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Deliverable D3.2

Adaptation of the optiSel R Package

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Abstract

As part of the Geronimo project, innovative breeding strategies are developed for certain local breeds that are implementing optimum contribution selection. The R package optiSel should be used for this purpose, which required an adjustment of the package's functionality. The researchers working with the local breeds were asked about the changes that would need to be made to the package, and the package was changed accordingly. The researchers then participated in a workshop in which they learned the basic functionality of the package, and successfully used the package for evaluating the data on the local breeds, they had available to them.

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1   Introduction

As part of the GEroNIMO project, innovative breeding strategies are developed for local breeds that combine all available phenotypic, pedigree, and genomic data. This is done at the example of the Slovenian Krškopolje pig breed, the French Nustrale pig breed, and the Noire de Challans chicken breed. The breeding goal for the pig breeds is to improve meat quality and welfare through selection for IMF, and through the reduction of the frequency of the $RYR1_{mut}$ allele while preserving genetic diversity. Genetic diversity should be preserved by constraining the increase in the pedigree- or marker-based kinship. For the chicken-breed, a pedigree-based assessment of the genetic diversity was planned, while for the pig-breed a marker-based assessment was planned.

The breeding programs of the breeds should be managed with optimum contribution selection, which required an adjustment of the optiSel R package for optimum contribution selection. In the course of the project, the researchers working with these breeds were asked about the changes that would need to be made to the package optiSel, and the package was changed accordingly. The request of the researchers was that the package should be able to control the frequencies of major QTLs (e.g. the RYR1 mutation) in the population. The availability of appropriate routines in the package was ensured. The researchers and doctoral students were invited to participate in a workshop in which they learned the functionality of the package, and successfully used the package for evaluating the data on the local breeds they brought with them.

2   The R package optiSel

The R package optiSel is a free software for optimum contribution selection which computes the optimum number of offspring per breeding animal, which can be downloaded as usual R packages. The software is able to optimize a certain quantity under various constraints. The current functionality of the software that is relevant to the project includes the maximization of genetic diversity, and the maximization of genetic gain in a selection index. In the second case, the increase in the mean kinship of the population can be constrained to increase in accordance with the desired effective size of the population. In any case, the increase or decrease of the frequencies of major QTLs per generation can be constrained, and an upper bound can be specified for the genetic contributions of the breeding animals.

Another functionality of the package that we encouraged to use for the Krškopolje pig breed is the detection of native chromosome segments, the computation of the native genetic contribution of each animal, and the inclusion of the native contribution as an additional trait in the selection index. This can later be extended towards other breeds as genomic information becomes available.

3 Conclusion

The R package optiSel is now working to the full satisfaction of the researchers and doctoral students who are working with the local breeds, as stated by them in the workshop that was held on 27th – 28th of April, 2022 by Robin Wellmann at the University of Hohenheim.