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Generalised sparse-group lasso for whole-genome regression and genomic selection

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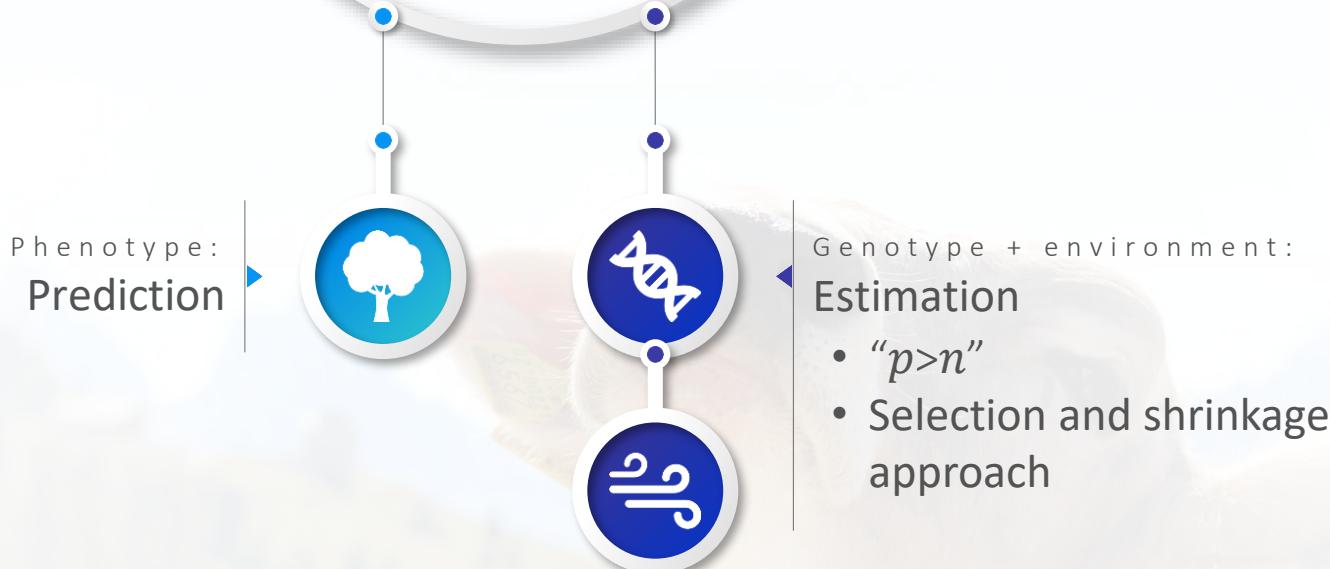
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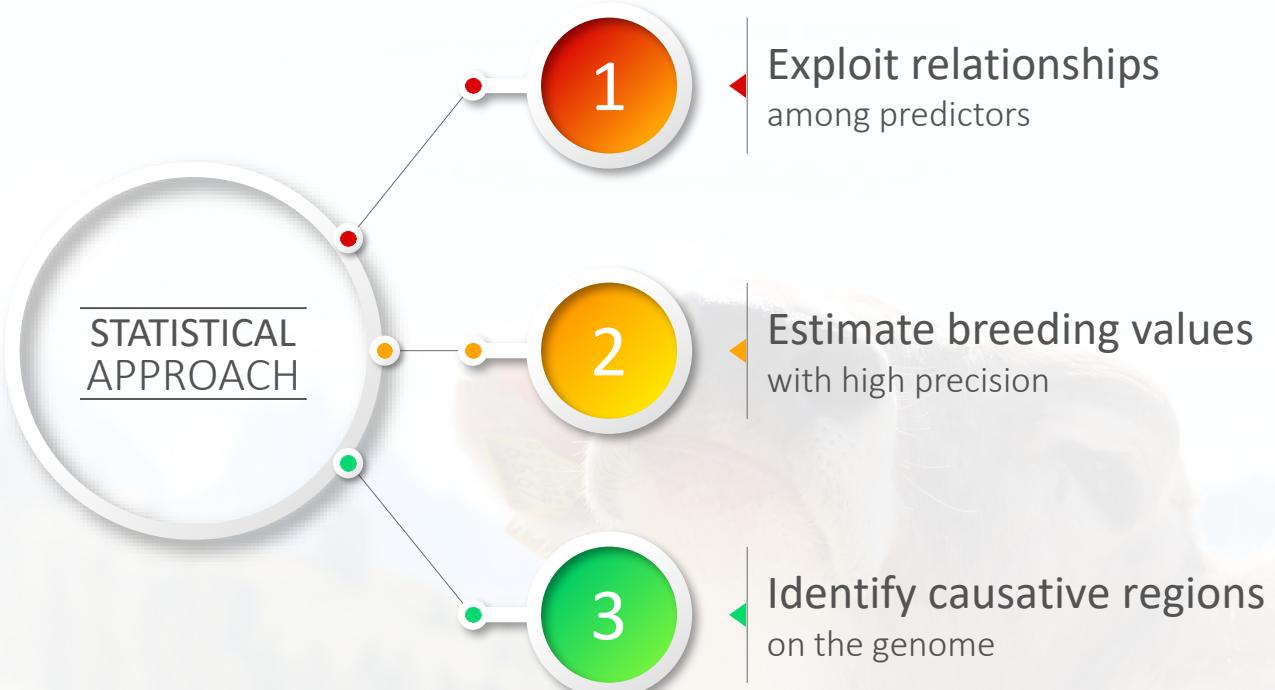
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BACKGROUND





