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ARTICLE

TVMM: an R package for testing hypothesis on mean vectors

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Abstract

The Multivariate Tests for the Vector of Means (TVMM) package has six functions: T2O function, which computes Hotelling original's T^2 test; T2Boot function, which computes the parametric bootstrap version of the original T^2 test; T2RobustBoot function, which computes the robust parametric bootstrap version of the T2Boot test; LRTTrace function, which computes the asymptotic version of the likelihood ratio test (*LRT*) using the trace operator; LRTTBoot function, which computes the parametric bootstrap version of the LRTTrace and the LRTTRBoot, which computes the robust version of the LRTTBoot. The alternative test versions of the *LRT* have the advantage of being valid for high-dimensional data. We describe the methods and illustrate the use of the TVMM package with real data on soil properties.

Keywords: High-dimension; Hypotheses; Alternative; Contaminated; Non-normal.

1. Introduction

It is a challenge to test hypotheses on a vector of non-normal and normal contaminated populations means. This challenge becomes even greater for large data (more observations than variables). Consider the problem of testing the following hypothesis

$$H_0 : \mu = \mu_0 \qquad \text{against} \qquad H_1 : \mu \neq \mu_0. \tag{1}$$

where μ is the vector of population averages and μ_0 is a vector of known constants. This problem is quite common in soil science, genetics, medicine, chemistry, among other areas (Marozzi, 2015, 2016; Wang *et al.*, 2013).

The TVMM package was build to assist in decision making about the mean vector in a p-variable population. The Hotelling T^2 test (Alves & Ferreira, 2019) is widely used in situations that involve making decisions about the vector of means. However, this test shows some restrictions due to the singularity of the covariance matrix since the test statistic can not be computed. Furthermore, under non-normality, this test is not suitable since assumptions such as homoscedasticity of the covariance matrix are violated. Another factor that can influence decision making through this test is the presence of outliers in the observed data. In this case, the vector of means and the matrix of sample covariances are highly influenced. Another alternative test widely (Ledoit & Wolf, 2002) used for testing the sample mean vector is the likelihood ratio test (LRT). However, this test also has the same restrictions as the T^2 Hotelling test.

Several proposals with adaptations of the T^2 test can be found at Mudholkar & Srivastava (2000), Tiku (1982), and Willems *et al.* (2002). Alternative adaptations proposed to the LRT test can be found at Marozzi (2015, 2016) and Wang *et al.* (2013) for the case of high-dimensional data, which arise when the number of variables (p) is greater than the number of observations (n). To get around the problems showed above, we built the TVMM package to provide users, in addition to the T^2 test itself, alternative tests even for high-dimensional data adapted from the T^2 test and LRT (Alves & Ferreira, 2019).

Finally, we emphasize that the main contribution of this paper is to introduce the user of statistical software R to the aforementioned TVMM package. It allows the user to perform tests on the vector of means where the assumptions are violated (non-normality) and also on high-dimensional data, where Hotelling's traditional T^2 test does not apply.

2. Methodology

2.1 The likelihood ratio test (LRT)

The likelihood ratio test (LRT) statistic is given by the following expression

$$-2\ln(\Lambda) = n[\ln|\boldsymbol{S} + \boldsymbol{H}| - \ln|\boldsymbol{S}|], \tag{2}$$

where $\boldsymbol{H} = (\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)(\bar{\boldsymbol{X}} - \boldsymbol{\mu}_0)^\top$ and ln is the natural logarithm. The $-2\ln(\Lambda)$ statistic follows a chi-square distribution with $s - r$ degrees of freedom. Consider $\Omega \in \mathbb{R}^s$ the unrestricted parametric space and $\Omega_0 \subseteq \mathbb{R}^r$ the restricted parametric space, with $\Omega_0 \subset \Omega$. In this case, $s = p + p(p+1)/2$ and $r = p$.

The T^2 test of traditional Hotelling will be presented in the 2.4.1 section.

