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# Closed Likelihood-Ratio Testing Procedures to Assess Similarity of Covariance Matrices

Francesca Greselin and Antonio Punzo

**Abstract** Different degrees of similarity can be devised among the  $k$  covariance matrices  $\Sigma_h$ , referred to  $k$  groups, using their spectral decomposition. In this paper we introduce a closed testing procedure allowing for a choice between eight patterns of covariances. The new methodology allows to disclose a richer information on the data underlying structure than the classical existing methods, and also a more parsimonious parameterization. An application on a real data set exemplify the proposal and shows its performances.

**Key words:** Eigenvalue Decomposition, Proportional Covariance Matrices, Common Principal Components, Closed Testing Procedures, Likelihood-Ratio Tests.

## 1 Introduction and motivation

This paper extends the study of similarity between  $k$  covariance matrices  $\Sigma_h$ , referred to  $k$  groups, under the assumption of multivariate normality. Consider  $p$  variables measured on  $n$  statistical units arising from  $k \geq 2$  different groups. Let  $x_1^{(h)}, \dots, x_{n_h}^{(h)}$  denote  $n_h$  independent observations, for the  $h$ th group, drawn from a normal distribution with mean vector  $\mu_h$  and covariance matrix  $\Sigma_h$ ,  $h = 1, \dots, k$ . Naturally,  $\sum_{h=1}^k n_h = n$ .

Suppose to be interested in making inference about  $\Sigma_1, \dots, \Sigma_k$ , with particular emphasis on their degree of similarity. In this paper, following Celeux and Govaert (1995), we develop an analysis of similarity between covariance matrices considering the decomposition  $\Sigma_h = \lambda_h \Gamma_h \Delta_h \Gamma_h'$ , ( $h = 1, \dots, k$ ), where  $\Delta_h$  is

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the scaled ( $|\Delta_h| = 1$ ) diagonal matrix of the eigenvalues of  $\Sigma_h$  sorted in decreasing order,  $\Gamma_h$  is the  $p \times p$  orthogonal matrix whose columns are the normalized eigenvectors of  $\Sigma_h$  ordered according to their eigenvalues and  $\lambda_h = |\Sigma_h|^{1/p}$ . Each component of the right side of (1) has a different geometric interpretation in terms of the group scatters:  $\Gamma_h$  governs the axes *orientation*,  $\Delta_h$  controls the *shape*, and  $\lambda_h$  denotes the *volume* of the ellipsoids of equal concentration. By allowing some but not all of these quantities to vary between groups, we obtain parsimonious and easily interpretable models which are appropriate to describe various practical situations. The resulting models give raise to the family  $\widetilde{\mathcal{M}} = \{EEE, VEE, EVE, EEV, VVE, VEV, EVV, VVV\}$ , where the three letters are respectively referred to volume, shape and orientation, and each of them can be equal (E) or variable (V) among groups.

In order to select the covariance structure in  $\widetilde{\mathcal{M}}$ , we define a closed multiple testing procedure characterized by local likelihood-ratio (LR) tests. Let  $\overline{\mathcal{M}} = \widetilde{\mathcal{M}} \setminus \{VVV\}$  be the closure, under intersection, of  $\mathcal{M} = \{VVE, VEV, EVV\}$ . For each  $M \in \overline{\mathcal{M}}$ , let us denote by  $H_0^M$  the corresponding null hypothesis. Thus, for example,  $H_0^{EEV}$  is the null hypothesis referred to EEV. We set model VVV as the benchmark (diagnostic), because it is the most general (less constrained) in  $\widetilde{\mathcal{M}}$ , requiring  $kp(p+1)/2$  parameters. This position allow us to define seven tests, the most *omnibus* as possible, which lay in a hierarchy. Rejection of  $H_0^M$  for all  $M \in \overline{\mathcal{M}}$ , implicitly leads to the “not rejection” of  $H_1^{VVV}$ .

