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Alternative Computational Arrangements on *g-Group* (g > 2) Profile Analysis

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***Abstract*—**Alternative and simple computational arrangements in carrying out multivariate profile analysis when more than two groups (populations) are involved are presented. These arrangements have been demonstrated to not only yield equivalent results for the test statistics (the Wilks lambdas), but they have less computational efforts relative to other arrangements so far presented in the literature; in addition to being quite simple and easy to apply.

***Keywords*—**Coincident profiles, g-group profile analysis, level profiles, parallel profiles, repeated measures MANOVA.

I. Introduction

THE term 'repeated measures' refers to multiple responses (observations) taken sequentially on the same subjects or processes with respect to a particular variable of interest. The set of variables may be a test battery that is administered to evaluate psychological traits or vocational skills in the social sciences. In the industrial setting, a process may be evaluated over several experimental conditions (treatments). If the repeated measures factor is quantitative (e.g., time), then Profile Analysis can provide an elegant interpretation of the data [1].

The term 'profile' comes from practice in applied work in which scores on a test battery are plotted in terms of graph or profile [2]. A profile can be thought of as a broken line that graphically joins interdependent observations – which are measured on the same experimental unit. An average profile consists of the average of the responses within each observational level. Profile analysis compares these average profiles from two or more populations (treatment groups).

Profile analysis is a specific style of Multivariate Analysis of Variance (MANOVA) (see, for example, [3]). It is a special application of MANOVA to repeated measures data; and it is otherwise referred to as Repeated Measures MANOVA (see, for example, [4]). Simply put, profile analysis is a stage-wise fashion of testing for equality of mean vectors between two or among more than two populations.

Ordinarily, in comparing more than two populations as in normal MANOVA, the populations mean vectors of the variable of interest are tested for equality. In profile analysis, however, the test for equality of population mean vectors is divided into several specific possibilities (see, for example, [5]). The primary hypothesis is;

(a) The populations mean profiles are parallel (that is, the profiles are similar).

Two other hypotheses that are contingent on this primary hypothesis are;

(b) The profiles are coincident (that is, the profiles are identical or superimposed)

(c) The profiles are level/horizontal/flat (that is, all the means are equal to the same constant).

This third hypothesis concerns the similarity of responses in all observation levels, independent of populations. It is typically relevant only if the profiles are parallel. If the profiles are not parallel, then at least one of them is necessarily not flat. Again, this third hypothesis is somewhat contingent on the second hypothesis being true.

The procedures of carrying out profile analysis with regard to the one-group and the two-group profile analyses (for both the univariate and multivariate contexts) have been established in the literature (see, for example, [5], [6]). Also, profile analysis has been carried out for more than two groups in the multivariate context, especially for three groups (see, for example, [3], [7]). However, the computational arrangements in the profile analysis (especially in the multivariate context when more than two groups are considered) are obviously cumbersome to most people (analysts); as the arrangements are somehow ambiguous and quite lengthy. For instance, the rationale for the choices of some of the matrices (like C and A; as used in [6]) are often not clear and probably arbitrary. More so, the computational arrangements for arriving at the values of the test statistics (in most cases, Wilk's lambda) for the three different hypotheses testing are quite cumbersome and lengthy, especially when the number of groups and number of variables increase.

This paper presentation, therefore, proposes alternative, simple, and direct computational arrangements in carrying out profile analysis for more than two groups in the multivariate context. It is a further improvement on [8] in the area of computational arrangements. This presentation will be referencing the data extracted from [9] as were also used in [7] in order to show that the alternative computational arrangements give equivalent results as the arrangements in [7].

We present in the next section the proposed arrangements aimed at reducing the computational complexities of the classical methods. Section III is devoted to a numerical example to demonstrate their equivalence to the classical methods in terms of the values of the test statistics; Section IV

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showcases some comparisons of the two arrangements; and we conclude in Section V.

