Some opportunities and challenges regarding SNP international evaluations

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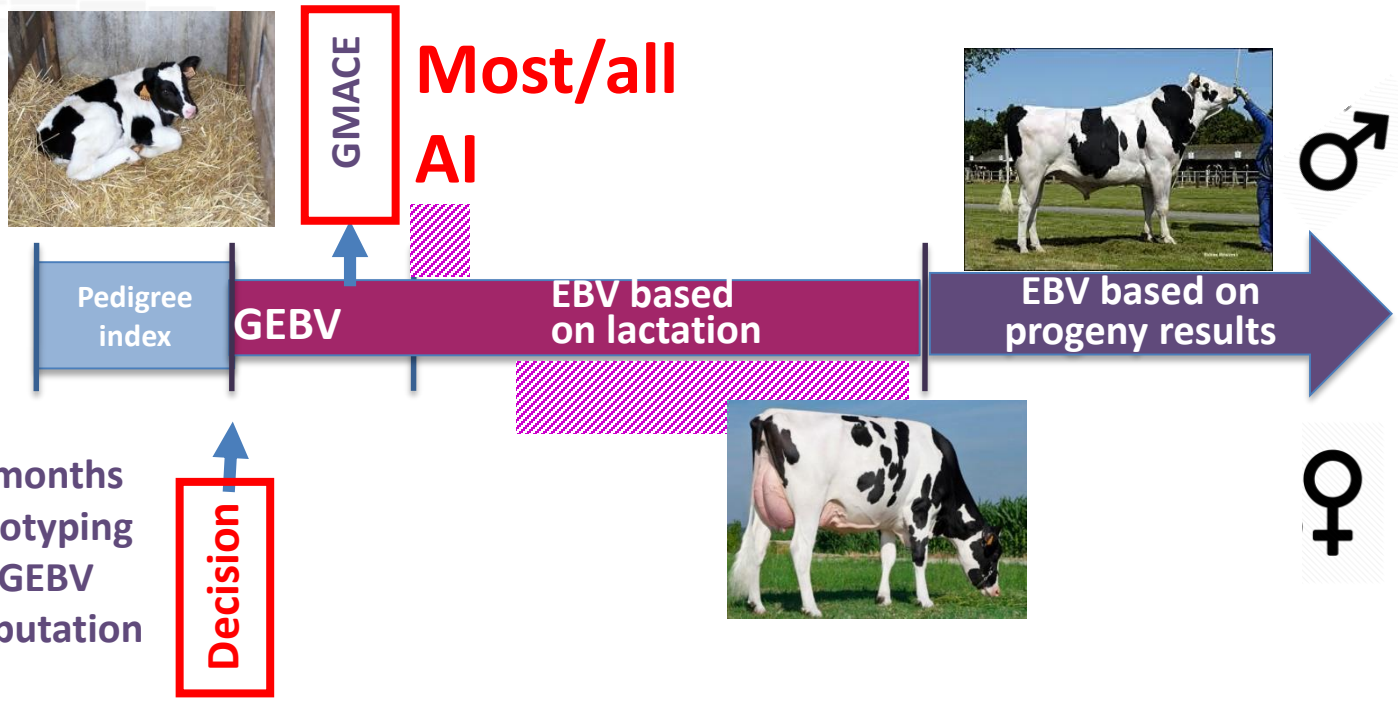
Genomic selection programmes in dairy cattle



- Impose to obtain GEBV more frequently
- Easy if we assume estimates of SNP effects are stable between two official evaluations

National genomic evaluations

- Two strategies :

Data ➔ BLUP ➔ DYD/DRP ➔ GBLUP ➔ GEBV ➔ SNP

ss

Data ➔ BLUP ➔ DYD/DRP ➔ SNP-BLUP ➔ SNP➔ GEBV

ss

- At national level, the first strategy becomes complex …

because of too many animals…

(In France, in August 2016, > 300,000 Holstein genotyped animals + number of genotyped females increases by ~20 to 30% a year)

➔ It does not make sense for quick use in genomic selection !

International genomic evaluations

➔More and more countries are moving towards SNP-BLUP

- GMACE is not really used, in particular in breeding programmes
- at international level, it is essentially viewed as a marketing tool…
- Heifers/cows GEBV do not benefit from GMACE

➔**SNP-MACE** is a big move towards:

- more reliable national GEBV
- easy to compute (quick)
- benefiting to all (including females)

Challenge 1 : redundant information = a big mess!

