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`

Computational techniques in animal breeding

by
Ignacy Misztal
University of Georgia
Athens, USA

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

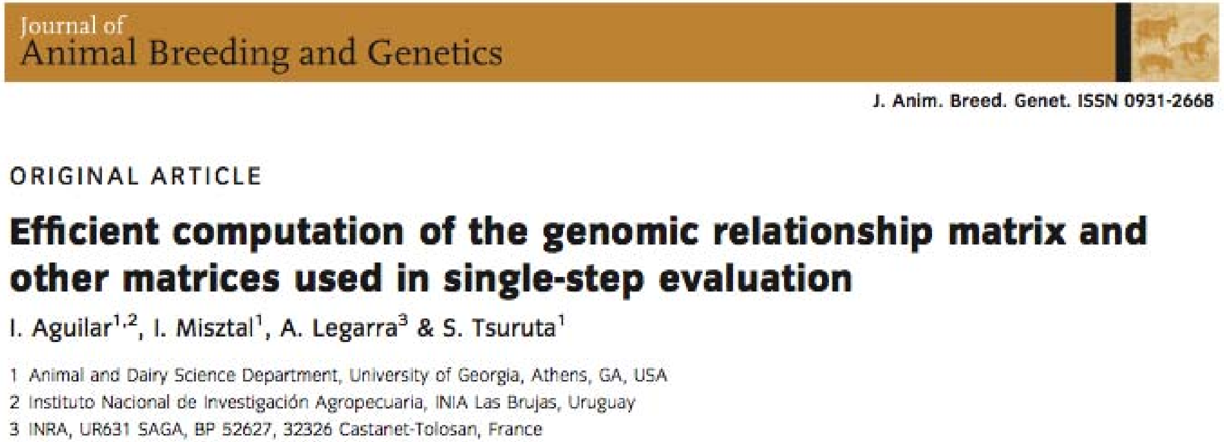
7th World Congress on Genetics Applied to Livestock Production, Montpellier, France

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 (Misztal et al. 2009)

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



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ORIGINAL ARTICLE

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

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2 Instituto Nacional de Investigación Agropecuaria, INIA Las Brujas, Uruguay
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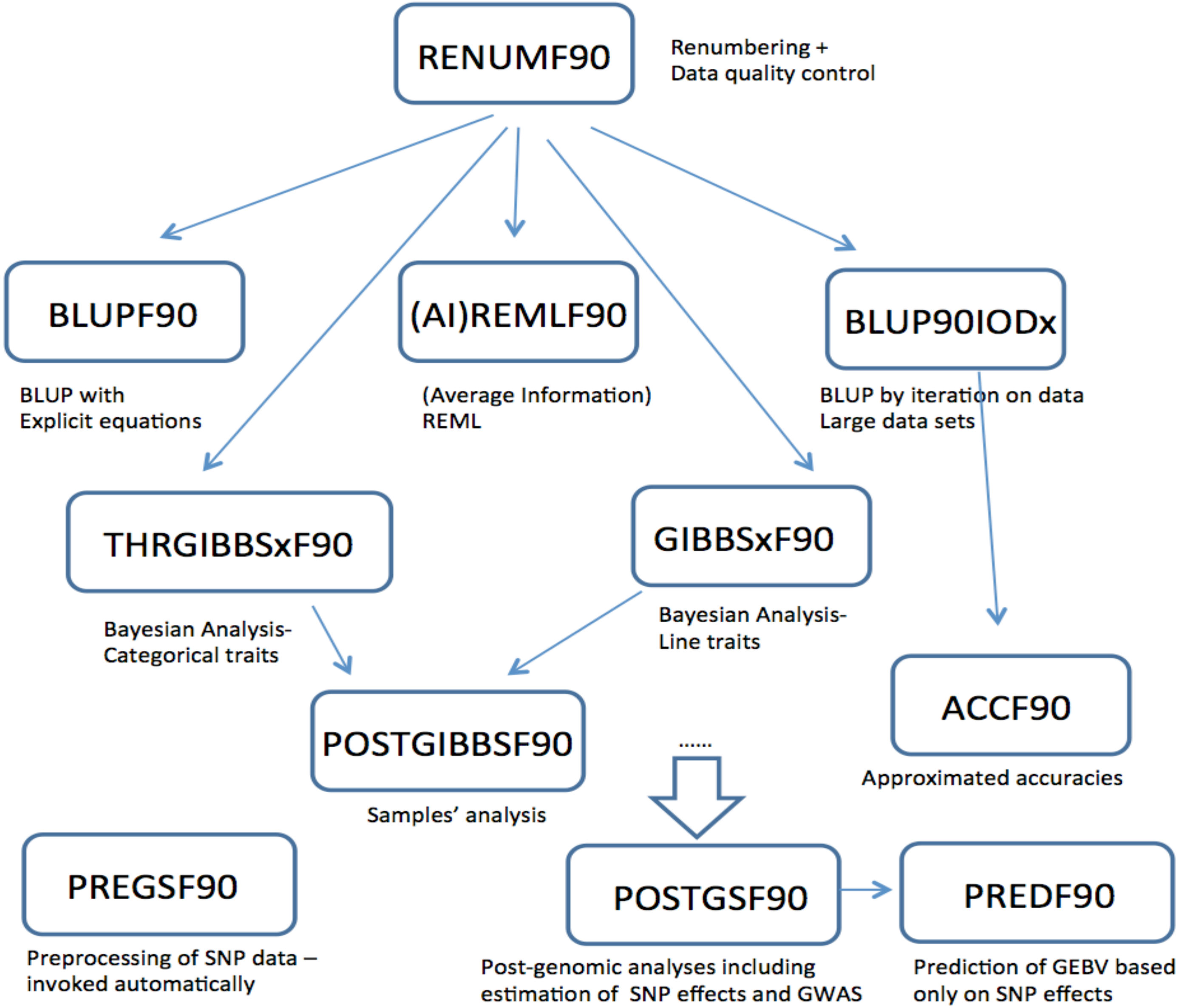


