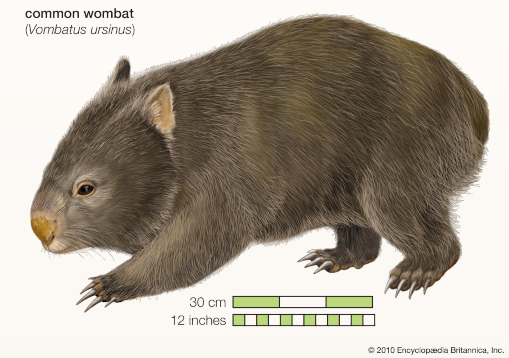


WOMBAT: A tool for estimation of genetic parameters – highlights and updates

Karin Meyer

Animal Genetics and Breeding Unit, University of New England, Armidale, Australia



Purpose

WOMBAT is a software package for linear mixed model analysis in quantitative genetics

- Focus on REML estimation of (co)variance components
- Targeted at animal breeding problems but suitable for many related applications
- Continuous traits

Recent changes & additions

- Version using long (8 byte) Integer variables
 - allows sparse storage of matrices with > 2.14 billion elements
- Options to override default program limits to suit individual analysis & RAM available
- Improved set-up steps for large analyses incl. faster build of the NRM inverse
- Implementation of GWAS via backsolving for marker effects from breeding values

Technical Details

- 'Super-nodal' factorisation, auto-differentiation & inversion of sparse coefficient matrix
- Written in FORTRAN
 - Compiled using ifort or gfortran; 64 bit
 - Parallelisation via OpenMP & Intel MKL routines (Linux version)

Main features



WOMBAT accommodates many different models & analyses and has multiple options for fine tuning
WOMBAT can handle large analyses with millions of equations

Analyses

- Uni- or multivariate REML estimation of variance components & genetic parameters
 - Full (default) or reduced rank estimates of covariance matrices
 - Penalised likelihood estimation to reduce sampling variance
- Prediction only (BLUP)
 - Direct solution
 - Iterative solution (very large problems)
 - Special option for single step models

Models

- Specify via parameter file:
- Fixed effect and covariables
 - Genetic effects
 - choice of relationship matrix
 - Maternal or paternal effects
 - Indirect ("social") genetic effects
 - Additional random effects
 - Genetic groups
 - Random regression
 - Factor-analytic models

Options

- Specify via command line or parameter file:
- Ordering of mixed model equations
 - Strategy to locate maximum of likelihood
 - Algorithm, iterates, convergence criterion
 - Parameterisation
 - Matrix storage: sparse or dense
 - Numerical settings, e.g. operational zeros
 - Pedigree checks & manipulation
 - Invoke auxiliary modules

Auxiliary modules

- Inversion of positive (semi-) definite matrices: sparse or dense mode
- 'Pooling' estimates of covariance components from analyses of subsets of traits
 - make matrices positive definite
- Simulation of records for given variances, data & pedigree structure
- Write out mixed model equation
- Sampling based approximation of standard errors for variance components
- GWAS (EMMAX type)
- H^{-1} & friends: Calculations of relationship matrices utilising genomic information
 - G , G^{-1} , A_{22} , A_{22}^{-1} , H^{-1} , $\log |H|$, $\text{Diag}(H)$
 - A^{-1} with Meta-founders, H^{-1} with unknown parent groups

Get it!

- Free download from **WOMBAT home page**
<http://didgeridoo.une.edu.au/km/wombat.php>
- Executable programs
 - Linux** (multi-threaded)
 - Windows**
- User Manual
 - PDF file** (A4)
 - Online version**
- Frequently Asked Questions**
- Suite of worked examples**



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