



## Some opportunities and challenges regarding SNP international evaluations

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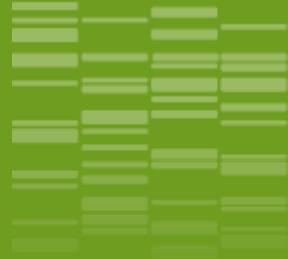
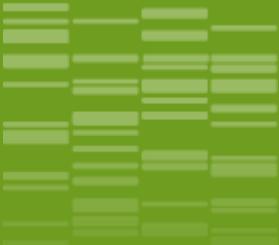
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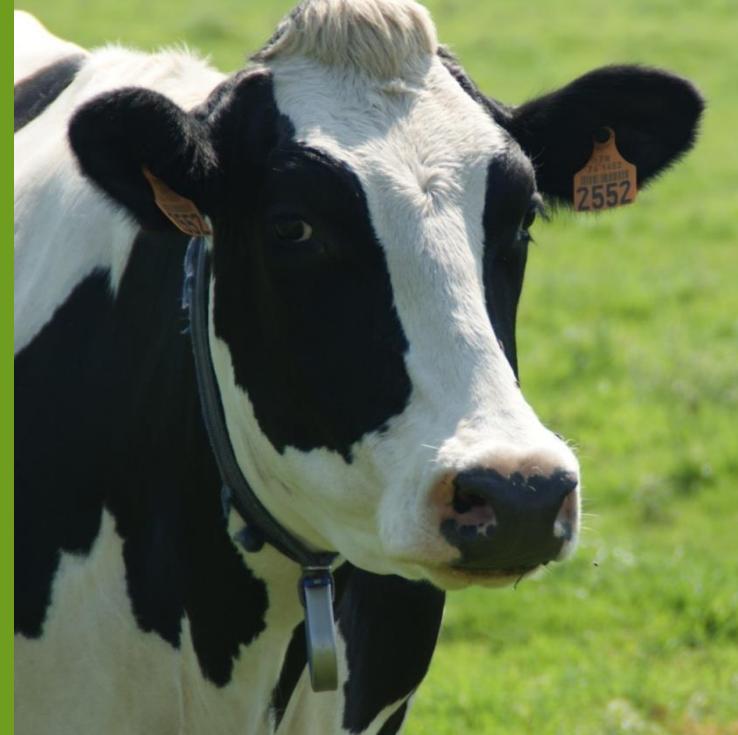
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# Some opportunities and challenges regarding SNP international evaluations

