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Estimating heritability and response to selection in the presence of phenotypic error

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Quantitative genetic analyses, such as the estimation of heritability or the response to selection, require measurements of phenotypic traits across multiple generations. This may be especially challenging in wild animal populations, where the measurement precision can suffer considerably.

Such imprecision leads to measurement error in phenotypic trait records, which is a possible cause for bias in the estimation of quantitative genetic parameters. Consequently, quantities that are derived from these estimates such as heritability and quantitative trait dynamics, are potentially biased as well.

Here we use simulated pedigrees to investigate the effect of phenotypic measurement error on the heritability of phenotypic traits and on their response to selection and we propose a method to take such error into account when fitting the animal model by adding a random effect to the model structure. In our simulated pedigrees, this correction provides estimates for parameters of interest which are unbiased with respect to the real simulated ones.

One of the main conclusions is that measurement error biases quantities that involve phenotypic variances, and that the error should therefore be modeled when interest centers around heritability and predictive models of evolutionary change, as estimated by the breeder's equation. Thanks to the proposed method, accounting for the error is relatively straightforward and merely requires the inclusion of an additional variance component in the animal model, which can be estimated if a certain type of “close” repeated measurement are available, while more “distant” repeats are used to isolate permanent environmental effects. Finally, we discuss why the Robertson-Price identity is robust against phenotypic measurement error, namely because it involves only genetic covariances that do not depend on random phenotypic fluctuations.