- Interbull MACE results (= phenotypes of RP animals) are used in all countries (= « Mike's *complications* »)
- Consortia share their reference populations
- Quite a few « strategic » bulls are genotyped in more than one consortium
- e.g., two countries:

Data → MACE → DYD/DRP → SNP-BLUP → SNP → **SNP**

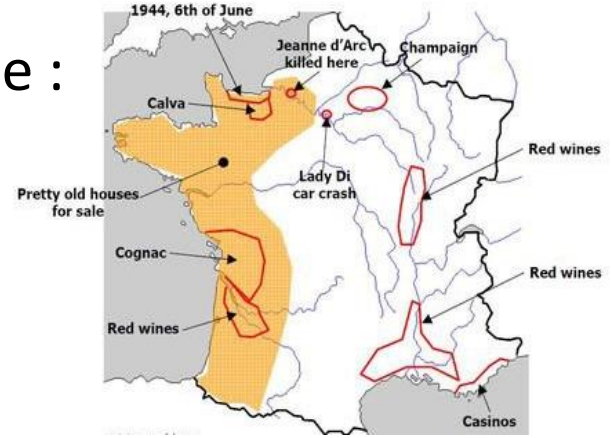
Data → MACE → DYD/DRP → SNP-BLUP → SNP → **MACE**

- Easiest : use national data only ? → disconnect from MACE

Challenge 2 : How to include results from countries with genomic evaluations deviating from GBLUP?

(+ SNP lists increasingly differ between countries)

e.g., France :



An example : our genomic model

QTL size	Genomic evaluation
Large Moderate Small	traced with markers ➔ haplotype effects $\hat{h}_j$ ➔ DGV = $\sum_{j=1,\ldots K}^{+} \hat{h}_j$
Tiny	Consider their sum only: $\hat{u} = \sum_{j'} \hat{m}_{j'} \sim N(0, \textbf{\textit{pedigree}}\ \text{relationship matrix})$ $\sim N(0, \textbf{\textit{genomic}}\ \text{relationship matrix})$

In practice…

$$g_i = \sum_{j=1}^{n} (h_{ij1} + h_{ij2}) + u_i$$

Trait dependent

Trait independent

$$g_i = \sum_{j=1}^{n} (h_{ij1} + h_{ij2}) + \sum_{j=1}^{k} (SNP_{ij1} + SNP_{ij2})$$

- Genomic relationships via EuroG10K chip:

  System size= constant

- Easy and fast evaluation once a week
- Causal variants easy to include

By the way…

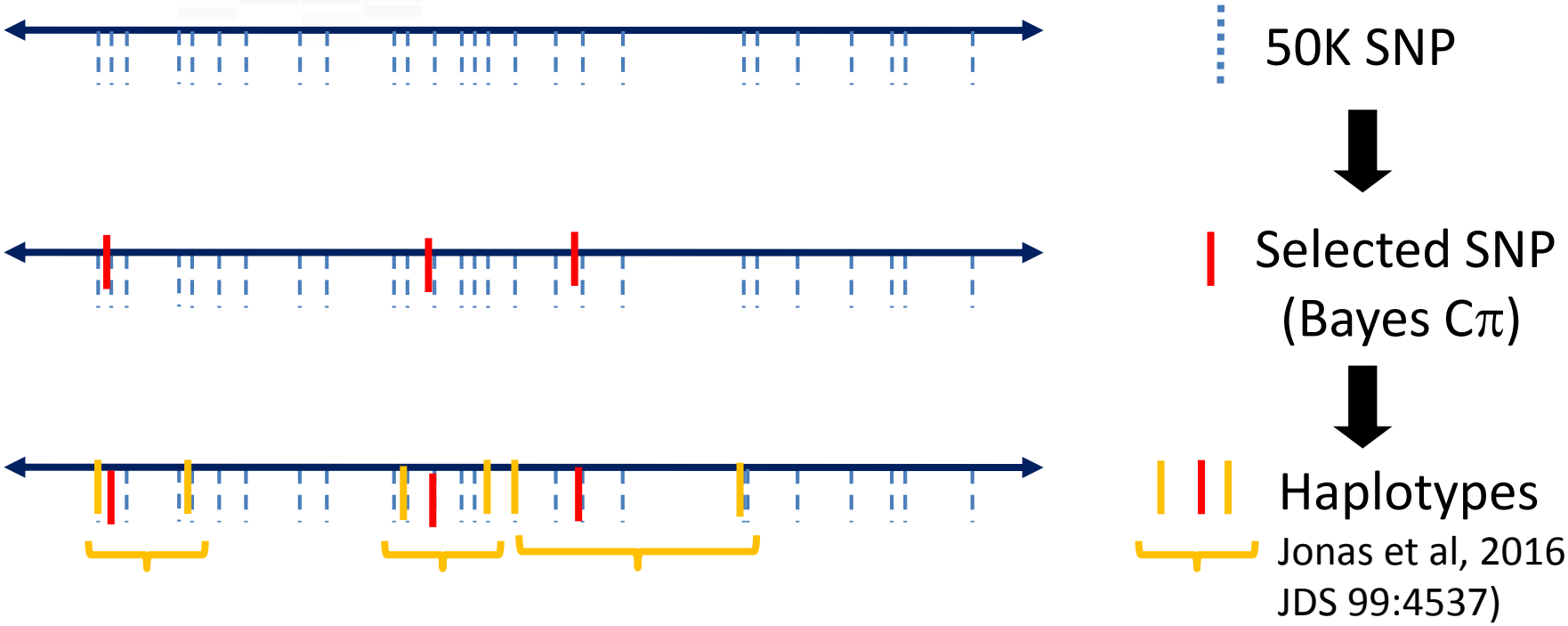
Challenge 3 : How do we deal with the « residual polygenic » component in an International SNP model?

