The effect of recombination rate on genomic selection in simulation

Handout to WCGALP 2022 talk

Martin Johnsson

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This handout contains an outline of the argument and the references for the "The effect of recombination rate on genomic selection in simulation" to be given at the World Congress of Genetics Applied to Livestock Production in Rotterdam 2022. For more details about the model and results, see the conference paper: M. Johnsson, A.M. Johansson, T. Klingström and E. Rius-Vilarrasa (2022) "The effect of recombination rate on genomic selection in simulation".

Introduction

Here are two perspectives on genomics in animal breeding: the sequence perspective and the statistical perspective, where you view the genome either as a sequence of DNA bases, or as a table of ancestry indicators. The power and usefulness of the statistical perspective is described in Lowe and Bruce (2019).

In our research on genome dynamics of livestock breeding, we investigate features of the genome that matter to genetic variation, and to the ability of genomics to capture it. Of course this relates to the classical questions about how variation is maintained and turned over. When we say "features of the genome", we mean chiefly recombination, mutation, population history. Historical natural selection might also be relevant; selection and population history interact with each other. Johri et al. (2022) have recently argued for modelling genome features in more detail when studying signatures of selection in population genetics.

We also want to emphasize the *dynamics*, how the genetic basis of complex trait changes over time with selection (something that we are painfully aware of as we need to spend the money to re-train our genomic selection models all the time) and the synthesis of these two perspectives; we want to think about the physical features of the genome as they are relevant to the structure of genetic variation. There is both classical and recent work that implicitly takes such a perspective, such as the computational models of Wientjes et al. (2022) and the equation-based models of Legarra et al. (2021).

The correlation between recombination rate and sequence variation is (observed in many species (Kern and Hahn 2018), and for example in pigs by Ros-Freixedes et al. (2022)) is a striking example of how genome features affect the distribution of genetic variation.

Results

Our simulations of illustrate how a high recombination rate is detrimental to genetic gain because it lowers genomic prediction accuracy. It also slightly improves long-term genetic gain by releasing genetic variance. We used AlphaSimR (Gaynor, Gorjanc, and Hickey 2021). Code is available at https://github.com/mrtnj/wcgalp2022_recombination.

Discussion

We used recombination landscapes based on Elferink et al. (2010) for the chicken genome and Ma et al. (2015) for the cattle genome. These maps are based on low to medium density SNP chip genotypes, whereas the real recombination landscape is likely to be much more fine-grained. However, theoretical work by White and Hill (2020) suggests that the fine-scale landscape might not matter much to the variation in relationship.

Battagin et al. (2016) studied the effect of recombination on genetic gain in a similar simulation setup, and our results on long-term genetic gain are qualitatively similar to theirs. However, they did not model the decline in genomic selection accuracy with higher recombination rate, which appear greater than the beneficial effect on genetic variance. The assumption that higher recombination rate, in general, would be good for breeding programs (e.g., as suggested in Johnsson et al. (2021)) seems to be mistaken.

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