

Implementation of genomic breeding values for novel traits such as feed efficiency through female nucleus reference populations

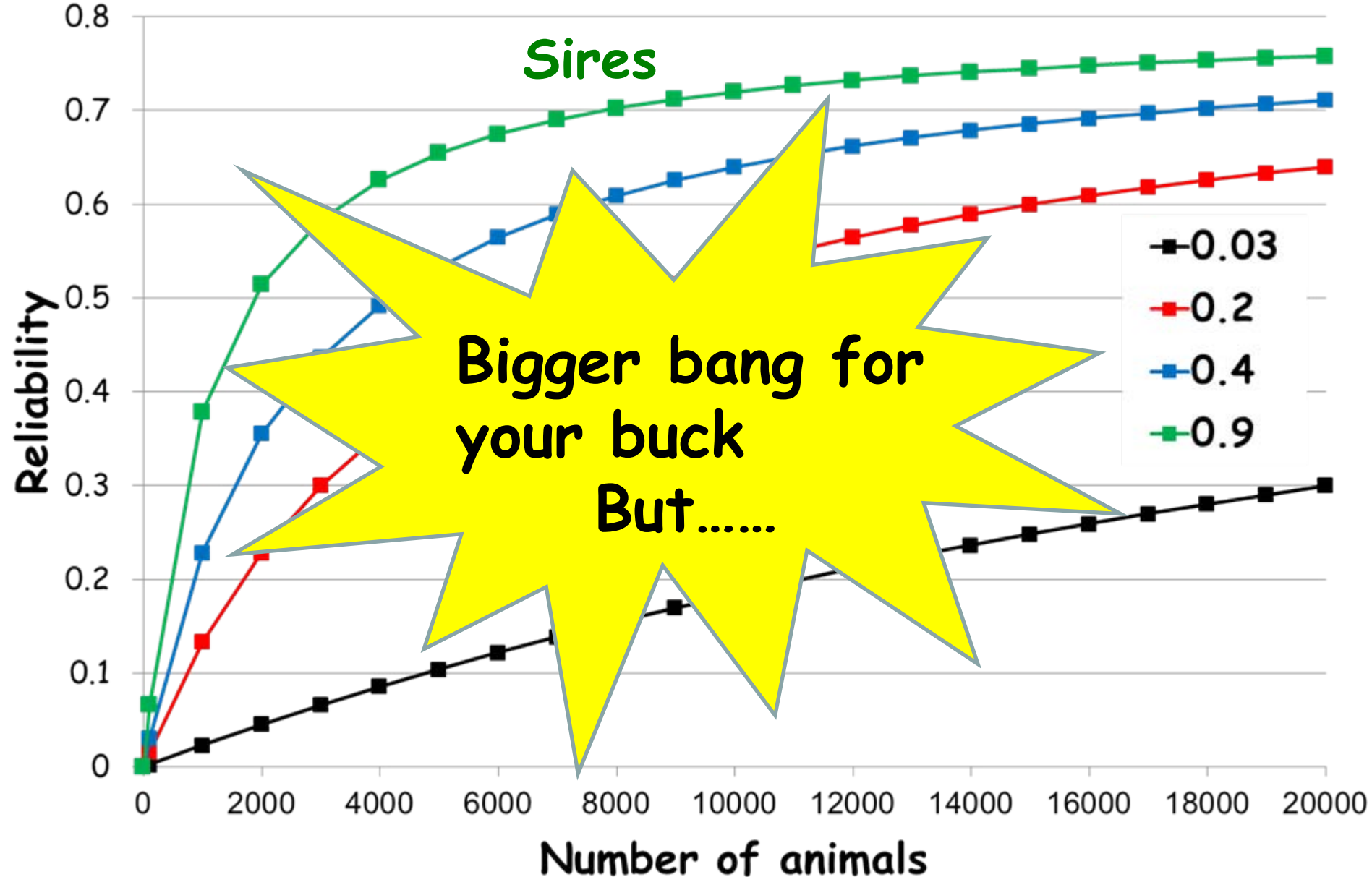
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Accuracy of genomic evaluations



