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Calibrating simulations of dominance variation in animal breeding: Case study in layer chickens

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In this contribution, we present the building blocks of a framework for stochastic simulations of additive and dominance genetic variation that reflect variation found in real-world datasets. Stochastic simulations are a cost-effective method for testing any novelty within a breeding programme *in silico* before actual experimental validation and eventual deployment in the real-world. Accordingly, to be informative as a hypothesis-generation and decision-making tool, the simulations should reflect real-world variation as close as possible. While additive genetic variation is a staple to many breeding methods and underlying simulations, dominance genetic variation is typically neglected, oversimplified, or simulated in an ad hoc manner. However, dominance variation is a vital genetic component of many breeding programmes, especially in the terms of inbreeding depression and heterosis. Here we showcase a framework for calibrating stochastic simulation of additive and dominance variation to reflect variation in a real-world dataset. To this end, we used SNP marker data and egg production phenotypes from a commercial layer chicken population to estimate additive and dominance genetic variances and inbreeding depression. We fitted both the full genomic directional dominance model and reduced dominance model (without the marker heterozygosity as a covariate) via Bayesian ridge regression. Furthermore, we built a framework of formulae and algorithms that use the real-world genetic parameters estimates to fine-tune a simulation, in particular the mean and variance of dominance degrees (relative magnitude of biological dominance effects compared to biological additive effects) and the number of quantitative loci. We evaluated a full grid across the parameter space to find the most credible inputs so that the resulting simulation reflected variation found in a real-world dataset. This work will enable fine-tunning of future simulation of animal breeding programmes influenced by additive and dominance variation.