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Exploring Non-Linear Genetic Relationships Between Correlated Traits

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Genetic evaluation has emerged as a crucial tool in livestock breeding, enabling decisions about which individuals to keep in a breeding program, based on a selection index that oftentimes considers multiple traits of commercial interest, and the accuracy of selection indexes depends on the accuracy of breeding values (BV) predicted by the model. Different traits may be affected by a same QTL region, resulting in a genetic correlation between such traits, and the current models used to perform genetic evaluations impose a linear genetic correlation between traits. However, if the genetic relationship between two traits is non-linear, the current models fail to comprise this assumption, resulting in less accurate predicted BV. A preliminary study with simulated data indicated that when using gaussian models (i.e. GBLUP) to evaluate two traits with the same heritability (0.3) and genetic correlation of 0.5, the estimated genetic correlation captured by the model was of 0.53 (SD=0.03) when the true genetic correlation was linear. However, when this correlation was non-linear (and in fact quadratic in this preliminary study), the captured correlation decreased to 0.46 (SD=0.02), and GBLUP failed to identify the non-linear genetic relationship. Methods able to account for non-linear genetic relationships between traits may increase the accuracy of predicted BV, and improve the individuals' final selection index, enabling more efficient breeding strategies. The non-parametric nature of machine learning (ML) methods provide the necessary flexibility to account for non-linear genetic correlations, and may thus provide new insights into the underlying genetic architecture of correlated traits. Our preliminary study indicated that, although prediction accuracy obtained with a two-trait ML model was comparable to that of GBLUP for both linearly and non-linearly correlated traits (0.52; SD=0.3 and 0.48; SD = 0.03 respectively), our ML approach was able to reveal the non-linear relationship between traits, an information of relevance to improve the selection index accounting for multiple traits.