Then, a primary concern for an MTP is the choice of a suitable *error rate* to control. We choose the *familywise error rate* (FWER); it is defined as the probability of committing at least one Type I error, and it is mostly employed when the number of elementary hypotheses is moderate, as in our case. We will employ *adjusted p-values* which are the natural counterpart, in the multiple testing framework, of the classical *p-values* (see, e.g., Bretz, *et al.*, 2009). We construct the MTP as a *closed testing procedure* (CTP) (Marcus *et al.*, 1976) because the latter are among the most powerful MTPs that strongly control the FWER at level  $\alpha$ . Further, they are a natural choice for our context, because they address a family of hypotheses that is closed under intersection.

Now, to assess the hypothesis  $H_0^M$  for  $M \in \overline{\mathcal{M}}$ , we employ the likelihood-ratio (LR) statistic

$$LR_M = -2 \ln \frac{L_M}{L_{VVV}} \quad (1)$$

that, under  $H_0^M$ , by the general theory of LR-tests is asymptotically distributed (when  $\min_{h=1, \dots, k} n_h \rightarrow \infty$ ) as a  $\chi^2$  with  $\nu_M$  degrees of freedom given by the difference in the number of (free) parameters  $\eta_{VVV}$  and  $\eta_M$  between VVV and  $M$ .

## 2 Testing for covariance similarity in the Crabs data

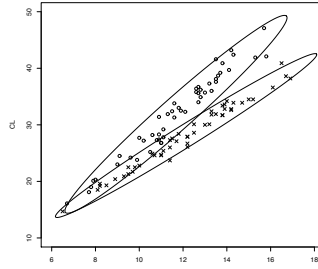
The crab data set of Campbell *et al.* (1974) on the genus *Leptograpsus*, consists in a sample of  $n = 100$  blue crabs, there being  $n_1 = 50$  males (group 1) and  $n_2 = 50$

females (group 2), each specimen having  $p = 2$  measurements (in millimeters) on the rear width (RW) and the length along the midline (CL) of the carapace. By Mardia's test, the two group-conditional distributions can be considered bivariate normal, while the LR-test of homoscedasticity rejects the null hypothesis at any reasonable significance level, giving a  $p$ -value  $p_{EEE} = 6.66 \cdot 10^{-15}$ .

Details on the decomposition (1) are shown in Table 1, while Fig. 1 displays the scatterplot of RW versus CL, in both groups.

**Table 1** Decomposition of  $\Sigma_h^{VVV}$ ,  $h = 1, 2$ , according to equation (1), for the two groups in the crabs data.

Group	Volume	Shape	Orientation
<i>males</i> ( $n_1 = 50$ )	$\lambda_1^{VVV} = 3.22274$	$\Delta_1^{VVV} = \begin{bmatrix} 17.54242 & 0 \\ 0 & 0.05700 \end{bmatrix}$	$\Gamma_1^{VVV} = \begin{bmatrix} 0.27256 & -0.96214 \\ 0.96214 & 0.27256 \end{bmatrix}$
<i>females</i> ( $n_2 = 50$ )	$\lambda_2^{VVV} = 2.24620$	$\Delta_2^{VVV} = \begin{bmatrix} 17.82737 & 0 \\ 0 & 0.05609 \end{bmatrix}$	$\Gamma_2^{VVV} = \begin{bmatrix} 0.37796 & -0.92582 \\ 0.92582 & 0.37796 \end{bmatrix}$

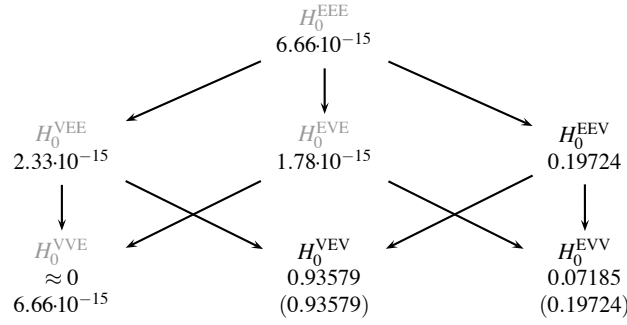


**Fig. 1** Scatterplot of variables RW and CL for  $n_1 = 50$  males and  $n_2 = 50$  females blue crabs (o denotes male and  $\times$  female). Ellipses of equal (95%) concentration are also superimposed.

