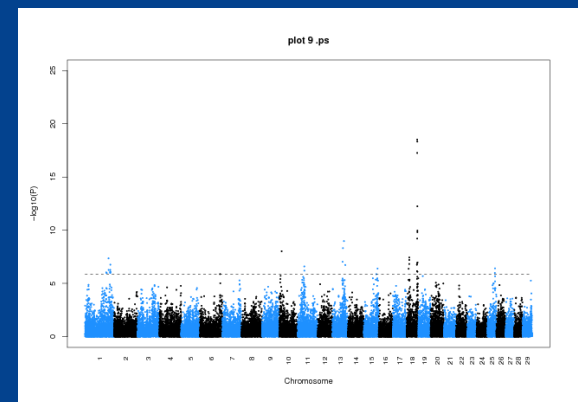
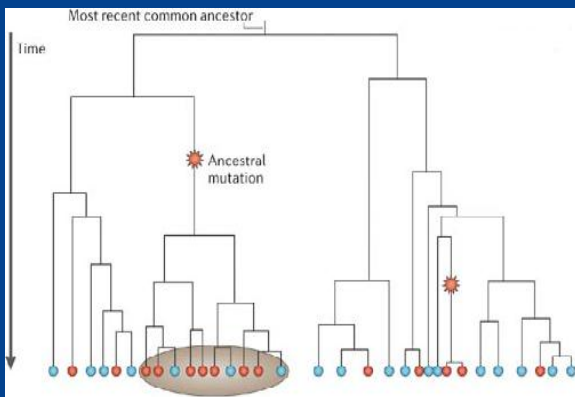


Mapping of Calving Traits in Dairy Cattle using Genealogy-Based Mixed Model

G. Sahana, B. Guldbrandtsen and M.S. Lund

Aarhus University, Faculty of Science and Technology, Molecular Biology and Genetics, 8830 Tjele, Denmark



Objectives

- › Detect associations between SNP markers and calving traits in Holstein cattle
- › Using a **novel** approach
 - › **Genealogy-based mixed model**

Animals, traits and markers

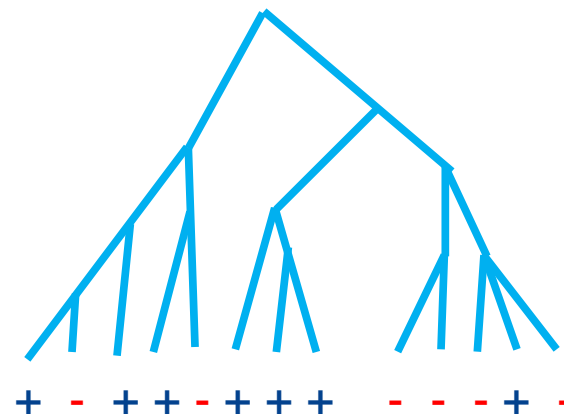
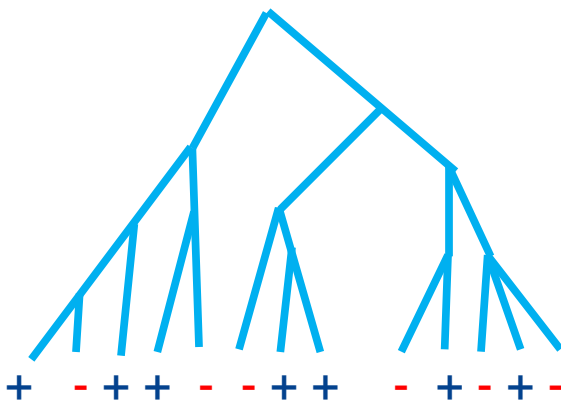
- › 4258 Holstein bulls
- › Traits
 - › Calving ease*
 - › Calf size*
 - › Stillbirth*
 - › Birth index
 - › Calving index
 - › * Both direct and maternal effects for first and 'later' lactations
- › 38,545 SNPs on 29 chromosomes