RENUMF90

Renumbering +
Data quality control

BLUPF90

BLUP with
Explicit equations

(AI)REMLF90

(Average Information)
REML

BLUP90IODx

BLUP by iteration on data
Large data sets

THRGIBBSxF90

Bayesian Analysis-
Categorical traits

GIBBSxF90

Bayesian Analysis-
Line traits

ACCF90

Approximated accuracies

POSTGIBBSF90

Samples' analysis

……

PREGSF90

Preprocessing of SNP data –
invoked automatically

POSTGSF90

Post-genomic analyses including
estimation of SNP effects and GWAS

PREDF90

Prediction of GEBV based
only on SNP effects

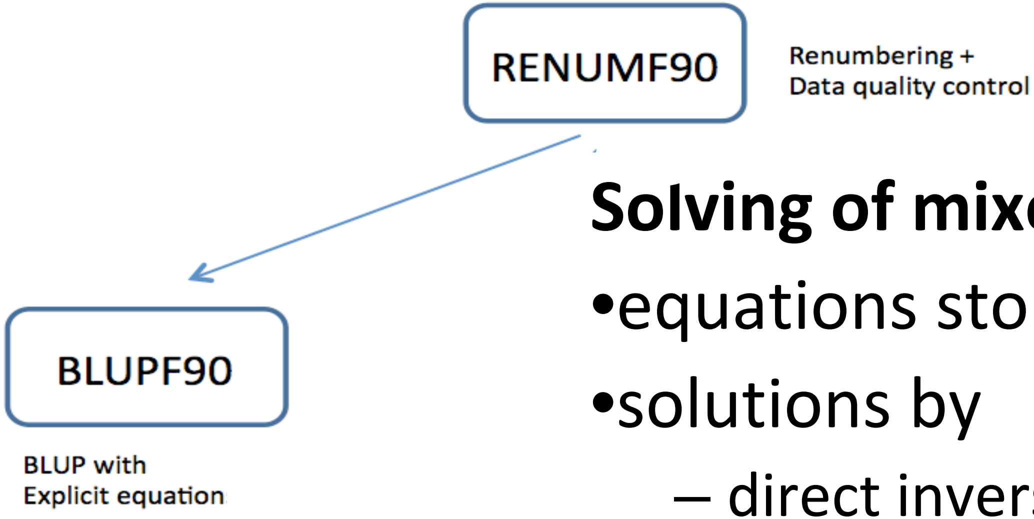
RENUMF90

Renumbering +
Data quality control

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)