TABLE I
REPEATED MEASURES LAYOUT FOR g-GROUP PROFILE ANALYSIS

Treatment Group	Experimental Units (Subjects)	Observation (Response) Level 1	2	⋯	p
	1	$[X_{111},$	$X_{112},$	⋯,	$X_{11p}]$
	2	$[X_{121},$	$X_{122},$	⋯,	$X_{12p}]$
1	⋮		⋮		
	n_1	$[X_{1n_11},$	$X_{1n_12},$	⋯,	$X_{1n_1p}]$
	Means, $\bar{X}_1' =$	$[\bar{X}_{11},$	$\bar{X}_{12},$	⋯,	$\bar{X}_{1p}]$
	1	$[X_{211},$	$X_{212},$	⋯,	$X_{21p}]$
	2	$[X_{221},$	$X_{222},$	⋯,	$X_{22p}]$
2	⋮		⋮		
	n_2	$[X_{2n_21},$	$X_{2n_22},$	⋯,	$X_{2n_2p}]$
	Means, $\bar{X}_2' =$	$[\bar{X}_{21},$	$\bar{X}_{22},$	⋯,	$\bar{X}_{2p}]$
	⋮				
	1	$[X_{g11},$	$X_{g12},$	⋯,	$X_{g1p}]$
	2	$[X_{g21},$	$X_{g22},$	⋯,	$X_{g2p}]$
g	⋮		⋮		
	n_g	$[X_{gn_g1},$	$X_{gn_g2},$	⋯,	$X_{gn_gp}]$
	Means, $\bar{X}_g' =$	$[\bar{X}_{g1},$	$\bar{X}_{g2},$	⋯,	$\bar{X}_{gp}]$
	Grand Means, $\bar{X}' =$	$[\bar{X}_1,$	$\bar{X}_2,$	⋯,	$\bar{X}_p]$

II. THE PROPOSED COMPUTATIONAL ARRANGEMENTS FOR PROFILE ANALYSIS

Let X_{ijk} ($i = 1, 2, \cdots, g; j = 1, 2, \cdots, n_i; k = 1, 2, \cdots, p$), be an observation (a response) in a repeated measures experiment, where, $i, j,$ and k stand for treatment group (population), selected subject in the i-th treatment group, and observation (response) level, respectively. Also, let

$$X_{ij}' = [X_{ij1},\ X_{ij2},\ \cdots,\ X_{ijp}] \tag{1}$$

denote the response vector for the j-th subject within the i-th treatment group; and

$$\bar{X}_i' = [\bar{X}_{i1},\ \bar{X}_{i2}, \cdots, \bar{X}_{ip}] \tag{2}$$

denote the mean response vector for the i-th treatment group. Consequently, the repeated measures layout for g-group profile analysis is as shown in Table I.

It is worthy of note that certain assumptions/conditions (see, for example, [4], [10]) must be met before profile analysis could be carried out on any set of data. In carrying out profile analysis, the null hypothesis of equality of population mean response vectors sought in the ordinary MANOVA; given by,

$$H_0: \underline{\mu_1} = \underline{\mu_2} = \cdots = \underline{\mu_g}$$

is (usually) divided into three specific possibilities; formulated in a stage-wise fashion;

Stage I: H_{01}: The profiles are parallel. Equivalently, that is;

$H_{01}: \mu_{1k} - \mu_{1(k-1)} = \mu_{2k} - \mu_{2(k-1)} = \cdots = \mu_{gk} - \mu_{g(k-1)}$; where $k = 2, 3, \cdots, p.$

Stage II: Given that the profiles are parallel, then;

- H_{02}: The profiles are coincident. Equivalently, that is;

$$H_{02}: \mu_{1k} = \mu_{2k} = \cdots = \mu_{gk};\ \ k = 1, 2, \cdots, p.$$

Stage III: Given that the profiles are coincident; then

- H_{03}: The profiles are level. Equivalently, that is;

$$H_{03}: \begin{matrix} \mu_{11} = \mu_{12} = \cdots = \mu_{1p} = \mu_{21} = \mu_{22} = \cdots = \mu_{2p} \\ = \cdots = \mu_{g1} = \mu_{g2} = \cdots = \mu_{gp} \end{matrix}$$

A. Test for Parallel Profiles

Prior to this test, plots are to be made of the mean response vectors (average profiles).