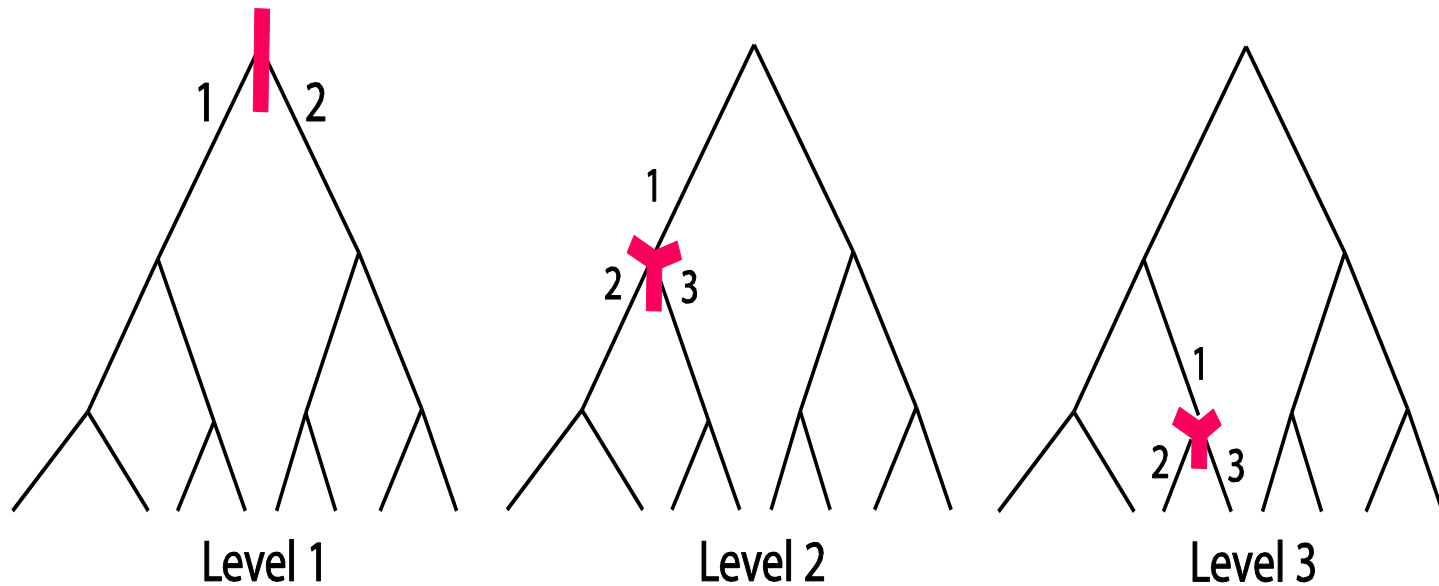
GENMIX – Genealogy based mixed model

Genealogy-based mapping

- › Trees are built based on marker information
- › H_0 : Trait values of individuals do not depend on their location in the genealogy
- › If the tree is similar to the true genealogy of the QTN, individuals in different parts of the tree will have different values
- › The level of significant clustering gives a score for the tree



Grouping Haplotypes



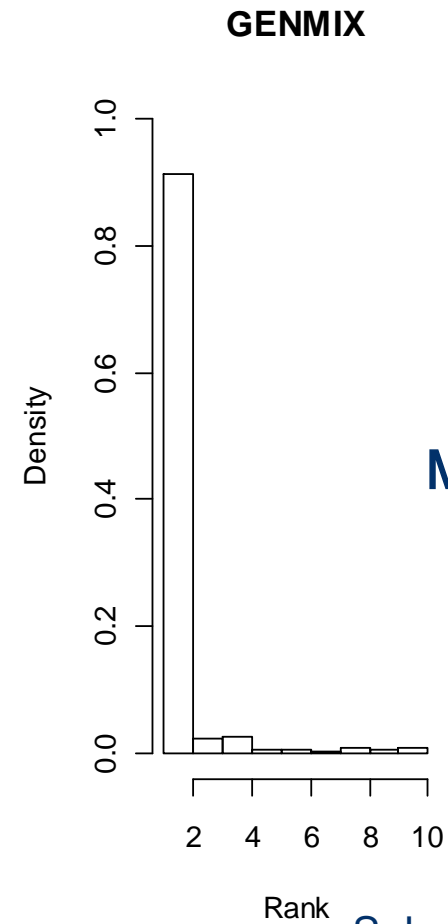
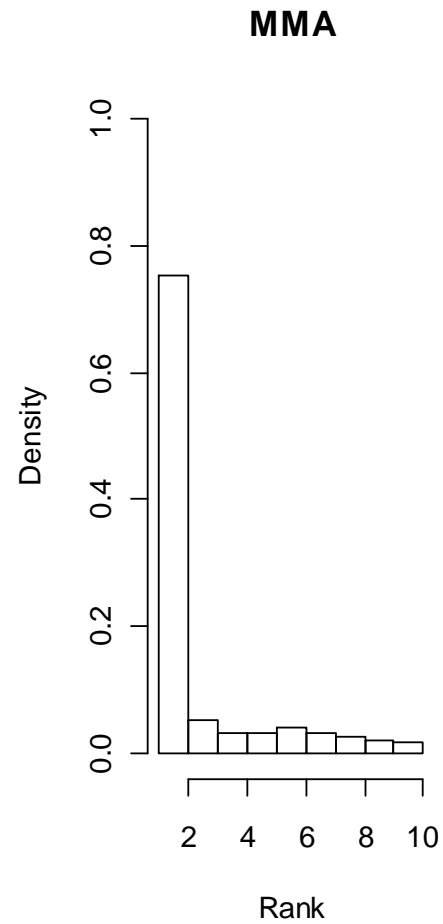
Model

