

MULTI-TRAIT DEEP LEARNING MODELS FOR GENOME-ENABLED PREDICTION OF TRAITS MEASURED ON HETEROGENEOUS SCALES IN PLANT BREEDING

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ABSTRACT

Genomic selection (GS) which was first proposed about 20 years ago, started to revolutionize plant breeding, its practical use is still difficult because of the numerous factors that affect its accuracy. The selection of the statistical machine learning approach is one such factor. In this study, the multi-trait Bayesian Best Linear Unbiased Predictor (GBLUP) model and the Gaussian kernel are used to explore the tuning process. Using the Japonica breeding program data sets, we investigated three tuning techniques: manual, grid search, and Bayesian optimization. We discovered that compared to manual tuning, employing grid search and Bayesian optimization increases prediction accuracy by 1.9 to 6.8%. Even if the increase in prediction accuracy in some circumstances may be slight, it is crucial to properly execute the tuning procedure in order to increase the accuracy of the GS approach, even though this necessitates more computer resources.

Kata Kunci: *kernels, multi-trait, Bayesian optimization, grid search, genomic selection*