WHOLE - GENOME REGRESSION

MODEL

OPTIMI-
SATION

$$y = X\beta + e$$

y phenotype vector

X marker-genotype matrix

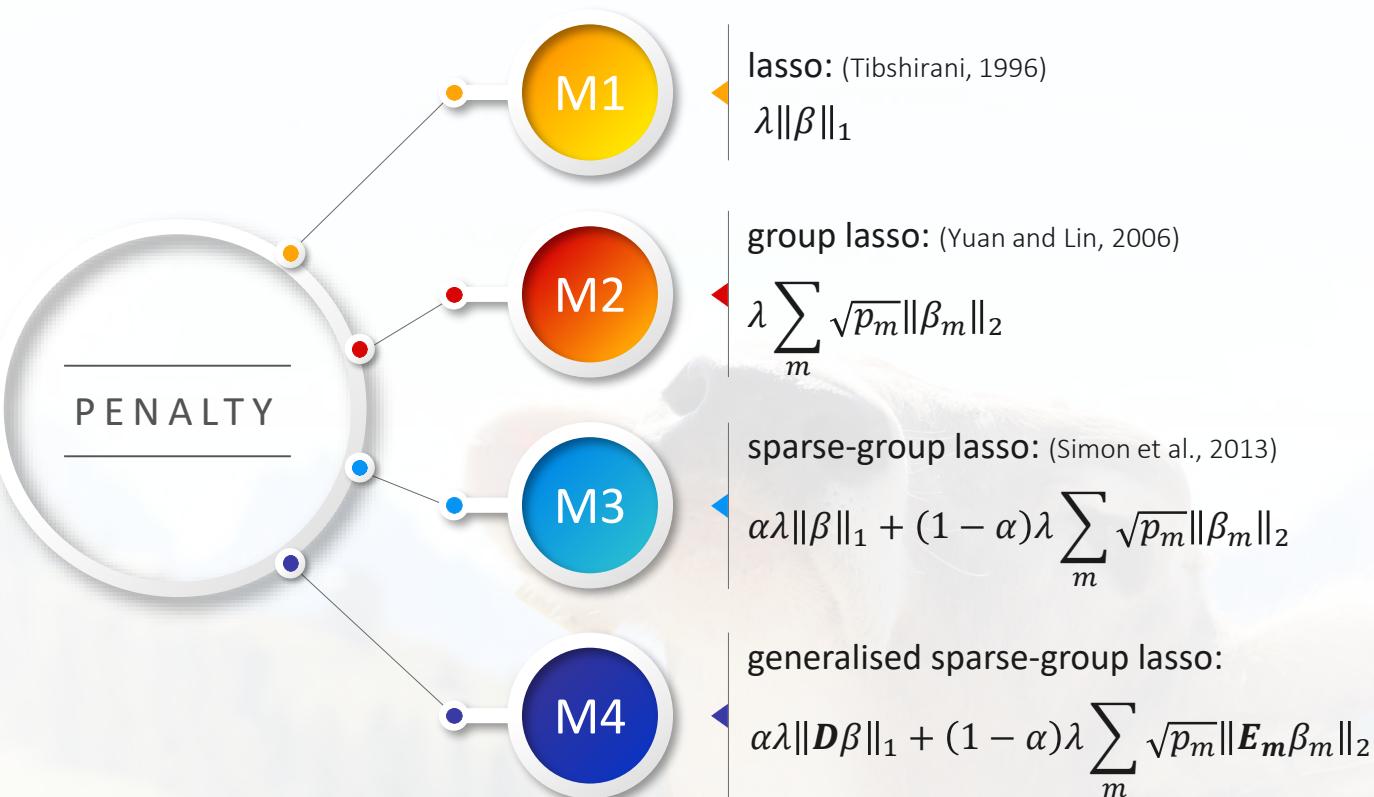
β vector of additive-genetic effects

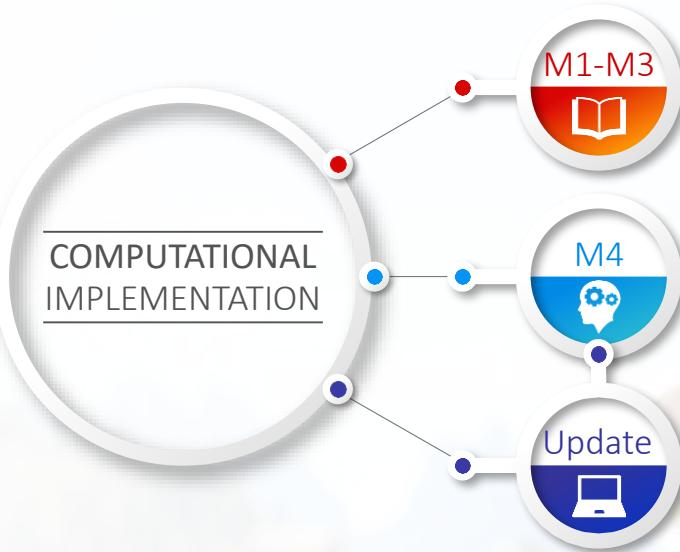
e vector of i.i.d. residuals

$$\hat{\beta} = \arg \min_{\beta} \left\{ \frac{1}{2n} \|y - X\beta\|_2^2 + \text{penalty} \right\}$$

(n -invariant formulation)







Proximal gradient descent

(backtracking line search, warm starts)

ADMM

(new variables: $\gamma = D\beta$, $\delta = E\beta$, w , new parameter ρ)

- ◀ Straight forward for $\beta^{(k+1)}$, $\gamma^{(k+1)}$, and $w^{(k+1)}$