$$y_i = \mu + a_i + q_{h1i}n_1 + q_{h2i}n_2 + e_i$$

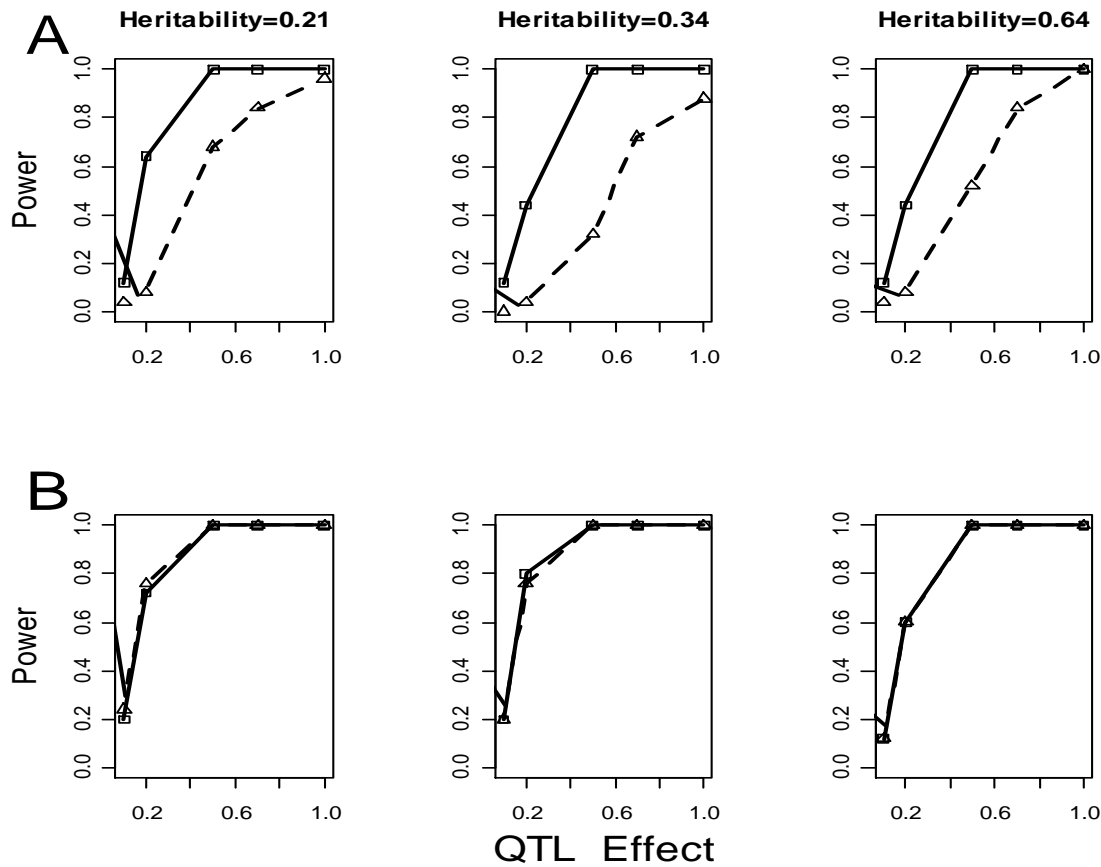
- $H_0: q_{h1i} = q_{h2i} = 0$
- Test using Wald test

