GMACE Pilot #4: Adjusting the National Reliability Input Data

P. G. Sullivan[1] and J. H. Jakobsen[2]
[1]Canadian Dairy Network, Guelph, ON, Canada
[2]Interbull Centre, Box 7023, SE-750 07 Uppsala, Sweden

Abstract

International standards do not exist for the approximation of national genomic reliabilities, which are used as input data for the GMACE international genomic evaluation system. The focuses of the present study were to develop a method of reducing differences among the national reliabilities approximated by different countries, to apply GMACE using modified national reliabilities, and to use cross-validations tests to determine if GMACE results could be measurably improved. A non-linear international regression model was applied to the average national reliabilities provided by countries for use in GMACE. Residuals of prediction for the average national reliabilities were smaller, indicating greater consistency among the approximations of different countries, for protein and stature relative to traits more difficult to evaluate, such as mastitis, stillbirths and cow conception rate. GMACE input reliabilities were modified by subtracting either some or all of the average prediction error for each combination of trait by country. The impacts of modifying the national reliabilities on GMACE results were relatively small. Predictability of national genomic evaluations by GMACE with only foreign genomic data as input, was essentially the same using either modified or unmodified national reliabilities. However, the international reliabilities produced by GMACE were more consistent if national reliabilities were modified as input and then the modifications were reversed for the GMACE reliability output. The approach was to essentially apply an international standardization of reliability on the way into GMACE and then a de-standardization back to each of the original national scales of expression on the way out.

Key words: genomics, international evaluation, GMACE, reliability, cross-validation

Introduction

Genomic variance estimates are a function of Mendelian sampling predictions and the corresponding reliabilities (Sullivan & Jakobsen, 2012). A bias in the estimation of national genomic reliabilities can directly impact genomic variance estimates and subsequent bull rankings from GMACE. A working group has been formed to review approximation methods for national genomic reliabilities. Currently there is no standard methodology to ensure consistency among the countries.

In a recent study (presented in Nantes, 2013) we quantified the potential impacts of biased input reliabilities on genomic variances and GMACE predictions, by simulating reliability biases. Using an international regression of the average reliabilities provided by countries, we derived expected values for the average reliability of each trait and country, then assumed deviations from expectation were biases. This is not strictly true, but allowed for a sensitivity analysis of the effects of changing input reliabilities on GMACE results.

The present study focused on which reliabilities should be used for GMACE in practice. The first objective was to refine the reliability predictions and regression of national reliabilities toward a globally standardized set of expectations. The second objective was to study the merits of using predicted (fully regressed) reliabilities, partially regressed reliabilities, or the provided (not regressed) reliabilities in GMACE. Cross-validation tests were used to compare the different approaches.

Material and Methods

Eleven countries participated with young bull GEBV data for as many as 37 different traits for the GMACE implementation run in

December 2013. These countries were Australia (AUS), Canada (CAN), Switzerland Red Holstein (CHR), Germany (DEU), Denmark-Finland-Sweden (DFS), France (FRA), Great Britain (GBR), Italy (ITA), the Netherlands (NLD), Poland (POL), and the United States (USA). Data were edited for variance estimation to minimize selection bias, by including only young GEBV bulls born between December 2008 and November 2011, without a classical MACE proof, and with sire and MGS having a MACE proof. This time interval was chosen to balance the goals of a sufficiently large variance estimation data set, minimal within-year selection bias, and the current population of young genomically tested bulls with no progeny.

Reliabilities are bounded between 0 and 100%, and increase at a decreasing rate. Thus, a non-linear model of prediction was used:

$$\exp(\overline{Grel_n}) = trait + b\sum rel\_loc + c\sum rel\_for + e$$

The predicted reliability was equal to:

$$\overline{Grel_p} = \log(trait + b\sum rel\_loc + c\sum rel\_for),$$

and the average difference between provided and predicted national genomic reliability was computed as: $res = \overline{Grel_n} - \overline{Grel_p}$. For individuals: $Grel_p = Grel_n - res$. The $\overline{Greln}$ was an average of the national genomic reliabilities for bulls born between August 2008 to July 2011. Traits in the prediction model included 37 of the usual MACE traits, but for the present report we show results for only six of the traits: protein (pro), stature (sta), somatic cell score (scs), mastitis (mas), direct stillbirth (dsb) and cow conception 1 (cc1). The $\sum rel\_loc$ was the sum of reliabilities for the local reference population, which were bulls with a national EBV submitted to MACE for the given trait, and coded as a reference bull for protein in the country's GenoList file provided to Interbull. The $\sum rel\_for$ was the sum of MACE reliabilities for the foreign reference population, which were bulls with a MACE proof based on only foreign EBV for the given trait, and coded as a reference bull for protein in the country's GenoList file.

The models being compared are summarized in Table 1. Model G, which was denoted as model rGM_ms(v) in Sullivan & Jakobsen (2012), was the operational model used by Interbull prior to the present study. Model GP used predicted (i.e. fully-regressed) reliabilities as input rather than the individual reliabilities provided by the countries. Using a different set of national reliabilities as input affects both the GMACE variance estimates used for scaling, and the relative weighting of national genomic evaluations when a bull has been evaluated in more than one country.

