

# Genomic reliability algorithm for a single step marker model

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# Outline

- Brief method outline
- Multi-breed adjustments
- Computational feasibility
- Results for 2 traits and 2 SNP panels
- Conclusions

# Method Outline

1. Build SNP marker MME and invert
2. Compute reliability for the genotyped animals and adjust for prediction  $R^2$  :  $Rel_g$
3. Compute reliability from using information source (IS) method:
  1. using only phenotypes of genotyped animals  $Rel_{ag}$
  2. using only phenotypes of non-genotyped animals:  $Rel_{ug}$
  3. using all phenotypes – when fitting a polygenic effect:  $Rel_a$

# Method Outline

- 4 . Compute reliability from genomics ( $Rel_g$ ) over and above pedigree and propagate through the entire pedigree (without updating the genotyped animals):  $Rel_{gg}$
- 5 . Compute total reliability ( $Rel_t$ )
  1. Genotyped animals: Combine  $Rel_g$  and  $Rel_{ug}$
  2. Non-genotyped animals: Combine  $Rel_{gg}$  and  $Rel_a$
- 6 . If fitting an polygenic effect in the model weight  $Rel_t$  and  $Rel_a$  by the proportions of total genetic variance assigned to the marker and polygenic effect

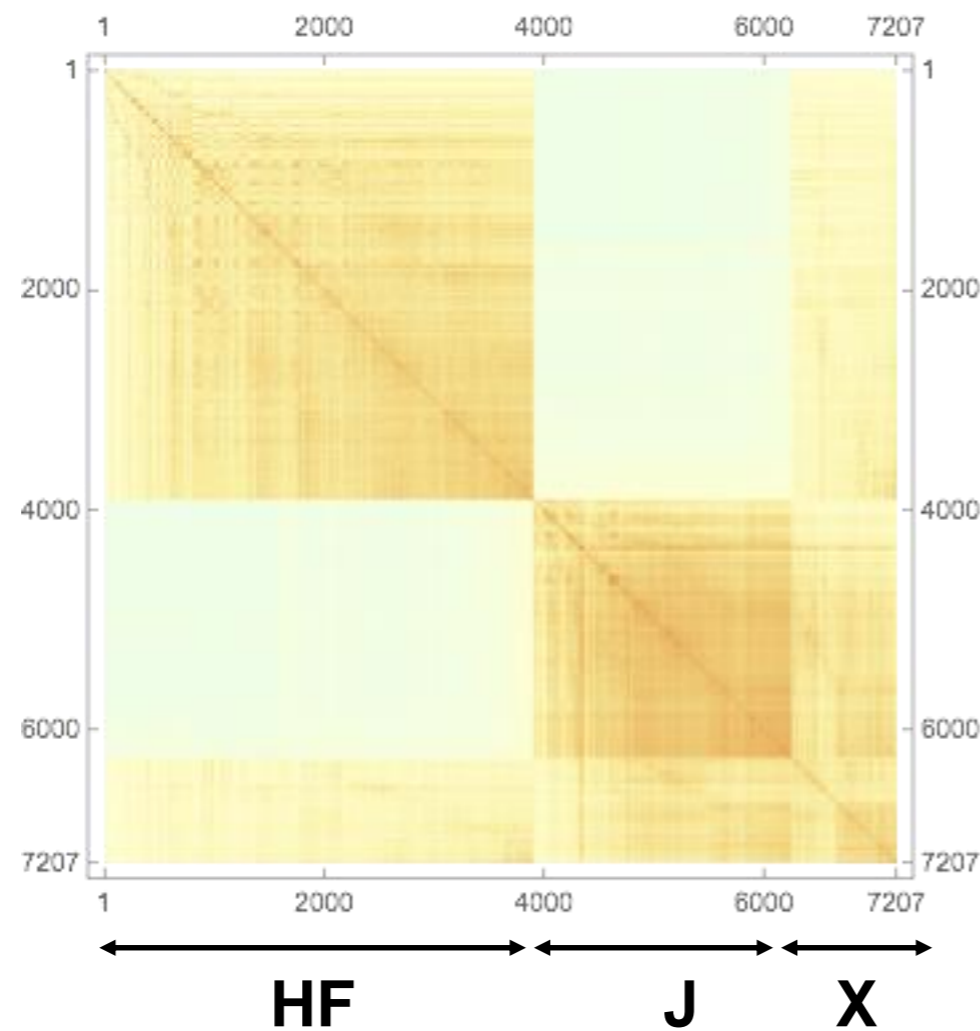
# Multiple breeds

- New Zealand
  - Mixture of Holstein Friesian, Jersey and crossbred animals (HFxJ)
  - SNP allele frequencies differ between the Holstein Friesian and Jersey breeds
  - Potentially impact the SNP marker reliability calculations

