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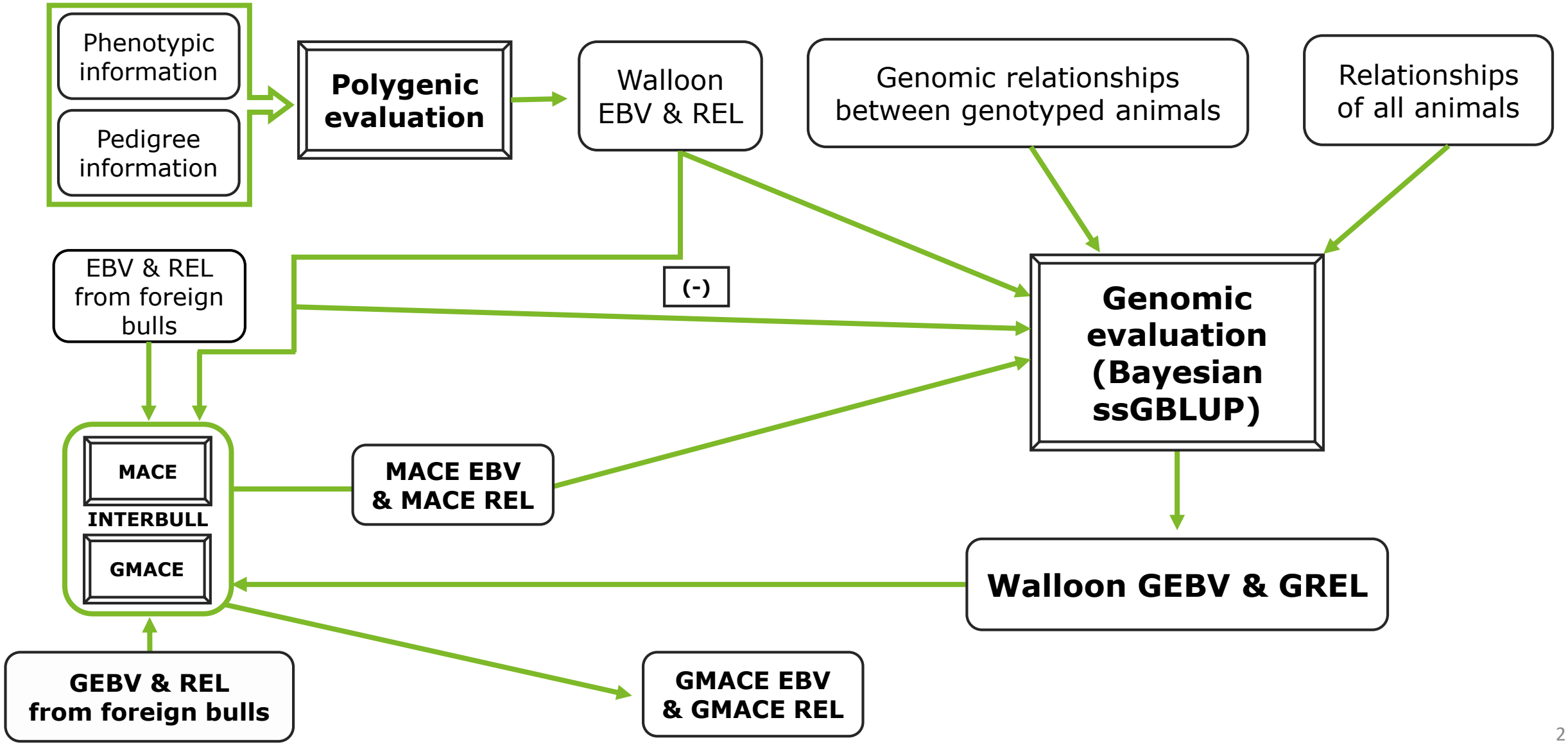
STRATEGY TO STABILIZE GEBV ESTIMATION UNDER A QUICKLY EVOLVING MIXED SIRE AND COW BASED REFERENCE POPULATION IN THE SINGLE-STEP EVALUATION SYSTEM OF THE WALLOON REGION OF BELGIUM

R.R. MOTA, S. NADERI, S. VANDERICK, F.G. COLINET, A. GILLON, P. MAYERES & N. GENGLER

CURRENT HOL EVALUATION IN BELGIUM



CURRENT SITUATION IN WALLONIA

- Gaps of 4 months between evaluations
- ~9,000 genotyped animals
- 20% expected increase each year

