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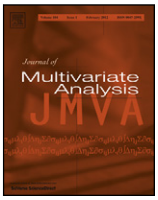

A parametric bootstrap approach for two-way ANOVA in presence of possible interactions with unequal variances[☆]

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ABSTRACT

In this article we consider the Two-Way ANOVA model with unequal cell frequencies without the assumption of equal error variances. For the problem of testing no interaction effects and equal main effects, we propose a parametric bootstrap (PB) approach and compare it with existing the generalized *F* (GF) test. The Type I error rates and powers of the tests are evaluated using Monte Carlo simulation. Our studies show that the PB test performs better than the generalized F-test. The PB test performs very satisfactorily even for small samples while the GF test exhibits poor Type I error properties when the number of factorial combinations or treatments goes up.

1. Introduction

In a two-way ANOVA model with factors *A* and *B*, it is customary to assume that the cell variances are the same even when they are not. In fact, it is well known that without the assumption of equal error variances, under the conventional Neyman–Pearson theory, exact tests for testing the effects of factors *A* and *B* do not exist. When variances are unequal, classical *F*-tests which are calculated under the equal error variance assumption will provide only approximate solutions for testing the effects of factors *A* and *B*. The sizes of classical *F*-tests are fairly robust against the assumption of equal variances when the sample sizes are equal [4]. When the sample sizes are different, the sizes of *F*-tests can substantially exceed the intended size. Moreover, they suffer from serious lack of power even under moderate heteroscedasticity. The generalized *F*-test [1] is a recently developed solution which is based on an extended definition of the *p*-values [10]. However, [7] observed in the literature of ANOVA that some asymptotic procedures and the generalized *F*-test perform satisfactorily for a small number of treatments and/or moderate to large samples. For one-way ANOVA, they proposed a parametric bootstrap (PB) approach as a solution. The PB approach has been applied to solve a number of problems when conventional methods are difficult to apply or fail to provide exact solutions; see, for example, [8,9,6].

For testing the interaction effect, [3] carried out a simulation study to compare the performance of the generalized *F*-test and the classical *F*-test when the number of factorial combinations of factors *A* and *B* is small. In this case, the generalized *F*-test performs better than the classical *F*-test. As already pointed out, for a bigger number of factorial combinations, the type I error probability of the generalized *F*-test may far exceed the nominal level. Therefore, it is important to develop

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a test procedure for the interaction effect and the main effect with satisfactory Type-I error rate and power regardless of number of factorial combinations and the sample sizes. In the present paper, we will develop a parametric bootstrap (PB) approach. Bootstrap approach is a type of Monte Carlo method applied on observed data [5]. The bootstrap methods can be in either parametric or nonparametric settings. However, the problems addressed in this paper are in a strict parametric setting, namely the two-way ANOVA model with the usual normality assumptions. Therefore, we only propose a parametric bootstrap approach.

This article is organized as follows. For testing no interaction effect to the two-way ANOVA model with unequal cell frequencies unequal error variances in Section 2 and compare it with the generalized F-test. For the tests on main effects, we also propose a parametric bootstrap (PB) approach in Section 3. The methods are compared with respect to Type I error rates and powers using Monte Carlo simulation. Comparison studies in Section 4 show that the PB test performs better than generalized F-test. Some discussion and further remarks are provided in Section 5.

2. Tests for the interaction effects

Consider the two-way ANOVA model with factors A and B, with factor levels $A_1, \ldots, A_a$ and $B_1, \ldots, B_b$, respectively giving a total of ab factorial combinations or treatments. Suppose a random sample of size n_{ij} is available from ijth treatment, $i = 1, \ldots, a; j = 1, \ldots, b$. Let $Y_{ijk}, i = 1, \ldots, a; j = 1, \ldots, b; k = 1, \ldots, n_{ij}$ represent these random variables and y_{ijk} represent their observed (sample) values. Assume that $n_{ij} > 1$ so that sample variances can be computed for each cell of the design. Sample mean and the sample variance of the ijth treatment are denoted by $\overline{Y}_{ij}$ and $S_{ij}^2, i = 1, \ldots, a; j = 1, \ldots, b$ respectively, where

$$\overline{Y}_{ij} = \frac{1}{n_{ij}} \sum_{k=1}^{n_{ij}} Y_{ijk} \quad \text{and} \quad S_{ij}^2 = \frac{1}{n_{ij} - 1} \sum_{k=1}^{n_{ij}} (Y_{ijk} - \overline{Y}_{ij})^2.$$

