

Institute: National Research Institute of Animal Production

Title: Breeding value prediction in dairy cattle using a single step model

Name of potential supervisor: prof. dr hab. Joanna Szyda

Background information:

The evaluation of animals' additive genetic merit called Estimated Breeding Values (EBVs), has for decades been a standard element of cattle breeding. Currently this process is carried out in two steps. First, Genomically Enhanced Breeding Values are predicted for selection candidates based on SNP (Single Nucleotide Polymorphism) genotypes. Prior to this procedure effects of SNPs need to be estimated based on the reference data set. Second, Conventional EBVs are predicted based on daughter phenotypes. In practice, two separate evaluations are needed - one for young animals without daughter information and one for older animals with daughter phenotypes. Such approach has several disadvantages. Combining SNP information, relatives' information and own phenotypic data is not optimal because effects of particular models are not estimated simultaneously. As a result, information from SNPs is not propagated to un-genotyped animals. A few years ago, a theoretical solution of this problem has been proposed, in the form of a single step genetic evaluation model, which allows for simultaneous utilization of SNP and phenotypic information. The application of the one-step model, the analysis of its predictive quality and the differences in prediction between the one-step and the two-step models is at the heart of the doctoral project.

The main question to be addressed in the project:

- Will the use of a one-step model result in more accurate estimates of breeding values
- Do the available programming tools allow for the effective implementation of the one-step model for particular types of traits, eg traits measured once during an individual's life, traits measured multiple times during lactation?
- Can the single-step model and input files preparation be more efficiently implemented using parallel programming syntax?

Information on the methods/description of work:

- Get acquainted with the Intel Fortran compiler, MKL library and the MiX-BLUP software.
- Pure polygenic single trait animal model eg. for stature including data preparation.
- Single trait SNP-BLUP model with DRP.
- Single trait G-BLUP model with DRP (6)
- Single step single trait lactation SNP-BLUP
- Single step single trait test-day SNP-BLUP for national data
- Single step single trait test-day SNP-BLUP including MACE data

Additional information:

requirements from the candidate

- The ability to work in the Linux operating system using the command line.

- The ability to create scripts in the bash shell.
- The ability to work with various software developed in open-source mode.
- The ability to program in C or Fortran languages at an intermediate level.
- Good knowledge of mathematical statistics.
- Very good working knowledge of English.
- Engagement in scientific work.
- Completed technical studies: bioinformatics, animal science, computer science, or related.

Place/name of potential collaborator:

- prof. Tomasz Suchocki, Wroclaw University of Environmental and Life Sciences

References:

- Liu Z, Goddard ME, Reinhardt F, Reents R. A single-step genomic model with direct estimation of marker effects. *J Dairy Sci.* 2014;97(9):5833-5850. doi:10.3168/jds.2014-7924
- Lourenco D, Legarra A, Tsuruta S, Masuda Y, Aguilar I, Misztal I. Single-step genomic evaluations from theory to practice: using snp chips and sequence data in blupf90. *Genes (Basel).* 2020;11(7):1-32. doi:10.3390/genes11070790
- Mrode R. Linear models for the prediction of animal breeding values. CABI Publishing