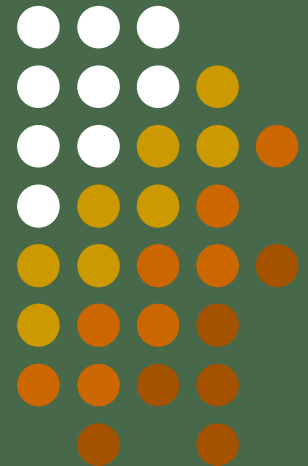


HAPLOTYPE ANALYSIS OF THE PROMOTER REGION OF BOVINE LTF GENE – SEARCHING FOR POSSIBLE ASSOCIATIONS WITH MILK TRAITS

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Presentation plan



- Introduction
- Material and Methods
- Results and Discussion
- Conclusions

Introduction



- real data – kind of challenge
- statistical analysis of the promoter region of bovine LTF gene



Material and Methods

- data source: Univerisity of Warmia i Mazury, Faculty of Animal Bioengineering, Department of Animal Genetics
- the real genotype and phenotype data set consisted of 377 individuals,
- 11 bi-alleic loci,
- phenotype: first lactation milk yields
- two approaches:
 - SNPs,
 - haplotypes.

Material and Methods

SNPs - BLUP estimation



$$y = \mu + \sum_i X_i g_i + e,$$

- assumption: random SNPs effects
- $E(\sigma_{g_i}^2) = 0.001$ (Meuwissen, Hayes, Goddard et al. 2001)
- mixed-model equations (Henderson et al. 1984)

Material and Methods

SNPs – Bayesian estimation



Two step analysis:

- data modelling:
 - BLUP,
 - variances of the chromosome segments: $\text{Var}(g_{ij}) = \sigma_{g_i}^2$
- combination of information from the prior assumption of variances of segments and from the data

(Meuwissen, Hayes, Goddard et al. 2001)