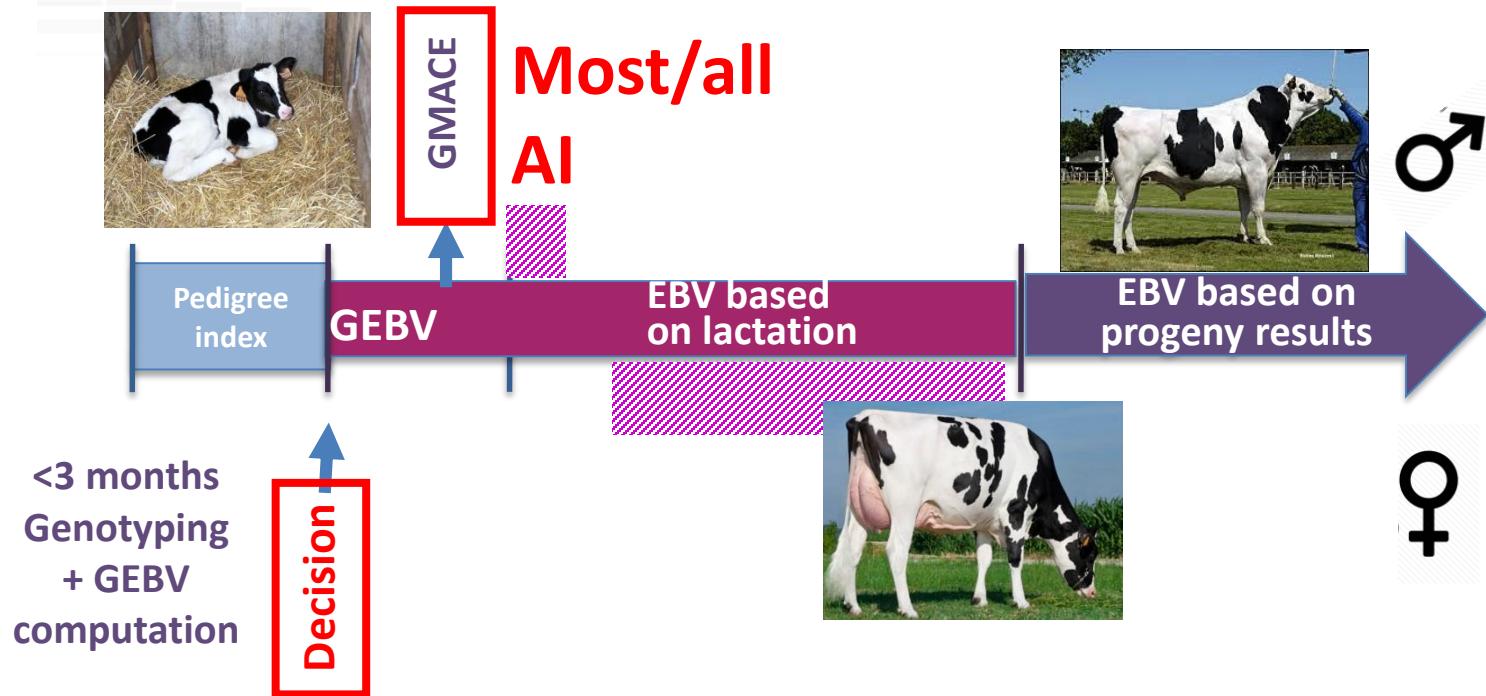


## Vincent Ducrocq

GABI, INRA, Jouy-en-Josas, France



# 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...

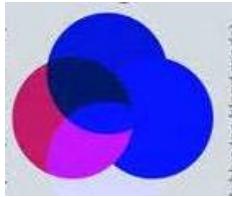
*(In France, in August 2016, > 300,000 Holstein genotyped animals  
+ number of genotyped females increases by ~20 to 30% a year)*

→ 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)

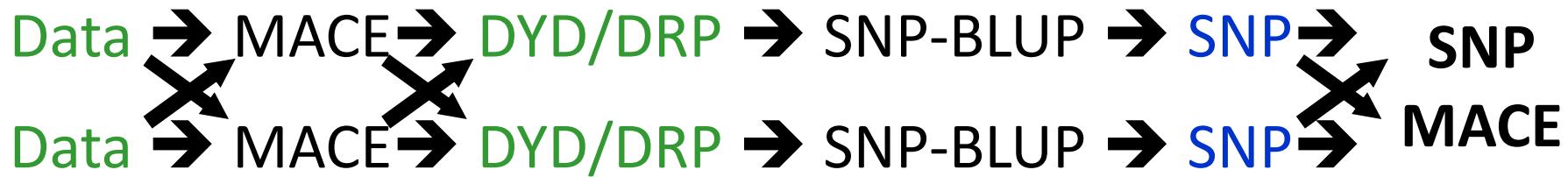




# Challenge 1 : redundant information = a big mess!



- 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:

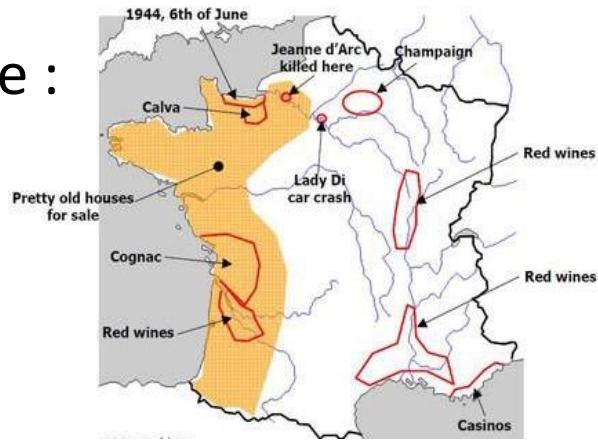


- Easiest : use national data only ? → disconnect from MACE



## 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	traced with markers → <b>haplotype effects</b> $\hat{h}_j$
Small	
Tiny	Consider their sum only: $\hat{u} = \sum_{j'} \hat{m}_{j'} \sim N(0, \cancel{\text{pedigree relationship matrix}}) \sim N(0, \text{genomic relationship matrix})$