2.2 The comedian robust estimator

Let X and Y be two random variables. Thus, Falk (1997) defined the robust estimator comedian by the following expression

$$COM(X, Y) = med[(X - med(X))(Y - med(Y))], \tag{3}$$

where the term "med" denotes the median. The comedian is an advantageous estimation method, since it always exists while $Cov(X, Y)$ requires the existence of the first two moments of X and Y. Besides that, it is symmetric, invariant to location and scale transformation. This means that $COM(X, aY + B) = aCOM(X, Y)$, where $a \in \mathbb{R}$ and B is a vector $n \times 1$ of constants. This estimator has also strong asymptotic consistency and normality (ibid.). The comedian generalizes the MAD (median absolute deviation) method, also introduced by Falk (ibid.), which can be obtained by making $X = Y$. The MAD will be useful for building the p-variant version of comedian.

Sajesh & Srinivasan (2012) provide the use of the p-variate version of the comedian estimator. Set $\boldsymbol{X}_{n\times p}$ as a data matrix with vector columns $\boldsymbol{X}_j$, $j = 1, 2, \ldots, p$. A comedian matrix $\boldsymbol{COM}(\boldsymbol{X}) = \{MAD(\boldsymbol{X}_i, \boldsymbol{X}_j),\ if\ i = j; COM(\boldsymbol{X}_i, \boldsymbol{X}_j),\ if\ i \neq j\}$ is a symmetric $p \times p$ matrix.

The comedian matrix has an issue of being non-positively defined, a requirement of a covariance matrix. To circumvent this problem, Maronna & Zamar (2002) adopted the following steps to obtain robust estimates for the mean vector and covariance matrix (Di Palma *et al.,* 2013):

1. let $\delta(X) = \boldsymbol{D}\boldsymbol{COM}(X)\boldsymbol{D}^\top$ be the median correlation matrix, where $\boldsymbol{D}$ is a diagonal matrix with elements $1/MAD(X_i)$, $i = 1, 2, ..., p$;
2. calculate the eigenvalues λ_i and eigenvectors $\boldsymbol{e}_j$ of the $\delta(X)$, $j = 1, 2, ..., p$ and let $\boldsymbol{E}$ be a matrix whose columns are the $\boldsymbol{e}_j'$s. Hence, $\delta(X) = \boldsymbol{E}\boldsymbol{\Lambda}\boldsymbol{E}^\top$, where $\boldsymbol{\Lambda} = diag(\lambda_1, ..., \lambda_p)$;
3. let $\boldsymbol{Q} = \boldsymbol{D}\boldsymbol{E}$, where $\boldsymbol{D}$ is defined in step 1 and $\boldsymbol{Z}_i = \boldsymbol{Q}^{-1}\boldsymbol{x}_i$, $i = 1, 2, ..., p$;
4. the robust estimators for the mean vector $\boldsymbol{m}(X)$ and covariance matrix $\boldsymbol{S}(X)$ are

$$\boldsymbol{S}(X) = \mathbf{Q}\boldsymbol{\Gamma}\mathbf{Q}^\top \quad \text{and} \quad \boldsymbol{m}(X) = \boldsymbol{Q}\boldsymbol{l} \tag{4}$$

where $\boldsymbol{\Gamma} = diag(MAD(\boldsymbol{Z}_1)^2, ..., MAD(\boldsymbol{Z}_p)^2)$ and $\boldsymbol{l} = (med(\boldsymbol{Z}_p))^\top$, $p = 1, \ldots, p$.

Estimates can be provided through an iterative process by replacing δ by $\boldsymbol{S}$ and repeating the steps 2, 3 and 4.

Both estimator are affine-equivariant estimator of location and scale, respectively, and the comedian covariance matrix is positive definite estimator as required. In addition, the estimates obtained by the COMEDIAN method have a high breaking point. The efficiency of the method increases with increasing data size (Sajesh & Srinivasan, 2012).

