

An Efficient Statistical Method for Genomic Selection

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Abstract: The high-throughput genotyping technology has generated a huge number of genomic markers that can be used for genomic selection. However, the large number of markers makes it difficult to estimate the breeding values. We propose to apply the penalized orthogonal-components regression method to estimate breeding values. As a supervised dimension reduction method, it can sequentially constructs linear combinations of markers, i.e. orthogonal components, such that these components are closely correlated to the phenotype. Such a dimension reduction is able to group highly correlated predictors and allows for collinear or nearly collinear markers. As shown in simulation studies, the proposed method is computationally efficient and provides accurate prediction when compared to existing methods. IN addition, the utility of the method was demonstrated through applications to real data.