Software - DMU

Precision



Power

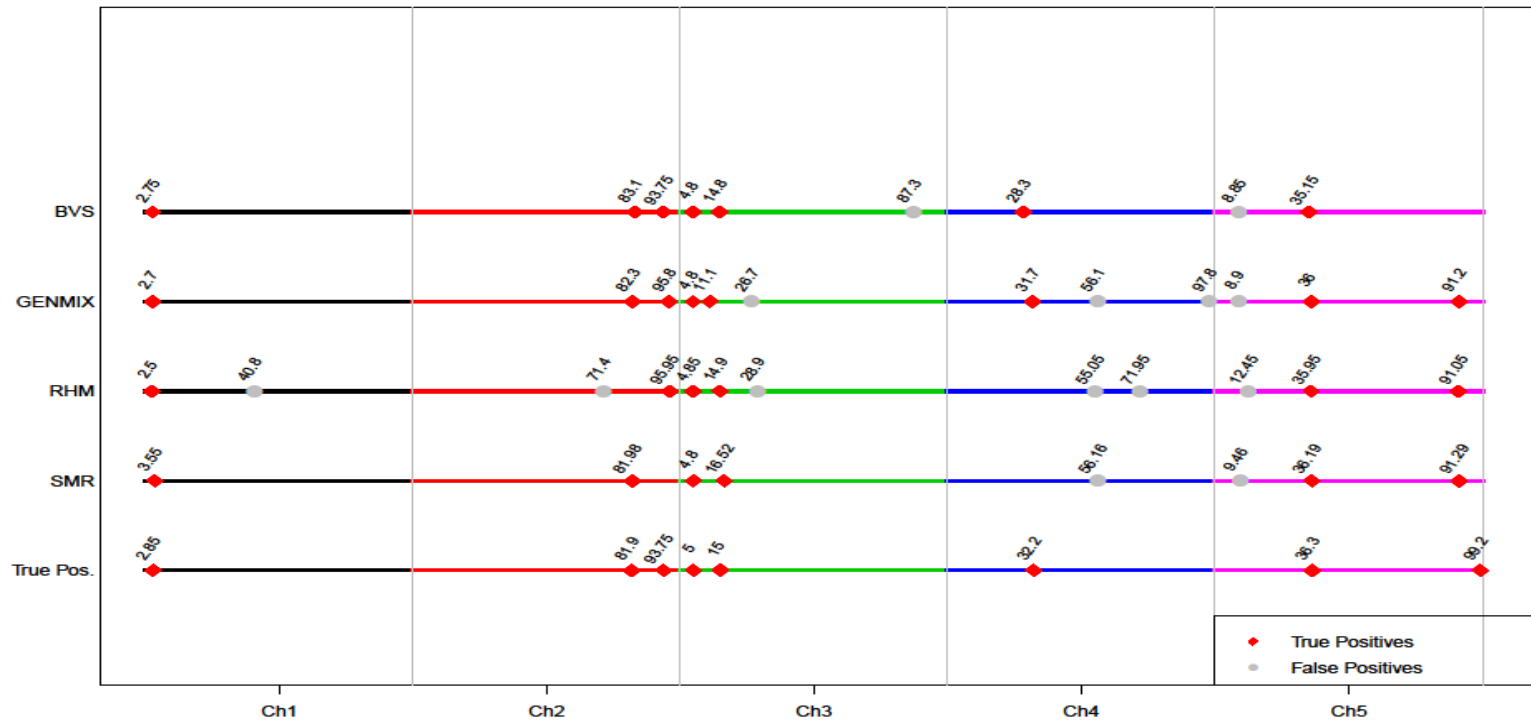


MAF=0.10

MAF=0.45

15th QTLMAS, Rennes, France

QTL localised by the four methods



Why GENMIX is more powerful

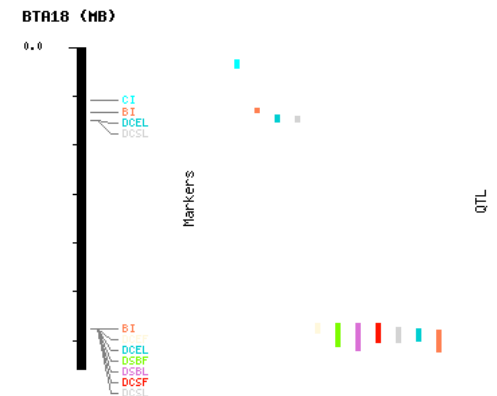
- › Haplotype clustering

- › Length based on possible recombination
- › Clustering based on genealogical history