The null hypothesis in Stage I;

$$H_{01}: \begin{bmatrix} \mu_{12} - \mu_{11} \\ \mu_{13} - \mu_{12} \\ \vdots \\ \mu_{1p} - \mu_{1(p-1)} \end{bmatrix} = \begin{bmatrix} \mu_{22} - \mu_{21} \\ \mu_{23} - \mu_{22} \\ \vdots \\ \mu_{2p} - \mu_{2(p-1)} \end{bmatrix} = \cdots = \begin{bmatrix} \mu_{g2} - \mu_{g1} \\ \mu_{g3} - \mu_{g2} \\ \vdots \\ \mu_{gp} - \mu_{g(p-1)} \end{bmatrix}$$

can be written as,

$$H_{01}: C\underline{\mu_1} = C\underline{\mu_2} = \cdots = C\underline{\mu_g}$$

where C is a contrast matrix given by;

$$\underset{[(p-1)\times p]}{C} = \begin{bmatrix} -1 & 1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & -1 & 1 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \cdots & -1 & 1 \end{bmatrix}. \tag{3}$$

H_{01} can be tested, in the usual one-way MANOVA fashion by employing the Wilks lambda statistic (Λ); which is most desirable (among it's equivalents like Pillai's trace, Hotelling-Lawley trace, and Roy's Greatest Root) because it can be converted exactly to an F-statistic (see, [3], [11]).

Employing the Wilks lambda criterion, therefore, H_{01} is to be rejected at the significance level, α if

$$\Lambda_1 = \frac{det.[CWC']}{det.[C(B+W)C']} \tag{4}$$

is too small; or alternatively, if it's equivalent F-statistic is greater than the F-critical value. For instance, where $(p-1) \geq 1$ and $g = 3$, the critical region will be;

$$\left(\frac{\sum_{i=1}^{g} n_i - p - 1}{p-1}\right)\left(\frac{1-\sqrt{\Lambda_1}}{\sqrt{\Lambda_1}}\right) > F_{2(p-1),\ 2(\sum_{i=1}^{g} n_i - p - 1);\ \alpha} \tag{5}$$

Furthermore, for cases where $g > 3$ and $p \geq 1$; as well as when $\sum_{i=1}^{g} n_i$ is large, a modification of Λ_1 due to Bartlett

[12] is employed (see, [5]). This is such that the critical region becomes;

$$-\left(n-1-\frac{(p+g)}{2}\right) In(\Lambda_1) > \chi^2_{p(g-1);\,\alpha} \quad (6)$$

The matrices B and W in (4) are, respectively, the Between (treatment) sum of squares and cross-products and the Within (residual) sum of squares and cross-products for the X_{ij}'s; and they are given as,

$$B = \sum_{i=1}^{g} n_i(\bar{X}_i - \bar{X})(\bar{X}_i - \bar{X})' \quad (7)$$

and

$$W = \sum_{i=1}^{g}\sum_{j=1}^{n_i}\left(X_{ij} - \bar{X}_i\right)\left(X_{ij} - \bar{X}_i\right)' \quad (8)$$

However, for ease of computation, (7) and (8) are re-written as;

$$B = G - \sum_{i=1}^{g} n_i(\bar{X}\bar{X}') \quad (9)$$

and

$$W = (D'D) - G \quad (10)$$

such that, for equal group sizes $(n_1 = n_2 = \cdots = n_g = n)$, G is given by

$$G = n(P'P) \quad (11)$$

and for unequal group sizes, G is given by

$$G = \sum_{i=1}^{g} n_i(\bar{X}_i\bar{X}_i') \quad (12)$$

The matrices D and P are such that

$$D = \begin{bmatrix} X_1' \\ X_2' \\ \vdots \\ X_g' \end{bmatrix} \quad (13)$$

and

$$P = \begin{bmatrix} \bar{X}_1' \\ \bar{X}_2' \\ \vdots \\ \bar{X}_g' \end{bmatrix} \quad (14)$$

where, for $i = 1, 2, \cdots, g$; and

$$X_i' = \begin{bmatrix} X_{i11} & X_{i12} & \cdots & X_{i1p} \\ X_{i21} & X_{i22} & \cdots & X_{i2p} \\ \vdots & \vdots & \ddots & \vdots \\ X_{in_i1} & X_{in_i2} & \cdots & X_{in_ip} \end{bmatrix} \quad (15)$$

If H_{01} is rejected, it would be concluded that at least one of the average profiles is significantly different. Consequently, it would rather be unreasonable to embark on testing the hypothesis of coincident profiles. Otherwise, proceed with the test.

