

BLUPF90 suite of programs for animal breeding with focus on genomics

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BLUPF90 suite of programs

- Collection of software for mixed-model computations
- Focus on breeding and genetics applications
- Features
 - Solving of mixed model equations
 - Variance component estimation
- Supports
 - general multiple trait
 - multiple effect
 - different model design per trait
 - correlated random effects

Birth

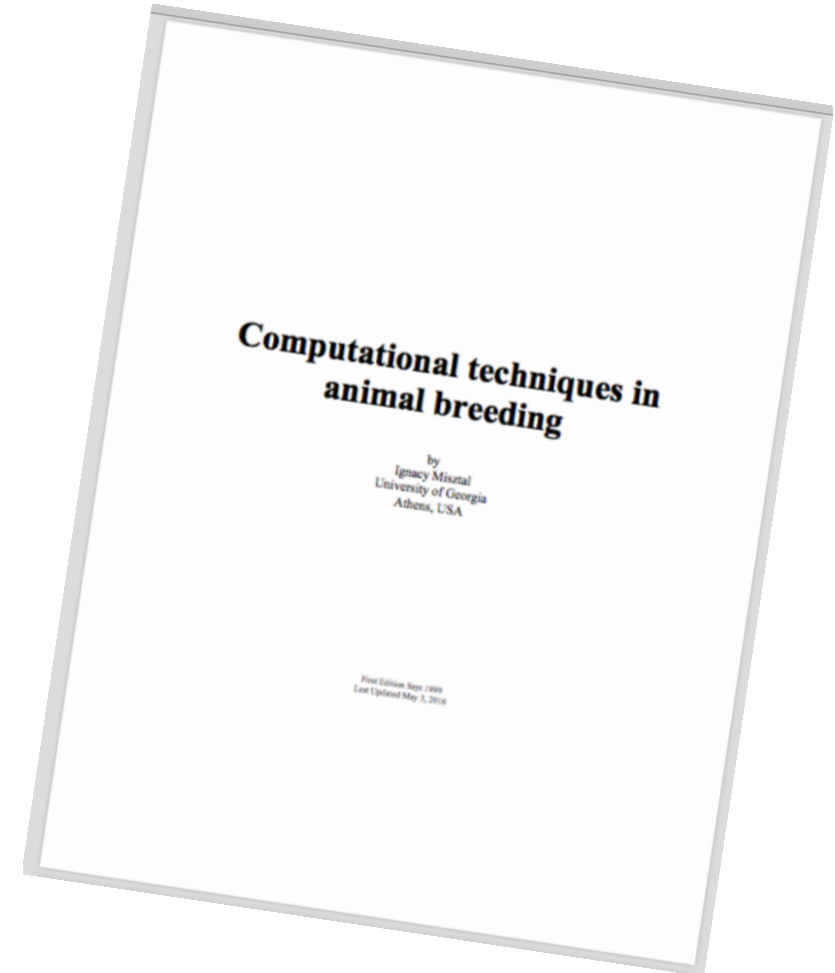
Developed to support a Fortran 90/95 programming course:

“Computational techniques in animal breeding”

University of Georgia, 1999 by I. Misztal

- BLUP program
 - solutions of mixed model equations
- Coded in Fortran 90/95 (F90)

BLUPF90

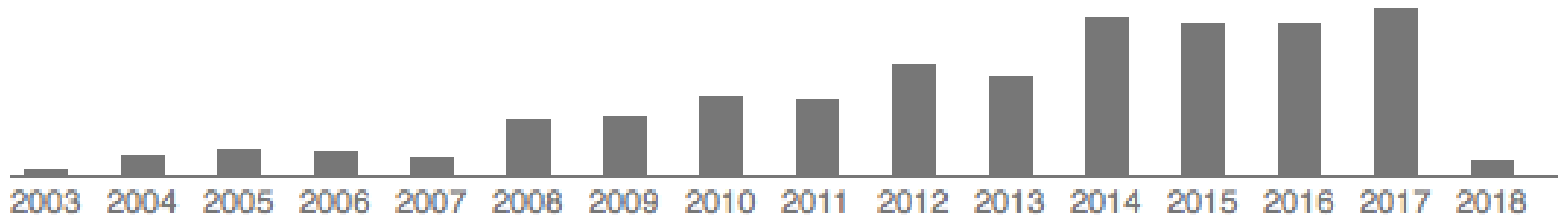


Original BLUP program evolved

- estimation of variance components (REML, Gibbs sampler)
- support for threshold models
- large scale genetic evaluations
 - computations of solutions
 - approximations of accuracy
- Instead of one big program, several programs are available
BLUPF90 family programs

