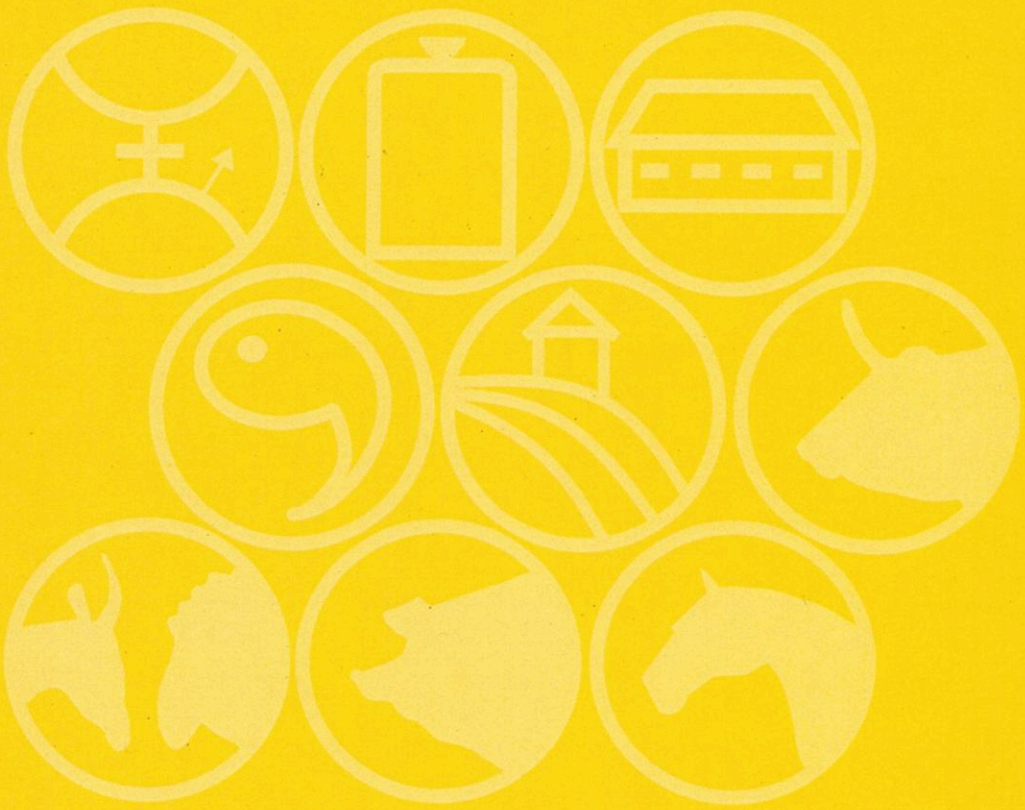
Book of Abstracts of the 63rd Annual Meeting of the European Federation of Animal Science



Book of abstracts No. 18 (2012)
Bratislava, Slovakia
27 - 31 August 2012

Effect of linkage disequilibrium, haplotypes and family relations on accuracy of genomic prediction

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Our objective was to investigate the effect of linkage disequilibrium (LD), haplotypes and family relationships on the accuracy of direct genomic values. A formula based on selection index theory was used to predict accuracies, using genomic relationships and information of a reference population (RF) of 529 genotyped cows. Four groups of selection candidates were simulated using increasing amounts of information: (1) allele frequency of RF (FREQ); (2) allele frequencies and LD pattern of RF (LD); (3) randomly drawing haploid chromosomes from RF (HAP); (4) animals from RF, thereby being the only group with real family relationships to RF (FAM). Accuracy of FAM was predicted using the remaining 528 animals as RF. At a heritability of 0.6, accuracies were on average 0.093±0.003 (FREQ), 0.168±0.006 (LD), 0.355±0.015 (HAP) and 0.577±0.064 (FAM). At a heritability of 0.1, relative differences between accuracies across groups were similar. FREQ used the same assumptions as the deterministic formula to predict accuracies of Daetwyler *et al.*, namely; no LD between loci, no relationships with RF and all loci have an effect. As a result, accuracies of this group were equal to predictions with the Daetwyler-formula. Variance of the accuracy of FAM was much higher compared to the other scenarios, due to much higher variances in relationships with animals in RF. Accuracies of FAM were on average more than 50% higher than the accuracy of HAP. It is concluded that level of relationship with RF has a much higher effect on the accuracy of direct genomic values compared to linkage disequilibrium per se. Furthermore, increasing length of haplotypes shared with animals in RF improves prediction accuracy, especially when multiple haplotypes are shared with one or more reference animals due to family relationships.

A software pipeline for animal genetic evaluation

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Genetic evaluation of animals is essential in any modern breeding program. This procedure usually involves many tools to deal with different aspects. Most of existing tools are independent programs and disconnected from others in terms of usage. Linking them into a complete process is challenging since each requires its own configuration in a specific format. Moreover, for large datasets the repeated manual parameterization is inefficient and error-prone. To address this issue, we have developed 'GEPipe', a software pipeline for genetic evaluation. Our objective is to automate the input parameterization and provide the integration of all involved components. GEPipe is a web-based application easily accessible from a web browser in the network. It is based on the principle 'less input more output' requiring from the user only a minimum set of data to maximize the output. Thus, with one single upload of PEST data and configuration files, six sub-systems (AGen, AfterBLUP, EvolveBLUP, PopRep, OptBS and ZwISSS) are automatically executed to generate different reports. As a result, GEPipe produces a complete documentation on the process of genetic evaluation: computing aggregate genotypes (AGen), analyzing and estimating BLUP (AfterBLUP), monitoring BLUPs over time (EvolveBLUP), creating population reports (PopRep), modeling and optimizing the structure of breeding programs (OptBS) and publishing breeding values (ZwISSS). This process helps breeders or breeding organizations with the quality management of their breeding programs. GEPipe and its sub-systems are freely released under the GPL license. The project is supported by funds of the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV) based on a decision of the Parliament of the Federal Republic of Germany via the Federal Office for Agriculture and Food (BLE) under the innovation support programme.