2.3 The exact binomial test

Type I error rates of tests were evaluated by Monte Carlo simulations. According to Oliveira and Ferreira (2010) these estimates are not error-free. Therefore, an exact binomial test is used to make the decision whether each of the modified or the original T^2 tests is considered exact, liberal or conservative. In this sense, considering a nominal level of significance of 1%, the following null hypothesis is tested

$$\mathrm{H}_0 : \alpha = 5\% \qquad \text{against} \qquad \mathrm{H}_1 : \alpha \neq 5\%. \tag{5}$$

The statistic of the exact binomial test (Cardoso de Oliveira & Ferreira, 2010) is given by

$$F = \left(\frac{z+1}{N-z}\right)\left(\frac{1-\alpha}{\alpha}\right), \tag{6}$$

where z is the number of rejection of the null hypothesis by one of the tests in the nominal significance level of α and N is the number of Monte Carlo simulations performed. Under the null hypothesis (5) the F_c statistic follows a F distribution with $\nu_1 = 2(N-z)$ and $\nu_2 = 2(z+1)$ degrees of freedom. If the null hypothesis is rejected and the type I error is considered significantly ($P \leq 0.01$) lower than the nominal level of α%, the test can be considered conservative; if the null hypothesis is rejected and the type I error is considered significantly ($P \leq 0.01$) higher than the nominal level of α%, the test can be considered liberal; and if the null hypothesis is not rejected, ($P > 0.01$), the test can be considered exact. In the next section we present our methodology used.

2.4 The TVMM package tests

The TVMM package has implemented some statistical tests, each with its particularity, which is useful in this decision making. The tests proposed here follow the same distribution properties as the original tests (T^2 and LRT). However, these distributions are asymptotic (approximate). To improve these distributional approaches, we built the parametric bootstrap versions of these tests. Besides, to circumvent possible problems with the presence of real outliers, we built the robust versions of these tests using the comedian (Falk, 1997) robust estimator. This estimator has the advantage of being location (average) and scale (covariance) (Maronna & Zamar, 2002) invariant. The multivariate version of this estimator is presented in Di Palma *et al.* (2013) and Sajesh & Srinivasan (2012).

However, before presenting them we remember that, in general, statistical tests are classified as conservative, exact, or liberal. We use the exact binomial test with $\alpha = 5\%$ to classify our tests (Cardoso de Oliveira & Ferreira, 2010) (see section 2.3). A test is considered acceptable or good if it is conservative or exact. If it is liberal, it must be discarded. All of our proposed tests were accurate in most of the scenarios, in which they were evaluated. In the other scenarios they were conservative (Alves & Ferreira, 2019). We will now present these tests. All tests presented here are acceptable (conservative or exact).

2.4.1 Hotelling's T^2 test

The T^2 test is widely used to test the hypotheses given in (1) and the expression of the statistic of the test is given by

$$T_c^2 = n(\bar{X} - \mu_0)^\top S^{-1}(\bar{X} - \mu_0). \tag{7}$$

where $\bar{X} = \sum_{j=1}^{n} X_j/n$ is the sample mean vector, $S = \sum_{j=1}^{n}(X_j - \bar{X})(X_j - \bar{X})^\top/(n-1)$ is the sample covariance matrix and n is the sample size. Under H_0 and with the hypothesis of normality and homoscedastic covariance matrix, T_c^2 as in (7) follows a T^2 distribution of Hotelling given by $(n-1)pF_{\alpha,p,n-p}/(n-p)$, where $F_{\alpha,p,n-p}$ is the upper quantile $100\alpha\%$ of the F distribution with p and $n-p$ degrees of freedom. Then, H_0 as in (1) is rejected if $T_c^2 > (n-1)p/(n-p)F_{\alpha,p,n-p}$.

As already mentioned, the T^2 test should be used in normally distributed populations where the number of p variables is less than the number of observations n $(p < n)$.