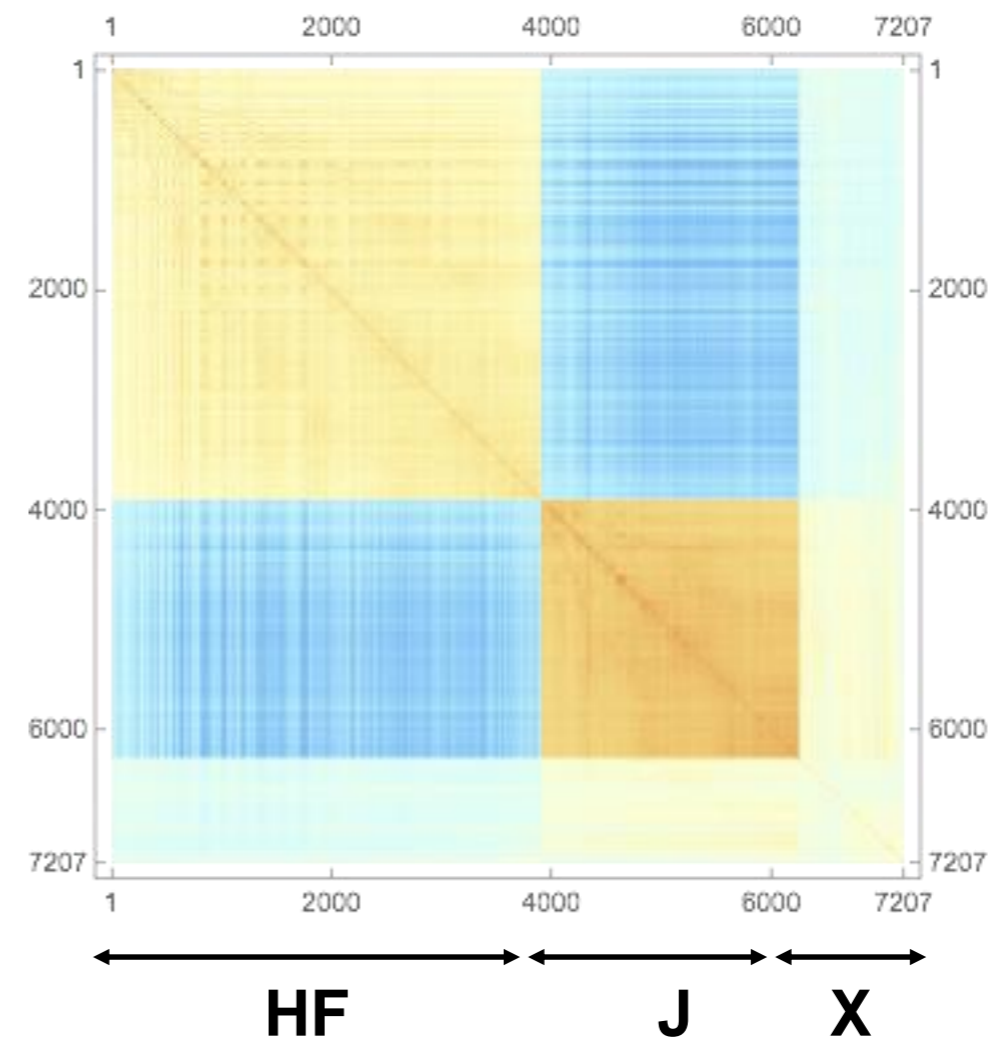
# Multiple breeds

- 7207 Sires with 3902 HF, 2356 J and 949 HFxJ
- 50k SNP panel (35k SNP)