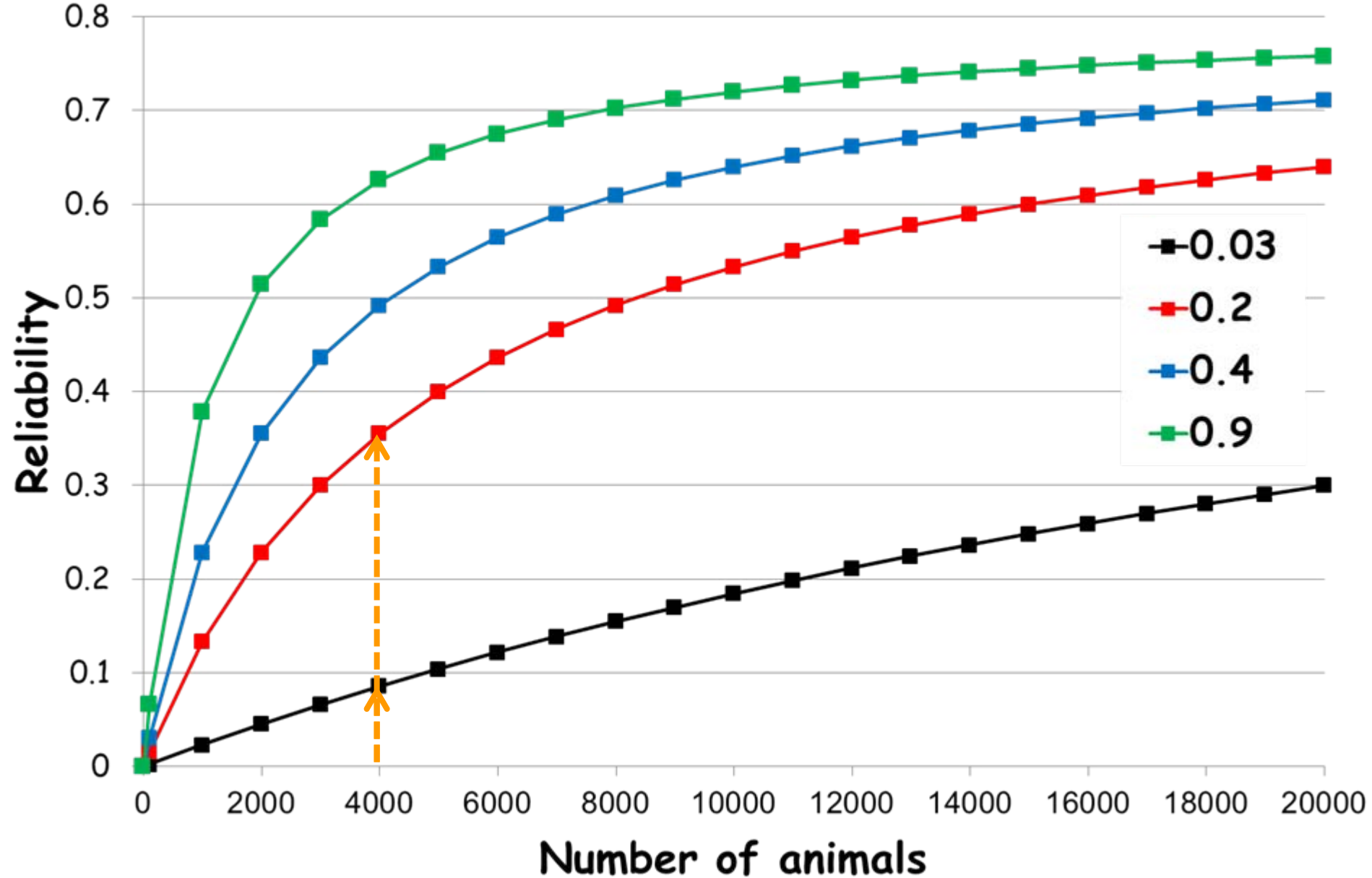
Limitations of bulls

1. A finite (slow growing) number of AI bulls
 - May be low AI usage (beef)
 - Natural mating bulls
2. High reliability bulls are usually elite
 - Need the good, the bad, and the ugly!
3. Limited to routinely recorded traits
 - Novel traits
4. Non-additive genetic effects
 - Intra- and inter-locus interactions

