

## Permutation Tests for Difference between Two Multivariate Allometric Patterns

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*(Accepted September 23, 1998)*

**Tzong-Der Tzeng and Shean-Ya Yeh (1999)** Permutation tests for difference between two multivariate allometric patterns. *Zoological Studies* 38(1): 10-18. Studies that include comparisons of multivariate allometric patterns between sexes, species, discrete growth stages, or geographic populations have gradually increased. Some statistical methods assume that compared groups share the same multivariate allometric pattern, so comparisons of multivariate allometric patterns also have to be performed before using these methods. Several methods have been used to detect the difference between 2 multivariate allometric patterns, but these methods lack an objective guide to test whether the 2 multivariate allometric patterns are the same or not. In this study, a permutation test was used to determine whether the difference of 2 patterns was significant or not. Four examples were used to explain and verify this test. The multivariate allometric pattern was estimated by the 1st eigenvector of the sample covariance matrix of the logarithmic measurement. The angle between the 2 first eigenvectors was taken as the test statistic. For each example, 5000 permutations were performed to assess the significance level. Finally, the effect of sample size difference on the permutation test was also examined. We found that all 1st eigenvalues explained the largest part of total variance and all 1st eigenvectors can satisfactorily interpret the multivariate allometric patterns. These tests can successfully detect the relationship between 2 multivariate allometric patterns in each example, so they can be a tool to test whether the difference of 2 multivariate allometric patterns is significant or not. Although this method is not sensitive to sample size differences, we still suggest that the sample size difference be as small as possible when using permutation tests to address this question.

**Key words:** First eigenvector, Angle, Allometry, Reorder.

Allometry is a method providing valuable information about evolutionary modifications of growth trajectories (Cock 1966, Klingenberg 1996). Studies on allometry trace to the pioneering work of Huxley (1932). He derived his formula of allometry,  $y = b x^\alpha$ , where  $x$  and  $y$  are trait measurements, and the constant  $\alpha$  is often called the allometric coefficient. Since generalization of allometry was proposed by Jolicoeur (1963), studies on multivariate allometric patterns of organisms have increased. Jolicoeur (1963) suggested that the 1st eigenvector extracted from the covariance matrix of logarithmic values reflects the multivariate allometric pattern. The 1st principal axis is the line passing through the greatest dimension of the concentration of data points of the multivariate

distribution (Legendre and Legendre 1983), but it need not represent the size component, except the coefficients in the 1st principal axis with the same sign (Jolicoeur and Mosiman 1960). This size component usually can represent sex, population, or species differences.

Three different levels of allometry are distinguished: static, ontogenetic, and evolutionary allometry. This classification has also been used in most comparisons between allometric levels (Cock 1966, Klingenberg 1996). Additionally, some statistical methods, e.g., Burnaby's method (Burnaby 1966) and shearing principal component analysis (PCA) for size correction (Humphries et al. 1981) or multiple groups PCA (Thorpe 1983) for ordination, assume that groups under consideration

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