- Ignore? ➔ suboptimal

  decrease accuracy, increase inflation

- The French way?

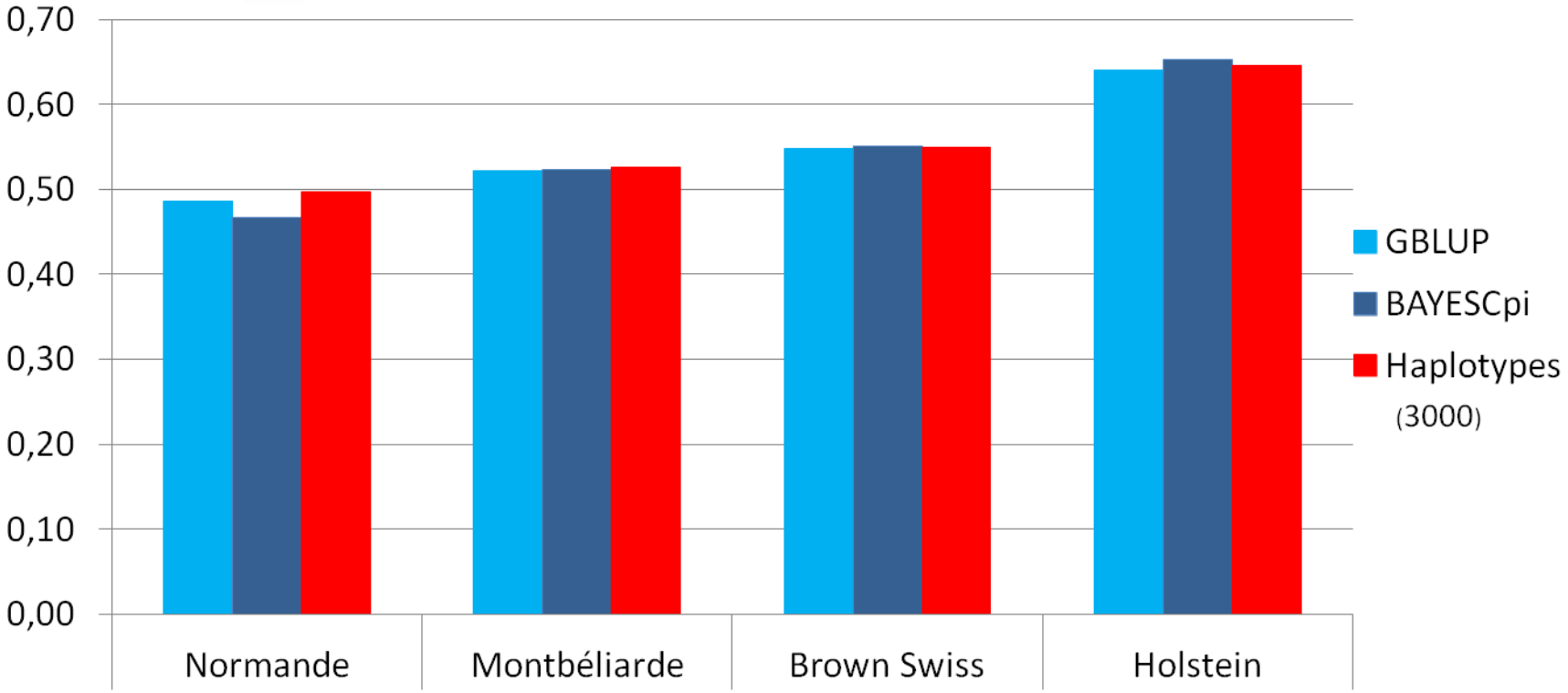
Back to challenge 2: another way to see it…