Considerations

1. What population size is required
2. Marginal benefit
 - Accuracy and economic benefit
3. Herd/animal selection

1. Population size required



1. Population size required

- theory v practice

1. Cost of phenotype procurement

2. Min reliability thresholds for publication

- LIC, NZ publish $EBV_{RFI} \sim 0.10$
- Re-consideration?

3. Bull selection risk management

- Bull teams

$$\text{Team Reliability}_{\text{UNREL}} = 1 - \left(\frac{1 - \overline{\text{rel}}}{n} \right)$$

$$\text{Team reliability}_{\text{HS}} = 1 - \left(\frac{n + 3}{4n} + \frac{\overline{\text{rel}} + (n - 1)\text{rel}_{\text{SIRE}}/4}{n} \right)$$

2. Marginal benefit

- Is there an easier & less expensive approach??
- What is the cost:benefit
 - May need to take cognisance of societal value
- Milk quality and milk infra-red spectroscopy (MIR)
 - Fatty acids gold standard: ~€70
 - MIR (98% accuracy for saturated fat): “free”
- Feed intake & MIR + pedometers

3. Herd selection

- Management representative of where the genetics will be used
- Genetics representative of candidate population
- Good data recording
 - Within-herd heritability
 - Contemporary group sizes
 - The good, the bad and the ugly
 - The young (long-term) and the old (short-term)

Cow selection procedure

1. Considerable genomic/genetic diversity within the reference population
 - Related to the candidate population
2. Phenotypic diversity

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Genomic selection: the option for new robustness traits?

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Australia - dairy

- 10,000 Holstein cows + 4000 Jersey cows
- Cows with multiple lactations favoured
- 4-8% improvement in reliability of genomic proofs
- 100 Ginfo herds
 - Selected on contribution of data to ADHIS
 - Genotypes on around 30k cows by June 2015
 - Designed to be an on-going reference population

Ireland - beef

- Little AI
- ~100,000 cows + 20,000 natural mating bulls
- Genotype 15% of herd
- Ensure minority breeds represented, first lactation cows, cow rank
 - 66% data quantity : 33% phenotypic diversity
 - Genomic/genetic diversity - no requirement for sire known

Ireland - beef

- Data quantity
 - Milk yield 5, fertility, 4, calving difficulty 1, carcass traits 1
 - Within a contemporary group
 - Maximum credit of 3 lactations
- Phenotypic diversity
 - Residual from the (fixed effects in the) genetic evaluation model
 - Included mate's direct genetic effects for milk yield and calving difficulty

International reference populations

- Many novel traits are expensive to measure (e.g., feed intake)
- Global Holstein breed has a small effective population size
- Individual country datasets of insufficient size to generate accurate genomic proofs
- Combined phenotypes and genotypes and account for genotype by environment interaction

International reference populations



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International genetic evaluations for feed intake in dairy cattle through the collation of data from multiple sources

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- **224,174 feed intake records**
 - 10,061 parity 1 to 5 records
 - 6,953 cows
 - +1,784 growing heifers
 - 9 countries



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Imputation of genotypes from low density (50,000 markers) to high density (700,000 markers) of cows from research herds in Europe, North America, and Australasia using 2 reference populations

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Conclusions

- Genomics will increase genetic gain
- What is the impact on other (non-recorded) traits?

- Cost sharing through international collaboration
 - Genotypes
 - Phenotypes
 - Ideas