Table 1. GMACE models of evaluation.

Model	Description
G	Current model in use for GMACE using provided reliability as input
GP	Model G using predicted reliability as input
GP.5	Input is a .5-regressed reliability (5*predicted + .5*provided)

Models GP.5 combines the ideas and merits of international standardization versus utilizing national expertise and customized information. Specific knowledge about the genomic evaluations customized by each country, including assumptions about polygenic variance, distributional properties of SNP, densities of SNP panels used for genotyping, number of SNP included for genomic evaluation, methods to blend SNP evaluations with EBV, etc. are considered in the $Grel_n$ provided by the countries, while differences in these factors are ignored in the predicted $Grel_p$. Thus an averaging of these two reliabilities is a fair compromise.

Table 2. Average genomic reliability ($\overline{Grel}$) and residual (*res*) by trait for Australia (AUS), Canada (CAN), Switzerland Red (CHR), Germany (DEU), Denmark-Finland-Sweden (DFS), France (FRA), Great Britain (GBR), Italy (ITA), The Netherlands (NLD), Poland (POL), and The United States (USA).

	Protein		Stature		Somatic Cell		Direct Stillbirth		Fertility CC1		Mastitis	
	$\overline{Grel}$	*res*	$\overline{Grel}$	*res*	$\overline{Grel}$	*res*	$\overline{Grel}$	*res*	$\overline{Grel}$	*res*	$\overline{Grel}$	*Res*
AUS	68.18	5.43	-	-	-	-	-	-	-	-	-	-
CAN	74.57	1.79	75.02	1.11	73.28	3.02	61.23	12.77	62.38	4.85	73.28	5.04
CHR	67.95	7.25	68.70	6.60	44.82	-13.74	-	-	66.86	18.72	44.82	-11.51
DEU	73.09	-3.47	71.04	-6.16	76.80	2.62	50.36	-3.35	44.92	-15.44	76.80	5.66
DFS	66.21	-5.69	74.02	0.87	67.23	-2.80	55.10	5.15	62.02	5.60	58.57	-7.58
FRA	70.56	-1.17	69.52	-3.58	68.28	-1.51	-	-	62.36	5.36	57.12	-5.54
GBR	63.12	-3.00	71.11	3.60	65.22	1.41	-	-	46.86	-4.97	65.22	3.57
ITA	74.00	4.01	72.54	1.27	71.87	4.21	-	-	-	-	71.87	6.25
NLD	66.15	-5.72	69.88	-3.64	71.37	1.36	31.07	-16.94	40.50	-16.96	59.82	-6.31
POL	64.78	2.52	63.96	0.23	65.02	4.80	-	-	-	-	65.02	6.99
USA	75.57	-1.29	76.27	0.29	72.12	-1.45	-	-	-	-	72.12	0.49

Cross-validation tests were conducted by country. Implied assumptions were that GMACE evaluations based on input data from only foreign scales were unbiased predictors of the excluded (i.e. cross-validated) national GEBVs for the given country, and that the national GEBV were also unbiased. Correlations and regressions of national GEBV on GMACE predictions were used as test statistics, but are not reported here. The main differences among models were in the relative scaling of evaluations between the different countries. To demonstrate these differences, we show estimates of Top Bull bias; the relative difference between a GMACE prediction of +3 standard deviations ($\boldsymbol{z} = \bar{X} + 3\sigma$) and the expected value for $\boldsymbol{z}$ based on cross-validation regression of national GEBV on GMACE: $\boldsymbol{w} = \hat{a} + \hat{b}x$, at the value $x = \boldsymbol{z}$. We define, as in Sullivan and Jakobsen (2012):

$$\text{TopBias} = 100\% * (\boldsymbol{z} - \boldsymbol{w}) / \boldsymbol{w}$$

Regression equations estimated with different levels of truncation selection on the x-variable (GMACE predictions) were similar, as expected, since regression estimates are not biased by selection on x. Therefore, to focus on key bulls of interest we used the regression equation for bulls with a GMACE prediction above +1σ to estimate TopBias (of a +3σ bull).

Results and Discussion

The average genomic reliability provided by countries and the differences from predicted reliability (*res*) are in Table 2. There was greater variation in *res* for the functional traits relative to protein and stature.

Modifying the reliability input had the expected impacts on genomic variance estimates (e.g. a decrease in reliability increased the variance estimate). Decreases in genomic variance estimates (lower gSD in

Table 3) caused decreases in values of TopBias (i.e. less positive or more negative), also as expected. There was, however, very little practical impact. The 95% confidence ranges across all countries were similar for the three models, and while there were individual cases of notable impact, there was no one model with consistently best results.