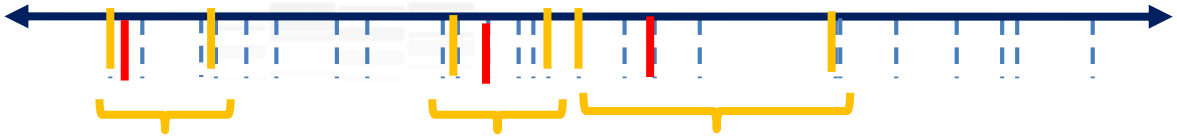
Expectations:

- More informative (haplotypes are more polymorphic)
- More stable over generations

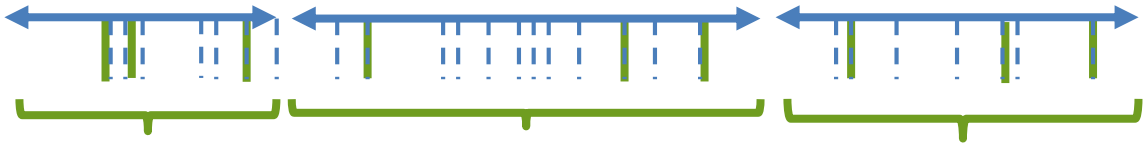
Validation results (27 to 41 traits /breed)



Can we do better ➔ haploblocks?