MAIN QUESTIONS

- How can we provide GEBV often to help breeders in early decisions?
- How can we stabilize GEBV when the reference population is constantly moving?
- Interim method through indirect predictions

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

D. A. L. Lourenco,*[2] S. Tsuruta,* B. O. Fragomeni,* Y. Masuda,* I. Aguilar,†
A. Legarra,‡ J. K. Bertrand,* T. S. Amen,§ L. Wang,§ D. W. Moser,§ and I. Misztal*

*Department of Animal and Dairy Science, University of Georgia, Athens 30602; †Instituto Nacional de Investigacion Agropecuaria, Canelones, Uruguay 90200; ‡Institut National de la Recherche Agronomique, UMR1388 GenPhySE, Castanet Tolosan, France 31326; and §Angus Genetics Inc., St. Joseph, MO 64506

INTERBULL BULLETIN NO. 53. Auckland, New Zealand, February 10 – 12, 2018

Tuning Indirect Predictions Based on SNP Effects from Single-Step GBLUP

D.A.L. Lourenco[1], A. Legarra[2], S. Tsuruta[1], D. Moser[3], S. Miller[3], and I. Misztal[1]
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INTERIM GENOMICALLY ENHANCED BREEDING VALUES

1. GEBV partition: mean, polygenic (a) and genomic terms (DGV) -> $\hat{\mathbf{u}} = \hat{\mathbf{m}} + \hat{\mathbf{a}} + \mathbf{DGV}$

2. SNP effect from DGV

3. GEBV prediction for young animals by combining the mean, polygenic and genomic (from SNPs) terms

GEBV PARTITION

$$\begin{bmatrix} \mathbf{1}'\mathbf{1} & \mathbf{1}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{1} & \mathbf{Z}'\mathbf{Z} + \mathbf{A}^{-1}k \end{bmatrix} \begin{bmatrix} \hat{\mathrm{m}} \\ \hat{\mathbf{a}} \end{bmatrix} = \begin{bmatrix} \mathbf{1}'\hat{\mathbf{u}} \\ \mathbf{Z}'\hat{\mathbf{u}} \end{bmatrix}$$

Applications of Linear Models in Animal Breeding

Charles R. Henderson

$$k = \frac{\sigma_e^2}{\sigma_a^2} = \frac{0.6\sigma_u^2}{0.4\sigma_u^2}$$

$$k = \frac{\sigma_e^2}{\sigma_a^2} = \frac{0.65\sigma_u^2}{0.35\sigma_u^2}$$

Christensen and Lund *Genetics Selection Evolution* 2010, **42**:2
http://www.gsejournal.org/content/42/1/2

GSE Genetics Selection Evolution

RESEARCH Open Access

Genomic prediction when some animals are not genotyped

Ole F Christensen*, Mogens S Lund

J. Dairy Sci. 102:1–8
https://doi.org/10.3168/jds.2018-15592

Technical note: **Methods for interim prediction of single-step breeding values for young animals**

E. C. G. Pimentel,* C. Edel, R. Emmerling, and K.-U. Götz
Institute of Animal Breeding, Bavarian State Research Center for Agriculture, 85586 Grub, Germany

SNP EFFECTS FROM DGV

$$\hat{\mathbf{e}} = \hat{\mathbf{u}} - (\mathbf{1}\hat{m} + \mathbf{Z}\hat{\mathbf{a}}) = \mathbf{DGV}$$