B. Test for Coincident Profiles

Under the assumption/tenability of parallel profiles, the profiles will be coincident only if the total heights, $\sum_{k=1}^{p}\mu_{1k}, \sum_{k=1}^{p}\mu_{2k}, \cdots, \sum_{k=1}^{p}\mu_{gk}$, are equal [5]. Therefore, the null hypothesis in Stage II can be written in the equivalent form;

$$H_{02}: 1'\underline{\mu_1} = 1'\underline{\mu_2} = \cdots = 1'\underline{\mu_g}$$

where

$$\underset{[1\times p]}{1'} = [1, 1, \cdots, 1] \quad (16)$$

Hence, this test is univariate, based on the univariate observations;

$$1'X_{ij}; i = 1, 2, \cdots, g \text{ and } j = 1, 2, \cdots, n_i.$$

Invariably, this is equivalent to performing a One-Way ANOVA on the subject totals. Timm [7] stated that the univariate and multivariate tests are equivalent, assuming parallelism. Nevertheless, the multivariate test approach would be preferred since the data have already been arranged in a multivariate configuration for the first test.

Employing the Wilks lambda criterion, H_{02} is to be rejected, at level of significance, α if

$$\Lambda_2 = \frac{det.[1'W1]}{det.[1'(B+W)1]} \quad (17)$$

is too small; or alternatively, if it's equivalent F-statistic is greater than the F-critical value. Generally, the critical region for H_{02} is given by;

$$\left(\frac{\sum_{i=1}^{g} n_i - g}{g-1}\right)\left(\frac{1-\Lambda_2}{\Lambda_2}\right) > F_{(g-1),(\sum_{i=1}^{g} n_i - g);\,\alpha} \quad (18)$$

and where the need arises, a modification of Λ_2 due to Bartlett [12] is carried out by simply replacing Λ_1 in (6) with Λ_2.

If H_{02} is rejected, it would be concluded that the profiles were not identical. Consequently, it would rather be unreasonable to embark on testing the hypothesis of coincident profiles. Otherwise, proceed with the test.

C. Test for Level Profiles

This test investigates whether all variables have the same mean, so that the common profile is level. That is, $\mu_1 = \mu_2 = \cdots = \mu_p$; and if this is so, the successive differences are zeros across the p variables. Invariably, the null hypothesis in Stage III can be written as;

$$H_{03}: C\underline{\mu} = \underline{0}$$

where the common mean vector, μ is estimated by the sample grand mean vector, $\bar{X}$.

Employing the Wilks lambda criterion, H_{03} is to be rejected at level of significance, α if

$$\Lambda_3 = \frac{det.[CWC']}{det.[C(B_\Psi + W)C']} \quad (19)$$

is too small; or alternatively, if it's equivalent F-statistic is greater than the F-critical value. The critical region for H_{03}, as given by [3], is;

$$\left(\frac{\sum_{i=1}^{g} n_i - (p-1)}{p-1}\right)\left(\frac{1-\Lambda_3}{\Lambda_3}\right) > F_{(p-1),(\sum_{i=1}^{g} n_i - (p-1));\,\alpha} \quad (20)$$

Under H_{03},

$$B_\Psi = \sum_{i=1}^{g} n_i(\bar{X}\bar{X}') \quad (21)$$

and where the need arises, a modification of Λ_3 due to Bartlett [12] is carried out by simply replacing Λ_1 in (6) with Λ_3.

If H_{03} is rejected, the conclusion thus becomes that all the means are not equal to the same constant. Otherwise, the profiles are level.

III. Example

The data extracted from [9] are used in this section to illustrate the multivariate computational procedures presented in the previous section. Timm [7] analyzed this same dataset (originally analyzed in [9] using univariate procedures) by employing a different set of multivariate methods. The data, which are shown in Table II, were as a result of an investigation on the influence of three drugs, each at a standard dosage, on learning. Fifteen subjects were assigned at random to the three drug levels so that five subjects were tested with each drug on three different trials. Thus, the number of groups is $g = 3$; the sample sizes for the three groups are $n_1 = n_2 = n_3 = 5$; and the number of dependent variables is $p = 3$.