Routine GMACE uses GEBV input from all countries, and leads to reliabilities that are consistently equal or higher than the input reliabilities. With cross-validations, however, the local GEBV are not included as input, making it less likely for GMACE reliabilities to be higher than the national. In the present study, this was especially true when GMACE results were based on input data from only one foreign country, or from two countries from the same national consortium. When data were available from several foreign countries, however, the average reliability from GMACE was generally higher than the national reliability (Table 4). As approximate reliabilities these do not guarantee higher true reliabilities. However, it can be concluded that GMACE results should be more accurate for bulls genotyped in more countries and in multiple genomic consortia. Using predicted equations to modify the national reliability input data (GP.5 vs G) generally improved the consistency of output reliabilities, relative to national, for bulls from different consortia. For example, reliability differences for dsb and cc1 were much more similar between "A 0 1" and "B 0 1" with model GP.5. GMACE rankings from either G or GP.5 can be used to identify foreign bulls that are best candidates for local re-genotyping, or to target an expanded sharing of selected genotypes among more countries.

References

Sullivan, P.G. & Jakobsen, J.H. 2012. Robust GMACE for young bulls – methodology. *Interbull Bulletin 45,* 3-7.

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Table 3. Bias (as a % of local GEBV) in the GMACE prediction of a top (+3 standard deviation) bull, for selected countries and 95% confidence ranges (L95 to U95) across all countries[y].

Country (n - Protein)	Model	Protein		Stature		Somatic Cell		Direct Stillbirth		Fertility CC1[y]		Mastitis	
		gSD[z]	Bias	gSD	Bias	gSD	Bias	gSD	Bias	gSD	Bias	gSD	Bias
CAN (35708)	G	84	-3	83	-3	81	-2	101	39	85	1	81	-1
	GP.5	85	-3	83	-3	82	-1	109	43	90	1	83	0
	GP	87	-3	84	-2	83	0	123*	50	95	2	84	1
USA (38756)	G	93	1	97	-3	96	1					96	1
	GP.5	93	1	97	-3	94	0					95	0
	GP	93	0	97	-3	93	-1					94	0
NLD (5957)	G	107	6	117	8	103	7	277*	24	105	46	87	21
	GP.5	103	5	114	8	103	7	78*	19	80	33	82	18
	GP	99	4	112	8	103	7	67*	16	68*	39	77	18
FRA (13579)	G	93	3	104	7	102	15			96	33	109	13
	GP.5	93	3	101	7	100	14			101	36	103	9
	GP	92	3	99	7	98	13			107	40	97	6
DEU (14430)	G	118	8	118	6	121*	7	94	-12	130*	8	121*	0
	GP.5	116	7	114	5	122*	7	86	-13	109	1	123*	2
	GP	114	7	110	5	122*	8	81	-13	96	-6	126*	3
DFS (854)	G	121*	11	121*	11	127*	12	108	40	149*	11	130*	24
	GP.5	116	10	120	12	124*	13	110	44	158*	9	120	27
	GP	112	9	120	13	121*	13	114	50	168*	8	112	24
All Countries		L95	U95	L95	U95	L95	U95	L95	U95	L95	U95	L95	U95
Confidence Range of TopBias	G	-18	31	-4	14	-6	21	-27	71	-7	50	-11	31
	GP.5	-18	32	-5	15	-5	21	-33	75	-11	50	-10	29
	GP	-18	31	-5	15	-5	21	-38	81	-15	54	-9	28

[z]gSD is the genomic estimate of SD as a percentage of the genetic SD used for MACE.
[y]one country was excluded for cc1 due to an extreme bias > 250% for all models.
*gSD truncated in these cases to the edges of the range [80-120].

Table 4. Average genomic reliability differences: GMACE with only foreign data, minus national.

Data[z]	Protein		Stature		Somatic Cell		Direct Stillbirth		Fertility CC1		Mastitis	
	G	GP.5	G	GP.5	G	GP.5	G	GP.5	G	GP.5	G	GP.5
A 0 1	-16	-11	-8	-5	-6	-3	-23	-11	-23	-16	-10	-6
B 0 1	-14	-19	-5	-10	-10	-10	-5	-11	-7	-13	-9	-9
A 1 0	-10	-9	-4	-4	-8	-7			-19	-18	-8	-6
B 1 0	-12	-14	-4	-5	-5	-5	-6	-10	-14	-16	-13	-11
A 0 2	-12	-8	-5	-2	-2	-1	-22	-10	-17	-12	-1	1
B 0 2	-6	-9	3	0	-5	-5			-13	-12	-4	-5
A 2 0	-7	-6	-2	-1	-4	-3					-4	-3
B 2 0	-6	-8	-1	-1	-1	-1			-8	-8	-3	-3
A 1 1	-4	-3	3	3	1	1			-11	-11	-1	0
B 1 1	-5	-8	4	2	1	1	4	-2	-1	-4	-2	-3
A 2 2	0	1	5	6	4	4					5	6
B 2 2	3	2	9	8	6	6			2	1	7	6
A 3 2	2	2	5	6	6	7					9	9
A 3 3	3	3	6	6	8	8					9	10

[z]A (CAN, GBR, ITA, USA) and B (DEU, DFS, FRA, NLD) are the 2 main consortia that share data for national genomic evaluations. The numbers for "Data" that follow A|B are the number of foreign countries, with a GEBV included in GMACE for the bull, from the same and different consortia, respectively. For example, A 3 1 is the group of bulls with a GEBV from all 4 countries in consortia A and 1 country in consortia B.