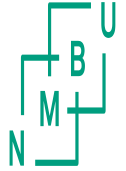


Linkage analysis based genomic relationships for optimum contribution selection



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Optimum Contribution sel¹

- Manages inbreeding
- Requires:

Genomic relationships:

- Calculated in many ways
- GRM => $F_{\text{hom}} \uparrow^2$
- Molecular Coanc.: $F_{\text{drift}} \uparrow$
- Linkage analysis G_{la} :
 - manages F_{hom} & F_{drift}
 - But computing $\uparrow \uparrow$

AIM:

Algorithm for large scale G_{la}

Results from 10 simulated generations:

Correl. with true IBD:	
A	0.49
$G_{\text{LA}}(3\text{gens})$	0.65
$G_{\text{LA}}(10\text{gens})$	0.97
GRM	0.87
Regression on true IBD (b)	
A	1.01
$G_{\text{LA}}(3\text{gens})$	0.96
$G_{\text{LA}}(10\text{gens})$	1.03
GRM	0.78

G_{la} Algorithm

- G_{la} versus A:
 - A : 50/50 inheritance
 - G_{la} : SNPs \rightarrow inherit.

Inheritance indicators (S):

- $S=1/2$: pat /maternal inheritance
- Need any locus with:
 1. Heterozygous parent
 2. Homozygous offspring
 3. Genotyped grandparents
 - Allele pat/maternal
- Impute remaining loci

Conclusions:

- Efficient G_{la} algorithm
 - $>10\text{k}$ G_{la} matrices
- Correl. to true IBD 0.97
- But with 3 generations genotyped: correl = 0.65
- No inflation bias

GRM:

- Correl. true IBD: 0.87
- Substantial inflation bias

References: ¹Meuwissen, J.Anim.Sci 75:934. ²Meuwissen et al. Front. Genet. 11:880.

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