# In practice...

The diagram illustrates the decomposition of a trait value  $g_i$  into two components. The first component,  $\sum_{j=1}^n (h_{ij1} + h_{ij2})$ , is highlighted with a blue border and labeled "Trait dependent". The second component,  $+ u_i$ , is circled in red and labeled "Trait independent". The third component,  $+\sum_{j=1}^k (SNP_{ij1} + SNP_{ij2})$ , is also circled in red and labeled "Trait independent".

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

- ❖ Genomic relationships via EuroG10K chip:  
**System size= constant**
- ❖ Easy and fast evaluation once a week
- ❖ Causal variants easy to include

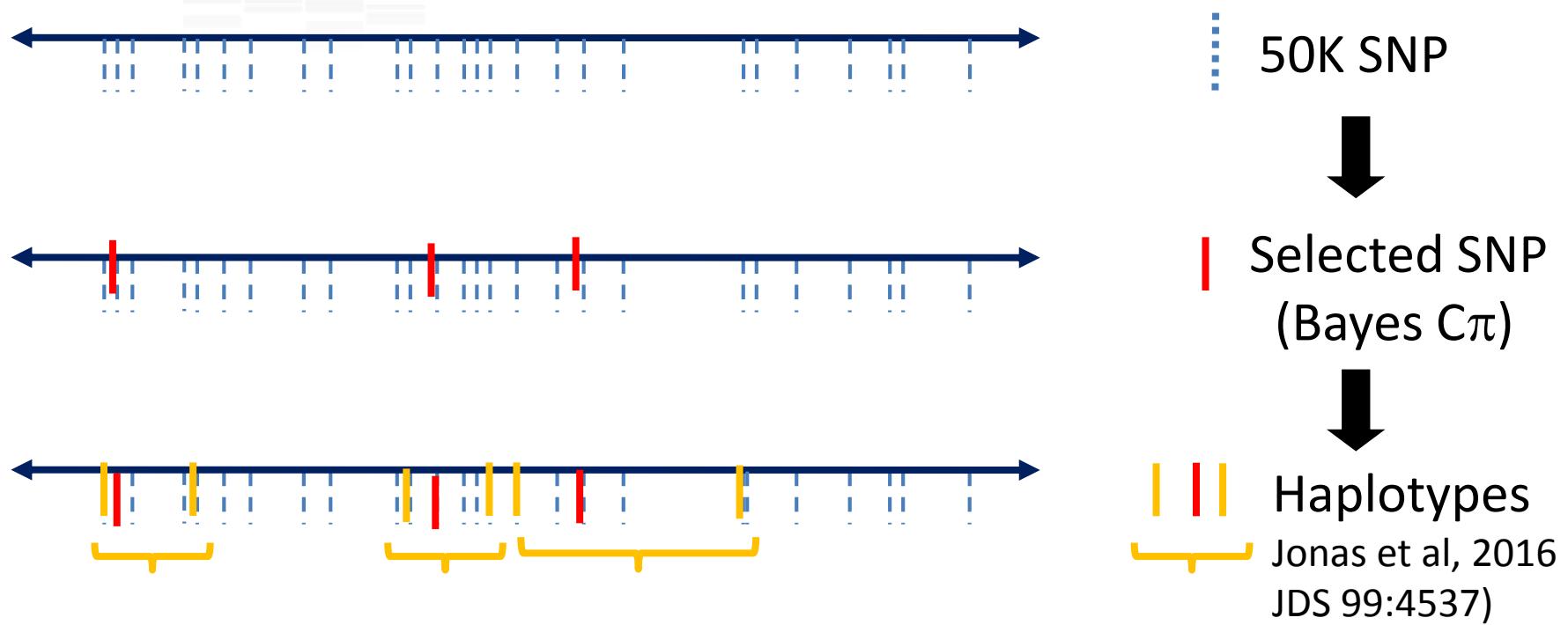
By the way...

