Applied Statistical Methods In Animal Science

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21.02.2022

Administration

- Course: 2 hours of lecture (2 V)
- Plan: 2 V $\rightarrow$ 1 U + 1 V (i.e., 1 hour of lecture intersperced with time to do exercises)
- Exercises: Work on problems in R
- Material: course notes, slides, solution to exercises
- Exam: written, date: 30.05.2022, 08:15-10:00

Objectives

The students

- are familiar with the properties of **fixed linear effects models**
- are able to analyse simple data sets
- know why least squares cannot be used for genomic selection.
- know the statistical methods used in genomic selection, such as
    - BLUP-based approaches,
    - Bayesian procedures and
    - LASSO.
- are able to solve simple exercise problems using the statistical framework R.

Program

Week	Date	Topic
1	21.02	Introduction
2	28.02	Linear Regression Models
3	07.03	Linear Fixed Effect Models
4	14.03	Model Selection
5	21.03	Pedigree BLUP
6	28.03	Variance Components
7	04.04	GBLUP - Marker-Effects Models
8	11.04	GBLUP - Breeding Value Models
9	18.04	**Easter Monday**
10	25.04	Lasso
11	02.05	SVM
12	09.05	Bayesian Approaches in Linear Regression Models
13	16.05	Bayesian Approaches in Linear Mixed Effects Models
14	23.05	Questions, Test Exam
15	30.05	Exams

Information

- Website: https://charlotte-ngs.github.io/asmss2022
- Topics for master thesis: will follow
- Exam: 30.05.2022 08:15 – 10:00

This Course

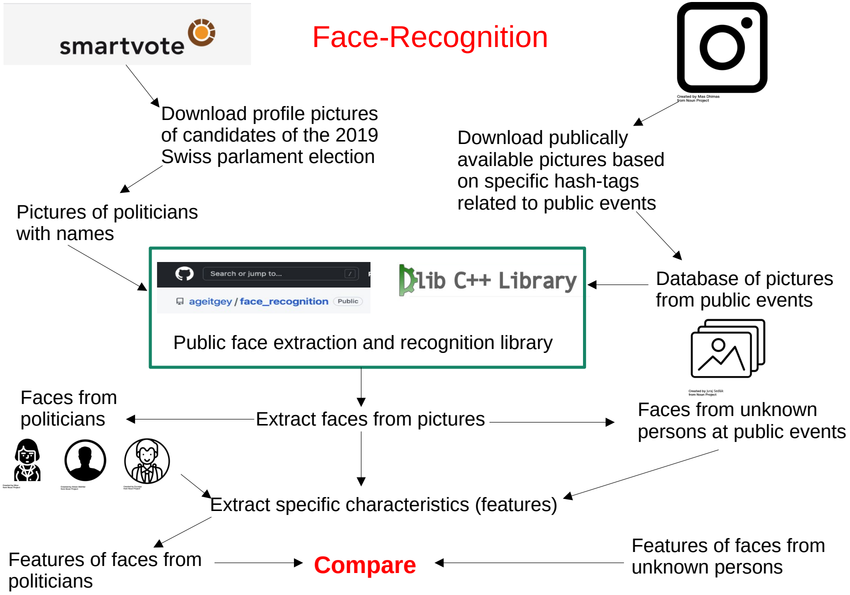
- Use dataset that is used to predict genomic breeding values and introduce four methods

1. Fixed Linear Effects Models - Least Squares
2. GBLUP - genomic version of BLUP
3. LASSO - still fixed linear effects model, but modified parameter estimation
4. Bayesian approach to estimate unknown parameter

Significance

- Why is this important?
- Is this only relevant for animal breeding?
- What about the rest of animal science?
- General trend of collecting data has led to development of `Big Data`
- Examples
  - Presidential campains in the US
  - Health care
  - Face recognition
  - Agriculture: Smart Farming
  - Animal Science

Face Recognition



Face-Recognition

Download profile pictures of candidates of the 2019 Swiss parlament election

Pictures of politicians with names

Created by Mas Dhimas from Noun Project

Download publically available pictures based on specific hash-tags related to public events

Database of pictures from public events

Created by Juraj Sedlák from Noun Project

Public face extraction and recognition library

Extract faces from pictures

Faces from politicians

Created by Nhor from Noun Project

Created by Simon Mettler from Noun Project

Created by Eucalyp from Noun Project

Faces from unknown persons at public events

Extract specific characteristics (features)