Although the LR-test for model VVV points out heteroscedasticity (with a practically null  $p_{EEE} = 6.66 \cdot 10^{-15}$ ), the scatterplot in Fig. 1 shows strong similarity between volume and shape of the two ellipses; accordingly, in Table 1, sample shape matrices appear to be similar as well as (to a lower extent) sample volumes. The orientation of the two ellipses in Fig. 1 shows a slight difference in the directions of their main axes, attested also in the values along the diagonal of the sample orientation matrices  $\Gamma_1^{VVV}$  and  $\Gamma_2^{VVV}$  in Table 1.

Results in Fig. 2 and Table 2 (see firstly the left six columns) corroborate the aforementioned considerations; in particular, at the 0.05-level, the EEV-model is not rejected since its components (EVV and VEV) are not rejected too. Also, in the comparison between  $q_{VEV}$  with  $q_{EVV}$ , it is interesting to note the incidence of the former which underlines a stronger degree of similarity between groups in terms of shape. On the contrary, some of the considered likelihood-based ICA (AIC, and also AIC<sub>3</sub>, and AICc) lean towards the more complex VEV-model with a loss of one parameter with respect to model EEV.

This paper underlines how some relevant configurations of similarity between covariance matrices  $\Sigma_h$ , referred to different normal groups, can be described by



**Fig. 2** Unadjusted and adjusted  $p$ -values (in round brackets) related to the closed LR-testing procedure applied to the crabs data. Rejected hypotheses, are displayed in gray.

**Table 2** Details on the closed LR-testing procedure, and some likelihood-based ICa applied to the crabs data. Bold numbers refer to the “not rejected” model(s) in  $\mathcal{M}$  at the 0.05-level (column of the adjusted values  $q_M$ ), and to the best model for each likelihood-based information criterion.

$M$	$\eta_M$	$LR_M$	$\nu_M$	$p_M$	$q_M$	$-2\ln L_M$	AIC	BIC	CAIC
EEE	3	69.0889	3	$6.66 \cdot 10^{-15}$		834.6112	840.6112	848.4267	851.4267
VEE	4	67.4247	2	$2.33 \cdot 10^{-15}$		832.9469	840.9470	851.3676	855.3676
EVE	4	67.8934	2	$1.78 \cdot 10^{-15}$		833.4156	841.4156	851.8363	855.8363
EEV	4	3.2466	2	0.19724		768.7689	776.7689	<b>787.1896</b>	<b>791.1896</b>
VVE	5	67.2897	1	$\approx 0$	$6.66 \cdot 10^{-15}$	832.8119	842.8119	855.8378	860.8378
VEV	5	0.0065	1	0.93579	<b>0.93579</b>	765.5287	<b>775.5287</b>	788.5546	793.5546
EVV	5	3.2403	1	0.07185	<b>0.19724</b>	768.7626	778.7626	791.7884	796.7884
VVV	6					765.5222	777.5223	793.1533	799.1533

considering the three-terms eigenvalue decomposition  $\Sigma_h = \lambda_h \Gamma_h \Delta_h \Gamma_h'$ . Each of these terms denotes specific geometric characteristics (volume, shape and orientation). This approach leads to eight different models by allowing each of the three terms to be common or not between groups. However, no statistical test to individuate the “correct” model among them exists and, still today, the omnibus Box’s  $M$ -test of homoscedasticity (versus heteroscedasticity) is widely used; unfortunately, being omnibus, after a rejection of the null hypothesis, it leaves the practitioner without any more information. In this paper such a gap has been covered by providing a closed testing procedure, using local likelihood-ratio tests, to assess the choice.

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