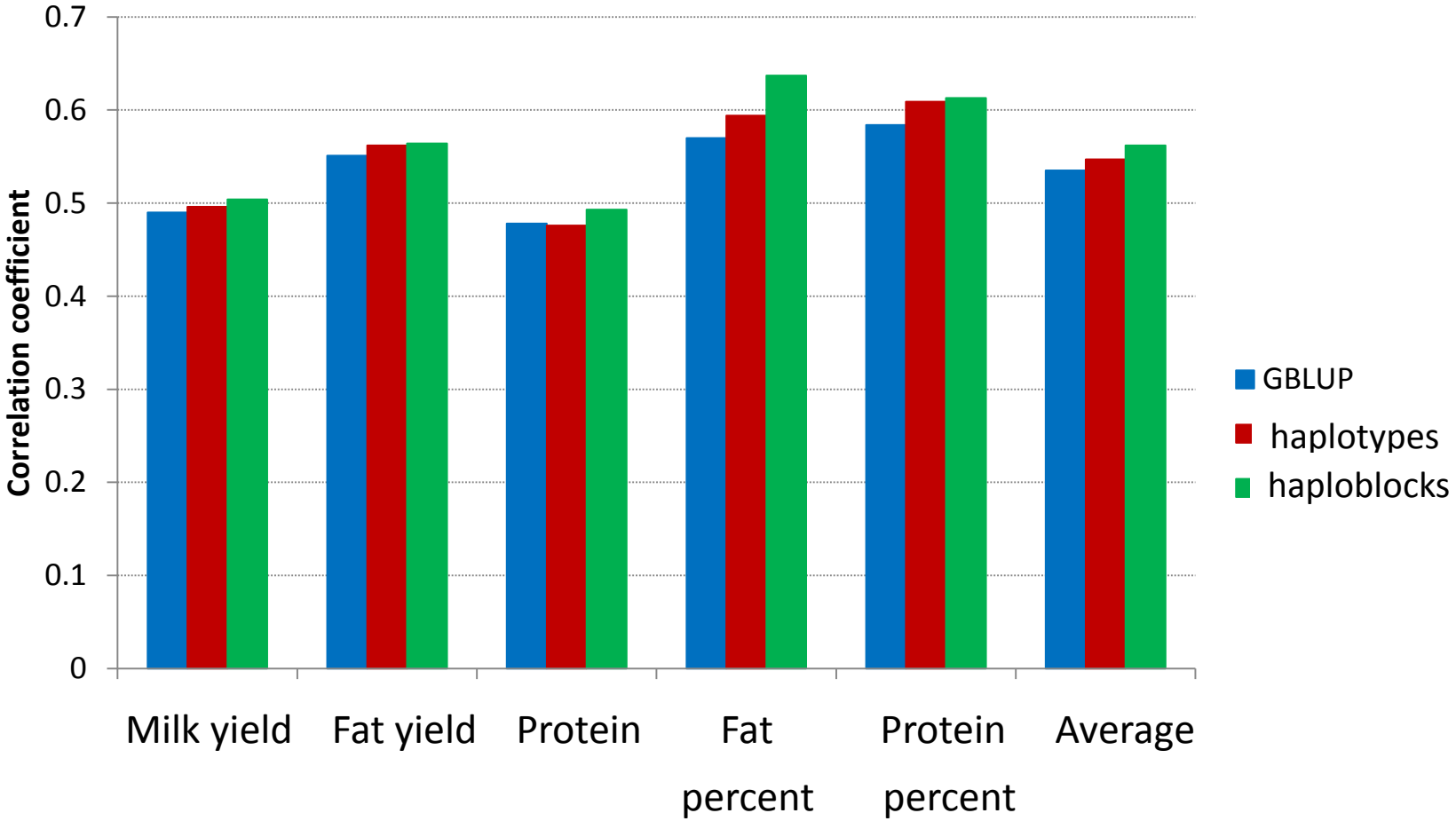
Haplotypes



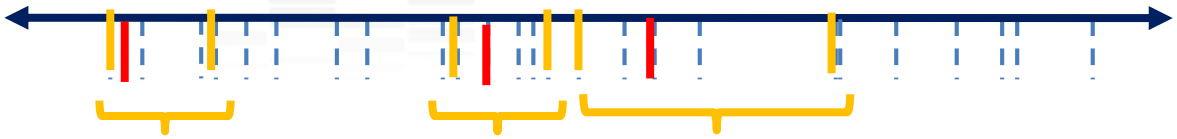
Haploblocks based on LD

(Jonas et al, 2017, in press)

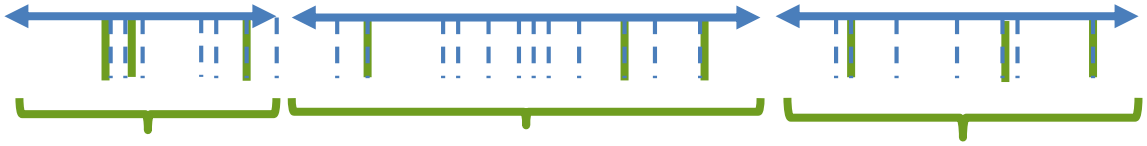
Validation results (Montbéliarde, 5 traits)



Can we do better ➔ haploblocks?

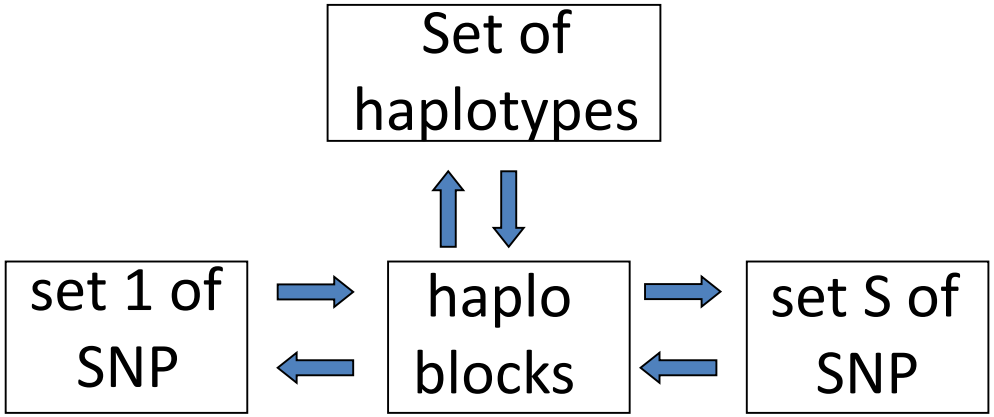


Haplotypes



Haploblocks based on LD

➔ A reason to prefer Mike's « **method 2b** » ?
= **international estimation of GEBV** of *haploblock* regions ?



Challenge 4 : will it make Interbull work simpler ?

