Using International Information In National Single Step Genomic BLUP In Swiss Dairy Cattle

Christian Stricker and Peter von Rohr

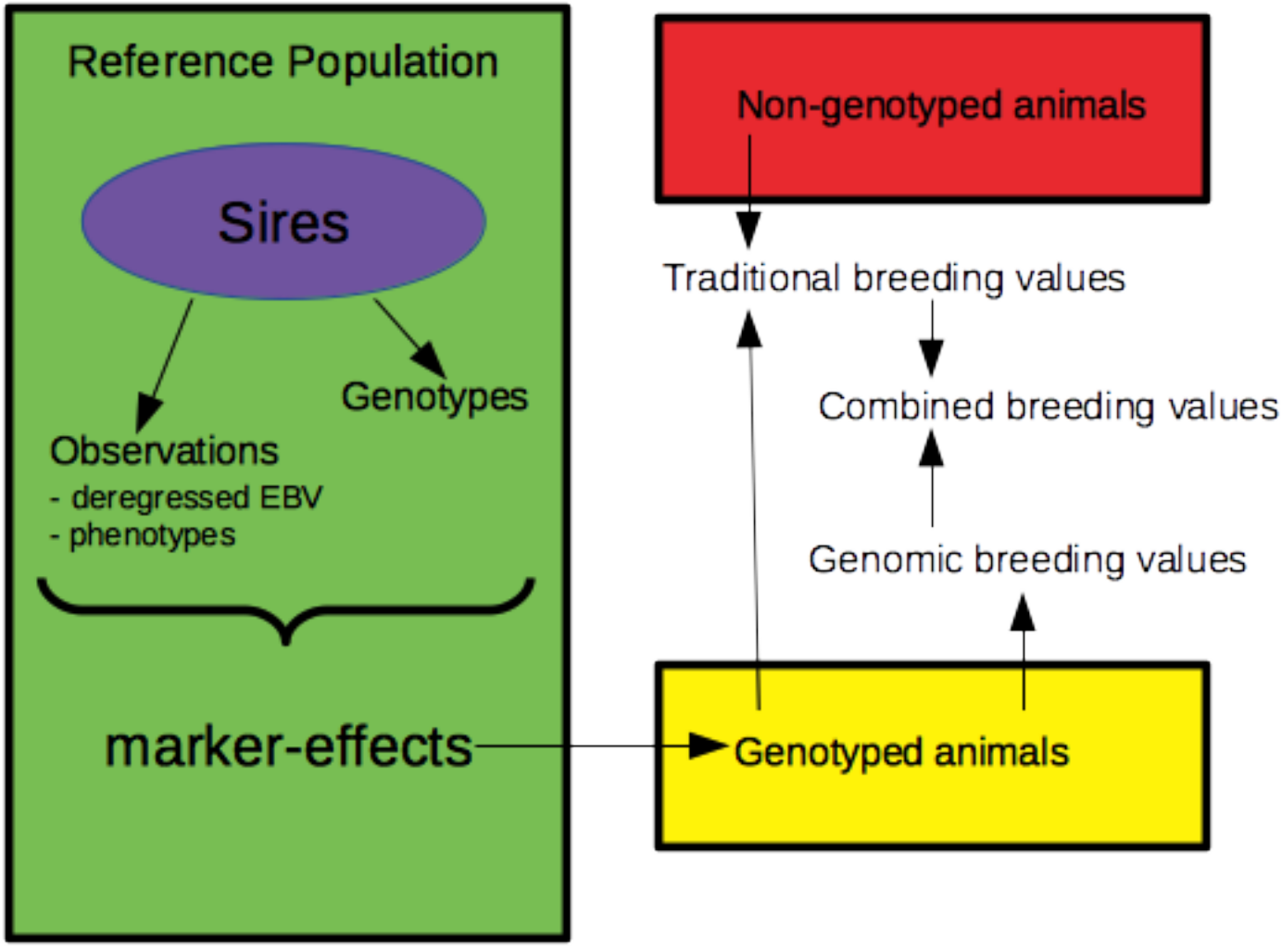
2018-06-06

Current Situation

In Swiss dairy cattle breeding, genomic breeding values are estimated using

- marker-effect models (MEM)
- Bayesian regression approach (Bayes $A - C$ and C_π)
- two-step procedure

Two-Step


Reference Population
Sires
Genotypes
Observations
- deregressed EBV
- phenotypes
marker-effects
Non-genotyped animals
Traditional breeding values
Combined breeding values
Genomic breeding values
Genotyped animals

