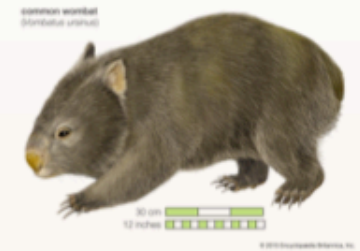# WOMBAT: A tool for estimation of genetic parameters – highlights and updates

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}, $\log|H|$, $\mathrm{Diag}(H)$
  - 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**

Click on links in bold to download