- No validation of genetic trend to worry about ??
- Validation?
- Need to find out when noise rather than new information is added to the system. How?
- Data management ?
- Fee system ?

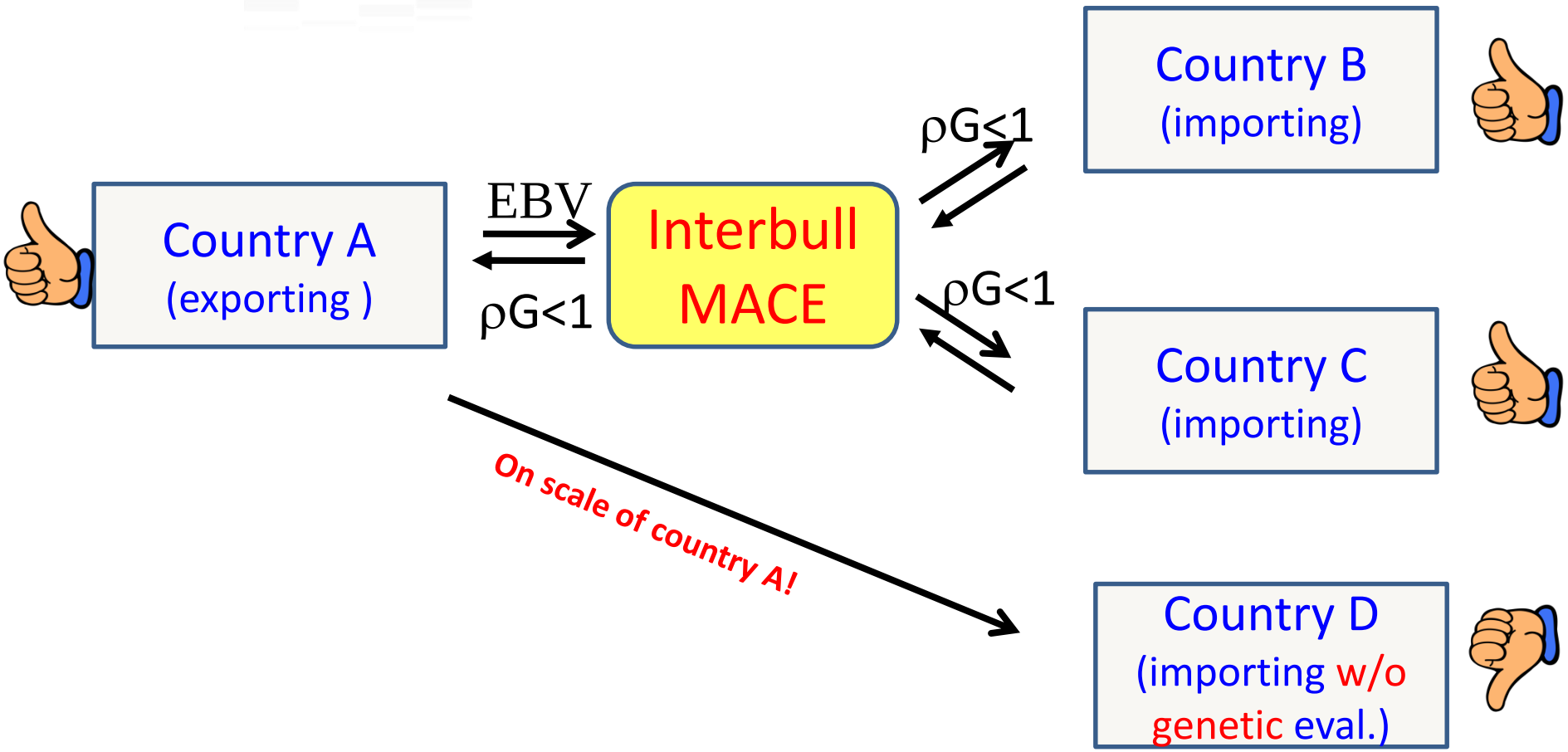
Challenge 5 : will it be accepted?

- So much effort to develop GMACE…
- Is SNP-MACE more politically acceptable than GMACE ?

