) - \mathbb{Z}^*(1+t)\right)^2 \mathrm{d}t.$$

Under Theorem 1 conditions, the process $\xi(t) = \mathbb{Z}^*(t) - \mathbb{Z}^*(1+t)$ $(t \in [0,1])$ is Gaussian with mean zero. Its covariance, $\mathbb{K}^*(s,t)$, is (also) a $L^2[0,1]$ function with $\mathbb{K}^*(s,t) = \mathbb{S}(s,t) - \mathbb{S}(s,1+t) - \mathbb{S}(1+s,t) + \mathbb{S}(1+s,1+t))$, where $\mathbb{S}(s,t)$ $(0 \leq s,t \leq 2)$ is the sample covariance function (covariance function of $X_\bullet$). Since, under really (and usual) mild conditions, it is known that $\sup_{(t,s)\in[0,2]\times[0,2]} |\mathbb{C}(s,t) - \mathbb{S}(s,t)| \to_n 0$ (a.s.), hence for $u \in \mathbb{R}$ we have $\mathcal{P}_X\{\mathcal{C}_n^* \leq u\} - \mathcal{P}\{\mathcal{C}_n \leq u\} \to_n 0$ ($\mathcal{P}_X$ denotes probability conditionally on the sample X).

An adequate convergence rate for the previous (punctual) convergence is sufficient in order to obtain the validity of the proposed bootstrap. To derive this result more extended discussion is required. Ferraty et al. (2010) proved the consistency of the naive and wild bootstrap for quite general semi-metrics in non-parametric (particularly smooth) regression with infinite-dimensional (functional) covariates. The recent paper of González-Manteiga and Martínez-Calvo (2011) provided a new input of this problem in the linear regression context and also for the naive and wild bootstrap. However, the used methods in both works cannot be directly translated to our topic (note that, unlike the estimators handled in these works, the limit distribution for $\mathcal{C}_n$ is not normal) and the way of applying these techniques on the repeated measures issue must be carefully considered. The works about general quadratic discrepancy bounds (see Hickernell, 1998 and references therein) and convergence rates for V-statistics (see, for example, Arcones and Giné, 1992) can be another interesting way to get uniform convergence for the proposed bootstrap which must also be deeply studied.

This resample algorithm takes advantage of the particular estimator properties and it is generalizable in order to approximate the distribution of general statistics. The most common general procedure, *permutation* test (see, for example, Good, 2000 or Munzel, 1999) implies that the relationship between each involved pair is the same (*interchangeability* assumption). Note that, although this is not a very strong assumption for the two-sample case, it is usually violated for the general k-sample problem. A direct adaptation for the permutation technique to the considered context is as follows

P_1 From a fixed partition of $[0,1]$, $\mathcal{T}$, compute $\mathcal{C}_n$.

P_2 Select B independent *permutation* samples, $\boldsymbol{X}_1^*, \ldots, \boldsymbol{X}_B^*$. Each consisting of n curves, $\boldsymbol{X}_b^* = \{X_1^{*,b}(t), \ldots, X_n^{*,b}(t)\}$ with $t \in [0,2]$ $(1 \leq b \leq B)$, where for $1 \leq i \leq n$, $X_i^{*,b}(t) = X_i(t)$ (with probability 1/2) or $X_i^{*,b}(t) = X_i(t + (-1)^{I_{[1,2]}(t)})$ (where $I_A(t)$ stands for the usual indicator function on the set A).

P_3 Compute the values of $\mathcal{C}_n^{*,b}$ with $b \in 1, \ldots, B$ ($\mathcal{C}_n$ on the permutation samples).

P_4 The distribution of $\mathcal{C}_n$ is approximated from $\mathcal{C}_n^{*,1}, \ldots, \mathcal{C}_n^{*,B}$. The final P-value is

$$P_P = \frac{1}{B}\sum_{b=1}^{B} I\{\mathcal{C}_n > \mathcal{C}_n^{*,b}\}.$$

The permutation algorithm involved the null in the resample process and it is useful in order to approximate the distribution (under the null) for general statistics.

4. Monte Carlo simulation study

In order to investigate the behavior of the proposed method, as usual, a Monte Carlo simulation study was carried out. Two different problems have been considered. In the first one, four different functions were proposed. Fig. 2 shows the different shapes of these curves:

1. $m_{0,1}(t) = \sqrt{6t/\pi}\,\mathrm{e}^{-6t} I_{[0,1]}(t)$
2. $m_{1,1}(t) = \sqrt{13t/(2\pi)}\,\mathrm{e}^{-13t/2} I_{[0,1]}(t)$
3. $m_{2,1}(t) = \sqrt{11t/(2\pi)}\,\mathrm{e}^{-11t/2} I_{[0,1]}(t)$
4. $m_{3,1}(t) = \sqrt{5}t^{2/3}\mathrm{e}^{-7t} I_{[0,1]}(t)$.

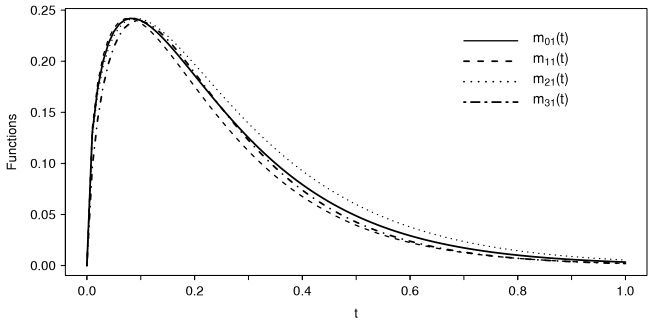

Fig. 2. Curves involved in the considered simulation models. The first curve (with $t \in [0, 1]$) is always $m_{0,1}$.

