

Can deep learning improve genomic prediction of complex traits?

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The genetic analysis of complex traits does not escape the current excitement around artificial intelligence, including a renewed interest in ‘deep learning’ (DL) techniques (e.g., Multilayer Perceptrons, MLPs). However, the performance of DL for genomic prediction of complex traits has not been comprehensively tested. To provide an evaluation of MLPs we used data from distantly related white Caucasian individuals ($n \sim 100k$ individuals, $p \sim 500k$ SNPs, $k=1000$) of the interim release of the UK biobank. We analyzed a total of nine phenotypes. We considered several configurations, from shallow to deep learners, and compared the predictive performance of MLPs with that of penalized linear regressions across different SNP densities. For height, a one layer MLP was slightly but consistently worse than linear methods such as lasso and ridge regression, whereas a deeper MLP was overall the worst performing strategy. For the rest of phenotypes, MLPs did not outperform penalized linear methods either. Analyses of SNP-importance scores showed that the one-layer MLP had scores similar to those of linear models. Moreover, for deep learners we found that many neurons were often inactive. We discuss reasons that may explain why linear models outperformed DL and avenues for improving the performance of DL for prediction of complex traits.