Information Exchange

In dairy breeds with gene-flow from foreign countries

- Exchange of genotypes
- Phenotypes not exchanged

$\rightarrow$ MEM evaluations based on de-regressed MACE breeding values

Single Step GBLUP

- In general BLUP is widely accepted in animal breeding
- Genomic BLUP (GBLUP) can be parametrized as MEM and as breeding-value model (BVM)
- In BVM the sum of SNP-effects is modelled as random component u
- Legarra et al. (2009) and Christensen and Lund (2010) showed single-step GBLUP approach

Comparison

$$y = Xb + Zu + e$$

Traditional Animal Model

u: random breeding values

$$Var(u) = A\,\sigma_u^2$$

A: genetisch-additive Verwandtschaftsmatrix

SSGBLUP

$$u = \begin{bmatrix} u_1 \\ u_2 \end{bmatrix}$$

u_1: non-genotyped animals
u_2: genotyped animals

$$Var(u_2) = G$$

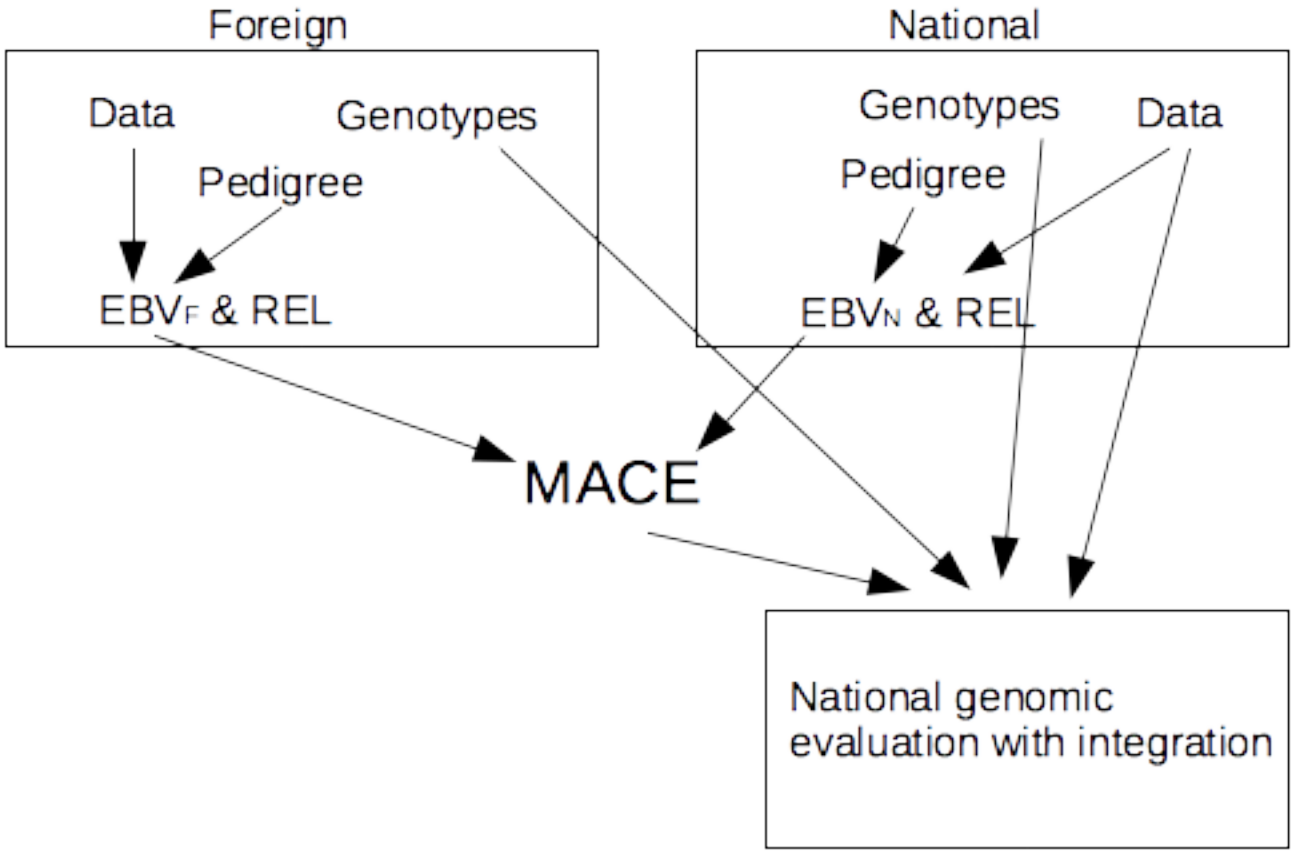
$$Var(u_1) = A_{11} + A_{12}A_{22}^{-1}(G - A_{22})A_{22}^{-1}A_{21}$$

$$Cov(u_1, u_2) = A_{12}A_{22}^{-1}G$$

G: genomic relationship matrix

Assume: $\sigma_u^2 = 1$

Combining Information Sources



Proposed Approach