The observed values of these random variables are denoted as $\bar{y}_{ij}$ and $s_{ij}^2, i = 1, \ldots, a; j = 1, \ldots, b$ respectively. Consider the two-way ANOVA model with unequal error variances:

$$\begin{aligned} &Y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijk} \\ &e_{ijk} \sim N(0, \sigma_{ij}^2), \quad i = 1, \ldots, a; j = 1, \ldots, b; k = 1, \ldots, n_{ij}, \end{aligned} \tag{2.1}$$

where μ is the general mean, α_i is an effect due to the ith level of the factor A, β_j is an effect due to the jth level of the factor B, and γ_{ij} represents an effect due to the interaction of the factor level A_i and the factor level B_j. Writing $Y_{ij} = (Y_{ij1}, \ldots, Y_{ijn_{ij}})'$, $Y = (Y_{11}', \ldots, Y_{1b}', Y_{21}', \ldots, Y_{2b}', \ldots, Y_{a1}', \ldots, Y_{ab}')'$, $\alpha = (\alpha_1, \ldots, \alpha_a)'$, $\beta = (\beta_1, \ldots, \beta_b)'$, $\gamma = (\gamma_{11}, \ldots, \gamma_{1b}, \gamma_{21}, \ldots, \gamma_{2b}, \ldots, \gamma_{a1}, \ldots, \gamma_{ab})'$, the model (2.1) can be written as

$$Y = \mathbf{1}_{n_{\ldots}} \mu + Z_1 \alpha + Z_2 \beta + Z_3 \gamma + e, \tag{2.2}$$

where $n_{\ldots} = \sum_{i=1}^a \sum_{j=1}^b n_{ij}$ and e is defined similarly to Y. The design matrices Z_1, Z_2 and Z_3 are given by

$$\begin{aligned} &Z_1 = \text{diag}(\mathbf{1}_{n_{1.}}, \ldots, \mathbf{1}_{n_{a.}}), \\ &Z_2 = [\text{diag}(\mathbf{1}_{n_{11}}', \ldots, \mathbf{1}_{n_{1b}}'), \text{diag}(\mathbf{1}_{n_{21}}', \ldots, \mathbf{1}_{n_{2b}}'), \ldots, \text{diag}(\mathbf{1}_{n_{a1}}', \ldots, \mathbf{1}_{n_{ab}}')]', \\ &Z_3 = \text{diag}(\mathbf{1}_{n_{11}}, \ldots, \mathbf{1}_{n_{1b}}, \mathbf{1}_{n_{21}}, \ldots, \mathbf{1}_{n_{2b}}, \ldots, \mathbf{1}_{n_{a1}}, \ldots, \mathbf{1}_{n_{ab}}), \end{aligned} \tag{2.3}$$

where $n_{i.} = \sum_{j=1}^b n_{ij}$, and $\mathbf{1}_k$ denotes the $k \times 1$ vector of ones, and $\text{diag}(M_1, \ldots, M_a)$ denotes a block-diagonal matrix with $M_1, \ldots, M_a$ along the blocks.

In order to have μ, α_i, β_j, and γ_{ij} uniquely defined, we need to have additional constraints. Let $w_1, \ldots, w_a$ and $v_1, \ldots, v_b$ be nonnegative weights such that $\sum_{i=1}^a w_i > 0$ and $\sum_{j=1}^b v_j > 0$. We consider the following constraints

$$\sum_{i=1}^a w_i \alpha_i = 0, \qquad \sum_{j=1}^b v_j \beta_j = 0, \qquad \sum_{i=1}^a w_i \gamma_{ij} = 0, \qquad \sum_{j=1}^b v_j \gamma_{ij} = 0. \tag{2.4}$$

In this section, we are interested in testing the following hypothesis

$$H_{0AB}: \ \gamma_{ij} = 0; \quad i = 1, \ldots, a, j = 1, \ldots, b \tag{2.5}$$

against its natural alternative hypothesis. From (2.1), the model for $\overline{Y}_{ij}$ is

$$\begin{aligned} &\overline{Y}_{ij} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \bar{e}_{ij}, \\ &\bar{e}_{ij} \sim N\left(0, \sigma_{ij}^2 / n_{ij}\right), \quad i = 1, \ldots, a; j = 1, \ldots, b, \end{aligned} \tag{2.6}$$