

The influence of the variance-covariance structure on the GWAS results

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Abstract

Genome-Wide Association Study (GWAS) is an analysis, which aims at finding relationships between genetic and phenotypic properties of plants. This study was completed with 509 wheat varieties and breeding lines observed during 2 vegetation seasons: 2017/18 and 2018/19 at four experimental stations belonging to two breeding companies. Genetic structure of the considered set of wheat accessions was analyzed by Tyrka et al. (2021) [1] and phenotypic data analyses are under preparation.

We perform a mixed model marker-trait association analysis in the context of multiple environments. This statistical analysis allows to specify four variance-covariance models for the set of environments as identity, diagonal, compound symmetry (cs) or uniform covariances with unequal variances (hcs). The problem is about the influence of the specified variance-covariance structure on significance of fixed marker effects. Smaller differences are observed between pairs diagonal-identity and cs-hcs.

All analyses were completed with Genstat 19 software [2].

Keywords

variance-covariance structure, Genome-Wide Association Study.

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References

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