# Genome-Wide Breeding Value Estimation with Elastic Net

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**RESULTS: Simulation Data** 

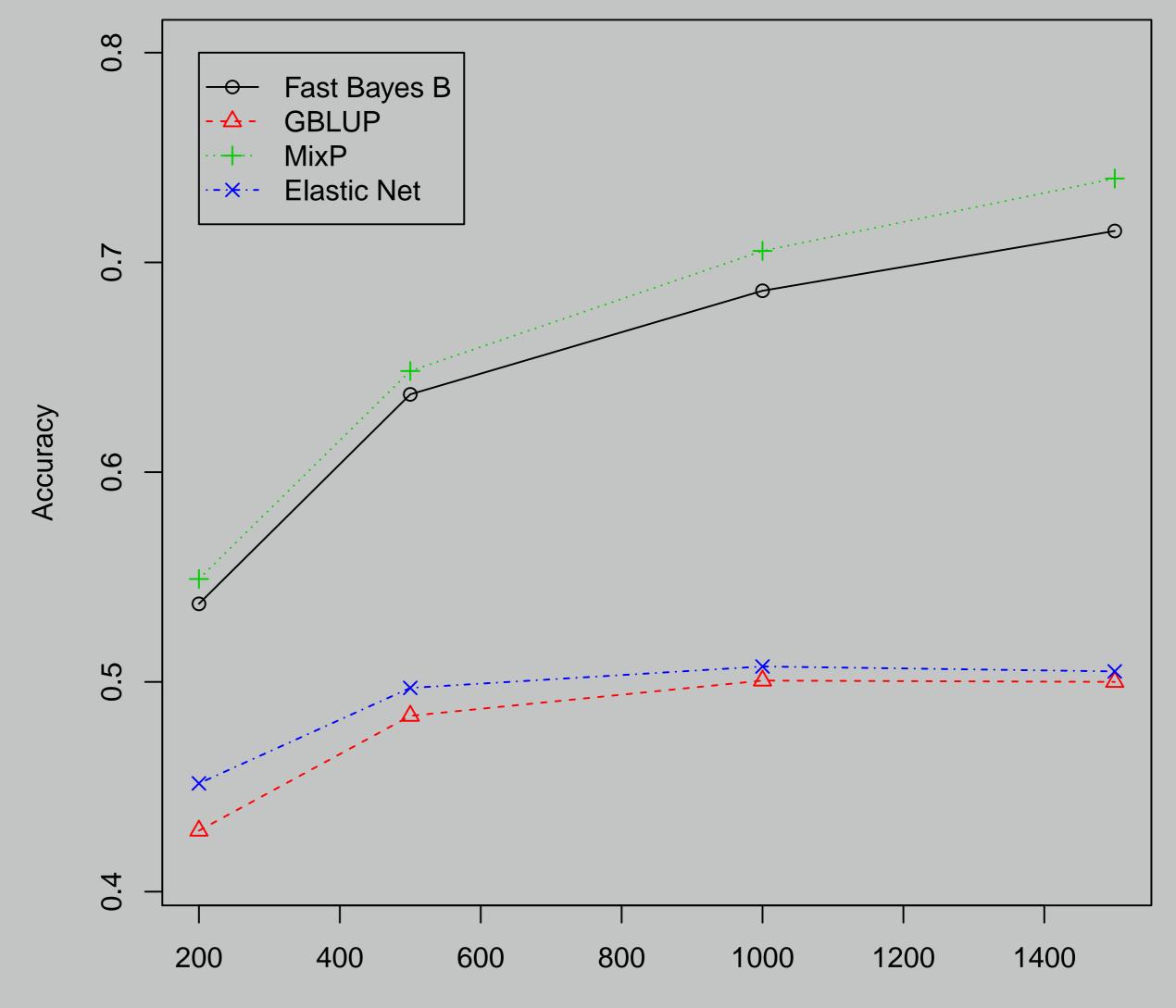
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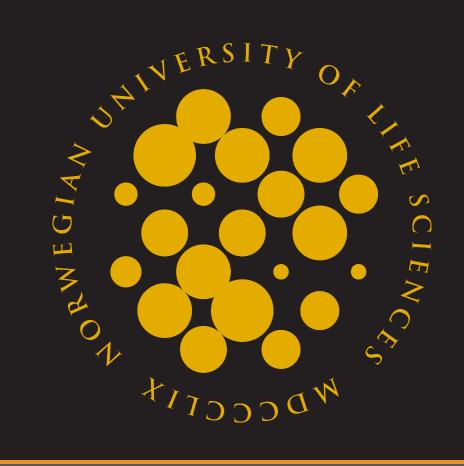
#### **OBJECTIVES**

To test the Elastic Net on GWEBV estimation with simulated and real data.

#### INTRODUCTION

- Genomic-wide breeding value (GWEBV) estimation is often facing with the problem of  $p \gg n$
- I.e., the number of genotype values to be estimated (p) is great greater than the number of phenotypic observations (n).





Α

- Several regularization methods were proposed to solve such problems, for example:
  - ► The Bayesian Lasso (Tibshirani, 1996).
  - ► The Elastic Net (Zou et al, 2005).

#### MATERIALS

## Simulation

- Based on a real pedigree of Norwegian Red Cattle
  - ▶ 8 generations
- ► 19,523 individuals.
- Ideal populations

#### Number of markers

comparison of accuracy of Fast-Bayes-B, GBLUP, MixP and Elastic Net Number of QTL simulated per chromosome is 5, which explain 2% of total phenotypic variance.

Accuracy is measured with the correlation coefficient between GWEBV and true values.

#### **RESULTS:** Wheat Data

Yield1234Fast Bayes B0.520.490.380.44GBLUP0.530.500.390.46MixP0.530.500.400.46Enet0.530.500.380.45

- Effective size  $N_e = 200$ .
- One 1M chromosome, 10<sup>8</sup> base pairs.
- Mutation rate  $10^{-8}/M/meiosis$ .
- ► Random mating of 10<sup>4</sup> generations.
- Genotypes of ideal populations were dropped through founders into the real pedigree.
   Newest 250 individuals are as validation set.
- ▷ 1,915 bulls are as training set.
- ⊳ 200 repeats.

METHODS

- Wheat data set (Crossa et al, 2010).
  - 599 wheat lines, 1,447(1,279) markers
    10 repeats of random 10-fold cross-validation

Accuracy is measured with correlation coefficient between GWEBV and phenotypic values.

No significant accuracy difference of different methods was observed.

### CONCLUSIONS

- With few QTL, the elastic net is better than GBLUP, but less accurate than MixP and Fast Bayes B.
- Its computation speed is at the same order of GBLUP and MixP.
- No accuracy difference between estimation methods was found in real wheat data.

#### REFERENCES

Crossa J et al., Genetics 2010, 186(2):713-724

The elastic net methods
 Data (X, y). X is the n × p predictor matrix of standardized variables; and y is the response vector.

$$\hat{\beta} = \arg\min_{\beta} \|\mathbf{y} - \mathbf{X}\beta\|^2 + \lambda_2 \|\beta\|^2 + \lambda_1 \|\beta\|_1$$

## Other methods for comparison

Fast Bayes B (Meuwissen et al, 2009)
 GBLUP (Meuwissen et al, 2001)

▷ MixP (Yu et al, 2011)

Meuwissen TH et al., Genetics 2001, 157(4):1819-29

Meuwissen TH et al., Genet Sel Evol 2009, 41:2

▷ Tibshirani R, J R Statist Soc B 1996, 58(1):267-288

▷ Zou H et al., J R Statist Soc B 2005, 67(2):301-320

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