2.4.2 The T^2 parametric bootstrap test

The T^2 parametric bootstrap test, called T^2_{PB} ($T2PB$), where PB is the same as parametric bootstrap, was constructed as follows. In step 1, from the original sample, we estimate the parameters $\boldsymbol{\Sigma}$ and $\boldsymbol{\mu}$, respectively, for $\mathbf{S}^*$ and $\bar{\mathbf{X}}^*$, where $\mathbf{S}^*$ and $\bar{\mathbf{X}}^*$ are the covariance matrix and the vector of traditional sample means. The test statistic is then calculated by

$$T^{*2} = n\left(\bar{X}^* - \mu_0\right)^\top \mathbf{S}^{*-1}\left(\bar{X}^* - \mu_0\right). \tag{8}$$

In step 2, using the estimated sample covariance matrix S^*, a sample of size n was generated from a normal distribution p -variate imposing H_0 and taking $\boldsymbol{\Sigma} = S^*$. Therefore a sample of size n is generated from a distribution $N(\mu_0, S^*)$. In step 3, for each bootstrap sample parametric the sample mean $\bar{X}_{PB}$ and the sample covariance matrix S_{PB} are estimated. In step 4, the test statistic is calculated by

$$T^2_{\mathrm{PB}} = n(\bar{\mathbf{X}}_{PB} - \mu_0)^\top \mathbf{S}^{-1}_{PB}(\bar{\mathbf{X}}_{PB} - \mu_0). \tag{9}$$

The steps 2 to 4 are repeated B times and a set of size $B+1$ is constructed with the B values of the test statistics calculated in (9) and the original value (8). The null distribution of the parametric bootstrap test is formed by this set. If the i-th member of this set is represented by T_i^2, $i = 1, 2, \cdots, B+1$, then the p-value is calculated as

$$p\text{-value} = \frac{\sum_{i=1}^{B+1} I(T_i^2 \geq T^{*2})}{B+1}, \tag{10}$$

where $I(T_i^2 \geq T^{*2})$ is an indicator function. The null hypothesis as in (1) will be rejected with a significance level of α if p-value $\leq \alpha$.

2.4.3 The T^2 robust parametric bootstrap test

The following steps were adopted in the construction of the T^2 robust parametric bootstrap test, called T^2_{RPB} (*T2RPB*), where *RPB* means robust parametric bootstrap. In the first 1, the estimators S^* e $\bar{X}^*$ are replaced by the respective robust comedian estimators S_R and $\bar{X}_R$ and the original statistic is then calculated

$$T^{*2} = n(\bar{\mathbf{X}}_R - \mu_0)^\top \mathbf{S}_R^{-1}(\bar{\mathbf{X}}_R - \mu_0). \tag{11}$$

In step 2 is similar to that reported in the previous test, where a sample of size n is drawn from a normal distribution $N(\mu_0, S_R)$. The third step is the same, but the sample mean and covariance matrix are denoted by $\bar{X}_{RPB}$ and $\mathbf{S}_{RPB}$. In step 4 the test statistic is then computed

$$T^2_{\mathrm{RPB}} = n(\bar{\mathbf{X}}_{RPB} - \mu_0)^\top \mathbf{S}_{RPB}^{-1}(\bar{\mathbf{X}}_{RPB} - \mu_0). \tag{12}$$

The same procedure as the previous test is performed and p-value is given by

$$p\text{-value} = \frac{\sum_{i=1}^{B+1} I(T_i^2 \geq T^{*2})}{B+1}, \tag{13}$$

where $I(T_i^2 \geq T^{*2})$ is an indicator function. The null hypothesis as in (1) is rejected with a significance level of α if p-value $\leq \alpha$.

As shown in the 2.4.1 section, Hotelling's T^2 test is not valid for high dimensional data ($p > n$). The same occurs with the adapted tests presented so far (T^2_{PB}, T^2_{RPB}). We then decided to build tests adapted to the *LRT* test, based on the works of Ledoit & Wolf (2002), which are valid for high-dimensional data. The main idea is to replace the determinant (generalized variance) of the matrices S e $S + H$, as in (2), by the total variance that is a corresponding feature and maintaining the same distribution properties as the *LRT* test.

