

Estimation of the Proportion of Genetic Variation Accounted for by DNA Tests

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et al.

Introduction

Validation of DNA Test

Yes/No: Does it work?

Emphasis on statistical significance

Proportion of Additive Genetic Variation
Accounted for by Test

Continuous measure of how well it works:
0 - 100%

Analyses estimate parameters necessary to
incorporate test info into NCE

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Technical

R_g = genetic correlation between MBV and trait

R_g^2 = proportion of additive genetic variance
accounted for by knowing MBV

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Aside

Details!!!!!!!!!!!!!!

See the proceedings paper

First part for statistically inclined

Last part includes ruminations on what it
all means (in layman's terms)

Will not attempt details today

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Technical: Estimators

1. Multiple trait model
MBV is indicator trait
2. Reduction in Sire Variance
Est. sire variance with & w/o adjusting for
MBV
3. Regression of Phenotype on MBV
Sort of like procedure of genomics
companies

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Technical: Estimators

1. Multiple trait model
2. Reduction in Sire Variance
3. Regression of Phenotype on MBV

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Technical: Simulation

Population: 100 sires w/ 10 prog./sire in 20 CG
 Heritability of trait: 0.1, 0.3, 0.5
 % of variation accounted for by MBV:
 4%, 16%, 36%, 64%
 500 replicates/combination
 Also duplicated for "MBV" which included non-additive effects (see proceedings)

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Technical: Results

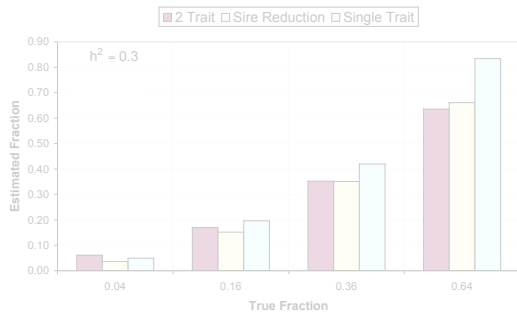
Example

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Fraction of Genetic Variance Accounted for by MBV

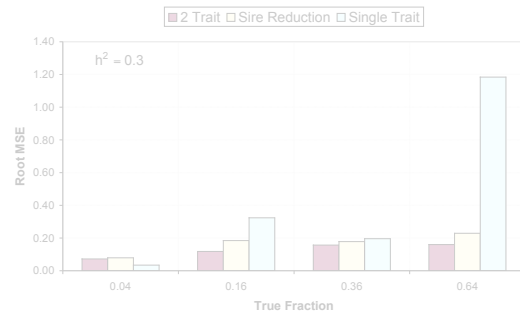


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Root MSE of Estimator



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Conclusions

All estimators performed similarly on average
 None were very precise at low h^2

Two trait model method more robust and is method of choice to estimate R_g^2

Used in Australia:

www.beefcra.com.au/aus-beef-dna-results

R_g^2 will be reported in future NBCEC "validations"

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