BLUPF90 and related programs (BGF90)

I. Misztal, S. Tsuruta, T. Strabel, B. Auvray, T. Druet & D.H. Lee. 2002
7th World Congress on Genetics Applied to Livestock Production, Montpellier, France



Scholar Google citations: 632

Genomic Era: Single-Step genomic evaluation

- Unified approach with pedigree, phenotypic and genomic information
- Pedigree-based relationships augmented by genomic relationship matrix (Miształ et al. 2009)

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \alpha H^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

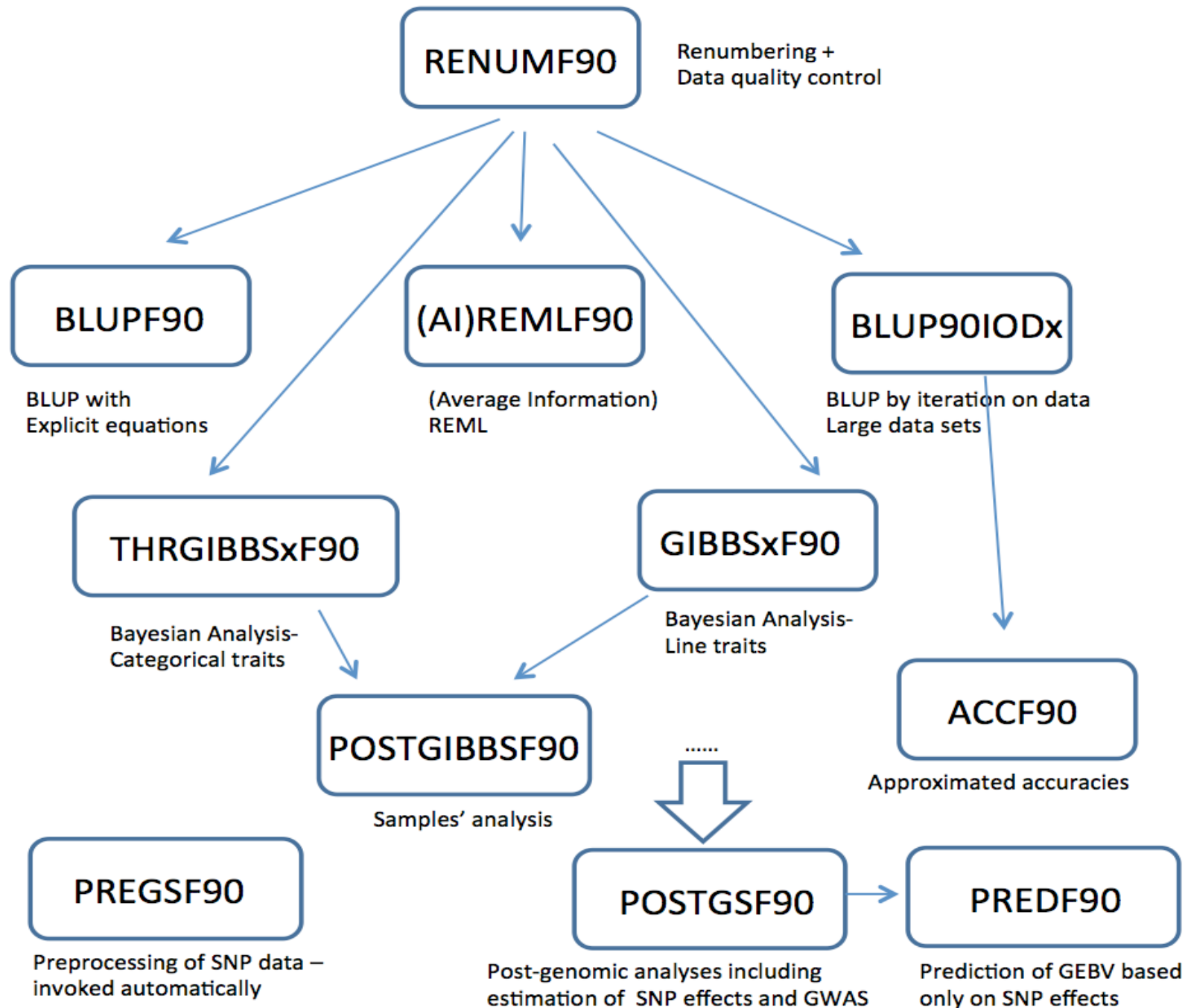
Efficient computation of the genomic relationship matrix and other matrices used in single-step evaluation