By (13) and (14);

$$D = \begin{bmatrix} 2 & 4 & 7 \\ 2 & 6 & 10 \\ 3 & 7 & 10 \\ 7 & 9 & 11 \\ 6 & 9 & 12 \\ 5 & 6 & 10 \\ 4 & 5 & 10 \\ 7 & 8 & 11 \\ 8 & 9 & 11 \\ 11 & 12 & 13 \\ 3 & 4 & 7 \\ 3 & 6 & 9 \\ 4 & 7 & 9 \\ 8 & 8 & 10 \\ 7 & 10 & 10 \end{bmatrix} \text{ and } P = \begin{bmatrix} 4 & 7 & 10 \\ 7 & 8 & 11 \\ 5 & 7 & 9 \end{bmatrix}$$

Also, computations using (3), (9), (10), (16), and (21), respectively, yielded the following matrices;

$$C = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \end{bmatrix};\ B = \begin{bmatrix} 23.387 & 8.397 & 10.050 \\ 8.397 & 3.407 & 5.050 \\ 10.050 & 5.050 & 10.000 \end{bmatrix};$$

$$W = \begin{bmatrix} 74 & 65 & 35 \\ 65 & 68 & 38 \\ 35 & 38 & 26 \end{bmatrix};\ 1' = [1, 1, 1];\ \text{and}$$

$$B_\Psi = \begin{bmatrix} 426.387 & 586.603 & 799.950 \\ 586.603 & 806.593 & 1099.950 \\ 799.950 & 1099.950 & 1500.000 \end{bmatrix}.$$

TABLE II
Edwards' Repeated Measures Data

Drug Group	Subjects	Trials 1	2	3
	1	2	4	7
	2	2	6	10
1	3	3	7	10
	4	7	9	11
	5	6	9	12
	Means	**4**	**7**	**10**
	1	5	6	10
	2	4	5	10
2	3	7	8	11
	4	8	9	11
	5	11	12	13
	Means	**7**	**8**	**11**
	1	3	4	7
	2	3	6	9
3	3	4	7	9
	4	8	8	10
	5	7	10	10
	Means	**5**	**7**	**9**
	Grand Mean	**5.333**	**7.333**	**10.000**

A. Testing for Interaction between Drugs and Trials (Parallel Profiles)

The plot of the mean vectors is as shown in [7]. The test hypothesis for this parallelism test is;

$$H_{01}: C\underline{\mu_1} = C\underline{\mu_2} = C\underline{\mu_3}$$

Equations (4) and (5) yielded $\Lambda_1 = 0.4608$; the equivalent F-statistic, for $g = 3$ and $p = 3$, to be 2.60; and the critical value, $F_{4,2;0.05} = 2.82$. Thus, H_{01} is not rejected; and the hypothesis of parallelism is tenable.

B. Testing for Significant Differences in Drugs (Coincident Profiles)

Since the hypothesis of parallelism was tenable, this test is worthwhile. The test hypothesis is;

$$H_{02}: 1'\underline{\mu_1} = 1'\underline{\mu_2} = 1'\underline{\mu_3}$$

Equations (17) and (18) yielded $\Lambda_2 = 0.84125$; the equivalent F-statistic to be 1.13; and the critical value, $F_{2,12;0.05} = 3.89$. Thus, H_{02} is not rejected; and the hypothesis of coincident profiles is tenable.

C. Testing for Significant Differences in Trials (Level Profiles)

This test is embarked upon since the hypothesis of coincident profiles was tenable. The test hypothesis is;

$$H_{03}: C\underline{\mu} = 0\ (\Rightarrow \mu_1 = \mu_2 = \cdots = \mu_8)$$

Equations (19) and (20) yielded $\Lambda_3 = 0.0839$; the equivalent F-statistic to be 70.97; and the critical value, $F_{2,13;0.05} = 3.81$. Thus, H_{03} is rejected; and the hypothesis of level profiles is not tenable.