2.4.4 The asymptotic *LRT* test with a trace

The asymptotic version of the *LRT* test, called *ATLRT* (Asymptotic Trace Likelihood Ratio Test), was obtained by directly replacing the determinant given in the expression (2) of the *LRT* test by the trace *tr* operator. So, the expression of this test is given by

$$T^2_{ATLRT} = n\left\{\log[tr(S^* + \boldsymbol{H})] - tr(S^*)\right\}, \tag{14}$$

where $\boldsymbol{H} = (\bar{X}^* - \mu_0)(\bar{X}^* - \mu_0)^\top$. Under H_0, as in (1) and normality, T^2_{ATLRT} has an asymptotic chi-square distribution with p degrees of freedom. The null hypothesis is rejected if $T^2_{ATLRT} \geq \chi^2_{\alpha;p}$, where $\chi^2_{\alpha;p}$, where $100\alpha\%$ is the upper quantile of a chi-square distribution with p degrees of freedom.

2.4.5 The *TLR* parametric trace bootstrap test

The T^2_{ATLRT} test is not guaranteed to follow an exact chi-square distribution with p degrees of freedom and p-various normality. To get around this issue, we proposed a parametric bootstrap version of the likelihood ratio test (*LRT*), called *TLRPBT* (Trace Likelihood Ratio Bootstrap Parametric Test). The steps for building this test are the same as those previously described in the *T2PB* test. The original test statistic has the following expression

$$T^{*2} = n\left\{\log[tr(\mathbf{S}^* + \mathbf{H}^*)] - tr(\mathbf{S}^*)\right\}, \tag{15}$$

where $\mathbf{H}^* = (\bar{\mathbf{X}}^* - \mu_0)(\bar{\mathbf{X}}^* - \mu_0)^\top$. The parametric bootstrap estimators $\mathbf{S}^*$ and $\bar{\mathbf{X}}^*$ are obtained from the original sample.

The test statistic expression is given by

$$T^2_{\text{TLRPB}} = n\left\{\log[tr(\mathbf{S}_{TLRPB} + \mathbf{H}_{TLRPB})] - tr(\mathbf{S}_{TLRPB})\right\}, \tag{16}$$

where $\mathbf{H}_{TLRPB} = (\bar{X}_{TLRPB} - \mu_0)(\bar{X}_{TLRPB} - \mu_0)^\top$. In this case, the expressions $\bar{\mathbf{X}}_{TLRPB}$ and $\mathbf{S}_{TLRPB}$ are the vector of averages and parametric bootsrap sample covariance matrix. The null hypothesis H_0 as in (1) will be rejected if the same conditions previously established in the *T2PB* test occurred.

2.4.6 The *TLR* robust parametric bootstrap test with trace

To get around the possible problems that can occur in the presence of real outliers, we have proposed the robust version of the previously presented *TLRPB* test, called *RTLRPBT* (Robust Trace Likelihood Ratio Bootstrap Parametric Test). The changes from the previously presented test (*TLRPB*) are that the original test statistic has the following expression

$$T^{*2} = n\left\{\log[tr(\mathbf{S}_R + \mathbf{H}_R)] - tr(\mathbf{S}_R)\right\}, \tag{17}$$

where $\mathbf{H}_R = (\bar{\mathbf{X}}_R - \mu_0)(\bar{\mathbf{X}}_R - \mu_0)^\top$. The comedian robust estimators for the vector of averages and covariance matrix $\mathbf{S}_R$ and $\bar{\mathbf{X}}_R$ are obtained from the original sample. The test statistic has the following expression

$$T^2_{\text{RTLRPB}} = n\left\{\log[tr(\mathbf{S}_{RTLRPB} + \mathbf{H}_{RTLRPB})] - tr(\mathbf{S}_{RTLRPB})\right\}, \tag{18}$$

where $\mathbf{H}_{RTLRPB} = (\bar{\mathbf{X}}_{RTLRPB} - \mu_0)(\bar{\mathbf{X}}_{RTLRPB} - \mu_0)^\top$. Here, $bar\ bfX_{RTLRPB}$ and $\bar{\mathbf{X}}_{RTLRPB}$ represent the vector of means and the robust sample covariance matrix. The null hypothesis H_0 as in (1) will be rejected if the same conditions previously established in the *TLRPB* test occurred.