**A Matrix**



**G Matrix**

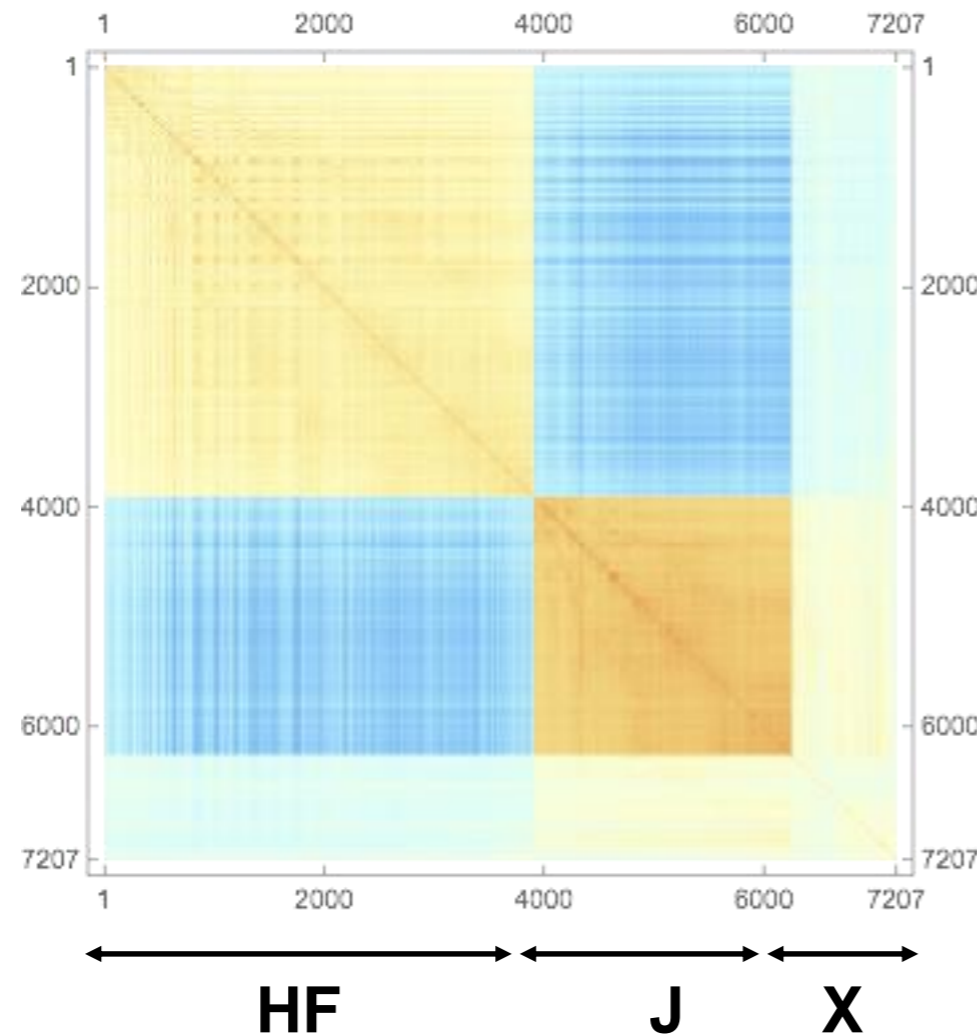


# Multiple breeds

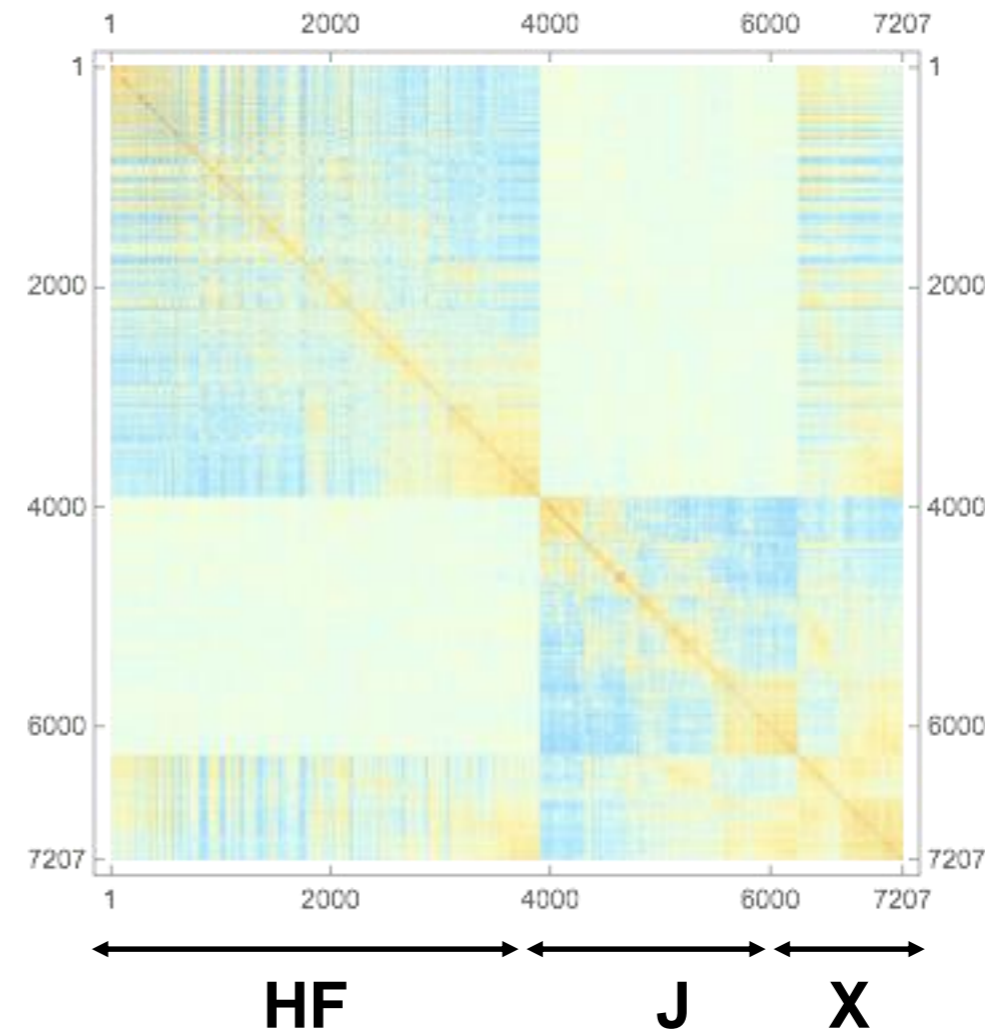
- Compute  $\mathbf{Z}$  as

$$(\mathbf{M}_i - 2\hat{p})/\hat{\omega} \text{ where } \hat{\omega} = \sqrt{2\Sigma\hat{p}(1 - \hat{p})} \text{ and } \hat{p} = \sum_{j=1}^m brd_j\bar{p}_j$$

**G Matrix**



**Breed Adjusted G Matrix**



# Examples

- New Zealand national population 29m animals
  - Dataset 1: 35K SNP on 140K animals
  - Dataset 2: 24K SNP on 70K animals (genotypes up to 2015)
  - 2 Traits
    - Liveweight  $h^2 = 0.35$ , 1.9m records
    - Fertility  $h^2 = 0.025$ , 16.4m records
- Prediction  $R^2$  adjustment was set to 0.85



