Validation of genomic reliability and gains from phenotypic updates

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Topics

- **Methods to compute genomic reliability**

  – **Summarized by Liu et al (2017)**

  – **GREL compared by Sullivan and Jakobsen (2014)**

- **Simple validation of genomic reliability**

  – **Do actual EBV changes agree with published REL?**

  – **Examples from USA and Intergenomics**

- **Gains in reliability from more frequent updates**

  – **Similar math can determine the value of re-estimating marker effects more often**

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REL calculation vs. validation

- **REL estimation**

  - **Adjust theoretical REL such as from SNP-BLUP-REL or from size of reference population**

  - **Use prediction error variance (PEV) because correlations are biased downward by selection**

- **REL validation**

  - **Similar to validating EBVs using truncated data**

  - **Examine published REL for 6 traits and Net Merit**

  - **Examine 3 breeds (HOL, JER, BSW) on USA scale**

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Genomic reliability theory

- **Selection reduces variance such that Var(EBV) < REL * Var(BV), but not prediction error variances (PEV):**

- **PEV = Var(EBV − BV) = (1 − REL) Var(BV)**

- **Variance of EBV differences are proportional to the difference in reliabilities regardless of selection. If EBV_1 and EBV_2 are earlier and later genomic evaluations with reliabilities REL_1 and REL_2, then**

- **$Var(EBV_2 − EBV_1) = (REL_2 − REL_1) Var(BV)$**

- **If REL_2 is known, high, and accurate, then solve for**

- **$REL_1 = REL_2 − Var(EBV_2 − EBV_1) / Var(BV)$**

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Data to validate genomic reliability

- **Published genomic evaluations from April 2014**

- **Published genomic evaluations from April 2017**

- **SD of difference in genomic PTAs**

- **REML estimates of true TA SD from Interbull MACE**

- **Example for Holstein protein validation bulls:**

- **Average published REL_1 was 0.76, REL_2 was 0.95, SD of change was 8.4, and REML TA SD was 17.5. The observed REL_1 for protein was calculated as**

- **Observed $REL_1 = 0.95 - (8.4)^2 / (17.5)^2 = 0.72$**

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Observed vs. published reliability, 2014

Trait	Observed	Published	Diff	Observed	Published	Diff
		Jerseys			Holsteins	
Milk	73	68	+5	72	76	-4
Fat	72	68	+4	74	76	-2
Protein	71	68	+3	72	76	-4
Longevity	47	55	-8	65	70	-5
SCS	64	62	+2	77	73	+4
Preg Rate	63	52	+11	69	68	+1
NetMerit	68	64	+4	68	73	-5
Average	65	62	+3	71	73	-2

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Observed vs. published reliability, BSW

| Trait	Observed	Published	Diff	Observed	Published	Diff
	Brown Swiss - USA			BSW - Intergenomics		
Milk	62	63	-1	70	68	+2
Fat	64	63	+1	76	68	+8
Protein	57	63	-6	66	68	-2
Longevity	57	55	+2	63	61	+2
SCS	64	59	+6	71	66	+5
Preg Rate	56	51	+5	67	58	+9
Average	60	59	+1	69	65	+4

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Discussion of BSW results

- Same software used by USA and Intergenomics

- Same data except PA in USA vs. Pedigree Index in IG

    – Bias from dam's PTA and extra weight on PA

    – Yield heritability reduced from 35% to 23% in Dec 2014

- Small test used only 41 bulls with > 50 US daughters

- Full test with all 475 IG bulls gave observed REL much more similar because USA and IG both have only PI for foreign MACE bulls

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Phenotypic update frequency

- **Suppose reliability increases steadily from REL_1 to REL_2 across a year.**

- **The gain in reliability from n updates per year (REL_n) instead of 1 annual update should average:**

- **$REL_n = .5 (REL_2 - REL_1) (n - 1) / n$**

- **Suppose bulls increase from 75% REL_1 to 91% REL_2 when 4 years old (no daughters to many daughters).**

- **Minimum gain is 0% with an annual update because the bulls would stay at 75% for the whole year.**

- **Maximum gain is 8% with instant updating. Bulls would average (75 + 91)/2 = 83% during that year.**

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HOL NM$ average reliability by age