The procedure to compute each artificial trajectory (sample sizes of $n = 25, 35, 50$ are considered), $X_i(t)$, is as follows: First, a thousand random points, $\{t_{j,1}\}_{j=1}^{1000}$, (following a uniform distribution, $\mathcal{U}[0, 1]$) are drawn and $X_i(t_{j,1}) = m_0(t_{j,1}) + \epsilon_{i,1}(t_{j,1})$ ($\epsilon_{i,s}(t)$ ($s = 1, 2$) are the error functions, they will be defined later) is computed. Another thousand random points, $\{t_{j,2}\}_{j=1}^{1000}$, are drawn from the same distribution and $X_i(1 + t_{j,2}) = m_l(t_{j,2}) + \epsilon_{i,2}(t_{j,2})$ is computed (the function m_l changes for the different considered models in Model 0 is $m_{0,1}$ (the null is true), in Model 1 it is $m_{1,1}$, in Model 2 it is $m_{2,1}$ and, finally, in Model 3 it is $m_{3,1}$). Three different type of error functions are considered. In the *normal* model, $\epsilon_{i,1}(t) = 20^{-1}\mathcal{B}_1(t)$ and $\epsilon_{i,2}(t) = \rho\epsilon_{i,1}(t) + 20^{-1}\sqrt{1-\rho^2}\mathcal{B}_2(t)$ (cases $\rho = 0, 1/4, 1/2$ are considered) where $\mathcal{B}_1$ and $\mathcal{B}_2$ are two independent standard Brownian Bridges. In the *lognormal* model, the error functions are computed in the same form but then, the functions $e^{\epsilon_{i,s}(t)}$ ($s = 1, 2$) (adequately centered) are added to the trajectories. Finally, in the *mixed* model, the exponential transformation is applied only to $\epsilon_{i,2}(t)$. When it is required, the residuals are truncated to zero (as minimum) and to the double of the real function (a bigger error would be inadmissible in real measures). On the other hand, in order to compute, numerically, the involved integral (steps B_1 and P_1), three different partitions of $[0, 1]$ are considered with the points $t_k = (I-1)^{-1}(k-1)$ ($1 \le k \le I$) and for $I = 26, 101, 251$. These grids are also employed in order to build the (discretization) process $\mathcal{Z}$ involved in the (Monte Carlo) asymptotic approximation.

Since the trajectories are drawn, the statistical power for the three described algorithms (based on the asymptotic distribution (labeled as *A*), on the bootstrap method (labeled as *B*) and on the permutation one (labeled as *P*)) are estimated from 5000 Monte Carlo replications. The *P*-values are estimated from 1000 replications ($B = 1000$) in the three studied methods.

Table 1 contains the rejection proportions ($\alpha = 0.05$) for Model 0 (the null hypothesis is true). In general, the nominal level is well respected in all considered situations for the asymptotic and, specially, for the permutation approximations. The employed partition seems not have any influence on the observed results. However, we must highlight that the Bootstrap method (*B*) often obtains the biggest results and its rejection proportions exceed the 6.5% in several cases (all of them with $n = 25$, the convergence is slow). In addition, even for $n = 50$, its observed rejection proportions are often larger than the upper bound of the usual 95% confidence interval (5.604% in the present case).

Table 2 is similar to the Table 1 for the Model 1 results. The observed differences among the statistical powers of the three studied methods are very small. The bootstrap (*B*) is always a bit better than the others, these (small) differences decrease when sample size increases. Remember that this method is lightly anticonservative for small sample sizes (slow convergence speed). The differences observed among different *I*'s are negligible (it never reaches 1%). Statistical power (logically) increases for the highest correlation between curves and, although the two source curves are quite similar, the results are very good and the statistical power is 1 for a variety of situations.

Table 3 shows the rejection proportions for Model 2. Although, a few are bigger, the statistical powers are similar than the observed ones in Table 2. We want to highlight that, when the residuals are from the exponential model, the rejection proportions are always 1 (Type II error is zero) even for the smallest considered sample size ($n = 25$). The observed differences among the different *I*'s are (again) negligible.

Finally, Table 4 depicts the estimated statistical powers for the Model 3. It is still not observed relevant differences among three different studied methods. The obtained results are also really good for $I = 251$ but it highlights that, in this case, the estimated statistical powers are strongly dependent on the considered grid. The quality of the integral estimations can be important depending on the shape of the involved curves and on where the differences between them are located.

The second studied problem is similar to the first one but the (four) considered functions were:

1. $m_{0,2}(t) = [\sin(2\pi t^2)]^5 I_{[0,1]}(t)$
2. $m_{1,2}(t) = [\sin(2\pi t^2)]^3 I_{[0,1]}(t)$
3. $m_{2,2}(t) = [\sin(2\pi t^2)]^7 I_{[0,1]}(t)$
4. $m_{3,2}(t) = [\sin(2\pi t^{(9/5)})]^3 I_{[0,1]}(t)$.

Fig. 3 shows the different shapes of the above curves.

Table 1
Observed rejection proportions for Model 0 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$).