$$\hat{\mathbf{g}} = \mathbf{DM}'\mathbf{G}^{-1}(\hat{\mathbf{e}})$$

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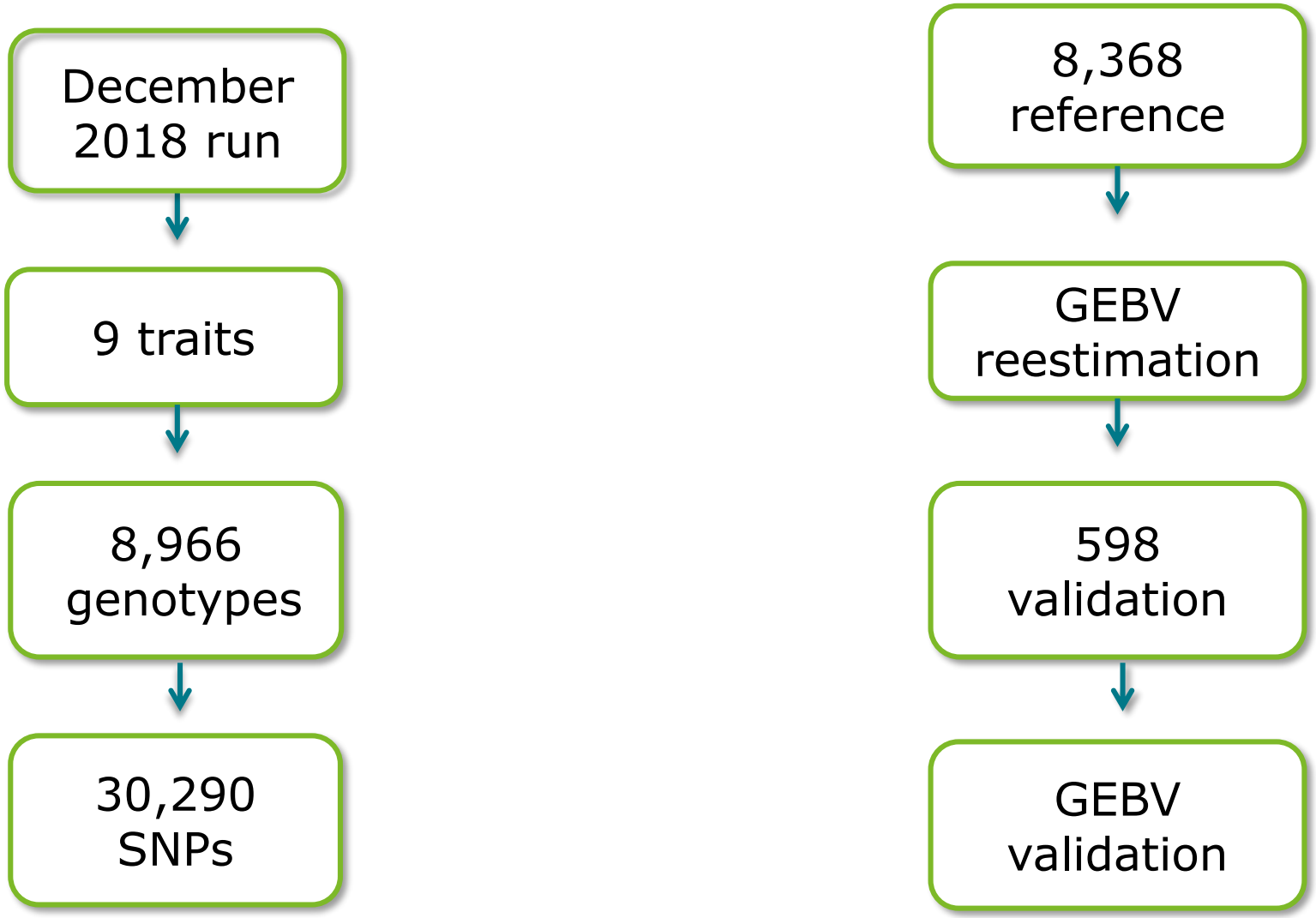
GEBV PREDICTION FOR YOUNG ANIMALS

