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On assessing contrasts between groups of animals

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Abstract

The main objective of assessing connectedness or linkage is to obtain an indication of the accuracy of comparisons between EBVs estimated in different herds or flocks. Several methods have been proposed to evaluate connectedness. Definition of connectedness is not always the same in those methods, and some of those methods can be very demanding computationally, which makes routine application difficult. The objective of this paper is to describe a straightforward method that assesses linkage across groups of animals, and to investigate the effect of heritability and the number of offspring from across flock sires on the prediction error (co)variance of flock means. The method is illustrated using a small example and Merino sheep data extracted from the Sheep Genetics Australia database.
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1. Introduction

Every genetic evaluation of animals partitions phenotypic expression of traits in animals into genetic, management, and other environmental causes. The genetic causes of phenotypic expression in animals are commonly known as estimated breeding values (EBVs). EBVs or combinations of EBVs (indexes) are estimates of an animal's genetic merit for a trait or a group of traits. Best linear unbiased prediction (BLUP) is widely used currently for estimating breeding values. Most genetic evaluation schemes involve models which fit a number of additive genetic effects for each animal, mostly in a multi-trait setting where a variety of phenotypic information is combined to predict genetic merit of animals on correlated traits. For example, OVIS, the Australian genetic evaluation scheme for sheep, currently used by Sheep Genetics Australia (SGA), provides EBVs for up to 49 traits simultaneously (Brown et al., 2000). When comparing EBVs we are not only interested in their values, but also in the amount of trust we can put in the EBVs. This is described by the accuracy of the EBV; the accuracy describes the value of the information used when calculating the EBV and is a

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function of its prediction error variance (PEV). The PEV of an EBV can be derived from the diagonal of the inverse of the coefficient matrix of the mixed model equations (MME) (Henderson, 1975). In order to calculate the prediction error variance of a difference (PEVD) between two EBVs, we also need their prediction error covariances (PEC), which is an off diagonal element of the inverse of the coefficient matrix of the MME.

To compare groups of animals or herds or flocks in the same analysis, the groups must be contrasted. This could be done directly or indirectly through comparison with other animals. This is referred to as connectedness or linkage; lack of contrast is called disconnectedness or being unlinked. A common problem for all extensively farmed livestock is the absence of such linkage. In dairy cattle populations, in which widespread use is made of artificial insemination (AI), herds or contemporary groups tend to be well connected genetically as a result of common use of relatively few sires. Such is generally not the case in beef cattle and sheep populations, as there are few AI programs, and flocks or herds are frequently isolated from each other geographically. Sire referencing schemes provide genetic links between populations and the common sires act as benchmarks for the different populations. Informal trade in sires and dams occurs often and provides genetic ties between small groups of herds or flocks. However, this trade is primarily market driven with the objective of assisting the breeding objective, not for the purpose of providing genetic links.

The main objective of assessing connectedness or linkage is to obtain an indication of the accuracy of comparisons between EBVs estimated for different herds or flocks in the one evaluation. Several methods have been proposed to evaluate connectedness. Connectedness is not always defined the same way in those methods, and some of those methods can be very demanding computationally, which makes routine application difficult. Fernando et al. (1983) proposed an algorithm to search for connected groups in a herd-year-season by sire layout which identifies groups of connected sires or herd-year-seasons, based on earlier work by Weeks and Williams (1964) and Petersen (1978). However this algorithm does not give a measure of how well the

connections are within each group. Kennedy and Trus (1993) argued that the most appropriate measure of connectedness would be to average PEV of all pair-wise EBV differences between animals in two contemporary groups. Other standards have been proposed, Laloë et al. (1996) compared PEV with two other statistical measurements of connectedness: a connectedness index which was initially proposed by Foulley et al. (1992) and the squared correlation between the predicted and the true difference of genetic values (CD). Laloë et al. (1996) concluded that CD provides a balance between the design and the information brought by the data, and is thus a method of choice to assess the quality of a genetic evaluation. Lewis et al. (1999) assessed linkage among flocks using a prediction error correlation between individual breeding values, these where then averaged across animals to get an idea of the amount of linkage in the across-flock evaluation. They show that this prediction error correlation decreases when connectedness between flocks improves. It is impossible to compare these correlations for all animals in a genetic evaluation with each other, but it is possible to compare group means. A connectedness rating was developed by Mathur et al. (2002) this rating was based on the prediction error variances of herd effects and the corresponding covariances. Roso et al. (2004) assessed the degree of connectedness among groups of bulls; different methods to assess connectedness were compared, their conclusion was that a linkage statistic based on the number of direct genetic links between groups was a good alternative to be used routinely. If the main objective of a linkage statistic is to identify groups where EBVs are poorly estimated in comparison to EBVs estimated for other groups so that necessary actions can be taken, then a method which assesses the accuracy of such comparisons is most appropriate. Once the groups where EBVs are poorly estimated are identified these disconnected groups can make use of sires from the connected group to ensure they become connected in the future.

The objective of this paper is to describe a straightforward method that assesses linkage across groups of animals and to investigate the effect of heritability and the number of offspring from across herd sires on the prediction error variance of flock means.