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.059	0.064	0.050	0.058	0.065	0.051	0.059	0.063	0.051
		1/4	0.054	0.059	0.045	0.053	0.060	0.047	0.053	0.061	0.048
		1/2	0.060	0.065	0.050	0.058	0.063	0.050	0.058	0.064	0.050
	35	0	0.056	0.059	0.048	0.057	0.060	0.051	0.057	0.062	0.049
		1/4	0.054	0.060	0.049	0.053	0.059	0.049	0.055	0.061	0.049
		1/2	0.054	0.059	0.045	0.053	0.060	0.047	0.053	0.061	0.048
	50	0	0.057	0.059	0.051	0.055	0.057	0.050	0.056	0.060	0.052
		1/4	0.051	0.053	0.046	0.052	0.054	0.049	0.051	0.053	0.047
		1/2	0.053	0.054	0.049	0.053	0.055	0.049	0.053	0.057	0.050
LogNormal	25	0	0.049	0.057	0.050	0.048	0.056	0.047	0.046	0.057	0.048
		1/4	0.047	0.056	0.047	0.048	0.057	0.046	0.049	0.056	0.048
		1/2	0.049	0.057	0.049	0.050	0.058	0.048	0.049	0.057	0.050
	35	0	0.048	0.053	0.050	0.047	0.053	0.049	0.050	0.055	0.048
		1/4	0.049	0.054	0.050	0.049	0.056	0.050	0.049	0.057	0.048
		1/2	0.050	0.060	0.053	0.053	0.058	0.053	0.051	0.059	0.053
	50	0	0.050	0.052	0.050	0.051	0.054	0.050	0.049	0.054	0.050
		1/4	0.053	0.056	0.053	0.053	0.056	0.053	0.054	0.056	0.053
		1/2	0.054	0.056	0.054	0.053	0.057	0.054	0.052	0.057	0.052
Mixed	25	0	0.051	0.061	0.050	0.053	0.062	0.050	0.054	0.060	0.050
		1/4	0.053	0.059	0.047	0.053	0.060	0.047	0.052	0.061	0.048
		1/2	0.058	0.065	0.052	0.059	0.068	0.053	0.061	0.066	0.053
	35	0	0.057	0.060	0.053	0.058	0.063	0.056	0.057	0.064	0.053
		1/4	0.055	0.058	0.050	0.056	0.059	0.053	0.056	0.061	0.050
		1/2	0.058	0.062	0.049	0.058	0.060	0.053	0.056	0.064	0.050
	50	0	0.053	0.055	0.052	0.054	0.055	0.050	0.052	0.057	0.050
		1/4	0.055	0.058	0.054	0.055	0.056	0.052	0.055	0.058	0.050
		1/2	0.053	0.056	0.049	0.052	0.056	0.049	0.054	0.055	0.048

Table 2
Observed rejection proportions for Model 1 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.523	0.541	0.489	0.527	0.543	0.495	0.524	0.543	0.493
		1/4	0.624	0.644	0.595	0.629	0.647	0.597	0.628	0.645	0.599
		1/2	0.808	0.822	0.786	0.811	0.823	0.788	0.812	0.825	0.790
	35	0	0.679	0.695	0.662	0.686	0.696	0.665	0.682	0.697	0.668
		1/4	0.787	0.796	0.769	0.789	0.801	0.777	0.788	0.801	0.776
		1/2	0.924	0.930	0.913	0.926	0.932	0.919	0.928	0.929	0.918
	50	0	0.821	0.825	0.805	0.822	0.830	0.814	0.822	0.830	0.811
		1/4	0.909	0.913	0.904	0.911	0.915	0.908	0.913	0.917	0.907
		1/2	0.982	0.984	0.982	0.985	0.987	0.983	0.985	0.987	0.984
LogNormal	25	0	0.989	0.992	0.992	0.989	0.993	0.991	0.989	0.993	0.991
Mixed	25	0	0.517	0.534	0.484	0.523	0.538	0.492	0.523	0.539	0.484
		1/4	0.768	0.785	0.749	0.771	0.787	0.751	0.771	0.789	0.755
		1/2	0.837	0.851	0.823	0.839	0.856	0.826	0.840	0.853	0.826
	35	0	0.665	0.680	0.642	0.671	0.679	0.648	0.671	0.682	0.649
		1/4	0.899	0.904	0.890	0.901	0.909	0.897	0.901	0.910	0.895
		1/2	0.946	0.950	0.940	0.950	0.954	0.946	0.952	0.955	0.946
	50	0	0.817	0.823	0.806	0.822	0.825	0.809	0.821	0.830	0.812
		1/4	0.979	0.981	0.978	0.980	0.981	0.979	0.981	0.981	0.979
		1/2	0.990	0.991	0.989	0.991	0.992	0.990	0.991	0.992	0.990

The procedure to compute each artificial trajectory and the considered correlations are the same as the ones used for the previous simulation problem (results described in Tables 1–4). Although, in this case, in order to make the problem more realistic, the errors have not been truncated and they were ten times larger than the previously used (i.e. the Brownian bridge involved on each $\epsilon_{*,*}(t)$ definition is multiplied by $1/2$ instead of by $1/20$). In addition, to simulate a more discretized scheme, the number of observed points was 100 (instead of 1000 used previously). The first curve is always from $m_{0,2}$ while the second curve is from $m_{0,2}$, $m_{1,2}$, , $m_{2,2}$ and $m_{3,2}$ in models 4, 5, 6 and 7, respectively.

Fig. 4 depicts, as a particular example (similar to Fig. 1), a simulation from the Model 7 with $\rho = 1/2, n = 25$ and mixed residuals. The curves are quite different and the null is easily rejected by the three proposed methods. The observed statistical power for this situation was 1.

