

## Compute Realized reliabilities of predictions from consecutive genetic evaluations using method LR

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Accuracies of genomic prediction are important to predict future genetic progress and to choose the adoption of different selection schemes, e.g. pedigree-based versus genomic ones. A method frequently used requires careful analysis of data involving cross-validation (e.g. hiding records and trying to predict them). Such methods for sheep and goats are very cumbersome and require access to raw data from genetic evaluation. We are essentially interested in accuracy at birth, when selection decisions are more important. The “LR” method (from Linear Regression) estimates these accuracies from sets of consecutive proofs. Pick a set of “focal” animals with same age and information - for instance, young rams or young females. The set has to consist on at least 50 animals for the results to be reliable. We compare genetic proofs (genetic evaluations) of these “focal” animals, at birth (“old” proofs), versus “more recent” proofs of the same animals, one (or more) years later, when they have more information (progeny records or own phenotype). The correlation between “old” and “most recent” proofs across the set of animals ( $r(w,p)$ ) is the ratio of initial and final accuracy such that the increase in accuracy from initial to final is  $(1/r(w,p)) - 1$ . For instance if  $r(w,p)$  is 0.8 it means that the accuracy increases by relative 25% from birth to the most recent evaluation. Thus high values of  $r(w,p)$  imply high accuracies at birth, and very low values imply that proofs at birth are little accurate.



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