

MASTER'S THESIS ANNOUNCEMENT

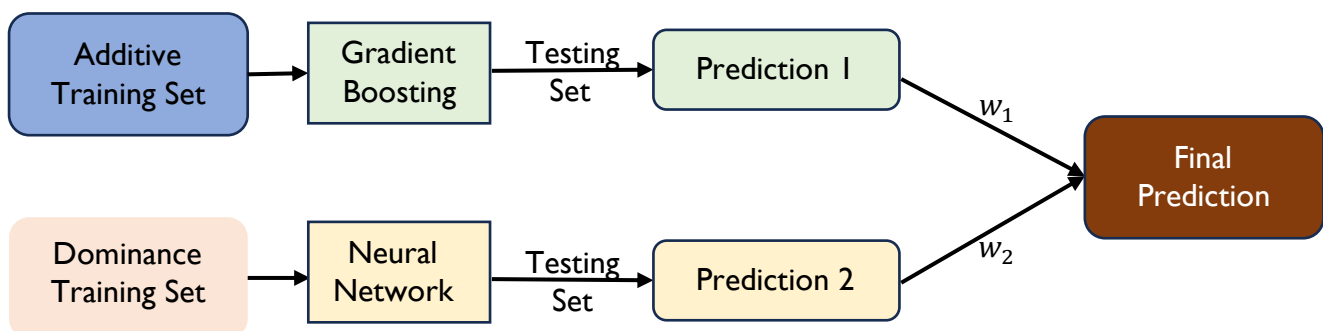
Non-additive Ensemble Machine Learning Methods in Genomic Prediction of Plant and Animal

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BACKGROUND

Research on trait genetics significantly impacts genomic model predictability. While classical models such as genomic best linear unbiased prediction (GBLUP) dominate plant and animal breeding, machine Learning methods (ML) are gaining traction for their superior handling of non-linear effects.



Despite ML's reputation, there have been novel efforts to boost its performance. Strategies include combining parametric and non-parametric techniques, innovative data transformations and application of Ensemble ML methods. Though outcomes vary, these approaches aim for more robust predictive frameworks, with some studies showing notable improvements while others face challenges.

MSC THESIS OBJECTIVES

- Analyse Genotypic and Phenotypic Data
- Compare the performance of additive-effect GBLUP and the GBLUP that accounts for both additive and dominance effects with ensemble ML methods.

REQUIREMENTS

- Basic understanding of quantitative and population genetics
- Proficiency in Python or R (Python is preferred)
- Basic knowledge of machine learning algorithms

APPLICATION

Please send your CV and a motivation letter to Bright Enogieru Osatohanmwun at bright.osatohanmwun@uni-goettingen.de. Note: You are encouraged to apply even if you do not meet all the requirements, as strong motivation is desired.