



Multivariate Analysis in Animal and Veterinary Sciences

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Abstract

Statistical techniques that simultaneously analyze several measurements in a single individual and that are related to each other are referred to as multivariate analysis. Various multivariate analysis techniques are used to study breed morphology and genetic diversity in animal and veterinary sciences.

Keywords: multivariate analysis, variables, biometric traits, breed

Introduction

The study of the relationships between more than two variables is known as multivariate analysis. It offers a range of tools to characterize and measure the relationship between several measured variables (Johnson and Wichern, 2007). Multivariate analysis makes it feasible to interpret data variance with much greater ease and helps gain a better understanding of biological relationships. Multivariate analysis techniques such as cluster analysis, principal component analysis and discriminant function analysis have been widely employed in studies of breed characterization and genetic diversity providing descriptive analysis of population differences by taking all variables into account and presenting an overview of the data (Dossa *et al.*, 2007). Animal Genetic Resources (AnGR) variety is substantially maintained through characterization, which is achieved by the analysis of morphological traits using these standard multivariate analysis techniques to evaluate the differences between and within breeds.

Some multivariate analysis techniques

Principal Component Analysis (PCA): It is a data reduction technique which highlights variation in a dataset. A dataset containing a large number of interrelated variables is transformed to a new set of uncorrelated variables called the principal components which are ordered in such a way that the first few maintain the majority of the variance found in each of the initial variables. The PCA makes data easier to visualize and understand by highlighting patterns in the dataset. The PCA have been used to study significant differences in biometric traits in different breeds and species of livestock to highlight breed morphology.

Discriminant Function Analysis (DFA): Decisions regarding naturally occurring group membership are made using this data reduction technique. To determine which variables from a set of predictors best predict group membership, DFA extracts a linear combination of variables that optimizes the differences between natural group means. Multivariate discriminant analysis of morphological traits is effective for a precise and objective discrimination of different population of livestock.

Cluster Analysis: The objective is to divide a sample of subjects into several groups according to a set of measured variables, with similar subjects being assigned to the same

group. It divides genotypes into groups or clusters, such that the members of the same cluster have strong degree of association between them while the members of different clusters have weak degree of association between them. It is frequently used for studying genetic diversity and to create core subsets from which individuals with comparable characteristics can be grouped into homogenous categories.

Canonical Correlation Analysis: It is a data reduction technique that calculates a linear combination between two sets of variables having highest correlation in order to assess their relationship. Canonical correlation analysis is able to analyze two variable sets simultaneously producing both structural and spatial meaning (Bilgin *et al.*, 2003). Since early selection is one of the modern selection programmes utilized for better production in animal, canonical correlation analysis has been used in numerous livestock studies to determine the relationship between two or more traits measured early in the life (Cankaya and Kayaalp, 2007).

Application in animal and veterinary sciences

Akbar *et al.* (2022) used PCA to evaluate different phenotypic characters in Thalli sheep breed of Pakistan. The PCA of morphometric traits showed that most of the variation was explained by principal component 1 (PC1) which had high values for withers height, body length and heart girth for both males and females. This indicated that selection of genetically elite animals depends greatly on morphometric traits. Vohra *et al.* (2017) applied PCA to 18 highly intercorrelated body biometric traits in Chhattisgarhi buffaloes of India to deduce the components that control body conformation which can further be used in phenotypic selection in breeding programmes. El Fadl *et al.* (2017) used linear discriminant analysis (LDA) to determine the most important predictors for the discrimination of tick-borne diseases (TBDs), particularly babesiosis and anaplasmosis and predict group membership from the predictors in Egyptian dairy cattle. Clinical signs such as oculonasal discharge, bloody feces, hemoglobinuria and respiratory rate were the strong predictors in the discrimination of babesiosis and anaplasmosis in the cattle herds with average rate of correct classification of 100% and 78.8%, respectively. Yadav and Vijh (2022) used discriminant analysis to identify the combination of independent phenotypic traits that distinguished Murrah from grade Murrah buffalo of India. The morphological variables including chest girth, head length, paunch girth, horn curliness, tail length, horn diameter, tail whiteness and distance between hip bones were more important and informative allowing for the assignment of animals into Murrah and grade Murrah populations, which would lower selection errors in future breeding and selection programmes. A study by Mote *et al.* (2019) to estimate genetic divergence of Gir crossbred cattle, FG (50% HF+50% Gir), IFG (FG Interse), FJG (50% HF+25% Jersey+25% Gir), IFJG (FJG Interse) and R (50%HF+12.50%Jersey+37.50%Gir) based on some important parameters showed that age at first conception, age at first calving, lactation milk yield, 300 days milk yield and lactation milk yield per day of lactation length contributed maximum to the total diversity. Two clusters were observed with one cluster having IFG, IFJG and R genetic groups and cluster two having FG and FJG genetic groups. Bayyurt *et al.* (2018) used canonical correlation analysis to examine the relationship between water holding capacity, pH and meat colour parameters as an indicator of meat quality in poultry of Turkey concluding that when water holding capacity and pH traits have high values, colour traits will also be high. Mokoena and Tyasi (2021) used canonical correlation analysis to study the association among some growth traits evaluated at birth and weaning time in non-descript goat kids of South Africa. It was found that withers height and heart girth contributed mostly at birth while body length and rump height at weaning. These traits were the most prominent and this information will assist the breeders to select the best animals at birth to improve performance at weaning.

Conclusion

By excluding variables that do not explain much of the variation, multivariate analysis increases its discriminating power. The use of these multivariate analysis techniques helps breeders in making a good decision regarding the selection of animals to improve production in breeding programmes.

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