Table 3
Observed rejection proportions for Model 2 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.609	0.626	0.581	0.609	0.631	0.580	0.610	0.628	0.582
		1/4	0.701	0.718	0.671	0.702	0.717	0.677	0.704	0.719	0.675
		1/2	0.866	0.873	0.853	0.870	0.880	0.856	0.868	0.880	0.856
	35	0	0.749	0.761	0.736	0.750	0.763	0.739	0.754	0.765	0.738
		1/4	0.840	0.846	0.827	0.841	0.853	0.830	0.842	0.851	0.831
		1/2	0.959	0.962	0.955	0.962	0.965	0.958	0.961	0.964	0.957
	50	0	0.895	0.898	0.888	0.896	0.901	0.889	0.895	0.899	0.889
		1/4	0.948	0.951	0.945	0.949	0.952	0.946	0.949	0.952	0.947
		1/2	0.995	0.995	0.995	0.995	0.995	0.993	0.994	0.995	0.994
LogNormal	25	0	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		1/4	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Mixed	25	0	0.838	0.850	0.827	0.840	0.852	0.829	0.839	0.854	0.830
		1/4	0.888	0.899	0.880	0.891	0.902	0.881	0.891	0.901	0.883
		1/2	0.932	0.942	0.928	0.936	0.946	0.928	0.935	0.943	0.929
	35	0	0.938	0.942	0.934	0.937	0.942	0.935	0.939	0.942	0.933
		1/4	0.967	0.968	0.965	0.966	0.970	0.965	0.968	0.969	0.966
		1/2	0.987	0.988	0.985	0.988	0.990	0.987	0.987	0.989	0.987
	50	0	0.991	0.991	0.990	0.992	0.991	0.991	0.991	0.992	0.991
		1/4	0.996	0.997	0.996	0.997	0.997	0.996	0.997	0.997	0.997

Table 4
Observed rejection proportions for Model 3 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.269	0.293	0.256	0.469	0.510	0.474	0.500	0.546	0.512
		1/4	0.363	0.393	0.357	0.681	0.719	0.691	0.720	0.761	0.740
		1/2	0.578	0.619	0.590	0.927	0.944	0.936	0.947	0.961	0.955
	35	0	0.385	0.404	0.374	0.736	0.765	0.747	0.779	0.810	0.793
		1/4	0.545	0.570	0.545	0.928	0.939	0.930	0.948	0.961	0.955
		1/2	0.831	0.857	0.835	0.997	0.999	0.998	0.999	1.000	0.999
	50	0	0.600	0.617	0.601	0.972	0.976	0.973	0.983	0.989	0.986
		1/4	0.811	0.833	0.822	0.999	1.000	0.999	0.999	1.000	1.000
		1/2	0.985	0.989	0.987	1.000	1.000	1.000	1.000	1.000	1.000
LogNormal	25	0	0.895	0.926	0.926	0.999	1.000	1.000	1.000	1.000	1.000
		1/4	0.991	0.994	0.995	1.000	1.000	1.000	1.000	1.000	1.000
	35	0	0.998	0.999	0.998	1.000	1.000	1.000	1.000	1.000	1.000
Mixed	25	0	0.428	0.466	0.439	0.800	0.835	0.821	0.836	0.872	0.860
		1/4	0.563	0.602	0.569	0.906	0.929	0.915	0.928	0.947	0.941
		1/2	0.647	0.679	0.650	0.952	0.967	0.964	0.969	0.980	0.975
	35	0	0.654	0.684	0.667	0.978	0.982	0.980	0.985	0.991	0.989
		1/4	0.792	0.810	0.801	0.991	0.995	0.995	0.995	0.997	0.997
		1/2	0.880	0.896	0.884	0.999	1.000	0.999	0.999	1.000	1.000
	50	0	0.915	0.928	0.924	1.000	1.000	1.000	1.000	1.000	1.000
		1/4	0.969	0.975	0.972	1.000	1.000	1.000	1.000	1.000	1.000
		1/2	0.994	0.995	0.995	1.000	1.000	1.000	1.000	1.000	1.000

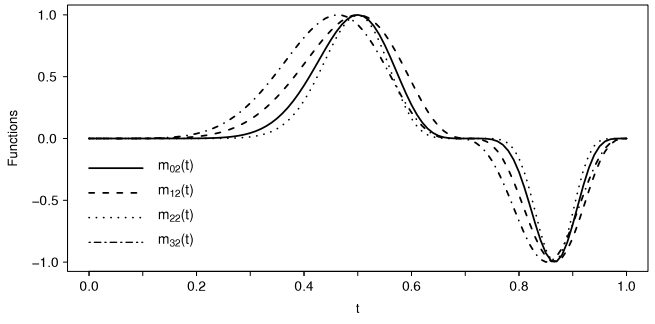

Fig. 3. Curves involved in the considered simulation models. The first curve (with $t \in [0, 1]$) is always $m_{0,2}$.