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Data Preparation

- Reads alphanumeric information
 - Phenotypes, Pedigree, Markers
- Prepares
 - renumbered files
 - parameter file } to be used in all programs
- Features
 - Trackback and extract pedigrees by generations
 - Inclusion of inbreeding in A^{-1}
 - Unknown parent groups
 - Merging effects (e.g. herd-year-season)

RENUMF90

Renumbering +
Data quality control

BLUPF90

BLUP with
Explicit equation

Solving of mixed model equations

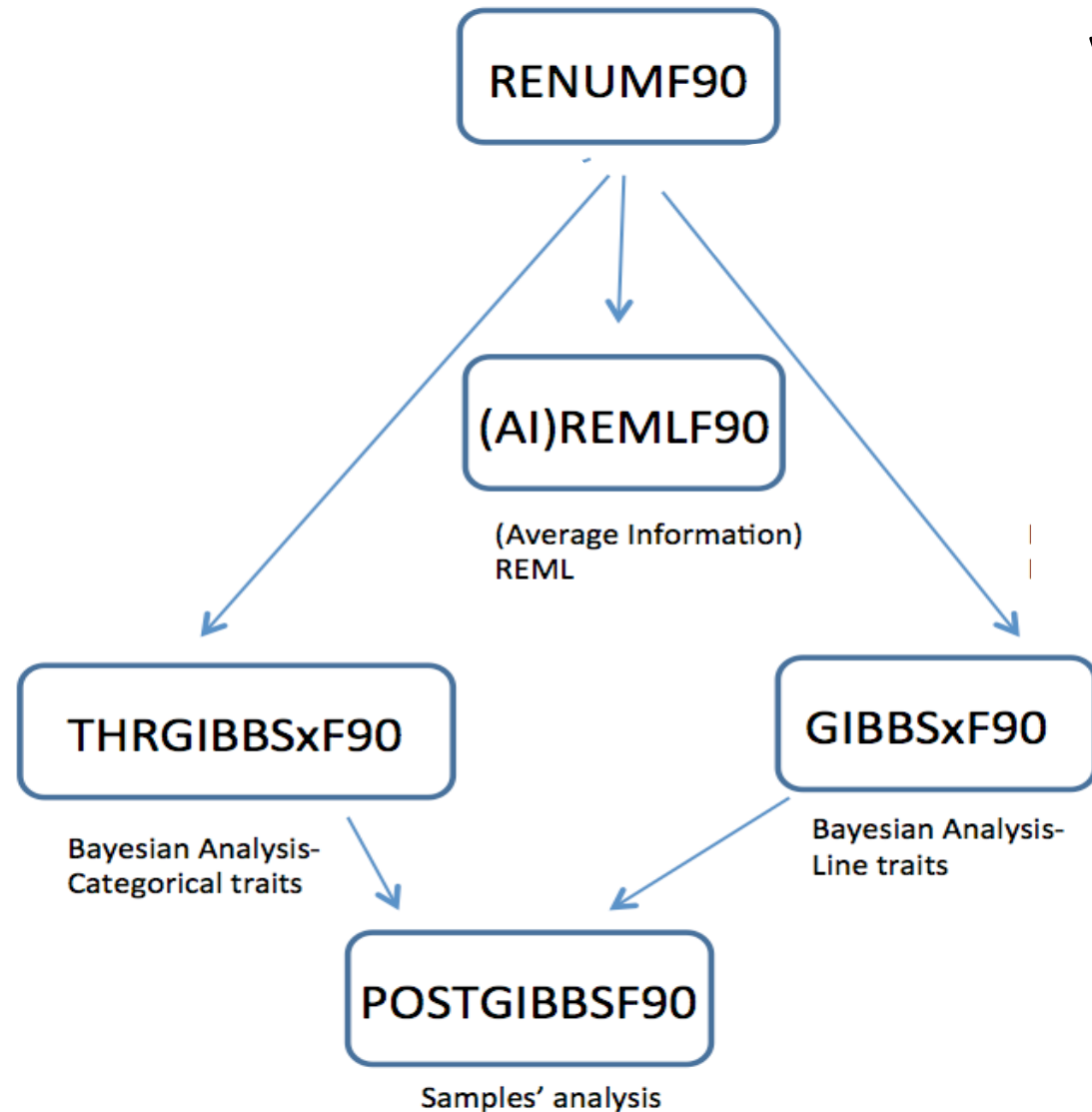
- equations stored in memory
- solutions by
 - direct inversion
 - iterative methods (PCG)
- prediction error (co)variances from the sparse inverse to derive accuracy
 - single/multiple trait animal models
 - random regression models
- supports heterogeneous residual variances