$$\mathbf{DGV}_{v} = \mathbf{M}_{v}\hat{\mathbf{g}}$$

$$\mathbf{GEBV}_{v} = \hat{\mathbf{m}} + \hat{\mathbf{a}} + \mathbf{DGV}_{v}$$

GEBV REESTIMATION AND VALIDATION



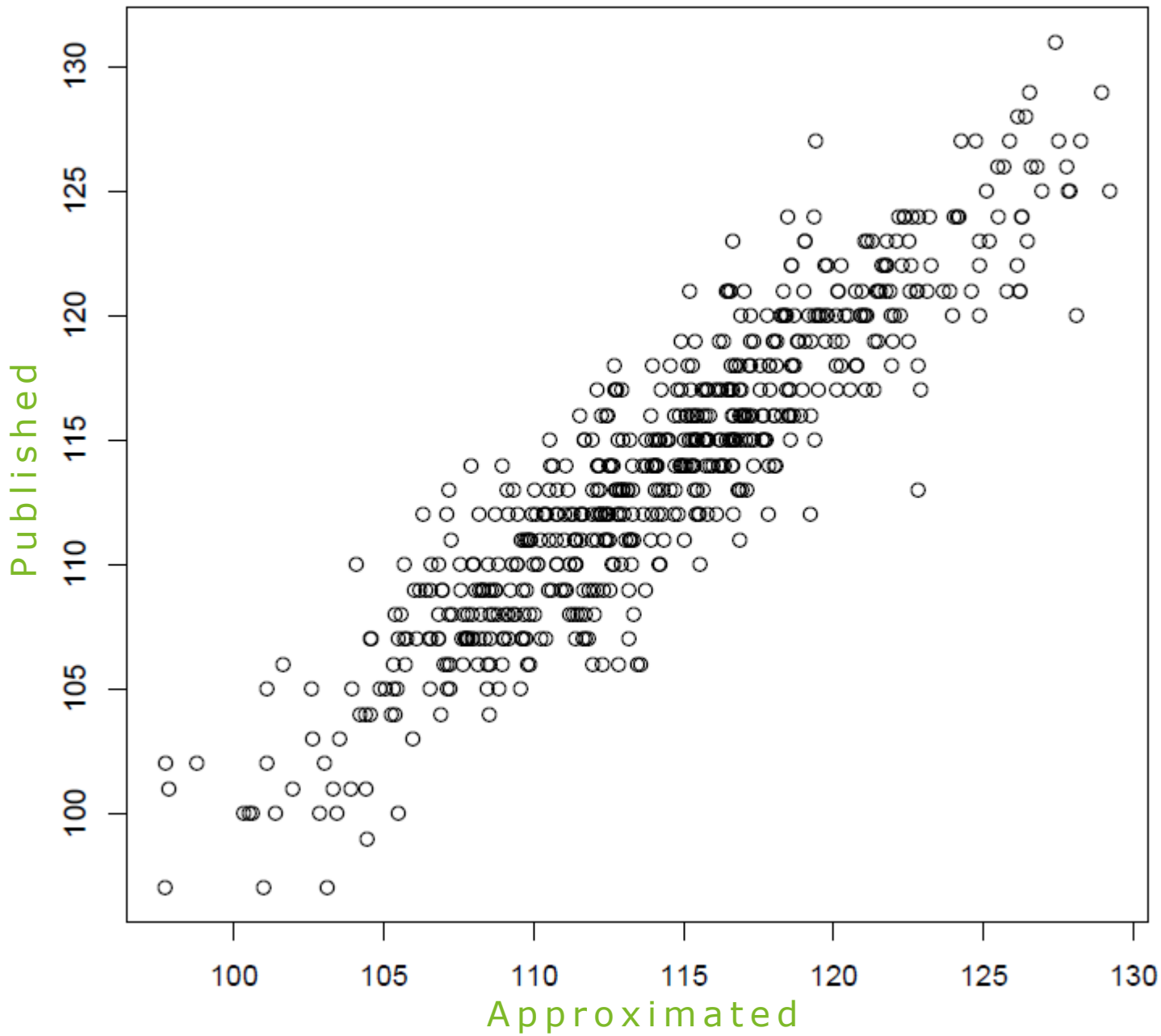
REESTIMATION RESULTS

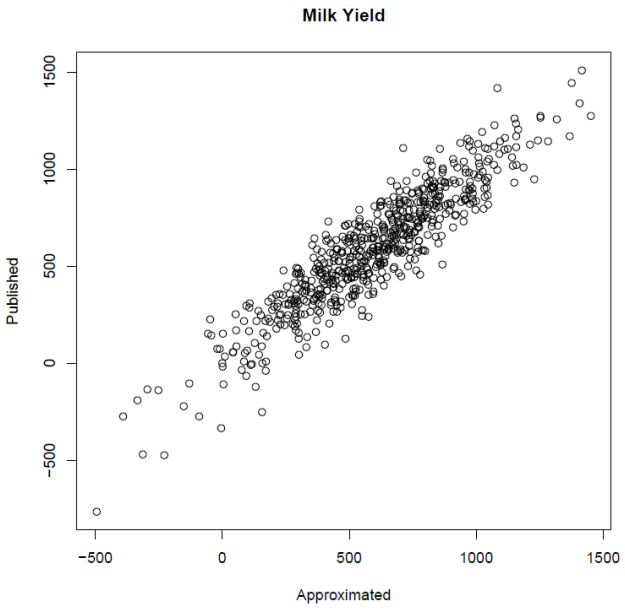
TRAITS	PUBLISHED	APPROXIMATED	RELATIVE DIFFERENCE (%)	CORRELATION
Milk yield	439.00±432.69	440.44±423.36	0.27	0.99
Fat yield	16.91±16.52	16.95±16.23	0.23	0.99
Fat percentage	-0.01±0.19	-0.01±0.19	0.00	0.99
Protein yield	13.20±14.11	13.27±13.78	0.44	0.99
Protein percentage	-0.02±0.10	-0.02±0.10	0.00	0.99
Somatic cell score	103.18±11.77	102.79±11.61	3.90	0.99
Longevity	105.03±9.50	104.71±9.49	3.20	0.99
Direct calving ease	100.05±8.29	99.99±8.22	0.60	0.99
Maternal calving ease	102.25±10.45	102.28±10.33	0.30	0.99