Material and Methods

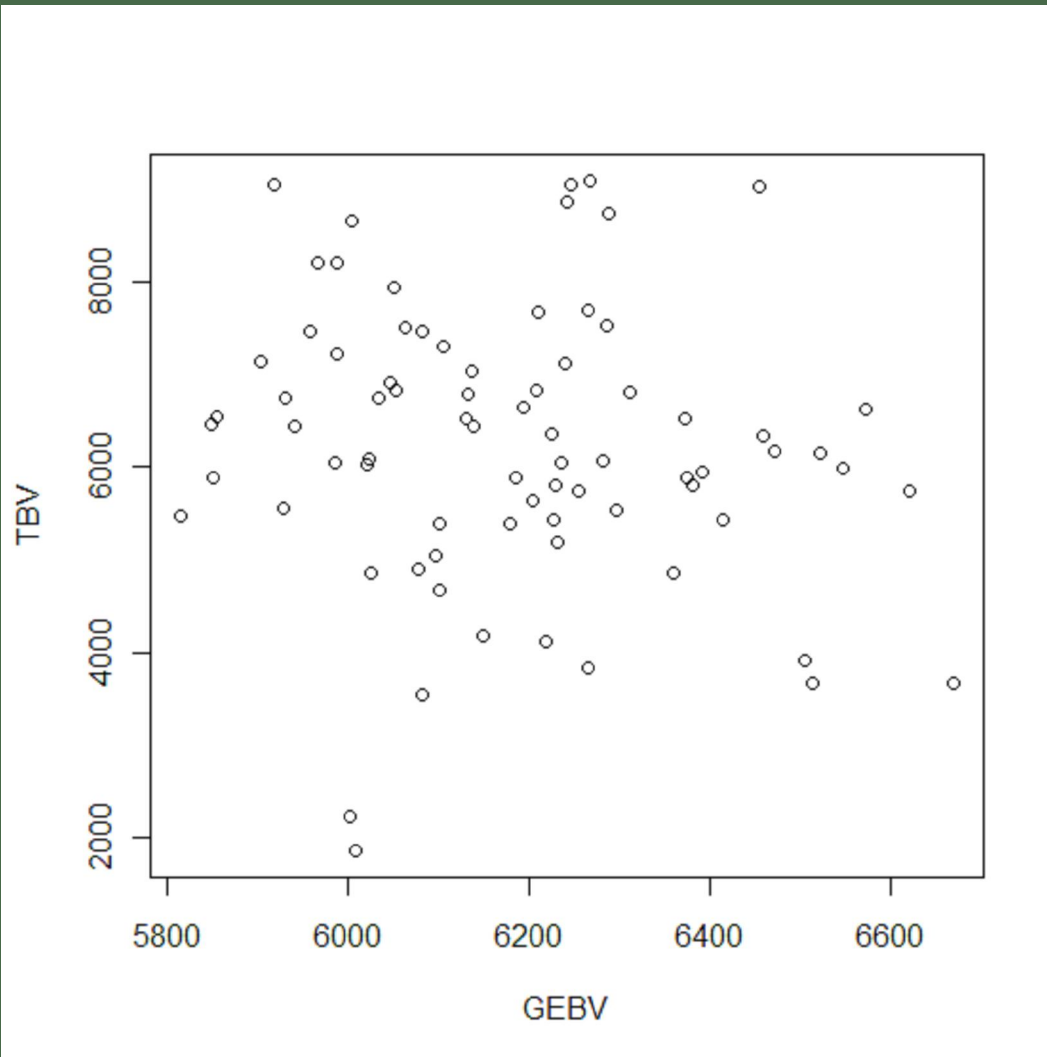
Haplotypes



- software used: HPLUS, authors: Sue Li, RJ Laws, LuePing Zhao (Fred Hutchinson Cancer Research Center)
- possibilities: haplotype estimation for bi- and multi-allelic markers, binary or continuous phenotypes, no limit in number of markers and samples
- continuous values of phenotypes \implies linear regression method