Random effects supported

- pedigree additive relationships (animal or sire model)
 - with or without unknown parent groups
 - with or without inbreeding
 - combined with genomic information ssGBLUP
- parental dominance
- metafounders
- relationships derived for honey bee production
- user defined matrices

Variance components programs

- REML
 - EM-REML – **REMLF90**
 - Average Information REML – **AIREMLF90**
 - standard errors of any function of variance components
- Gibbs sampling
 - highly optimized for storage of mixed model equations and block sampling:
 - for multiple traits **GIBBS1F90**
 - multiple traits and random correlated effects **GIBBS2F90**
 - and heterogeneous residual variances **GIBBS3F90**
 - and multiple trait threshold-linear traits **THRGIBBS1F90**
 - with heterogeneous residual variance **THRGIBBS3F90**



Sparse-dense matrix efficient methods

- key feature of the BLUF90 programs
 - sparse matrix module with **efficient programming of sparse matrix computations**
 - FSPAKF90 (Misztal & Perez-Enciso 1998) interface to FSPAK (Perez-Enciso *et al.*, 1994)
- With single-step GBLUP
 - large blocks of dense matrices deteriorate the performance of the FSPAK subroutines
- Module YAMS (Masuda *et al* 2014)
 - detects dense blocks in MME
 - rearrange computations using dense operations with optimized and parallelized subroutines.
- Drastically reduction of computing time for variance component (REML), and exact accuracies by inversion.

Genomic information

- Single-step GBLUP included in **all programs**
- **PREGSF90**
 - interface to process the genomic information
 - set of quality control on genotypes
 - provides several outputs to detect possible errors with genotypes
 - creation and inversion of matrices (e.g. G , G^{-1} , A_{22} , A_{22}^{-1})
- **POSTGSF90**
 - solutions from ssGBLUP used to backsolve estimates for SNP effects
 - can be used to predict interim DGVs for newly genotyped individuals using **PREDF90**
- **SEEKPARENTF90**
 - Validation and discovery of paternity using genomic information

Large scale genetic evaluations programs

- **BLUP90IOD**

 - compute solutions for large scale genetic evaluations

 - iteration on data with the preconditioner conjugate algorithm solver

- Modified versions provide support

 - heterogeneous residual variance

 - multiple breed evaluation

 - optimized preconditioners for random regression models

 - threshold-linear models.

- Single-step genomic evaluations

 - full storage of $\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}$

 - APY method with sparse inverse of \mathbf{G}^{-1}

 - efficient sparse implementation of \mathbf{A}_{22}^{-1}

 - unknown parent groups in ssGBLUP

RENUMF90

Renumbering +
Data quality control

BLUP90IODx

BLUP by iteration on data
Large data sets

ACCF90

Approximated accuracies

Single-step GBLUP in large scale evaluations

Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus¹

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Implementation of genomic recursions in single-step genomic best linear unbiased predictor for US Holsteins with a large number of genotyped animals

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- Performance data
 - BW & WW: 6 M records
 - PWG: 3.4 M records
- Pedigree data:
 - 8.2 M animals
- Genotype data
 - 81 K animals

- Performance data
 - Final score: 11 M records
- Pedigree data:
 - 10 M animals
- Genotype data
 - 570 K animals

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Software

Download

You can find the latest release of BLUPF90 family of programs at the following page.

- [Repository for BLUPF90 programs](#)
(64 bit Linux versions updated on October 10, 2017)

Documentation & Support

The BLUPF90 manual and the other documentation on the programs are available at the *dokuwiki*. For help, questions and bug reports, please visit the Yahoo Group.

- [Dokuwiki for BLUPF90 Family of Programs](#) for documentation
- [Blupf90 discussion group at yahoo.com](#) for support

<http://nce.ads.uga.edu/software/>

Summary

- BLUPF90 suite is a collection of software for mixed-model analysis with focus on breeding and genetics applications
- Great flexibility of models including multiple-trait, random correlated effects and linear-threshold models
- Genomic analyses using single-step GBLUP are fully integrated in all programs with efficient optimizations for large scale genetic evaluations.

Summer Course 2018

***Programming and computer algorithms in animal breeding with
a focus on single-step GBLUP and reality of genomic selection***

May 7th to May 25th, 2018

University of Georgia, Athens, GA