- › Mixed-model analysis

- › Method of choice when samples have complex pedigree structure
- › Able to control type I error

Mapping QTL for calving traits

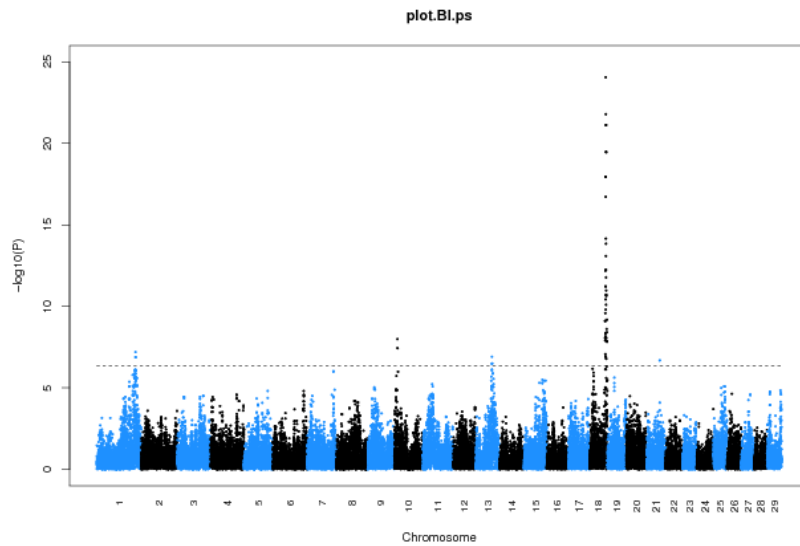


Calving QTL detected

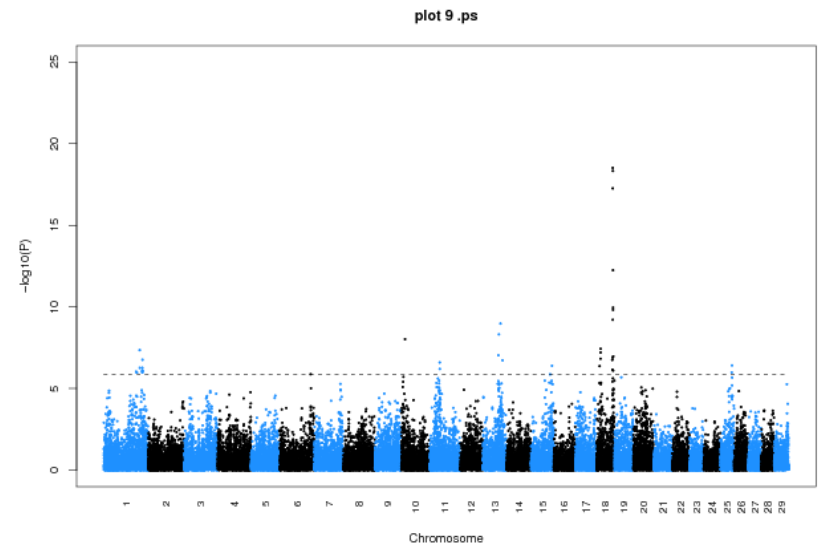
Trait	No. Of QTL	Chromosomes
Birth Index	8	1, 10, 11, 13, 15, 18,
Calving Index	13	1, 4, 8, 10, 13, 19, 20, 23, 25, 26
Calving ease (Direct)	13	1, 6, 11, 12, 13, 15,, 17, 18, 21, 25
Calving ease (Maternal)	10	3, 4, 6, 8, 9, 10, 19, 20, 23, 25, 26
Calf size (Direct)	24	1, 3, 4, 5, 7, 9, 10, 12, 13, 18, 19, 20, 25, 26
Calf size (Maternal)	5	3, 4, 6, 9, 15
Stillbirth (Direct)	3	13, 18
Stillbirth (Maternal)	13	3, 5, 6, 7, 9, 12, 13, 15, 19, 20, 23



Comparison with Mixed Model analysis



GENMIX



MMA

Conclusions

- › We have presented a powerful new approach for association mapping which outperformed mixed model analysis
- › Used that new method for mapping QTL for calving traits
- › Identified several QTL for all the calving traits. These will be further followed for gene mapping.