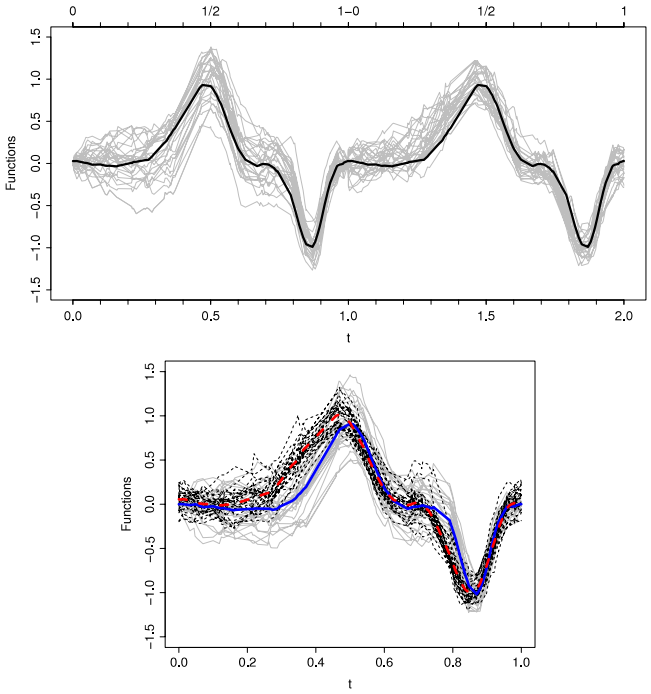

Fig. 4. Artificial example from Model 7 with $\rho = 1/2$, mixed errors and $n = 25$. The upper plot depicts the trajectories (gray lines) and the average curve under the null (wide black curve) for $t \in [0, 2]$). Lower plot shows $m_i(t)$ (gray lines) and $m_i(1 + t)$ (dashed black lines) with $t \in [0, 1]$ ($1 \leq i \leq n$), and the respective average curves (wide lines).

Table 5 (similar to Table 1) contains the observed rejection proportions for Model 4 (null hypothesis is true). In general, the results are not quite different than the observed ones in Model 0. The nominal level is also well respected in most of the considered situations for the asymptotic and, specially, for the permutation approximations. In addition, the employed partition seems not have any influence on the results. However, like it has been observed for the first considered problem, the Bootstrap method (B), it is anticonservative, specially, for Normal residuals.

Table 6 shows the obtained results in Model 5. Three statistical methods achieve quite similar statistical powers. The scheme does not vary in a relevant way from the observed one, previously, in Table 2 (Model 1). The bootstrap (B) is usually bit better than the others (this method is also lightly anticonservative). Note that, for LogNormal and Mixed residuals, the power is really high even for $n = 25$ and $\rho = 0$. In these cases, the results are optimum (all the observed powers are 1) for $n \geq 35$.

The observed statistical powers for Model 6 are showed in Table 7. Curves involved in this case, $m_{0,2}$ and $m_{2,2}$, are really close to each other (see Fig. 3) and, for several of the residuals, correlations and sample sizes considered, the observed statistical powers are moderate. All methods work similarly. As usual, the used partition seems to be not relevant for the final result.

Finally, Table 8 contains the observed statistical powers for Model 7. The observed results are even better than the Table 6 ones (Model 5). The rejection percentage is 1 for all considered situations even for $\rho = 0$.

5. Considerations for the *k*-sample case

There exist several ways to generalize $\mathcal{C}_n$ to the k-sample case. Perhaps, the most direct way is the one employed by Kiefer (1959) and, recently, by Martínez-Camblor and de Uña-Álvarez (2009) given by,

$$\mathcal{C}_n(k) = \sum_{j=1}^{k} n \int_0^1 \left(X_\bullet(t + (j-1)) - \bar{X}_\bullet(t)\right)^2 \mathrm{d}t,$$

where $X_\bullet(t) = n^{-1} \sum_{i=1}^{n} X_i(t)$ with $t \in [0, k]$ and $\bar{X}_\bullet(t) = k^{-1} \sum_{j=1}^{k} X_\bullet(t + (j-1))$ with $t \in [0, 1]$ and $1 \leq j \leq k$ (note that $\mathcal{C}_n = 2\mathcal{C}_n(2)$).

It is not difficult to develop a similar result to Theorem 1 for the above statistic. Arguing as in Martínez-Camblor et al. (unpublished manuscript) the following result can be derived.

Theorem 2. *Assume that $X_i(t) = m(t) + e_i(t)$ with $1 \leq i \leq n$, are n independent trajectories from a L^2-processes (defined on $[0, k]$), with $\mathbb{E}[e_i(t)] = 0$ (for $t \in [0, k]$) and covariance function $\mathbb{C}(s, t)$. Then, if $m(t) = m(t + (j-1))$ $\forall t \in [0, 1]$ and with*

Table 5
Observed rejection proportions for Model 4 (the null is true) (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$).

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.056	0.062	0.047	0.057	0.063	0.047	0.054	0.062	0.050
		1/4	0.051	0.059	0.044	0.050	0.058	0.044	0.053	0.059	0.045
		1/2	0.059	0.064	0.051	0.058	0.066	0.053	0.057	0.065	0.052
	35	0	0.057	0.061	0.052	0.056	0.061	0.052	0.056	0.060	0.052
		1/4	0.054	0.061	0.050	0.055	0.061	0.049	0.055	0.061	0.050
		1/2	0.061	0.065	0.057	0.064	0.068	0.060	0.064	0.068	0.057
	50	0	0.056	0.060	0.053	0.057	0.063	0.053	0.057	0.062	0.056
		1/4	0.055	0.060	0.052	0.056	0.059	0.054	0.056	0.058	0.052
		1/2	0.050	0.053	0.047	0.050	0.052	0.045	0.051	0.052	0.044
LogNormal	25	0	0.049	0.055	0.050	0.049	0.055	0.050	0.050	0.058	0.051
		1/4	0.052	0.061	0.050	0.050	0.059	0.053	0.050	0.059	0.051
		1/2	0.049	0.056	0.051	0.050	0.056	0.052	0.049	0.059	0.052
	35	0	0.054	0.057	0.054	0.055	0.057	0.054	0.055	0.059	0.054
		1/4	0.050	0.056	0.050	0.049	0.056	0.051	0.050	0.055	0.050
		1/2	0.047	0.050	0.048	0.047	0.052	0.049	0.047	0.053	0.046
	50	0	0.048	0.051	0.049	0.047	0.051	0.050	0.048	0.052	0.051
		1/4	0.054	0.058	0.054	0.053	0.057	0.054	0.053	0.055	0.053
		1/2	0.052	0.056	0.050	0.052	0.054	0.051	0.050	0.054	0.051
Mixed	25	0	0.058	0.066	0.057	0.058	0.064	0.055	0.057	0.065	0.054
		1/4	0.056	0.064	0.055	0.056	0.064	0.052	0.055	0.064	0.052
		1/2	0.057	0.064	0.055	0.057	0.065	0.054	0.056	0.063	0.054
	35	0	0.054	0.062	0.055	0.055	0.060	0.054	0.055	0.060	0.054
		1/4	0.057	0.064	0.054	0.055	0.063	0.055	0.057	0.063	0.054
		1/2	0.056	0.063	0.055	0.056	0.061	0.056	0.056	0.060	0.056
	50	0	0.055	0.057	0.054	0.053	0.057	0.053	0.053	0.056	0.053
		1/4	0.055	0.059	0.053	0.056	0.057	0.053	0.054	0.059	0.052
		1/2	0.056	0.060	0.051	0.055	0.059	0.050	0.057	0.059	0.051

