

Detecting the Association of Single Nucleotide Polymorphisms and Prediction of Future Yields for a Growth Trait Using a Mixed Model with Orthogonal Polynomials

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The main aim of this study is the detection of association between SNPs and a quantitative growth trait in the situation where a trait value for each individual is measured at five different time points. In order to account for the correlation between the consecutive measurements a mixed model, which describes each effect using the 4th order Legendre orthogonal polynomials, is fitted. In this model, the SNPs are modeled as fixed effects while the environment as a random effect. The maximum likelihood estimates of all model parameters are obtained using the EM algorithm and the assessment of the significance of the additive effects of each SNP is based on the Likelihood Ratio Test with P values corrected for multiple testing. For each significant SNP, we calculate the percent of the total variance contributed by that SNP. Moreover, by using a fixed model with orthogonal polynomials, which simultaneously incorporates effects of all the SNPs we are able to predict future trait values.