Features of faces from politicians

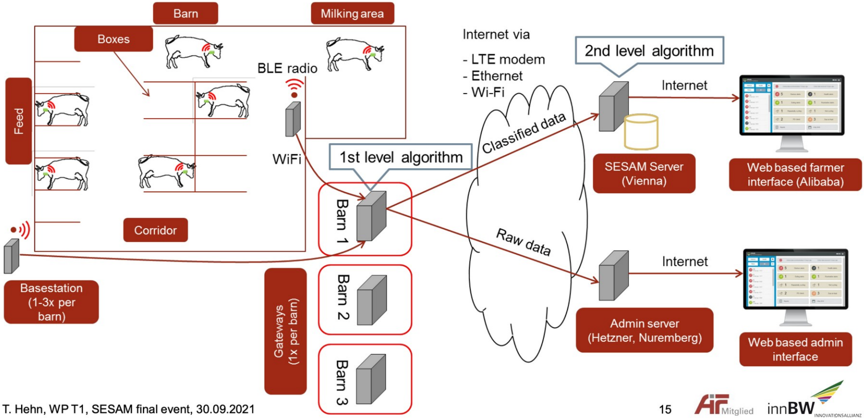
Compare

Features of faces from unknown persons

Smart Farming

- Automated Milking Systems (AMS): Collection of data
- Sensor systems: SESAM (DigiDairy as follow-up)
- CFIT: automated gathering of feed intake data

SESAM


Barn
Milking area
Boxes
Feed
BLE radio
WiFi
Corridor
Basestation (1-3x per barn)
Gateways (1x per barn)
1st level algorithm
Barn 1
Barn 2
Barn 3
Internet via
- LTE modem
- Ethernet
- Wi-Fi
Classified data
Raw data
2nd level algorithm
Internet
SESAM Server (Vienna)
Web based farmer interface (Alibaba)
Internet
Admin server (Hetzner, Nuremberg)
Web based admin interface

CFIT

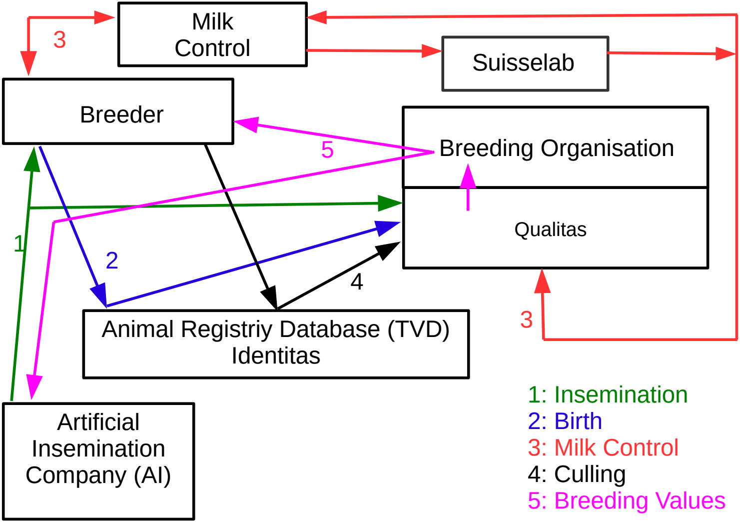
Use video image analysis for

- cow identification
- collection of feed intake data

Traditional Animal Breeding

- Before 2006
- Data collected for other purposes were used to predict breeding values
- Predicted breeding values as side-product

Data Logistics



1: Insemination
2: Birth
3: Milk Control
4: Culling
5: Breeding Values

Genomic Selection

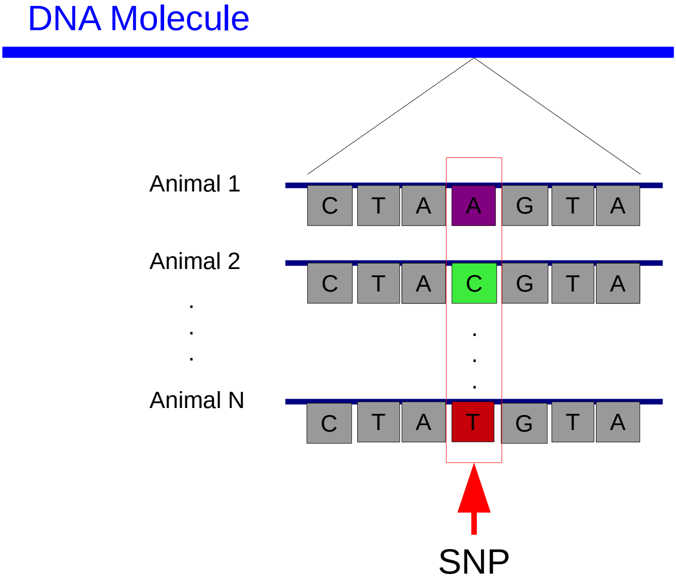
- Same goal as in traditional breeding: Find animals with best genetic potential as parents of next generation
- New: use additional source of information
- **Genomic** information
    - spread accross whole genome
    - single nucleotide polymorphisms (SNP)
- Introduction:

“> Meuwissen THE, Hayes BJ, Goddard ME (2001) Prediction of total genetic value using genome-wide dense marker maps. Genetics 157:1819–1829”

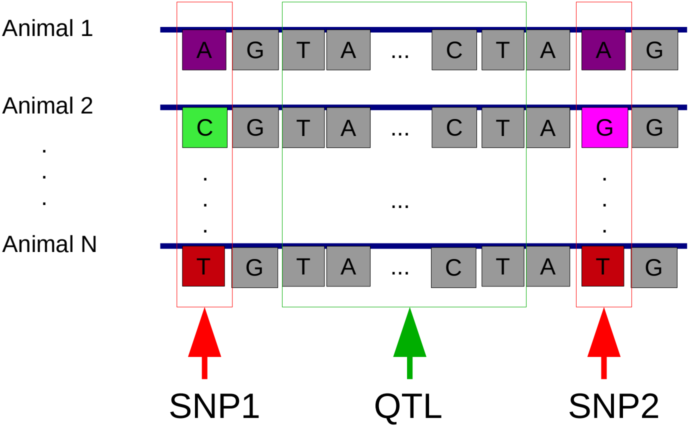
- Popularisation:

“> L. R. Schaeffer. Strategy for applying genome-wide selection in dairy cat- tle. Journal of Animal Breeding and Genetics, 123(4):218–223, 2006. ISSN 09312668. doi: 10.1111/j.1439-0388.2006.00595.x.”

SNP


DNA Molecule
Animal 1
C T A A G T A
Animal 2
C T A C G T A
.
.
.
Animal N
C T A T G T A
SNP

QTL


Animal 1
A G T A ... C T A A G
Animal 2
C G T A ... C T A G G
Animal N
T G T A ... C T A T G
SNP1
QTL
SNP2

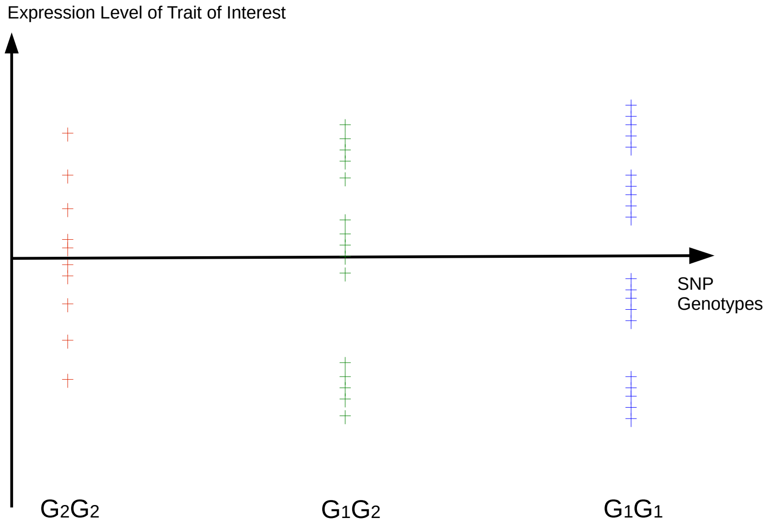
Linkage

- Flanking SNPs and QTL not independent passed on from parents to progeny
- Favorable QTL-allele linked with a given SNP-allele
- QTL is unknown, but use SNPs close to QTL as information for selection

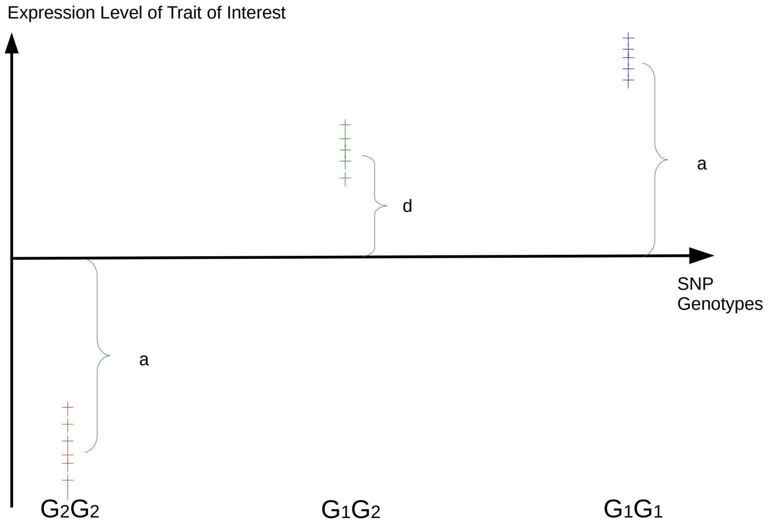
Monogenic Model

- Assume quantitative trait is influenced by one locus only
- Locus is bi-allelic → two alleles (G_1 and G_2) and three genotypes
- Look at Distribution of trait values for three different genotypes