- Benefit to all: higher reliability of SNP effects
  higher reliability of GEBV for both sexes
- Open new horizons for understanding what we do (detection and use of causal variants, source of GxE, multibreed genomic evaluation,…)

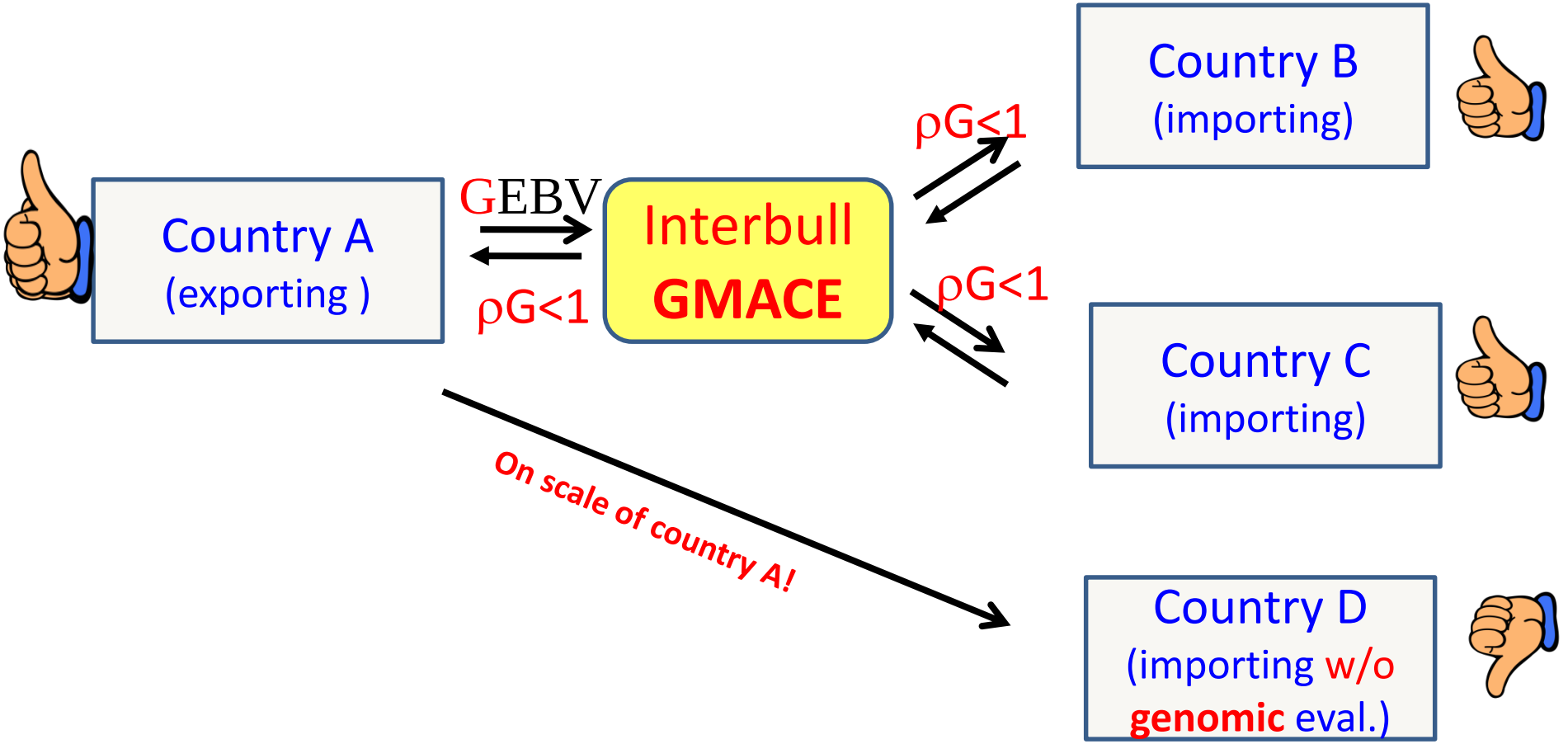
Will it be enough ?