Table 6
Observed rejection proportions for Model 5 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.684	0.716	0.693	0.680	0.712	0.686	0.681	0.712	0.686
		1/4	0.881	0.903	0.890	0.877	0.898	0.884	0.873	0.895	0.885
		1/2	0.976	0.984	0.978	0.978	0.985	0.983	0.979	0.983	0.982
	35	0	0.896	0.907	0.899	0.889	0.904	0.894	0.891	0.904	0.897
		1/4	0.986	0.988	0.987	0.987	0.988	0.988	0.986	0.989	0.987
	50	0	0.994	0.994	0.994	0.993	0.994	0.993	0.993	0.994	0.994
LogNormal	25	0	0.990	0.992	0.993	0.991	0.993	0.993	0.989	0.994	0.992
		1/4	0.999	0.999	0.999	0.999	0.999	0.999	0.998	1.000	0.999
Mixed	25	0	0.995	0.996	0.997	0.996	0.999	0.999	0.997	0.997	0.997
		1/4	0.997	0.997	0.997	0.997	0.997	0.997	0.997	0.997	0.997
		1/2	0.999	0.999	0.999	0.999	0.999	0.999	0.999	0.999	0.999

$j \in 1, \ldots, k$ (null hypothesis), we have the convergence

$$\mathcal{C}_n(k) \xrightarrow{\mathcal{L}}_n \sum_{l\in\mathbb{N}} \sum_{j=1}^{k} \lambda_{j,l} \mathcal{N}_{j,l}^2, \tag{10}$$

where $\{\{\lambda_{j,l}\}_{j=1}^{k}\}_{l\in\mathbb{N}}$ are k non-negative number sequences satisfying (for each $1 \le j \le k$) that $\lambda_{j,1} \ge \lambda_{j,2} \ge \cdots \ge \lambda_{j,k} \ge \cdots \ge 0$ and $\sum_{l\in\mathbb{N}} \lambda_{j,l}^2 < \infty$ and $\{\boldsymbol{N}_l = (\mathcal{N}_{1,l}, \ldots, \mathcal{N}_{k,l})\}_{l\in\mathbb{N}}$ is a sequence of k-dimensional, normal distributed random variables whose marginals follow a standard normal distribution.

Proof. The first part of the proof is similar to the Theorem 1 one. According with the results exposed above, there exists a Gaussian process, $\mathcal{Z}$, with zero mean and covariance function $\mathbb{C}(s, t)$ defined on $[0, k]$ such that

$$\mathcal{C}_n(k) \xrightarrow{\mathcal{L}}_n \sum_{j=1}^{k} \int_0^1 \left(\mathcal{Z}(t + (j-1)) - \bar{\mathcal{Z}}(t)\right)^2 \mathrm{d}t \tag{11}$$

Table 7
Observed rejection proportions for Model 6 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	0.227	0.248	0.221	0.223	0.246	0.219	0.225	0.243	0.214
		1/4	0.305	0.341	0.310	0.314	0.341	0.305	0.309	0.339	0.310
		1/2	0.501	0.537	0.499	0.494	0.524	0.490	0.487	0.523	0.496
	35	0	0.321	0.342	0.319	0.316	0.334	0.315	0.312	0.334	0.313
		1/4	0.460	0.489	0.461	0.463	0.488	0.463	0.460	0.482	0.465
		1/2	0.733	0.757	0.738	0.718	0.741	0.729	0.722	0.744	0.724
	50	0	0.523	0.546	0.528	0.510	0.526	0.509	0.512	0.526	0.504
		1/4	0.724	0.737	0.730	0.724	0.744	0.729	0.723	0.740	0.731
		1/2	0.938	0.954	0.944	0.936	0.943	0.942	0.940	0.947	0.942
LogNormal	25	0	0.531	0.565	0.553	0.548	0.580	0.574	0.551	0.585	0.573
		1/4	0.762	0.792	0.786	0.767	0.797	0.790	0.770	0.796	0.793
		1/2	0.944	0.958	0.957	0.936	0.949	0.950	0.937	0.949	0.952
	35	0	0.738	0.760	0.753	0.759	0.775	0.773	0.759	0.779	0.778
		1/4	0.941	0.953	0.958	0.936	0.950	0.951	0.936	0.949	0.951
		1/2	0.997	0.998	0.997	0.997	0.997	0.998	0.996	0.997	0.998
	50	0	0.924	0.932	0.931	0.933	0.939	0.939	0.934	0.939	0.940
		1/4	0.994	0.995	0.994	0.994	0.995	0.995	0.995	0.995	0.996
Mixed	25	0	0.251	0.277	0.255	0.255	0.280	0.263	0.250	0.279	0.257
		1/4	0.357	0.391	0.373	0.357	0.394	0.368	0.355	0.388	0.369
		1/2	0.433	0.462	0.445	0.444	0.472	0.452	0.441	0.470	0.456
	35	0	0.402	0.420	0.409	0.397	0.427	0.409	0.399	0.426	0.411
		1/4	0.561	0.594	0.582	0.561	0.590	0.577	0.561	0.591	0.577
		1/2	0.686	0.713	0.704	0.701	0.725	0.713	0.699	0.724	0.714
	50	0	0.601	0.621	0.614	0.611	0.630	0.625	0.604	0.628	0.618
		1/4	0.802	0.814	0.817	0.799	0.817	0.811	0.796	0.812	0.809
		1/2	0.919	0.925	0.925	0.915	0.927	0.923	0.921	0.934	0.925

