***Estimation of variance components and prediction of genetic (BLUP) values***

* ATBK - Animal Breeders Toolkit
* ASREML estimates variance components under a general mixed model in multivariate, spatial, repeated measures, multi-environment and genetic analyses by REML. Detailed documentation included.
	+ ASREML - A discussion group for the [AsREML software](http://www.metla.fi/info/vlib/forestgen/software.htm#asreml). The address of the list is asreml@chiswick.anprod.csiro.au. To sign up, send a message to: asreml-request@chiswick.anprod.csiro.au, with the word "subscribe" in the body of the message.
* [BENDOPT and BENDPDF:](http://www.boku.ac.at/nuwi/popgen/software.htm#odce) two programs implementing different approaches of the so-called "BENDING" procedure
* [DFREML](http://agbu.une.edu.au/~kmeyer/dfreml.html) by [Karin Meyer](http://agbu.une.edu.au/~kmeyer/homepage.html). Estimates of (co)variance components through a derivate-free method. Programs are provided as fortran source code for DOS and Unix. The compressed executable is ~ 2720 Kb. [Info](http://nitro.biosci.arizona.edu/zbook/volume_1/program_details/dfreml.txt).
* [DMU](http://chuck.agsci.colostate.edu/wais/logs/agdg2316.html) by Just Jensen. Multivariate mixed model analysis. Versions available for IBM, Unix and PC.
* [GRAMBLUP](http://nce.ads.uga.edu/~xin/gramblup.html) - General Purpose Reduced Animal Model Multiple Traits BLUP Program. Download. Some [info](http://nitro.biosci.arizona.edu/zbook/volume_1/program_details/gramblup.txt).
* [HLM](http://www.gamma.rug.nl/catalog/multi.html#HLM) - estimation of maximum likelihood estimates of the variance-covariance components. Commercialware.
* JAA - Mixed model program using iteration on data with support for animal model. Download
* JSPFS - single-trait REML program for animal models using sparse matrix solver. Download.
* [MIXED procedure](http://www.pop.psu.edu/~liny/hlm.html) in SAS. [FAQs.](http://www.sas.com/service/techsup/faq/stat_proc/mixeproc.html) - [Curt Finley's comments](http://chuck.agsci.colostate.edu/wais/logs/agdg20.html) on the usefulness of SAS PROC MIXED for animal breeders (on the [animal breeders discussion group](http://chuck.agsci.colostate.edu/))
* MTCAFS (MTC) - multitrait REML estimation of variance components program by canonical transformation, with support for multiple random effects. Download.
* [MTDFREML](http://chuck.agsci.colostate.edu/cvantass/mtdfreml.html) (**M**ultiple **T**rait **D**erivate **F**ree **RE**stricted **M**aximum **L**ikelihood) by [Curt VanTassel](http://chuck.agsci.colostate.edu/cvantass). Estimates of variance components and BLUP solutions to mixed model equations.
* [MTGSAM](http://chuck.agsci.colostate.edu/cvantass/mtgsam.html) Multiple Trait Gibbs Sampler for Animal Models
* [Quercus](http://www.cbs.umn.edu/eeb/quercus.html) calculates maximum Likelihood estimates of fixed effects and variance components. Supplied as Pascal source code for Unix and VMS platforms. [Info](http://nitro.biosci.arizona.edu/zbook/volume_1/program_details/quercus.txt).
* [PIGBLUP](http://www.une.edu.au/abri/pig.htm) is a modern genetic evaluation system for pigs
* [VARCL](http://www.medent.umontreal.ca/multilevel/varcl.html) - an interactive software package for variance component analysis of hierarchically structured data by maximum likelihood. Commercialware.
* [VCE](http://dad.fao.org/dad-is/tools/software/vce/eg.htm) -- Multivariate multimodel REML estimation of variance components. Fortran source code for Unix platforms. .

