

# Efficient computation of genomically-enhanced inbreeding coefficients

P. Faux & N. Gengler

University of Liege, Gembloux Agro-Bio Tech, Department of Agricultural Science – Gembloux, Belgium

Contact: Pierre.Faux@ulg.ac.be

## Background

- In livestock species, inbreeding impacts animal performances:
  - Inbreeding depression
  - Loss of genetic diversity
- A good estimation of an animal's inbreeding coefficient requires the knowledge of both paternal and maternal lineages
- Inbreeding may be underestimated due to lacks or inconsistencies in pedigree
- Dense genotypes (over 50k SNPs) are genomic fingerprints of animals that may help to overcome underestimations

## Material & Methods

### Methods

- Inbreeding coefficient (Wright, 1922) is half of the relationship coefficient between parents
- Genomic relationships are created using dense genotypes (e.g. Leutenegger et al., 2006; VanRaden, 2008)
- Legarra et al. (2009) proposed a method to combine pedigree-based and genomic relationships:

$$H = \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G - A_{22})A_{22}^{-1}A_{21} & A_{12}A_{22}^{-1}G \\ GA_{22}^{-1}A_{21} & G \end{bmatrix}$$

G = genomic relationship matrix

A = pedigree-based relationship matrix (indices 1 and 2 respectively for non-genotyped and genotyped animals)

H = combined relationship matrix

- Diagonal of H is  $1 + F_G$  where  $F_G$  is the genomically-enhanced inbreeding coefficient
- Computation of H is computationally demanding beyond 10k animals in population
  - quadratic increase of memory to store H
  - cubic increase of time for inversion of  $A_{22}$

## Material

- Tests on the dairy cattle population from Luxembourg (397,743 animals)
- Among them, 440 sires are genotyped

**Objective:** We aim to make an efficient use of dense genotypes in estimation of inbreeding coefficients

## Conclusions

- Computation of genomically-enhanced inbreeding coefficients is fast and does not require high memory
- Use of genomic information helps to better estimate the inbreeding level of the whole population

## Implementation

- The method of Colleau (2002) is used to compute  $A_{22}$ , the product  $A_{12}$  times  $A_{22}^{-1}$  and the pedigree-based inbreeding coefficients
- The method of Faux and Gengler (2013) is used to compute the inverse of  $A_{22}$
- Computations of H is restricted to diagonal elements
- Any genomic relationship matrix can be used

Computation of pedigree-based inbreeding coefficients of all n animals in population (n-by-1 vector)

Loading of matrix G (n<sub>2</sub>-by-n<sub>2</sub> matrix)

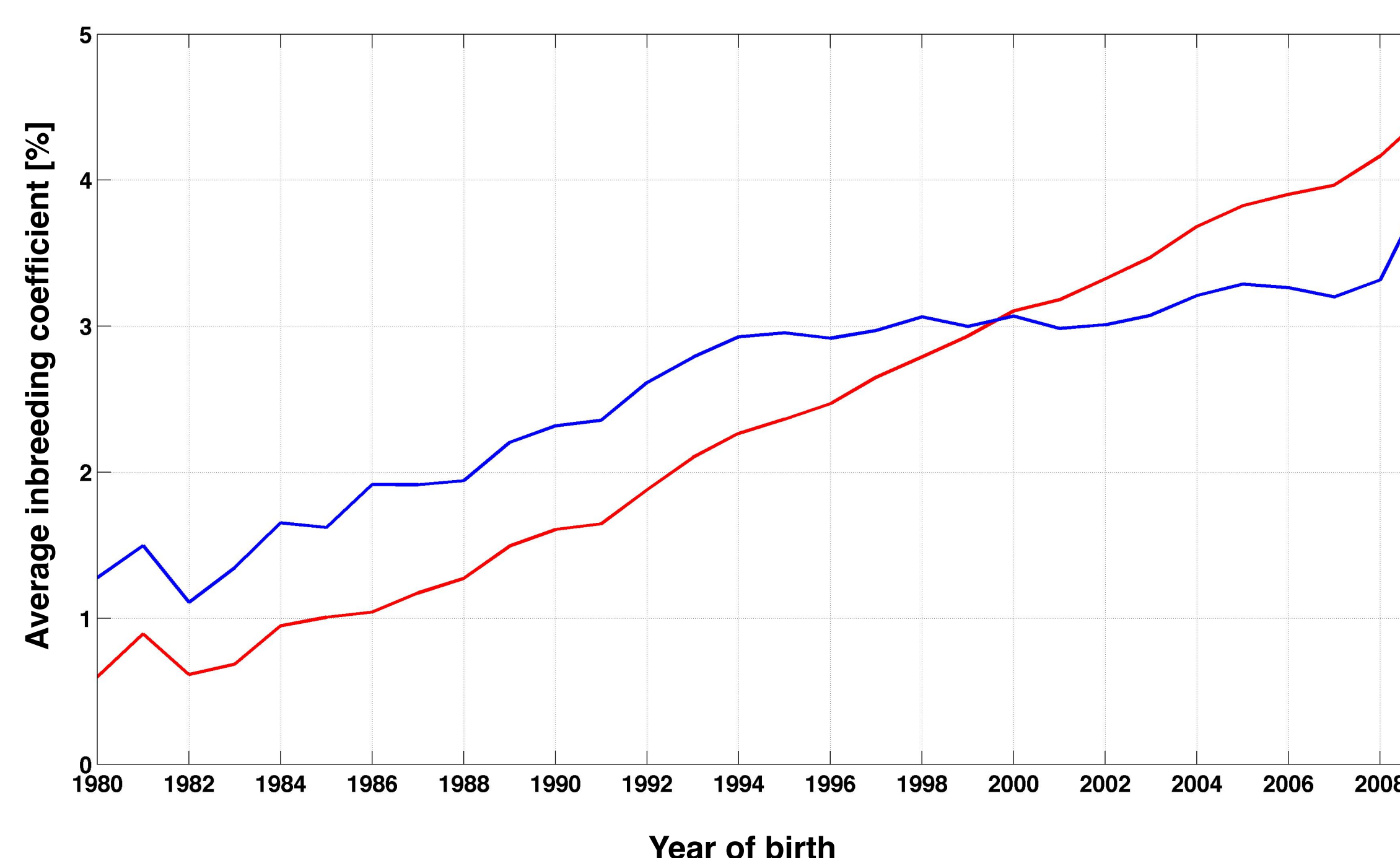
Computation of  $A_{22}$  (n<sub>2</sub>-by-n<sub>2</sub> matrix) and its subtraction of G

Inversion of  $A_{22}$  (stored in the same matrix)

Product of  $A_{12}$  by  $A_{22}^{-1}$  (n<sub>1</sub>-by-n<sub>2</sub> matrix)

Genomic adjustment of the inbreeding coefficients

## Results



**Figure 1.** Evolution of the average inbreeding coefficients of dairy cattle from Luxembourg, born between 1980 to 2009, considering all animals with at least 10 generations known for each parent, with (blue) or without (red) genomic information.