Table 8
Observed rejection proportions for Model 7 (5000 iterations) for different residual types (normal, lognormal and mixed), correlation structures ($\rho = 0$, $\rho = 1/4$ and $\rho = 1/2$) and different sample sizes ($n = 25$, $n = 35$ and $n = 50$). The statistical power in the omitted rows is always 1.

Residuals	N	ρ	$I = 26$			$I = 101$			$I = 251$		
			A	B	P	A	B	P	A	B	P
Normal	25	0	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		1/4	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
LogNormal	25	0	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		1/4	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Mixed	25	0	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
		1/4	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

where $\bar{\mathcal{Z}}(t) = k^{-1}\sum_{j=1}^{k}\mathcal{Z}(t+(j-1))$ $(1 \le j \le k)$. From the properties of the Gaussian process and arguing as in Theorem 1, for each $j \in 1, \ldots, k$, $\xi_j(t) = \mathcal{Z}(t+(j-1)) + \bar{\mathcal{Z}}(t)$ $(t \in [0,1])$ is a centered Gaussian process with covariance $\mathbb{K}_j(s,t) \in L^2[0,1]$. Therefore we can derive the equality

$$\int_0^1 \xi_j(t)^2 \mathrm{d}t = \sum_{l\in\mathbb{N}} \lambda_{j,l}\mathcal{N}_{j,l}^2, \tag{12}$$

where $\{\lambda_{j,l}\}_{l\in\mathbb{N}}$ $(j \in 1, \ldots, k)$ is a non-negative sequence satisfying $\lambda_{j,1} \ge \lambda_{j,2} \ge \cdots \ge \lambda_{j,s} \ge \cdots \ge 0$ and $\sum_{l\in\mathbb{N}}\lambda_{j,l}^2 < \infty$ and $\{\mathcal{N}_{j,l}\}_{l\in\mathbb{N}}$ $(j \in 1, \ldots, k)$ is a sequence of independent random variables following a standard normal distribution.

From (11) and (12) we can derive that

$$\mathcal{C}_n(k) \xrightarrow[n]{\mathcal{L}} \sum_{l\in\mathbb{N}}\sum_{j=1}^{k}\lambda_{j,l}\mathcal{N}_{j,l}^2.$$

Hence, to prove (10) is enough we need to prove that the k-dimensional random vectors $\{\boldsymbol{N}_l = (\mathcal{N}_{1,l}, \ldots, \mathcal{N}_{k,l})\}_{l\in\mathbb{N}}$ are normal distributed. We equivalently prove that, for each $f \in \mathbb{N}$, $\sum_{j=1}^{k} a_j\mathcal{N}_{j,f}$ follows a normal distribution for each $a_1, \ldots, a_k \in \mathbb{R}$. Note that, for each (fixed) $f \in \mathbb{N}$, we have that

$$\mathcal{Z}_f^*(t) = \{a_1(\mathcal{Z}(t) - \bar{\mathcal{Z}}(t))e_{1,f}(t), \ldots, a_k(\mathcal{Z}(t+(k-1)) - \bar{\mathcal{Z}}(t))e_{k,f}(t)\},$$

is a k-dimensional centered Gaussian process where, for each $j \in 1, \ldots, k$, $\{e_{j,l}(t)\}_{l\in\mathbb{N}}$ is the convergent orthonormal sequence of deterministic functions associated with the respective Karhunen–Loève decomposition. Hence for each $j \in$

$1, \ldots, k$,

$$a_j e_{j,f}(t) \sum_{l \in \mathbb{N}} \sqrt{\lambda_{j,l}} e_{j,l}(t) \mathcal{N}_{j,l} = a_j (\mathcal{Z}(t + (j-1)) - \bar{\mathcal{Z}}(t)) e_{j,f}(t).$$

For each $j \in 1, \ldots, k$, we can assume that $\lambda_{j,f} \neq 0$ (if $\lambda_{j,f} = 0$, the respective $\mathcal{N}_{j,f}$ does not intervene on $\xi_j(t)$ (Eq. (12)) and it can be chosen (freely) independently with $\{\mathcal{N}_{i,f}\}_{i \neq j}$ $1 \leq i \leq k$). Therefore for the orthonormal sequence properties, for each $f \in \mathbb{N}$, we can derive the equality

$$\sum_{j=1}^{k} a_j \mathcal{N}_{j,f} = \int \sum_{j=1}^{k} \frac{a_j}{\sqrt{\lambda_{j,f}}} (\mathcal{Z}(t + (j-1)) - \bar{\mathcal{Z}}(t)) e_{j,f}(t) \mathrm{d}t.$$

Because the right side of the previous equation is a Gaussian variable, the k-dimensional random vectors $\{\boldsymbol{N}_l = (\mathcal{N}_{1,l}, \ldots, \mathcal{N}_{k,l})\}_{l \in \mathbb{N}}$ are normal distributed and the proof is concluded. □

Theorem 2 (like Theorem 1) provides the convergence ratio for the statistic $\mathcal{C}_n(k)$ but, due the parameters $\lambda_{j,l}$ ($1 \leq j \leq k$ and $l \in \mathbb{N}$) are still unknown, it is not useful in order to obtain a final significance. However, Eq. (10) allows us to develop a Monte Carlo procedure, similar than the one described in the Section 2, which lets us approximate the final P-value.

