

RDBLK Example Data

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SYNOPSIS

To illustrate the implementation of the RDBLK program we provide the beef cattle weaning weight data used in the study by Munilla and Cantet (2015) as an example. Users can execute the programs using these files as input data, and should obtain the same results as reported in the paper.

DATA

The data set belongs to the firm ‘Estancias y Cabañas Las Lilas’, from Argentina, and it is comprised of 5,501 records of Hereford calves weaned at about 6 months of age. These calves expand a genealogy of 6,681 individuals. The data set is composed by 604 maternal families.

MODEL

The model of fit is the ‘Maternal animal model with environmental dam–offspring correlation’ (cf. Munilla and Cantet, 2015). In this particular implementation, we fit the following fixed effects: sex (SX, two levels), age of dam (AOD, 5 levels), contemporary group (CG, 87 levels) and age at measurement (AGE, in days, as a covariate). To achieve full rank, we set to zero the last level of SX and AOD effects. The model also included random maternal permanent environmental effect (MPE) on 2,016 dams.

INPUT

The program requires three input files with specific formats.

- » Parameter file (mandatory name: 'param.txt'): defines the model of fit and set up Bayesian analysis implementation. Each program (i.e. RDBLK_GS and RDBLK_GIW) requires a slight different input parameter file. The difference is because the RDBLK_GIW fits a modified model, referred to as the 'operational' model. The user should notice that this version speeds up execution time considerably. In addition, it allows setting different prior degrees of belief for the additive genetic variances (cf. Munilla and Cantet, 2012). Within this example directory we have only included the input parameter file for the RDBLK_GS program. The input parameter file for executing the RDBLK_GIW version can be retrieved from the corresponding binary file directory. Notice that in both cases the input file is thoroughly annotated to understand how to input each piece of information.
- » Data file (mandatory name: 'dat.txt'): each line must contain the information for each recorded individual. The order of columns must agree with the order in which the effects were defined in the parameter file: fixed effects followed by random effects. All classificatory effects, including MPE, must be coded with numbers from 1 to the number of levels. Direct and maternal genetic effects' columns must be placed together after the MPE effect. Individuals and dams ID must match the ones used in the pedigree file. The last column is for the record. Up to date, the program only allows single trait models. **IMPORTANT:** the

first column must be a sex identifier, coded as an indicator variable: 1 = male, 2 = female. This is mandatory, as the program use this field to sort the input file by maternal families.

- » Pedigree file (mandatory name: 'ped.txt'): a pedigree file is also required, identifying individual, sire and dam. Individuals in the pedigree file must be numbered uniquely and consecutively from the oldest to the youngest, starting from 1. The file must be sorted by individual.

DISCLAIMER

Please report any problem to: munilla@agro.uba.ar

REFERENCES

- » Munilla and Cantet. 2012. J. Anim. Breed. Genet. 129:173–187.
- » Munilla and Cantet. 2015. J. Anim. Sci. 93:1–10.