3. The TVMM package

The current version of the TVMM package, which is available in the CRAN repository, contains the functions that describe the tests presented in the 2.4 section. The details are now displayed.

3.1 The `T20` function

This function performs the traditional Hotelling's T^2 test and its arguments are presented, `T20(X, mu0)`:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested.

3.2 The `T2Boot` function

This function performs the T^2 parametric bootstrap test (*T2PB*) and its arguments are presented, `T2Boot(X, mu0, B=2000)`:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested;
- `B`, the number of resamples bootstrap parametric which must be at least equal to 2000.

3.3 The `T2RobustBoot` function

This function performs the T^2 robust parametric bootstrap test (*T2RPB*) `T2RobustBoot(X, mu0, B)` and its arguments are presented:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested,
- `B`, the number of resamples bootstrap parametric which must be at least equal to 2000.

3.4 The `LRTTrace` function

This function performs the asymptotic *LRT* test with trace (*ATLRT*) and its arguments are presented, `LRTTrace(X, mu0)`:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested.

3.5 The `LRTTBoot` function

This function performs the test *LRT* parametric bootstrap with trace (*TLRPBT*) and its arguments are presented, `LRTTBoot(X, mu0, B)`:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested,
- `B`, the number of resamples bootstrap parametric which must be at least equal to 2000.

3.6 The `LRTTRBoot` function

This function performs the *LRT* robust parametric bootstrap test with trace (*RTLRPBT*) and its arguments are presented, `LRTTRBoot(X, mu0, B)`:

- `X`, a matrix $n \times p$ containing n observations and p variables. It should not contain missing values (`NA`),
- `mu0`, a vector containing the mean population to be tested,
- `B`, the number of resamples bootstrap parametric which must be at least equal to 2000.

3.7 The `guiTVMM` function

This function has as main objective to provide the user with an interactive guide in which the user can perform all the functions previously presented. This function also features a graphical output (histogram) that aims to provide the user with a visual interpretation of the decision made (acceptance or rejection) around the null hypothesis as in the expression (1). Their arguments are showed using `guiTVMM(gui = TRUE)`:

- `gui`, logical argument, `TRUE` or `FALSE`. The default is `TRUE`.

4. Application to real data

In this section, the proposed methodology was applied to two real data sets: the first that deals with the contents of sand and clay from Capoeira Nova, in the Amazon, Brazil, available at Ferreira (2018); the second deals with nutrients and soil properties in the municipality of Benjamin Constant, located in the northwest of the Amazon (www.biosbrasil.ufla.br).

4.1 Application to bivariate data ($p = 2,\ n = 30$)

We want to verify that the Capoeira Nova soil has an average sand and clay content equal to that of a forest population (see Table 1), at a level of 5% of significance. An exploratory analysis was previously carried out and we verified that the variables sand and clay are correlated and the data do not show normal p-variable according to the Royston test. There was also the presence of outliers in the data.

Table 1. Sand and clay contents in a Capoeira Nova soil in the Amazon, Brazil.

sand	clay	sand	clay	sand	clay
11	38	20	32	13	47
24	25	18	34	28	32
16	49	17	39	11	45
18	34	30	32	27	36
5	64	45	24	7	59
11	40	11	50	42	23
17	38	41	21	21	35
9	40	22	36	48	21
13	40	14	32	12	36
53	21	25	28	31	32

According to Ferreira (2018), it is known that in a forest soil the average levels of sand and clay content have values equal to 14 and 42, respectively. So, in possession of the samples collected of sand and clay contents in a new capoeira soil, in the Amazon, the hypotheses to be tested are $H_0 : \boldsymbol{\mu} = \boldsymbol{\mu}_0 = [14, 42]^\top$ *versus* $H_1 : \boldsymbol{\mu} \neq \boldsymbol{\mu}_0 = [14, 42]^\top$. The tests *T2*, *T2PB*, *T2R*, *T2RPB*, *ATLRT*, *TLRPBT* and *RTLRPBT* have been applied (see section 2.4).

