Interim genomic prediction considering newly acquired genotypes and phenotypes

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Interim genomic prediction

- Development of an approach for computing interim GEBV
    - by considering newly acquired genotypes AND phenotypes
    - for:
        - Genotyped but non-phenotyped animals
        - Genotyped and phenotyped animals
        - Non-genotyped but phenotyped animals

Proposed approach

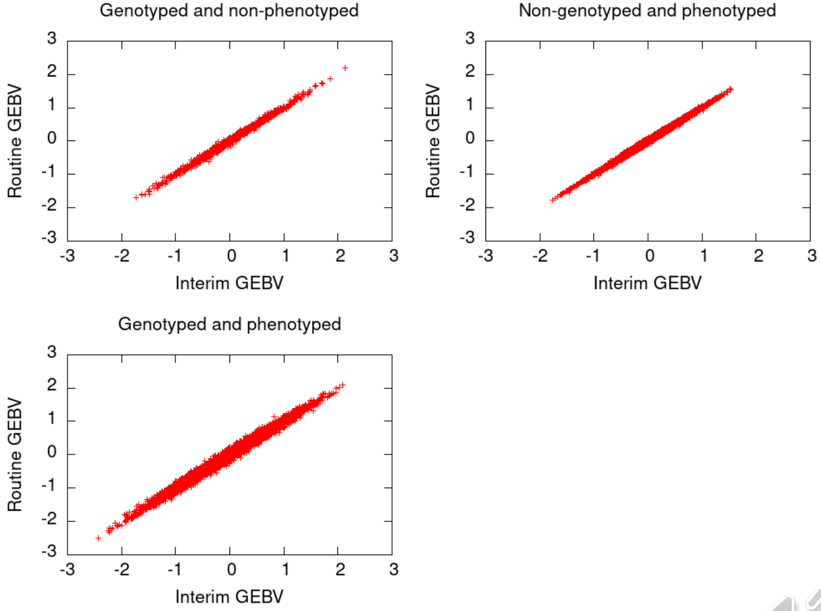
- MME similar to Pedigree-BLUP

$$p(\mathbf{u}) = N(\mathbf{0}, \mathbf{A}\sigma_u^2) \rightarrow p(\mathbf{u}) = N(\boldsymbol{\mu}, \mathbf{A}^*\sigma_u^2)$$

$\boldsymbol{\mu}$ = vector of (imputed) DGV

$\mathbf{A}^*$ = modified pedigree relationship matrix

Trait 1



Proposed approach

- Can consider both newly acquired genotypes and phenotypes
- Efficient and accurate
- Equivalent to ssGBLUP
    - Assuming same estimated SNP effects!

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Thank you!

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