RDBLK User's guide

Fortran 95 Library RDBLK

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AUTHOR

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SYNOPSIS

> This program set-up and solves single-trait maternal animal mixed model equations when dam-offspring residuals are correlated and, thus, the error covariance matrix R has a block diagonal structure. Further, it creates a Markov chain via iterative Monte Carlo simulation using a single-site systematic Gibbs sampler algorithm. Ultimately, the main goal is to estimate the (co)variance components under a Bayesian approach.

DETAILS

> » Two implementations of the program are possible: 1. Maternal animal model with environmental dam–offspring correlation; 2. Operational model (speeds up execution time). See Munilla and Cantet (2015) for details.

> » Driven by an input parameter file used to define the model of fit and the parameterization of the Bayesian analysis. Also, requires input data and

pedigree files.

» Admits both, categorical factors and (nested) covariates for the fixed effects.

» Support multiple incidence matrices, identically and independently distributed (iid) random effects, and random animal effects (inbred populations).

» Support a positive semi-definite system of equations. However, a full rank reparameterization for fixed effects is recommended to avoid numerical inaccuracies. It also admits to define an effect as a contrast using negative values in the data file.

» Theoretical background on Bayesian statistics and Gibbs sampling algorithm is based on Sorensen and Gianola's book (2002, ch.13).

TECHNICAL NOTES

» Sparse storage of the system of equations.

» Use an adaptive Griddy Gibbs sampler algorithm (Ritter and Tanner, 1992) to sample from the unknown full conditional density of the dam–offspring correlation parameter. (NOTE: the implementation of an alternative algorithm would be an interesting option to increase the efficiency of the program. If you are interested in collaboratively undertake the task, please contact the author).

USAGE

The program is intended to be executed under either Windows (64 bits) or

Linux environment. For each of the two implementations and OS a self-contained directory with the binary file and the input parameter file template are provided. This directory should be downloaded in the user's system and executed together with the data and pedigree files (see below). In addition, source codes are also provided. To compile the files, a Fortran 95 compiler is required.

INPUT

The program requires three input files. See the directory "example" to illustrate how these files should be formatted.

» Parameter file (.txt): defines the model of fit and set up Bayesian analysis implementation (a template of the parameter file is provided together with the binary file).

» Data file (.txt): a data file is required with a line for each recorded individual (see example directory for details).

» Pedigree file (.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. The file must be sorted by individual.

OUTPUT

Upon execution the program delivers the following files:

» CVC-CHAIN.txt: List the values of each (co)variance parameter drawn in each round of the Gibbs sampler.

» SOLUTIONS.txt: [Optional] If requested, it delivers the solutions of the MME obtained before the execution of the Gibbs sampler. The solutions are based on the (co)variances parameters set in the input parameter file as staring values.

» Dat1.sal: Deliver the data file sorted by maternal families.

» ERROR FILE.txt: Flag inconsistencies found in the pedigree file.

EXAMPLE

To illustrate the implementation of the program a directory with the beef cattle weaning weight data used in the study by Munilla and Cantet (2015) is provided as an example. An annotated file is also provided to detail how to format the data and the input parameter files.

DISCLAIMER

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

REFERENCES

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