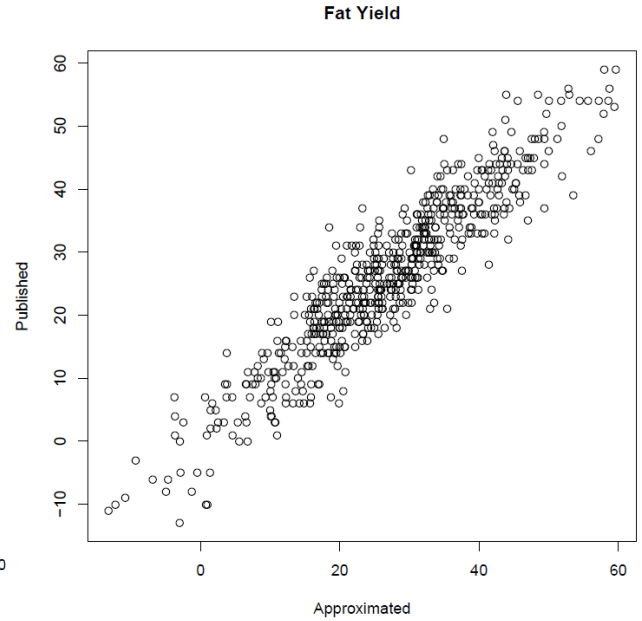
VALIDATION RESULTS

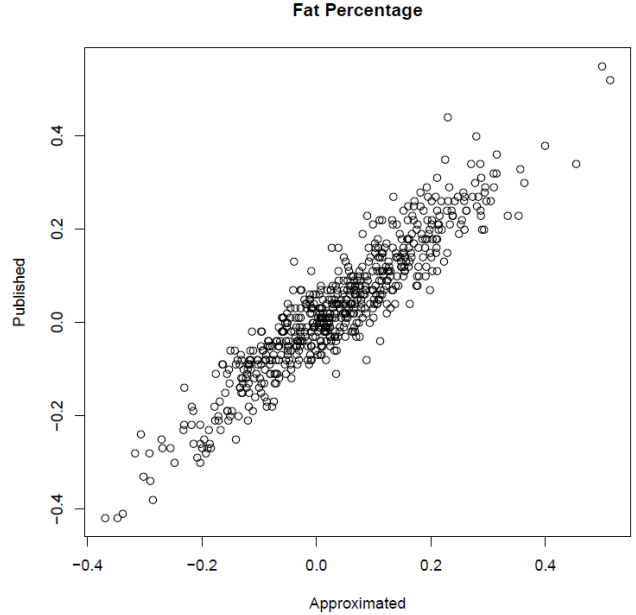
TRAITS	PUBLISHED	APPROXIMATED	RELATIVE DIFFERENCE (%)	CORRELATION
Milk yield	593.20±311.16	595.52±301.71	0.43	0.92
Fat yield	26.10±13.00	26.60±12.88	2.82	0.93
Fat percentage	0.03±0.14	0.04±0.13	0.05	0.93
Protein yield	19.98±10.65	20.27±10.08	1.81	0.93
Protein percentage	-0.01±0.09	-0.01±0.07	0.01	0.94
Somatic cell score	109.52±8.56	109.84±8.59	3.20	0.91
Longevity	113.81±5.97	114.22±5.88	4.10	0.91
Direct calving ease	103.18±6.32	102.66±6.23	5.20	0.94
Maternal calving ease	110.20±8.14	110.79±7.82	5.90	0.94