Results

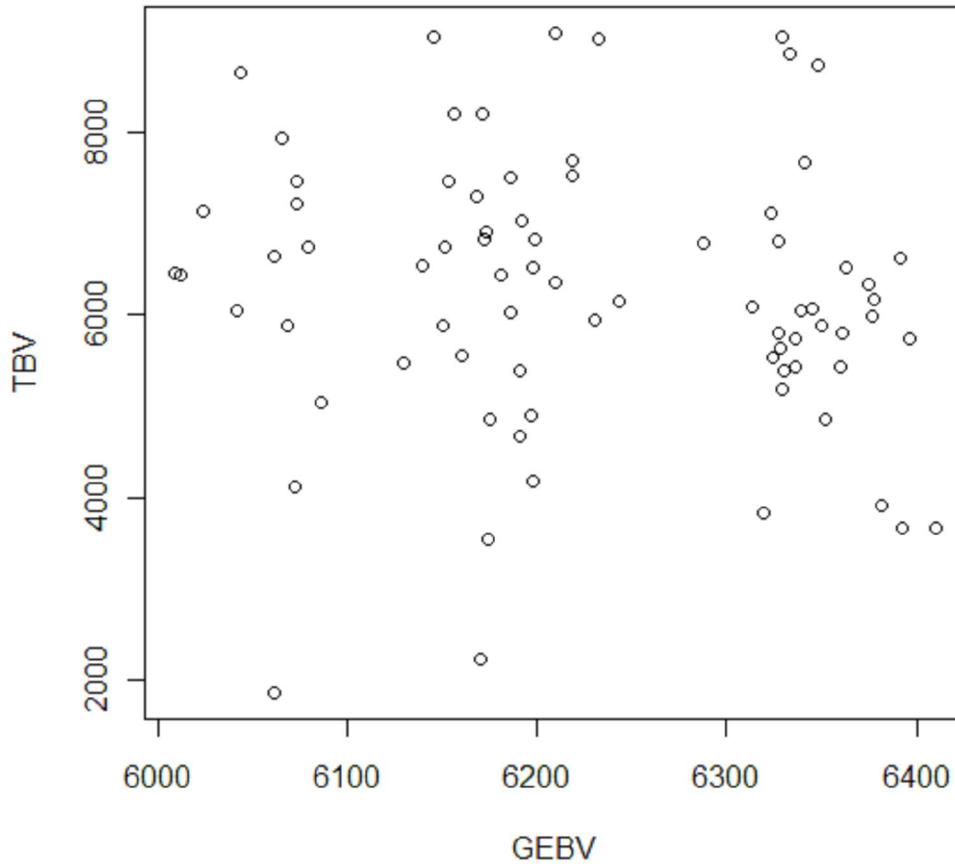
BLUP estimation



correlation
between true and
predicted values:
- 0.13

Results

Bayesian estimation



correlation
between true and
predicted values:
- 0.12

Results

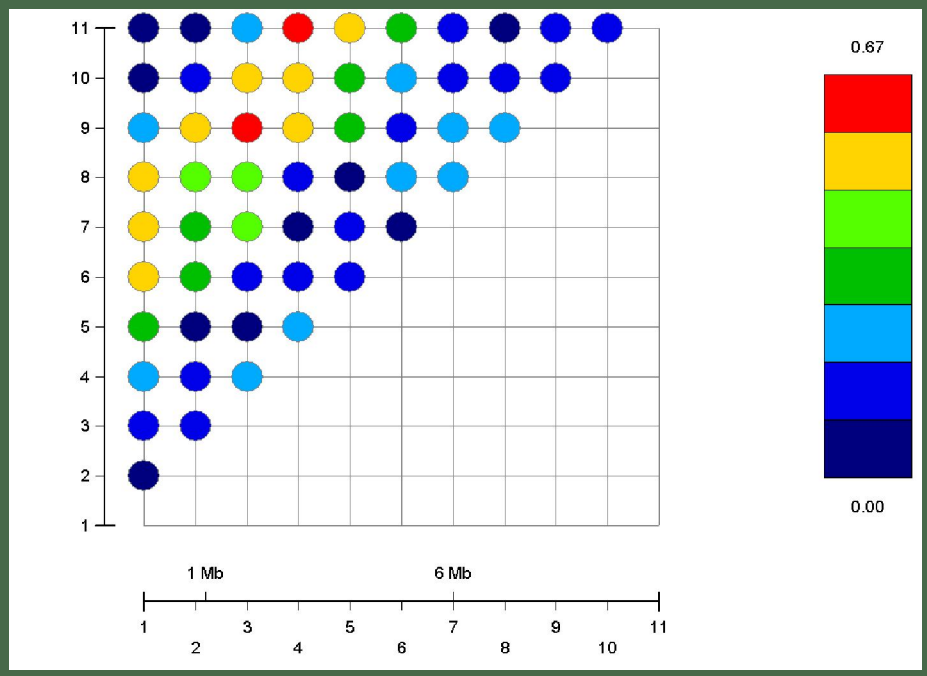
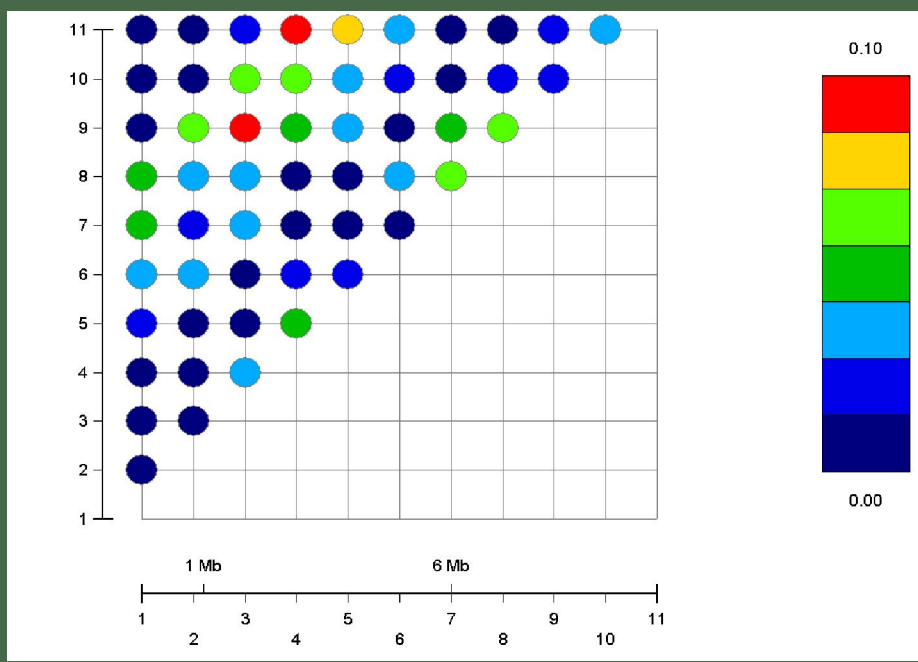
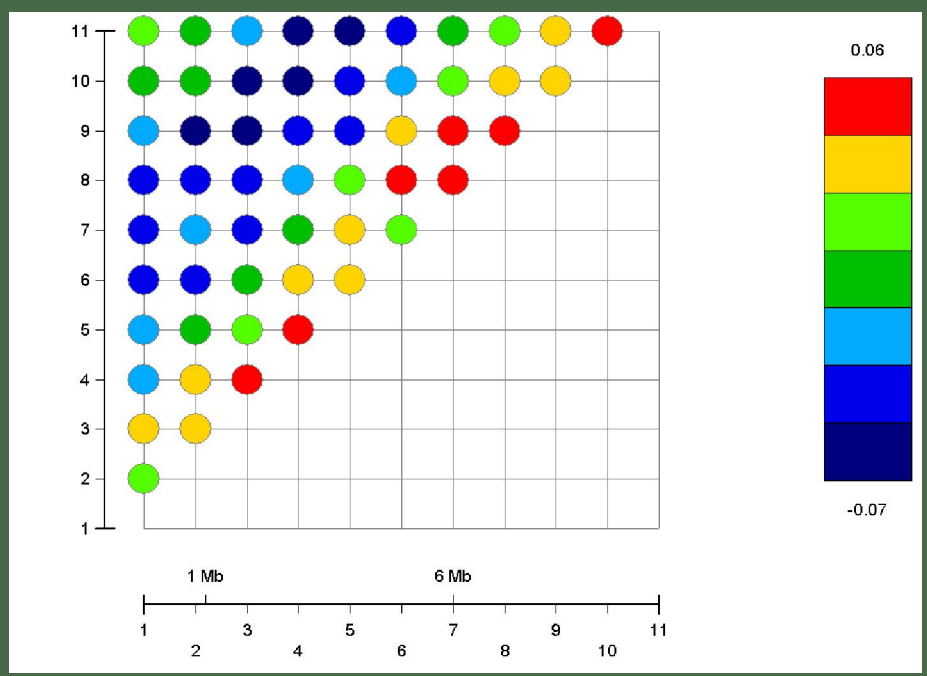
HPLUS estimation



- 4 attempts \implies elimination of insignificant haplotypes
- final result: ALL haplotypes insignificant
- significant level = 16% \implies at least one significant haplotype



D Discussion LD



r^2

D'

Conclusions



- non – informative SNPs
- insignificant effects of haplotypes
- low LD \implies close to equilibrium \implies low variation
 \implies problem with finding association with phenotypes
- data set not large enough?

Thank you
for your attention!

