

Single-step evaluation for calving traits with 1.5 million genotypes: SNP-based approaches

J. Vandenplas, R. Veerkamp, R. Evans, M.P.L. Calus &
J. ten Napel



Single-step SNPBLUP

- Prediction of
 - genomic breeding values for genotyped and non-genotyped animals
 - SNP effects
- Main difference with ssGBLUP
 - No computation of a genomic relationship matrix (or its inverse)

Single-step SNPBLUP

- Two ssSNPBLUP variants explored

Solutions	Liu et al. (2014)	Mantysaari and Stranden (2016)
SNP effects	✓	✓
Aggregate GEBVs		
Ungenotyped	✓	✓
Genotyped	✓	X
Residual polygenic	X	✓

Aim

Investigation of the performance of

two ssSNPBLUP approaches

using

a multi-trait dataset and >1.5 million genotypes

ICBF evaluation for calving traits

Same data and model as previous presentation

Number of	
Traits	6
Records (until 2015)	3,221,888
Pedigree animals	10,359,131
Genotypes	1,512,383
SNPs	50,855
Equations	137,753,736



ICBF evaluation for calving traits

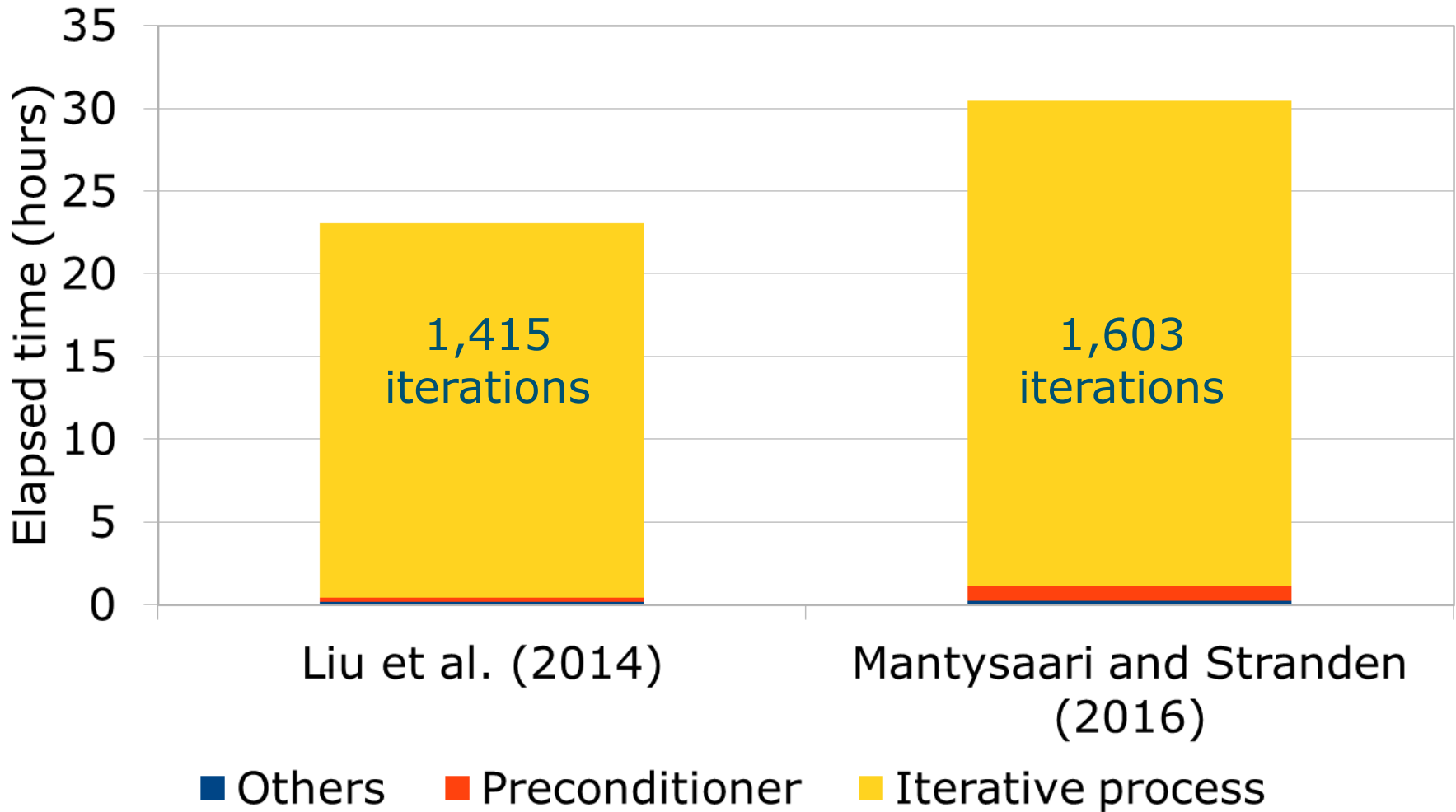
- Direct and maternal genetic effects for all traits
- Genetic groups (breed fractions) as regressions
- SNP effects
 - Current allele frequencies
 - Both direct and maternal genetic effects
- Residual polygenic effect: 5%



Software

- PCG solver + second-level diagonal preconditioner
 - ➔ “A diagonal preconditioner for solving single-step SNPBLUP efficiently”, Session 65, Abstract p. 595.
 - Convergence: Relative residual $<10^{-6}$
- All data in memory to allow parallelization
 - Records
 - Pedigree relationship matrix
 - Compressed genotypes (4 SNPs/1byte; Plink format)
- Multi-threaded (10 threads) Fortran program

Performance



Performance

	Liu et al. (2014)	Mantysaari and Stranden (2016)
Number of iterations	1,415	1,603
Total time (h)	23.0	30.4
Time/iteration (s)	56.4	64.6
Time (s) for 1 multiplication of the genotype matrix	26.2	26.0
Peak memory (RAM; GB)	93	109
Genotypes (GB)		35.8

Single-step SNPBLUP

- **Achievable** for routine evaluations
 - **Convergence properties** need to be investigated
 - Other threshold/convergence criterion?
 - **Software**
 - Still **under development** (preconditioner, time, RAM)
 - **Low** amounts of **memory** and **I/O**
 - Shared-memory **parallelisation**
- **Suitable** for current hardware

Conclusions

■ Routine ssSNPBLUP?

- **Achievable** within reasonable time
 - With large genotype datasets
 - With current hardware
- Requires an **adapted** (but simple) **PCG solver**
- **Liu et al.** (2014) approach
 - Seems to be the **most efficient** ssSNPBLUP approach

Take-home message of the 2 presentations

- Single-step evaluations

- ssGBLUP_**APY** / ssGTBLUP (Ismo Stranden)
- ss**SNP**BLUP

→ All currently **achievable**, even with >1.5 million genotypes

- Still room for **improvement**

- Convergence - preconditioner
- Time / memory



World Congress on
Genetics Applied
to Livestock Production



Rotterdam | The Netherlands
3 - 8 July 2022



WCGALP 2022

**QUALITY, INCLUSIVE,
ATTRACTIVE AND MODERN.
WITH A DUTCH TOUCH.**

IMPORTANT DATES

12 January 2022: Deadline abstract submission
1 March 2022: Deadline early bird registration

www.wcgalp2022.com

Thank you!