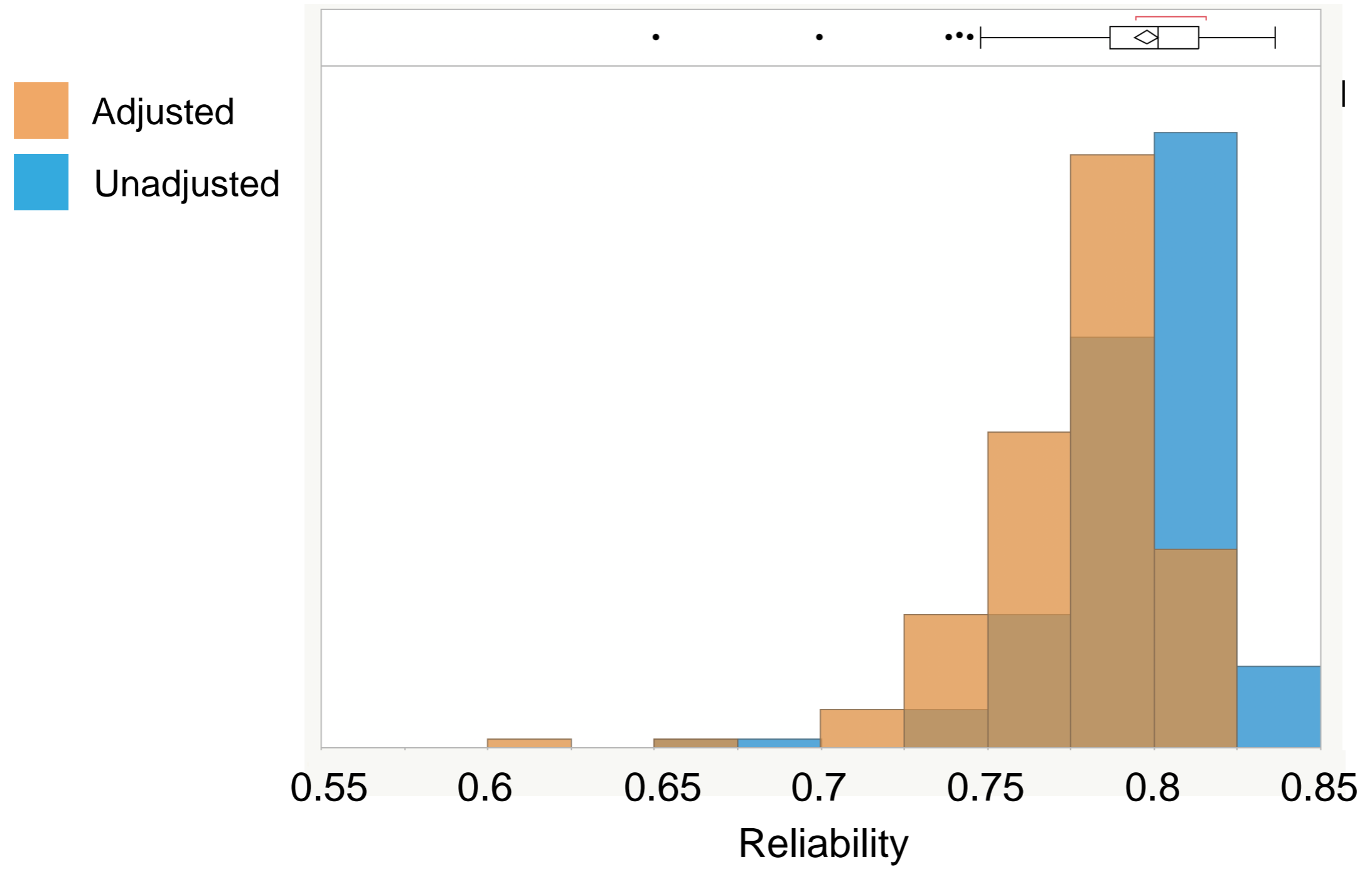
# Multiple breeds

- Results of breed adjustments on SNP reliability for live weight
  - Last three sire birth year cohorts with no daughters
  - Similar results observed for fertility

Young Sires	A Matrix	35k SNP and 140K N	
		SNP	SNP breed adjusted
Holstein Friesian	0.34	0.73	0.73
Jersey	0.37	0.80	0.77
HF x J	0.34	0.75	0.75

# Multiple breeds

## Reliability distributions for Jersey



# Computation Time

	35K SNP 140K Genotypes	24k SNP 70K Genotypes
Breed Adjustment	19m:12s	6m:16s
SNP Reliability	61m:39s	15m:40s
Reliability all animals	0m:58s	0m:55s
Total	81m:41s	22m:51s

# Computation Time

24 Cores Simultaneously

- SNP Reliability
- Inverse of SNP equations
- Direct computation of the individual animal reliabilities from the SNP  
 $(\mathbf{ZC}^{22}\mathbf{Z}')_{ii}$
- Iterative computation of the individual animal reliabilities from the SNP  
 $\mathbf{z}_i\mathbf{C}^{22}\mathbf{z}'_i$

35k SNP 140k N	24k SNP 70k N
4m:10s	1m:24s
44m33s	10m:17s
106m15s	29m:55s

# Results Liveweight

		35K SNP 140K N	24k SNP 70K N
Proven Sires	A Matrix	0.85	0.85
	Genomic	0.88	0.87
Young Sires	A Matrix	0.34	0.34
	Genomic	0.62	0.42

# Results Fertility

		35K SNP 140K N	24k SNP 70K N
Proven Sires	A Matrix	0.56	0.56
	Genomic	0.61	0.62
Young Sires	A Matrix	0.28	0.28
	Genomic	0.39	0.34

# Conclusions

- Method is computational feasible for our national data set
- For very large numbers of genotyped animals computing in individual reliabilities  $(\mathbf{ZC}^{22}\mathbf{Z}')_{ii}$  from the marker model inversion may be problematic

# Conclusions

- In multi-breed genomic analysis adjusting the SNPs for breed mean and variance appears to be useful in avoiding reliability discrepancies caused by breed SNP frequency differences



# Conclusions

- The method provides sensible reliabilities for the examples provided for this talk
- The method provides a way to incorporate genomic reliabilities for non-genotyped animals

Post-Doc Position available at Livestock Improvement  
NZ in genomic evaluation

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