Two considered nonparametric techniques are directly generalized to the k-sample case. In the case of the permutation test (P), step P_2 must be adequately changed (it is straightforward) to the k-sample case. For the bootstrap method (B), under the null, we have the equality,

$$\mathcal{C}_n(k) = \sum_{j=1}^{k} n \int_0^1 (X_\bullet(t + (j-1)) - m(t + (j-1)))^2 \, \mathrm{d}t - kn \int_0^1 \left(m(t) - \bar{X}_\bullet(t)\right)^2 \mathrm{d}t,$$

which is a direct analogy (for the $\mathcal{C}_n(k)$-statistic) of the formula in (9). Taking into account this point in the step B_3 we obtain a k-sample generalization for the bootstrap method.

6. Conclusions

Functional data analysis (FDA) has been the focus of numerous and interesting works along the last few years. Because the number of areas in which this kind of data appears is increasing, FDA earns interest and, recently, most of the usual statistical methods have been adapted to this context (the references are uncountable (including special issues of several journals like Computational Statistics, Journal of Multivariate Analysis or Computational Statistics and Data Analysis), see for example the recent papers of Park et al., 2009, Delicado, 2011 or Rosen and Thompson, 2009). It seems there is a clear and direct the relationship between FDA and LDA but, in addition FDA is also connected with other statistical fields. Recently, González-Rodríguez et al. (in press) built a bridge between fuzzy data and a special subset of a functional Hilbert space. From this result, the developed methods for the statistical analysis of fuzzy data can be considering techniques for functional data analysis and vice versa.

This paper is concerned with the generalization of repeated measures to the functional setting. The data nature makes this problem equivalent to compare the equality among different pieces of the whole curve. Both the parametric and the nonparametric approaches are considered. From the usual parametric case (additive model) the asymptotic distribution is derived. Of course different resampling methods have been studied for FDA (see, for example, Fan and Lin, 1998 or Cuevas et al., 2006). We used the quadratic distance properties and develop a resampling plan similar to the used one in Martínez-Camblor et al. (unpublished manuscript). The main particularity of this method is that the null is not taken into account at the resample moment but at computing the statistic (bootstrap) values (this algorithm can also be used with other (particular) distances, see, for example, Martínez-Camblor, 2010). The usual permutation procedure is also considered.

The Monte Carlo Simulation study depicts the high ability of these procedures to detect differences between the original curves even for small samples. The convergence of the bootstrap method is slower than the permutation one and makes it (lightly) anticonservative for small sample sizes, as consequence, it is (lightly) more powerful than the two other procedures, although, in general, the observed statistical powers for the six (three in each problem) studied methods are quite similar in all considered scenarios.

Of course, absolutely continuous functions are not considered in practice and, an artificial discretization of the curves is made in order to compute the proposed statistic. Different grids have been considered. All of them are simple equidistant partitions of the interval [0, 1] with different number of points (cases $I = 26$, 101 and 251 were considered). In Models 0 (null hypothesis), 1 and 2, and in the problem two models (4, 5, 6 and 7) the used grid it is not relevant for the final result, the observed differences among the powers obtained for the grids are negligible in all studied cases. However, the situation changes drastically in Model 3, the obtained results depend on the grid. The lost of power for the smallest I is important, therefore, it seems that, depending on the shape of the curves (and where the differences between them are located), we must be careful with the required precision for the numerical computations.

It seems that the repeated measures functional approach allows detecting whether different curves are from the same source or not. The studied method obtains really good results (high statistical powers) although the differences between

the underlying curves are not large even for small sample sizes. However, simulations not shown here suggest that, for very small sample size ($n \leq 15$), the nominal level is not respected and the studied test (its bootstrap and asymptotic approximations) is too anticonservative. Although in most of the considered models, the role of the grid involved in the discretization process (required in order to solve the numerical components of the algorithm) seems negligible, in Model 3 it is shown that this grid can be really important to obtain adequately (optimum) results. When the numerical errors are too *rude* (corresponding with the smallest value of I), the achieved powers are poor (compared with the obtained ones for the biggest value of I). The computational cost derived from a tight grid can be decreased by using an efficient point selection (not an equidistant one). Simulations (not shown here) which use a grid which takes into a count the shape of the involved functions (with $I = 26$) reach the same statistical powers than the obtained ones for the best grid.

The intense activity on FDA research leaves the fields of application (see Epifanio and Ventura-Campos, 2011 for a recent input) and the possibility of methodology improvement always open. For instance, in order to solve the considered problem, one can apply different (and perhaps better) approaches. The k-nearest neighbor method of Burba et al. (2009) or the local linear ideas of Barrientos-Marin et al. (2010) are different possible ways to address this topic.

Acknowledgments

The first author is specially grateful to Susana Diaz-Coto whose patient ear and wise counsel have improved this work. We are really grateful to the Editor and the anonymous reviewers whose comments and suggestions have improved the paper.

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