 ***Population genetics***

* [GSED](http://www.uni-forst.gwdg.de/forst/fg/publicat.htm) - a program for the characterization of genetic structures in population genetic investigations
* [BOTTLENECK](http://www.ensam.inra.fr/~piry/) is a program for detecting recent effective population size reductions from allele data frequencies
* [ECO-GENE](http://www.rrz.uni-hamburg.de/OekoGenetik/software.htm) for a comprehensive evaluation of human influences on the genetic system
* [FSpeed Fast Inbreeding Computation Software](http://www.tenset.co.uk/fspeed/) - Windows program for rapidly computing the inbreeding of all individuals in a breeding population. Free version available.
* [GDA](http://biology001.unm.edu/~lewisp/gda.html): Software for the Analysis of Discrete Genetic Data
* GENEPOP computes estimates of classical population parameters. [Info](http://www.curtin.edu.au/curtin/dept/biomed/teach/genepop/web_docs/)
* [GENETIX](http://www.univ-montp2.fr/genome-pop/genetix.htm) - a set of programs computes several basic parameters of population genetics such as Nei's D and H, Wright's F-statistics (the Weir-Cockerham's and Robertson-Hill's estimators), and linkage disequilibrium D
* [Population and Quantitative Genetics Software](http://wbar.uta.edu/software/software.htm)

 ***Survival analysis***

* [The Survival Kit V3.0](http://www.boku.ac.at/nuwi/popgen/softskit.htm)by Vincent Ducrocq & Hans Sölkner. Cox and Weibull model, estimation of fixed and random effects (time-dependent), estimation of hyperparameters of the distribution of the random effects, estimation of breeding values. Suitable for large applications.

 ***QTL mapping & linkage analysis***

* [An Alphabetic list of Genetic Analysis Software](http://linkage.rockefeller.edu/soft/list.html)
* [Dendrome's QTL mapping software site](http://s27w007.pswfs.gov/qtl/software.html)
* Pedros's directory of [biomolecular research tools](http://www.public.iastate.edu/~pedro/research_tools.html)
* [POPGENE](http://www.ualberta.ca/~fyeh/index.htm), a program for population genetics analysis
* [DnaSP](http://www.bio.ub.es/~julio/DnaSP.html) - DNA Sequence Polymorphism
* [PLABQTL](http://probe.nalusda.gov:8000/otherdocs/jqtl/jqtl1996-01/utz.html) - a program for composite interval mapping of QTL
* [LAMARC](http://evolution.genetics.washington.edu/lamarc.html) is a package of programs for computing likelihoods for samples of data (sequences and electrophoretic polymorphisms) from populations
* QTL Cartographeris a package of programs that will aid in locating the genes that control quantitative traits using a molecular map of markers
* [MQTL](http://gnome.agrenv.mcgill.ca/tinker/mqtl.htm): Software for simplified composite QTL interval mapping in multiple environments
* [MSIM](http://gnome.agrenv.mcgill.ca/tinker/msim.htm): Software for Automated Simulation of genetic markers and QTL
* DISPAN, a software for the analysis of allozyme data. Info.
* [Multimapper](http://www.rni.helsinki.fi/~mjs/) / Bayesian QTL mapping software for inbred lines (distributed as C source code)

 ***Other***

* [Miscellaneous free software, shareware, and demos](http://www.graphpad.com/www/sharewar.htm)
* [CompuPed](http://www.compuped.com/) - a genetic heritage information database management system for serious animal breeders, geneologists and pedigree fans.
* [Cyrillic](http://www.cherwell.com/ProdHome/cyrilhome.html) - pedigree drawing software with tools for managing genetic data
* [Journal of Statistical Software](http://www.stat.ucla.edu/journals/jss/)
* [ODCE](http://www.boku.ac.at/nuwi/popgen/software.htm)Optimum Design of Crossbreeding Experiments
* GNU Fortran (G77)- a free fortran compiler (beta). (See also [the list of other fortran compilers](http://www.fortran.com/fortran/compilers.html))
* KIN (ftp site): Software for Computing Kinship Coefficients, by N. Tinker and D. Mather.
* [ACEDB](http://s27w007.pswfs.gov/Homepage/acedb-faq.html) - database system used to collect information regarding the molecular biology of the genome. Available as source code for various platforms
* [CBE - Crossbreeding Effects](http://www.boku.ac.at/nuwi/popgen/softcbe.htm)