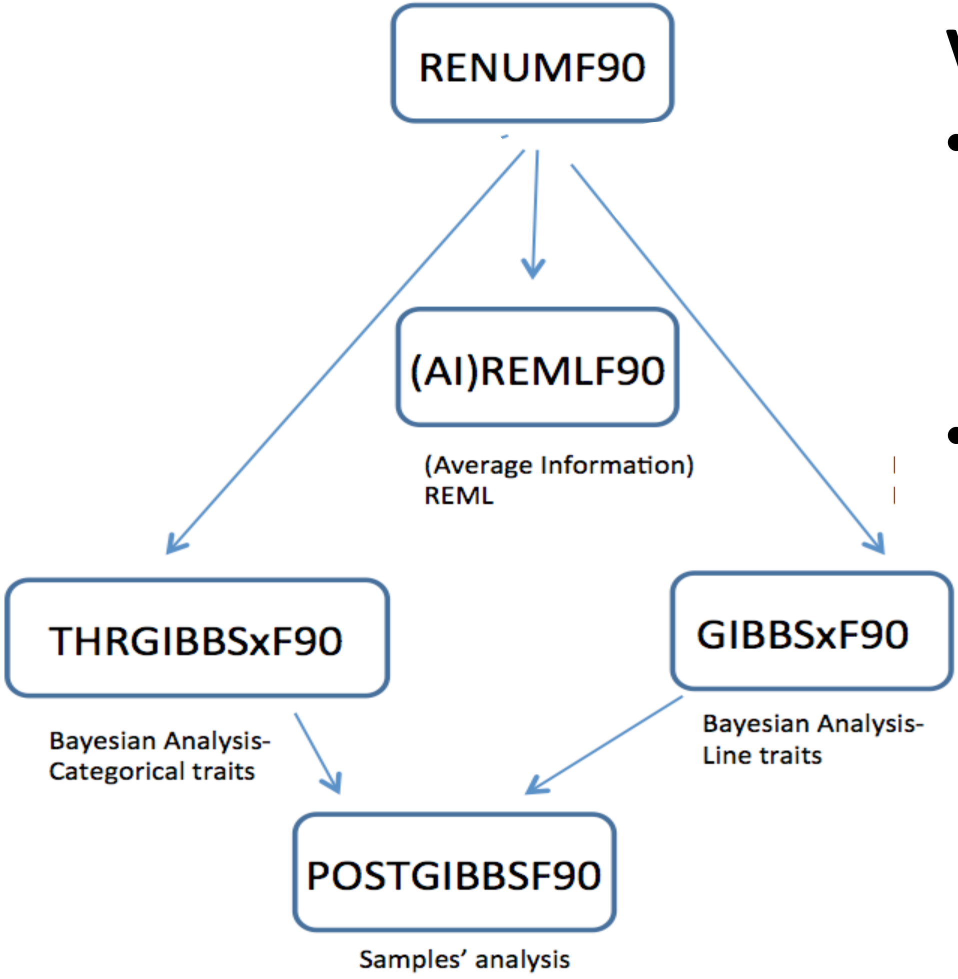


Solving of mixed model equations

- 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


RENUMF90

(AI)REMLF90

(Average Information) REML

THRGIBBSxF90

Bayesian Analysis- Categorical traits

GIBBSxF90

Bayesian Analysis- Line traits

POSTGIBBSF90

Samples' analysis

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

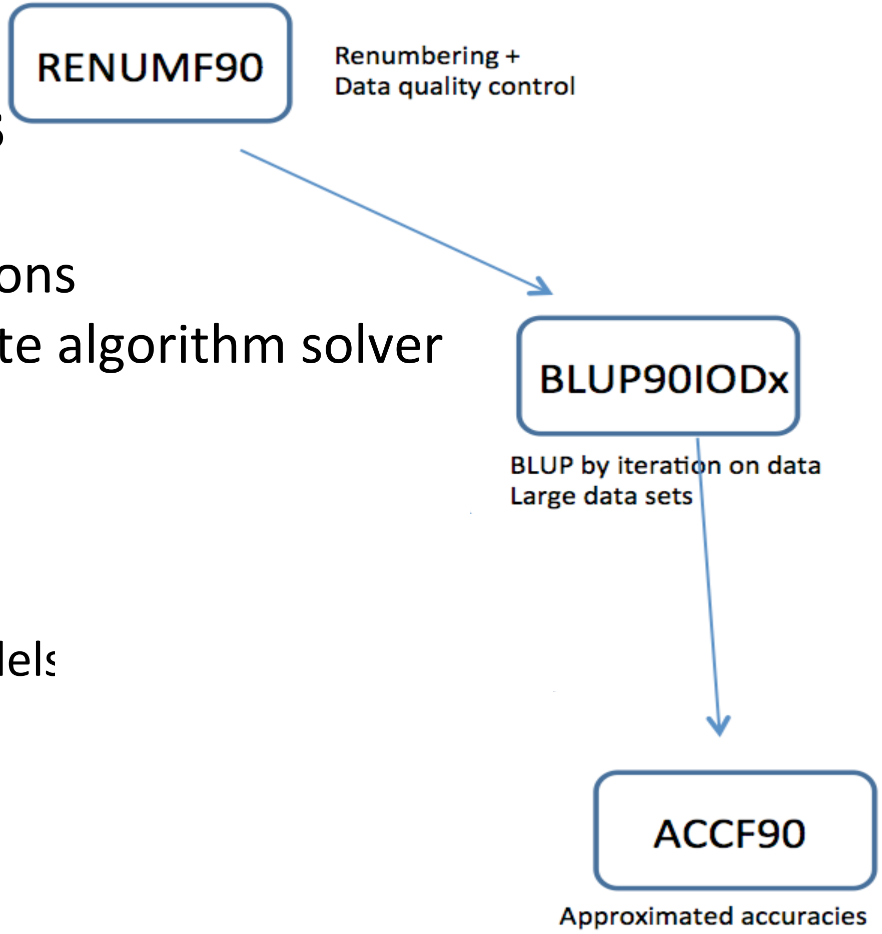
- **BLUP90IOD**

  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

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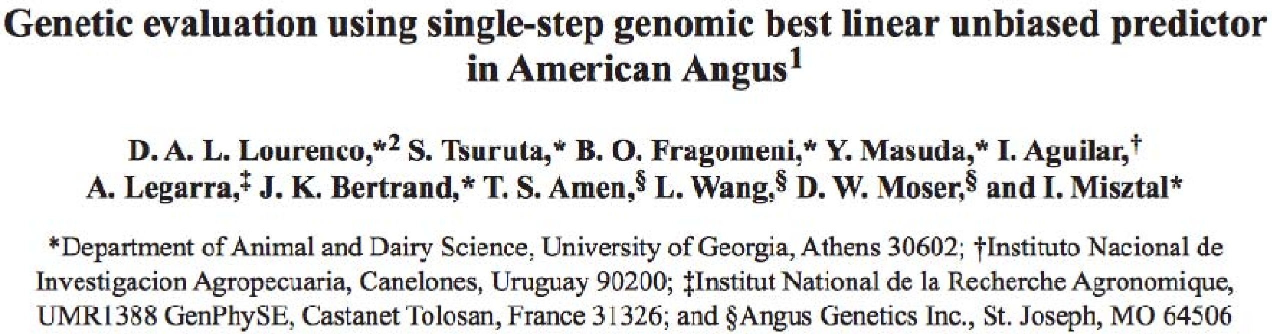
Large data sets

ACCF90

Approximated accuracies

Single-step GBLUP in large scale evaluations



Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus[1]

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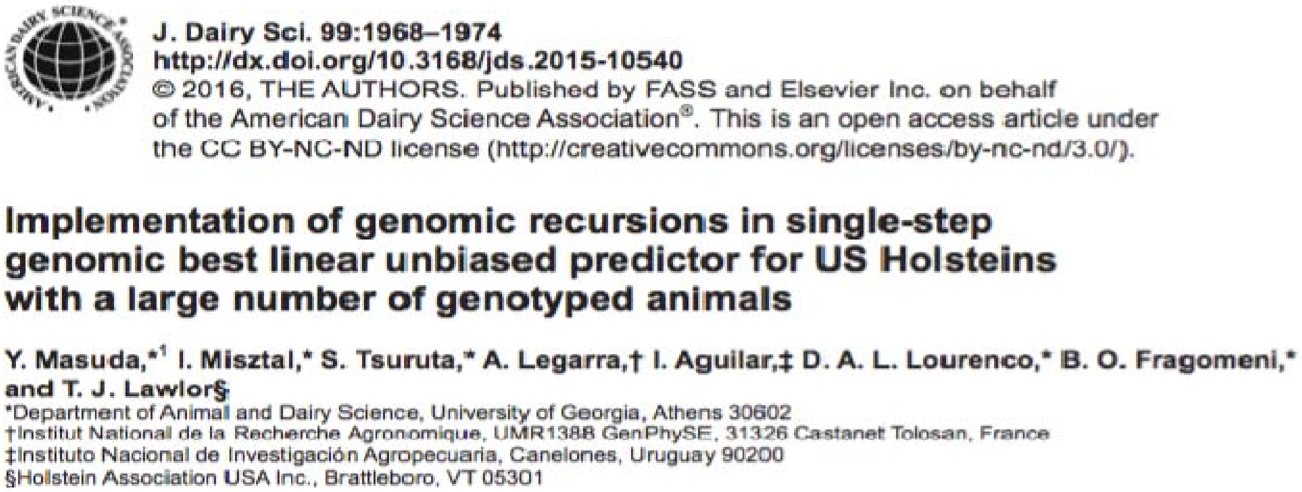
- **Performance data**
  - BW & WW: 6 M records
  - PWG: 3.4 M records
- **Pedigree data:**
  - 8.2 M animals
- **Genotype data**
  - 81 K animals



J. Dairy Sci. 99:1968–1974
http://dx.doi.org/10.3168/jds.2015-10540

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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§Holstein Association USA Inc., Brattleboro, VT 05301

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

ANIMAL BREEDING AND GENETICS GROUP

UNIVERSITY OF GEORGIA

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