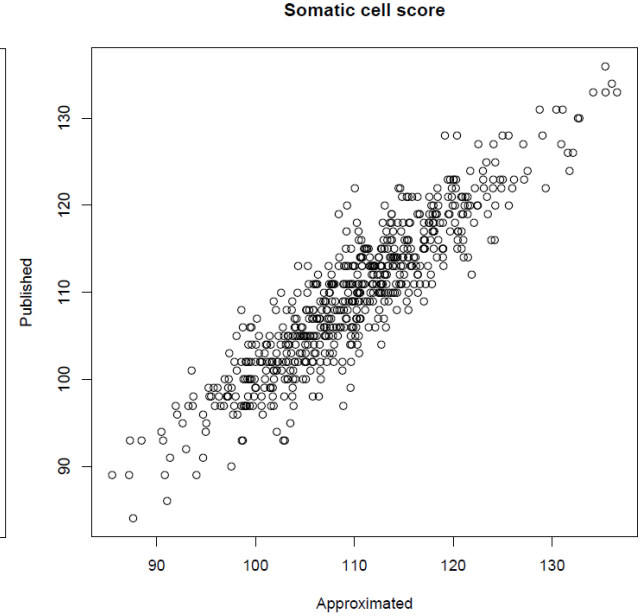
Longevity

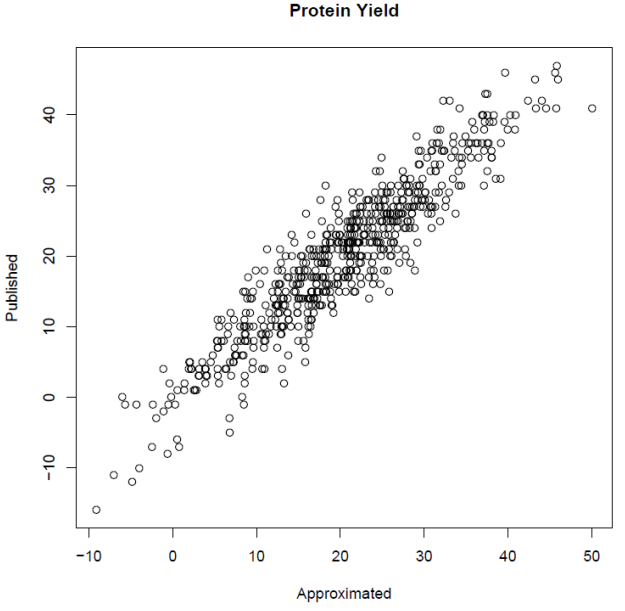

Published
100
105
110
115
120
125
130
Approximated
100
105
110
115
120
125
130

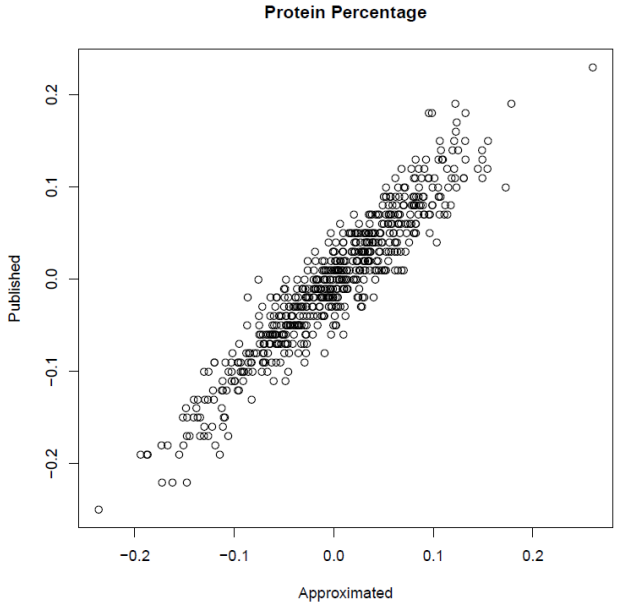

Milk Yield
Published
Approximated
−500
0
500
1000
1500


Fat Yield
Published
Approximated
−10
0
10
20
30
40
50
60


Fat Percentage
Published
Approximated
−0.4
−0.2
0.0
0.2
0.4


Somatic cell score
Published
Approximated
90
100
110
120
130


Protein Yield
Published
Approximated
−10
0
10
20
30
40
50


Protein Percentage
Published
Approximated
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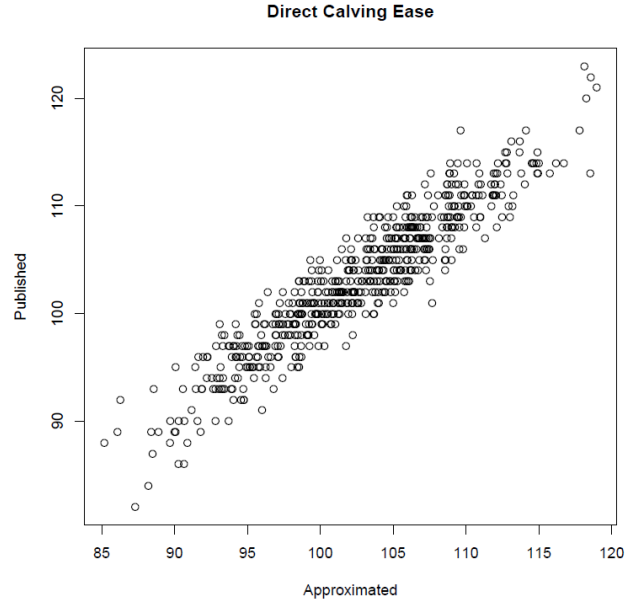
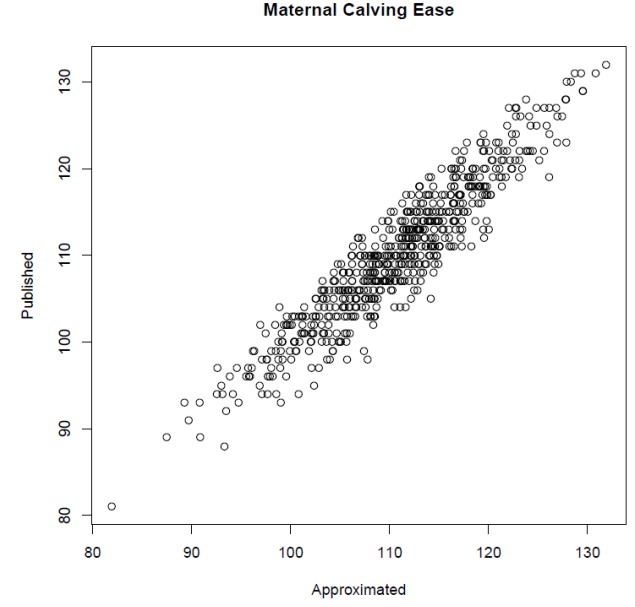
−0.1
0.0
0.1
0.2


Direct Calving Ease
Published
Approximated