4.1.1 Application of TVMM package

Table 2 shows that all tests took the same decision to reject the null hypothesis H_0. However, since the assumption of p-variate normality is not met, we suggest choosing the result of the *TLRPBT* because this was the most powerful among all tests evaluated in Alves and Ferreira (2019).

Table 2. Tests for the vector of population means for the levels of sand and clay in a Capoeira Nova soil, in the Amazon.

Test	Statistics	P-value	Decision
T2	11.93406	0.00802	Reject H_0
T2PB	11.93406	0.00899	Reject H_0
T2RPB	45.19158	0.00049	Reject H_0
ATLRT	9.21556	0.00997	Reject H_0
TLRPBT	9.21556	0.00299	Reject H_0
RTLRPBT	7.11871	0.02848	Reject H_0

4.2 High-dimensional data ($p = 19,\ n = 16$)

The objective here is to verify if there is a difference between the average sample levels and the average levels of nutrients and soil properties measured in pristine forest areas (pristine forest) (PF), in the municipality of Benjamin Constant, in the Amazon, Brazil.

4.2.1 Presentation of the data

The data in question is part of the project "Conservation and Sustainable Management of Below-Ground Biodiversity" (GSM-BGBD) and was taken from the site Bios Brazil (www.biosbrasil.ufla.br). The study area is located in the municipality of Benjamin Constant, northwest of the Amazon, and is bordered by Brazil, Colombia, and Peru. An exploratory analysis of the data was previously carried out and it was found that they are correlated, do not show multivariate normality, and have outliers. The studied soil nutrients are active acidity values (pH), total Nitrogen (N), Phosphorus (P), Potassium (K), Calcium (Ca), Magnesium (Mn), Aluminum (Al), potential acidity ($H + Al$), exchangeable bases (SB), effective cation exchange capacity ($CTCt$), potential cation exchange capacity ($CTCT$), base saturation (V), aluminum saturation (m), organic material (MO), zinc (Zn), iron (Fe), manganese (Mn), Copper (Cu), Boron (B) and Sulfur (S). Table 3 presents the observations for each variable of interest.

Table 3. Levels of nutrients and soil properties in pristine forest areas (Benjamin Constant, Amazon, Brazil).