Phenotypic update frequency

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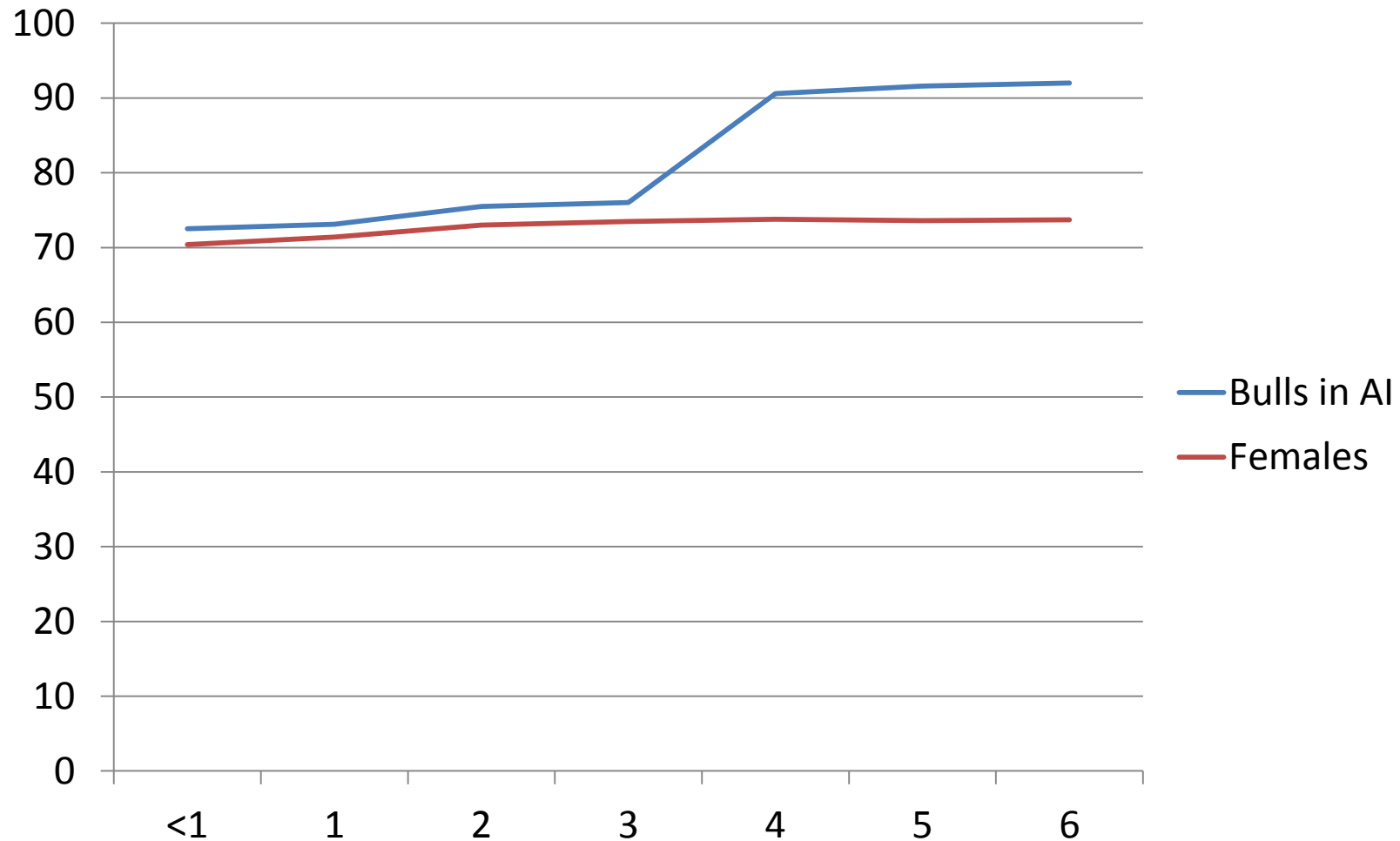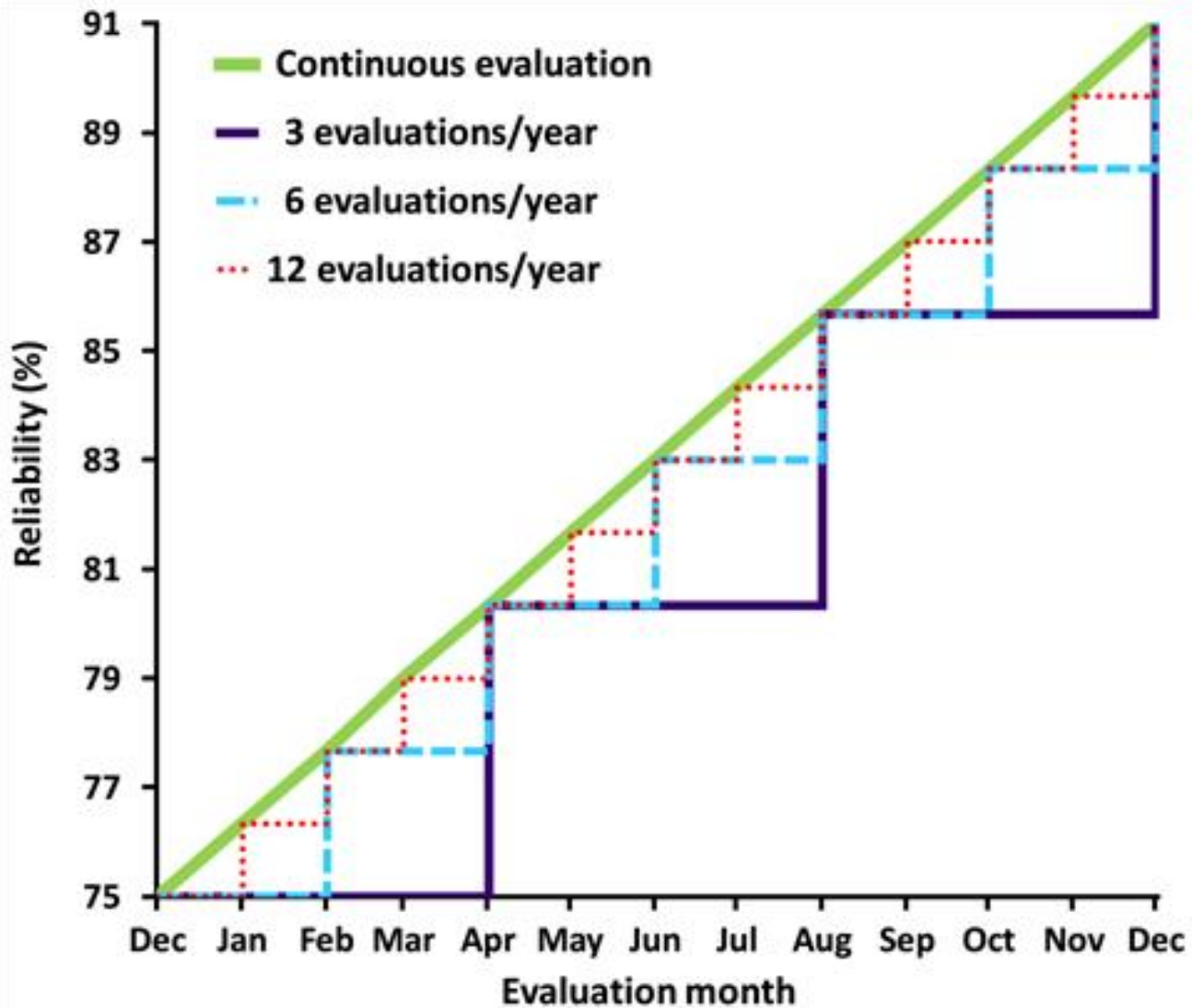
Reliability gains by update frequency

Frequency	Updates	Young REL	Marginal Gain	Proven REL	Marginal Gain
Annual	1	73.0		75.0	
6 months	2	73.5	0.5	79.0	4.0
4 months	3	73.7	0.2	80.3	1.3
3 months	4	73.8	0.1	81.0	0.7
2 months	6	73.83	0.03	81.6	0.6
Monthly	12	73.92	0.09	82.3	0.7
Weekly	52	73.98	0.06	82.8	0.5
Daily	365	73.99	0.01	82.97	0.17
Instant	∞	74.0	0.01	83.0	0.03

Assuming that REL begins at 75% and is 91% 1 year later for proven bulls and begins at 73% and is 75% 1 year later for young bulls.

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Conclusions

- **Exact calculation of genomic reliability is hard, but validation is easy**

- **Published USA REL averaged 2% too high for HOL, 3% too low for JER, and 1% too low for BSW**

- **Published Intergenomics REL averaged 4% too low for BSW traits because observed REL were higher**

- **Updating marker effects more frequently than 3 times per year could improve average REL up to 2.5% for recently proven bulls but < 0.3% for young animals**

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