85
90
95
100
105
110
115
120


Maternal Calving Ease
Published
Approximated
80
90
100
110
120
130

NEXT STEPS

1. Develop a core, high quality, “stable” reference population
2. Generate high quality SNP effects to estimate DGV
3. Generate appropriate GEBV for non-reference population animals
4. Efforts to generate REL based on the approach promoted by INTERBULL

ACKNOWLEDGEMENTS

LIÈGE université Gembloux Agro-Bio Tech

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Wallonie Bruxelles international WBI

GPLUSE Genotype plus Environment Integration for a more sustainable dairy production system

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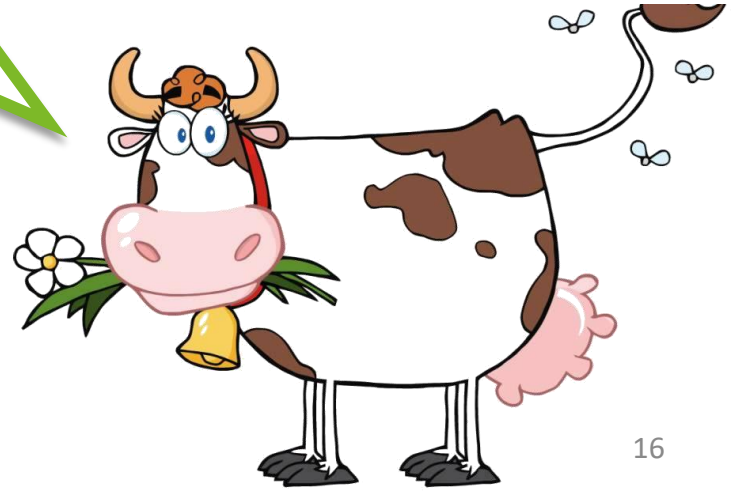

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