- ◀ Assumption for $\delta^{(k+1)}$: group structure in $(D + E)\beta$
- ◀ $D = I$
- ◀ E block diagonal, $E_m^T E_m = (I_{m \times m} K)^{-1}$, K ... covariance matrix

1000 individuals

10 families
100 half sibs per family



466 SNPs
2 chromosomes
233 SNPs per chromosome



100 experiments

$$\text{SIMULATION}$$
$$y = X\beta + e$$



3 different numbers of QTL:
1, 3, or 9 groups per chromosome



3 traits with different heritabilities
 $h^2 \in \{0.1, 0.3, 0.5\}$



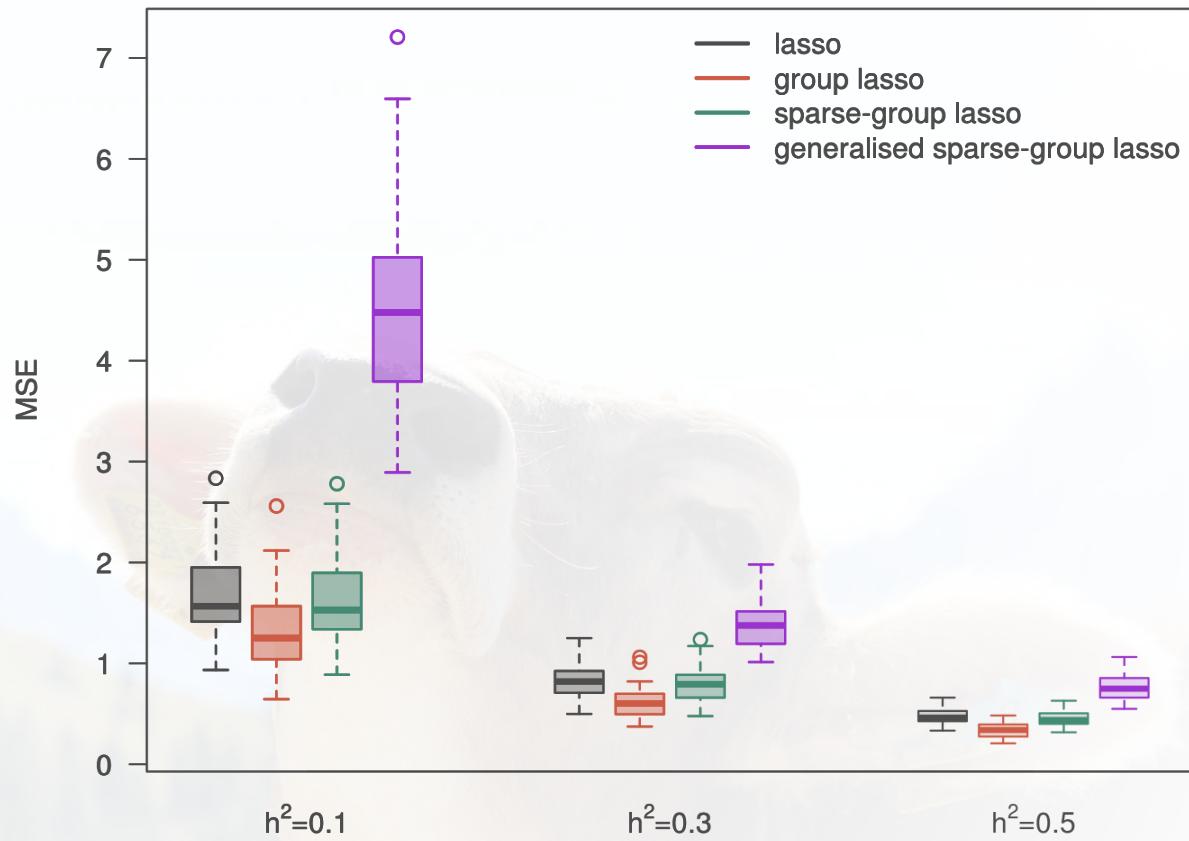
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RESULTS

