

Some models of genomic selection

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Several models for solving the well-known problem of genomic selection are proposed when the number of DNA-markers (SNPs) is typically 10-100 times the number of individuals in the sample and SNPs may be correlated. The models use Steptoe x Morex barley mapping population as an example. The first group of the models exploits the Bahadur representation for computing the probability mass functions of genotypes. The second group uses an obvious modification of the Lasso method. Imprecise statistical models are also considered as a tool for simplifying computationally hard algorithms.