IV. Results

In this section, the outcomes of the three different tests in I vis-à-vis the newly Proposed Computational Arrangements (***PCA***) in II are placed side-by-side in comparisons with the outcomes of the tests vis-à-vis the computational arrangements in [7] (otherwise referred to, in this paper, as the Classical Arrangements (***CA***)). These comparisons are presented in Table III.

Given our example, the matrices Y, X, and $\hat{B}$ using the classical arrangements (as were used in [7]) are

$$Y = \begin{bmatrix} 2 & 4 & 7 \\ 2 & 6 & 10 \\ 3 & 7 & 10 \\ 7 & 9 & 11 \\ 6 & 9 & 12 \\ 5 & 6 & 10 \\ 4 & 5 & 10 \\ 7 & 8 & 11 \\ 8 & 9 & 11 \\ 11 & 12 & 13 \\ 3 & 4 & 7 \\ 3 & 6 & 9 \\ 4 & 7 & 9 \\ 8 & 8 & 10 \\ 7 & 10 & 10 \end{bmatrix}; \quad X = \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix} \text{ and } \quad \hat{B} = \begin{bmatrix} 4 & 7 & 10 \\ 7 & 8 & 11 \\ 5 & 7 & 9 \end{bmatrix}$$

TABLE III
COMPARISONS OF ***CA*** WITH ***PCA***

S/N	***CA***	***PCA***	***Remark***
1	$\Lambda_1 = 0.4602$	$\Lambda_1 = 0.4608$	PCA is equivalent to CA
2	$\Lambda_2 = 0.84197$	$\Lambda_2 = 0.84125$	PCA is equivalent to CA
3	$\Lambda_3 = 0.0839$	$\Lambda_3 = 0.0839$	PCA is equivalent to CA
4	$Q_h = (C\hat{B}A)'[C(X'X)^{-1}C'](C\hat{B}A)$	$B = G - \sum_{i=1}^{g} n_i(\bar{X}\bar{X}')$	PCA has reduced computational effort than CA
5	$Q_e = A'Y'[I - X(X'X)^{-1}X']YA$	$W = (D'D) - G$	PCA has reduced computational effort than CA
6	Different Q_h and Q_e are computed for each of the three tests.	B and W are computed only once, and the same are used in three tests; except in the third test where B_Ψ is used.	PCA has reduced computational effort than CA
7	C and A are chosen; and their structures and compositions vary in the three tests.	C is not chosen but predetermined; and the same C is used where applicable.	PCA has reduced computational effort than CA
8	The dimension of the component, $I - X(X'X)^{-1}X'$ of Q_e is $(m \times m)$; where $m = \sum_{i=1}^{g} n_i$. Given our example, $m = 15$.	The dimension of the highest square matrix is $(p \times p)$. Given our example, $p = 3$.	PCA has reduced computational effort than CA

Furthermore, the matrices C and A are such that when testing for parallel profiles,

$$C = \begin{bmatrix} 1 & 0 & -1 \\ 0 & 1 & -1 \end{bmatrix} \text{ and } A = \begin{bmatrix} 1 & 0 \\ -1 & 1 \\ 0 & -1 \end{bmatrix};$$

when testing for coincident profiles,

$$C = \begin{bmatrix} 1 & 0 & -1 \\ 0 & 1 & -1 \end{bmatrix} \text{ and } A = \begin{bmatrix} 1 \\ 1 \\ 1 \end{bmatrix};$$

and when testing for level profiles,

$$C = \begin{bmatrix} \frac{1}{3} & \frac{1}{3} & \frac{1}{3} \end{bmatrix} \text{ and } A = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ -1 & -1 \end{bmatrix}.$$

V. Conclusion

We have presented alternative computational arrangements in carrying out profile analysis for more-than-two groups in the multivariate context. These arrangements were demonstrated on the same data in [9] analyzed in [7]; and the numerical values of the respective test statistics (Λ) for the three different tests conducted under profile analysis are equivalent to those derived by the computational arrangements of [7]. Our results also show that the proposed computational arrangements actually have reduced computational efforts than the classical arrangements when carrying out profile analysis for more-than-two groups in the multivariate context.

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