MEAN SQUARED ERROR



- 1 group of QTL per chromosome
- Equal effect sizes within groups ("simplified scenario")
- $\alpha = 0.95$



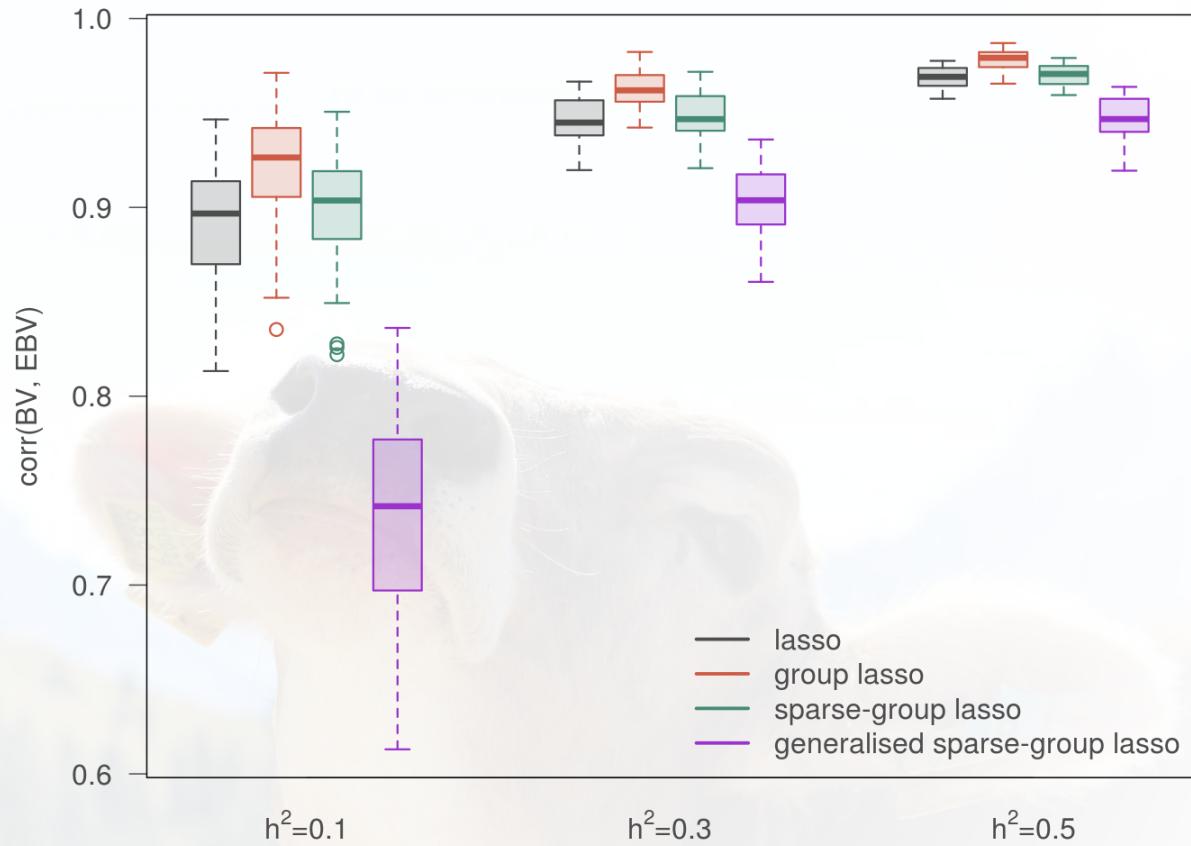
CORRELATION BREEDING VALUES



1 group of QTL
per chromosome

Equal effect sizes
within groups
("simplified scenario")

$\alpha = 0.95$



DISCUSSION AND OUTLOOK

Thank you very much.

$$\begin{aligned}\alpha(D\beta - \gamma) + (1 - \alpha)(E\beta - \delta) &= 0 \\ \rightarrow \quad \binom{D}{E}\beta - \binom{\gamma}{\delta} &= 0\end{aligned}$$

Decoupled updates for γ and δ

Theoretical correlation
(Wittenburg et al., 2016)



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