

WOMBAT - A tool for mixed model analyses in quantitative genetics by REML

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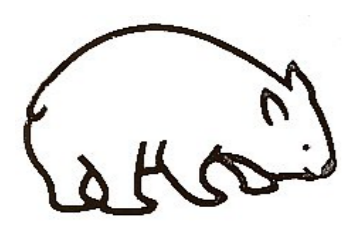
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Summary. WOMBAT is a computer program for quantitative genetic analyses of continuous traits, fitting a linear mixed model. It estimates covariance components and the resulting genetic parameters by restricted maximum likelihood.

Introduction

Modern analyses to estimate genetic parameters and covariance components for continuous traits generally fit a linear, mixed model. Restricted maximum likelihood (REML) is a preferred method of estimation. Advantages over traditional, analysis of variance type methods include that different types of relationships can be utilised in estimating genetic variances, that fixed and random effects are fitted simultaneously, and desirable statistical properties of the estimators.



WOMBAT is a program to carry out such analyses. It allows for a wide range of models, accommodating numerous traits, multiple fixed and random effects, selected genetic covariance structures, random regression models and reduced rank estimation.

The program

WOMBAT is a single program, written in Fortran 95. The user interface comprises a parameter file and command line options.

Parameter file

WOMBAT acquires all information on the analysis to be carried out through a mandatory parameter file. This needs to be set up following a specific set of simple rules. Information needed includes:

- The names of input files
- The layout of the data file
- The model of analysis

Example: Parameter file

```
COM Example 2 from DFREML - Bivariate analysis
ANAL MUV 2
PEDS muexped.d
DATA muwex2.d GRP
TRNOS 1 2
traitno 2
animal 0
generation 4
sex 2
NAMES weight fintake
END
MODEL
FIX generation
FIX sex
RAN animal NRM
TR weight 1
TR fintake 2
END
VAR animal 2
4.9 1.0 6.0
VAR residual 2
1.7 1.0 12.6
```

- Starting values for the covariance components to be estimated

Run options

The behaviour of WOMBAT can be modified at run time through a variety of command line options. These allow choice of:

- Level of output
- Parameterisation
- Method to reorder mixed model equations
- REML algorithms
- Convergence criterion/number of iterates
- Additional calculations

Example: Run options

```
wombat -v --aireml22,0.001 --logdia bivar.par
```

Computing

WOMBAT incorporates state-of-the-art numerical procedures to ensure both computational efficiency and reliable maximisation of the likelihood ($\log \mathcal{L}$) function. Features include:

- Dynamic allocation of arrays → limits on size of the mixed model determined by memory available
- Sparse matrix storage & manipulation
- High quality re-ordering of mixed model equations to minimise 'fill-in'
- Fast computation of inbreeding coefficients & numerator relationship matrix
- 'Average information' REML with backtracking to ensure an increase in $\log \mathcal{L}$
- 'Parameter expanded' & standard expectation maximisation algorithms

The Linux versions of WOMBAT have been compiled using a commercial compiler with a high degree of optimisation. They have fast execution times and are suitable for the analysis of large data sets.

Extras

In addition to estimation of covariance components, several auxiliary tasks can be performed:

- WOMBAT can be used as a simple prediction (BLUP) program.
- WOMBAT provides the facility to replace observations with simulated data sampled from a multivariate normal distribution.
- WOMBAT is set up to pool results from analyses of subsets of traits by 'iterative summation of expanded part matrices'.

Output

WOMBAT generates multiple output files with 'standard' names. Information provided includes:

Example: Output

```
Program WOMBAT: Estimates of covariance components
=====

Example 2 from DFREML - Bivariate analysis
Analysis type      : "MUV 2"
Data file          : "muwex2.d"
Pedigree file      : "muexped.d"
Parameter file     : "wombat.par"

No. of traits      =      2
No. of records     =     568
Maximum log L      =   -915.885

**** Estimates for RE 1 "animal" ****
No. of levels      =     329
Covariance structure = NRM
Order of fit       =      2
Covariance matrix
1      5.0422
2    -0.47615      6.3692
Eigenvalues of covariance matrix
Value      6.52      4.89
(%)        57.16     42.84
Matrix of correlations and variance ratios
1      0.6165
2    -0.0840      0.2912
Covariances/correlations & approx. sampling errors
4 COVS A 1 1      5.042      1.889      vrat      0.616      0.163
5 COVS A 1 2    -0.476      1.995      corr      -0.084      0.355
6 COVS A 2 2      6.369      3.904      vrat      0.291      0.161
```

- Summary information on the data & pedigree structure
- Estimates of covariance matrices & genetic parameters together with their approximate standard errors
- Estimates for all fixed and random effects fitted and the corresponding 'residuals'.

Material available

The Program

WOMBAT is available as a pre-compiled ('executable') program, for a number of common computing environments.



Linux 32-bit and 64-bit, including 'generic' versions for older distributions and processors



Windows 32-bit to run under Cygwin



Windows 32-bit to run in CMD window

The Manual

User notes for WOMBAT are available as a .pdf file.

The Examples

A suite of worked examples, representing types of analyses common to animal breeding applications, is provided. Examples comprise data, pedigree and parameter files (input), as well as output files generated by WOMBAT.

All material can be downloaded (free of charge) from the WOMBAT homepage.



WOMBAT Home Page

agbu.une.edu.au/~kmeyer/wombat.html