International genetic evaluations

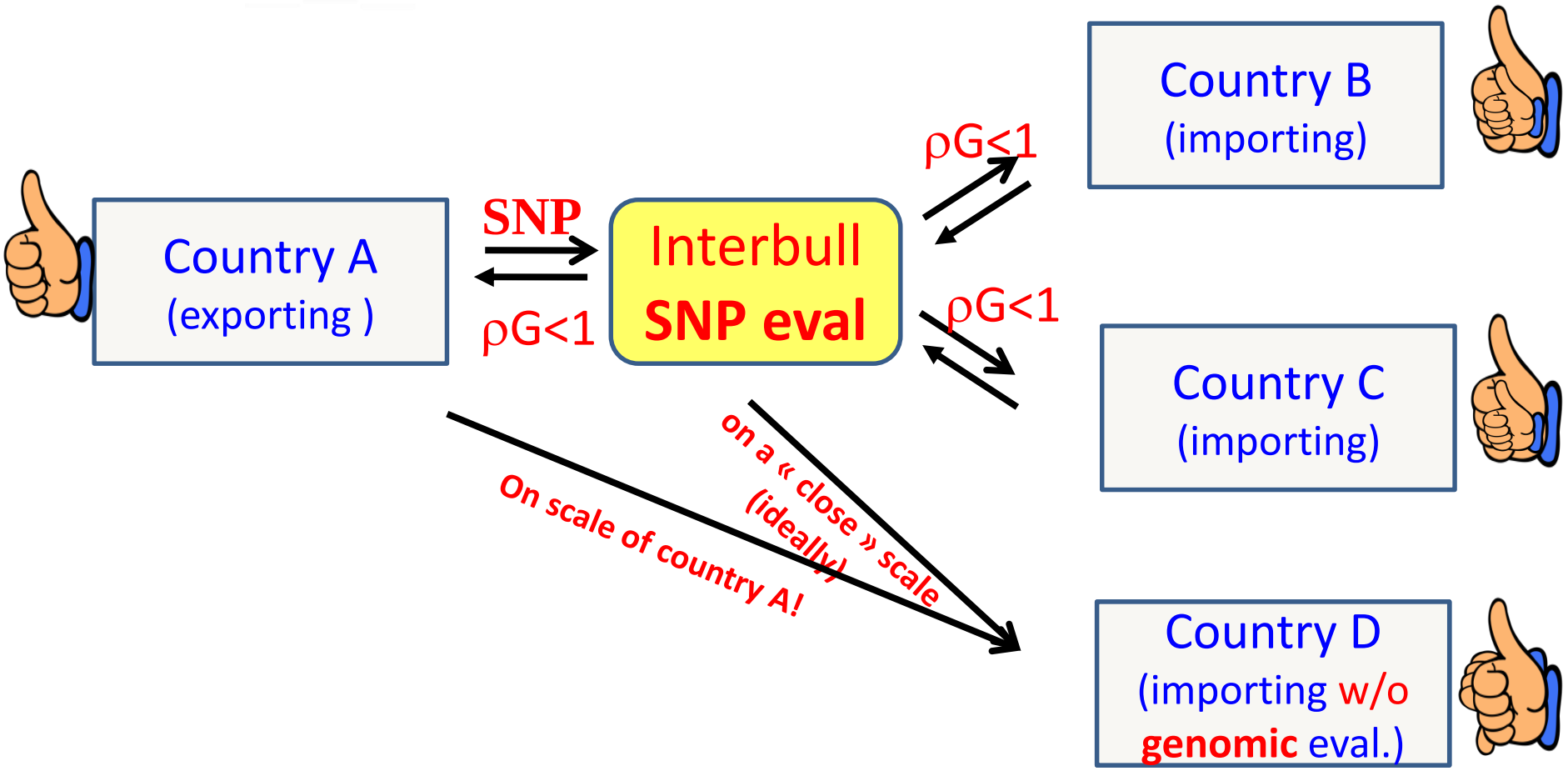


International genomic evaluations

Initially Now …



International SNP evaluations

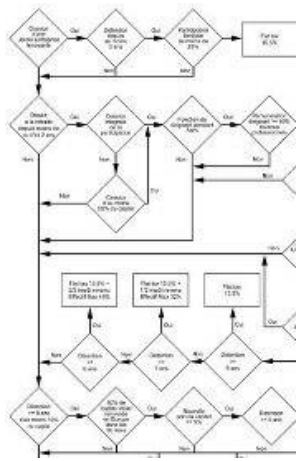


Summary

- Challenge 1 : redundant information
- Challenge 2: national genomic evaluations differing from GBLUP or with different sets of SNP
- Challenge 3: inclusion of a « residual polygenic » effect
- Challenge 4: Interbull chores and monitoring
- Challenge 5: acceptability …

Summary

- Opportunity 1: added reliability for all (incl. females)
- Opportunity 2: end of the Interbull « white elephant » ?
  (« Rube Goldbert machine », « usine à gaz »)
- Opportunity 3: genomic selection in countries without national genomic evaluation yet
- Opportunity 4: easier multibreed evaluations?
- Opportunity 5: understand genetic background (causal variants, G x E, …)



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