pH	P	K	Ca	Mg	Al	H+Al	SB	CTC	CTC	V	m	MO	Zn	Fe	Mn	Cu	B	S
4.5	4.6	78.0	6.2	2.3	4.4	19.1	8.7	13.1	27.8	31.3	34.0	1.5	4.6	210.0	69.7	2.0	0.3	14.3
4.7	4.9	74.0	4.9	2.7	4.4	17.1	7.8	12.2	24.9	31.3	36.0	1.5	5.4	158.0	57.7	1.2	0.4	6.2
4.4	3.7	69.0	1.9	2.0	5.6	21.4	4.1	9.7	25.5	16.0	58.0	1.2	1.7	162.0	64.1	0.7	0.3	4.9
4.5	3.7	52.0	2.7	1.9	5.2	21.4	4.7	9.9	26.1	18.1	52.0	1.6	1.5	128.5	50.7	1.2	0.4	4.9
4.5	3.1	36.0	3.7	1.3	5.3	21.4	5.1	10.4	26.5	19.2	51.0	1.3	1.4	277.0	49.7	1.2	0.2	4.5
4.2	3.4	55.0	1.3	1.2	6.8	26.7	2.6	9.4	29.3	9.0	72.0	1.4	2.5	322.5	9.4	1.5	0.1	12.8
4.7	5.5	47.0	3.0	1.0	6.1	19.1	4.1	10.2	23.2	17.7	60.0	1.0	2.0	208.8	137.7	1.3	0.2	6.2
4.4	4.9	48.0	3.9	2.0	6.2	23.9	6.0	12.2	29.9	20.1	51.0	1.8	9.4	173.5	104.9	1.1	0.3	9.8
4.4	4.6	67.0	2.8	2.5	6.8	26.7	5.5	12.3	32.2	17.0	55.0	1.6	9.6	144.5	64.6	1.2	0.4	5.8
4.5	4.6	53.0	4.3	1.6	4.2	19.1	6.0	10.2	25.1	24.0	41.0	2.2	17.9	191.0	72.1	1.0	0.4	7.1
4.2	2.3	74.0	1.9	2.2	9.3	33.4	4.3	13.6	37.7	11.4	68.0	2.0	3.7	338.5	52.6	2.2	0.7	6.2
4.5	2.3	63.0	6.0	3.0	7.5	29.9	9.2	16.7	39.1	23.5	45.0	1.8	3.3	124.1	81.6	1.6	0.3	5.8
4.2	3.7	70.0	2.7	1.3	8.1	26.7	4.2	12.3	30.9	13.5	66.0	1.6	2.9	207.5	45.8	1.3	0.3	7.1
4.5	4.0	86.0	5.1	2.9	4.2	19.1	8.2	12.4	27.3	30.1	34.0	2.2	14.0	125.6	106.6	3.3	0.1	8.4
4.7	3.7	84.0	8.0	3.0	3.3	15.3	11.2	14.5	26.5	42.3	23.0	2.1	13.5	125.1	89.1	1.2	0.3	3.3
4.3	4.3	56.0	2.3	1.2	7.5	26.7	3.6	11.1	30.3	12.0	67.0	2.0	11.8	155.5	58.1	2.3	0.0	5.4

A hypothesis test was carried out to check if there are significant differences between the sample levels of the measured soil attributes and the population hypothesized mean levels. The hypotheses to be tested are $H_0 : \mu = \mu_0$ *versus* $H_1 : \mu \neq \mu_0$. The tests *ATLRT*, *TLRPBT* and *RTLRPBT* were applied. Here $\mu_0 = [4.9, 3.6, 76.4, 6.1, 2.5, 3.0, 13.0, 8.8, 11.9, 21.8, 43.6, 25.3, 1.9, 6.7, 157.6, 53.9, 2.0, 0.2, 6.9]^\top$.

Table 4 shows the results obtained when the adapted *LRT* tests are applied to this data. The proposed tests present different decisions under the acceptance of the null hypothesis H_0. While the *ATLRT* test tells us that we should not rejectH_0, the other two tests *TLRPBT* and *RTLRPBT* lead to the decision to reject H_0. It is worth mentioning that the *ATLRT* test, despite controlling the type I error, has low power and is not recommended. Therefore, a decision must be made according to the *TLRPBT* and *RTLRPBT* tests. As the *TLRPBT* test is the most powerful in all scenarios evaluated in Alves and Ferreira (2019), the researcher must make his decision based on this test.

5. Issues: guiTVMM function

We also highlight that the TVMM package has the same tests implemented in an interactive guide, which can be called with the *guiTVMM* function. It will not be presented here and help for using this guide can be found at https://rpubs.com/Henriqueufla/617206.

Table 4. Tests for the vector of population means for nutrients and soil properties of Benjamin Constant, northwest of the state of Amazonia.

Test	Statistic	p-value	Conclusion
ATLRT	6.09636	0.99768	Do not reject H_0
TLRPBT	6.09636	0.00499	Do not reject H_0
RTLRPBT	5.63033	0.03648	Do not reject H_0

Note: all tests controlled the type I error.

6. Considerations

The TVMM package presents versatility in use. The user can choose the syntax of the R language itself or choose the interactive guide. The last option ensures that the user does not need to have a high level of understanding of the R language. Also, in the future versions of the package, we intend to add the mobile and web interface versions so that the range of use of the package increases, further facilitating the interaction with the TVMM package.

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