Distribution No Effect



Distribution With Effect



Breeding Value

- Definition: Two times deviation from large number of offspring from population mean
- Assume: Hardy-Weinberg equilibrium
- Compute population mean as expected value of genotypic values
- Compute expected genotypic value of offspring for each of the three parental genotypes
- Assume purely additive loci, hence $d = 0$

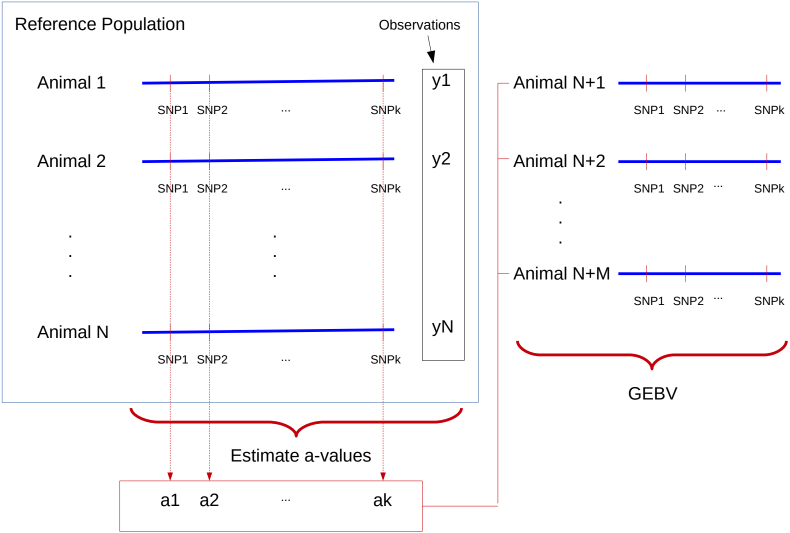
Genomic Breeding Value

- Take into account many loci
- Approximate unknown QTL with linked SNP
- Estimate *a*-effects from monogenic model
- Compute genomic breeding values for all loci based on *a* effects

Two Approaches

1. Two Step Procedure (used currently in Swiss Dairy Cattle)
2. Single Step

Two Step



Reference Population

Observations

Animal 1

SNP1 SNP2 ... SNPk

Animal 2

SNP1 SNP2 ... SNPk

.
.
.

Animal N

SNP1 SNP2 ... SNPk

y1

y2

yN

Estimate a-values

a1 a2 ... ak

Animal N+1

SNP1 SNP2 ... SNPk

Animal N+2

SNP1 SNP2 ... SNPk

.
.
.

Animal N+M

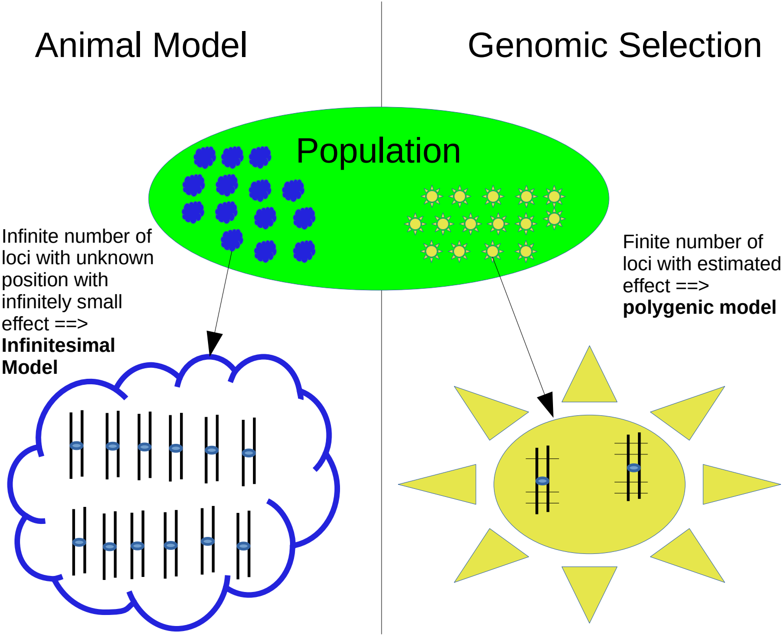
SNP1 SNP2 ... SNPk

GEBV

Single Step

- Combine all information into one single BLUP-based analysis
- Problem: Determine covariance between animals with and without genomic information

Summary: Traditional versus Genomic Selection



Animal Model

Genomic Selection

Population

Infinite number of loci with unknown position with infinitely small effect ==> **Infinitesimal Model**

Finite number of loci with estimated effect ==> **polygenic model**