## 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?

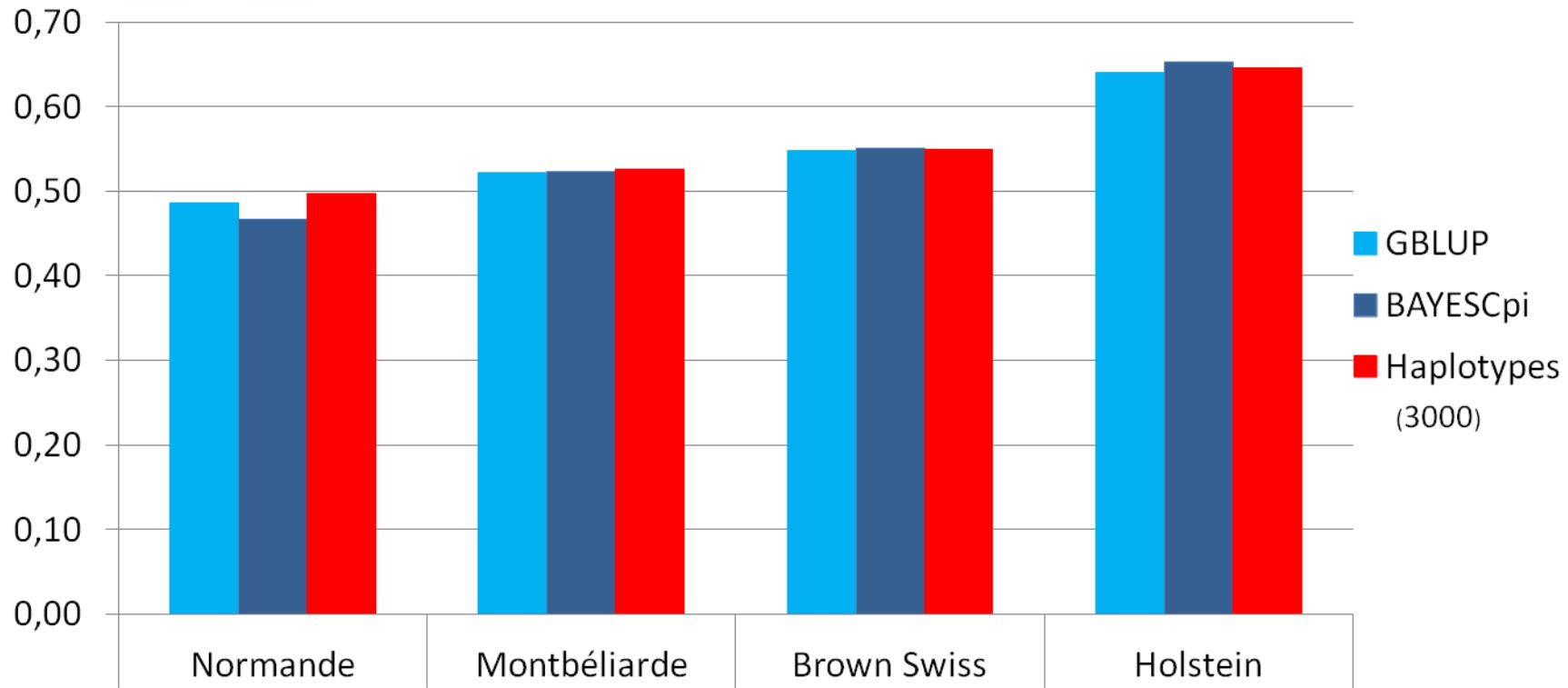
# Back to challenge 2: another way to see it...



Expectations:

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

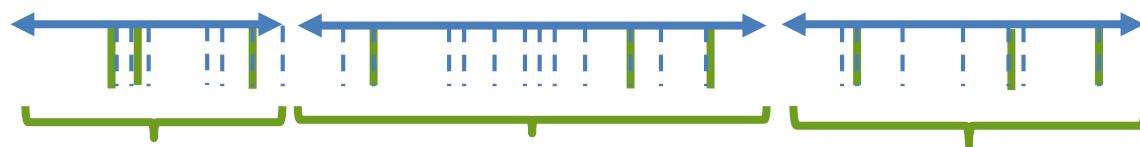
# Validation results (27 to 41 traits /breed)



# Can we do better → haploblocks?



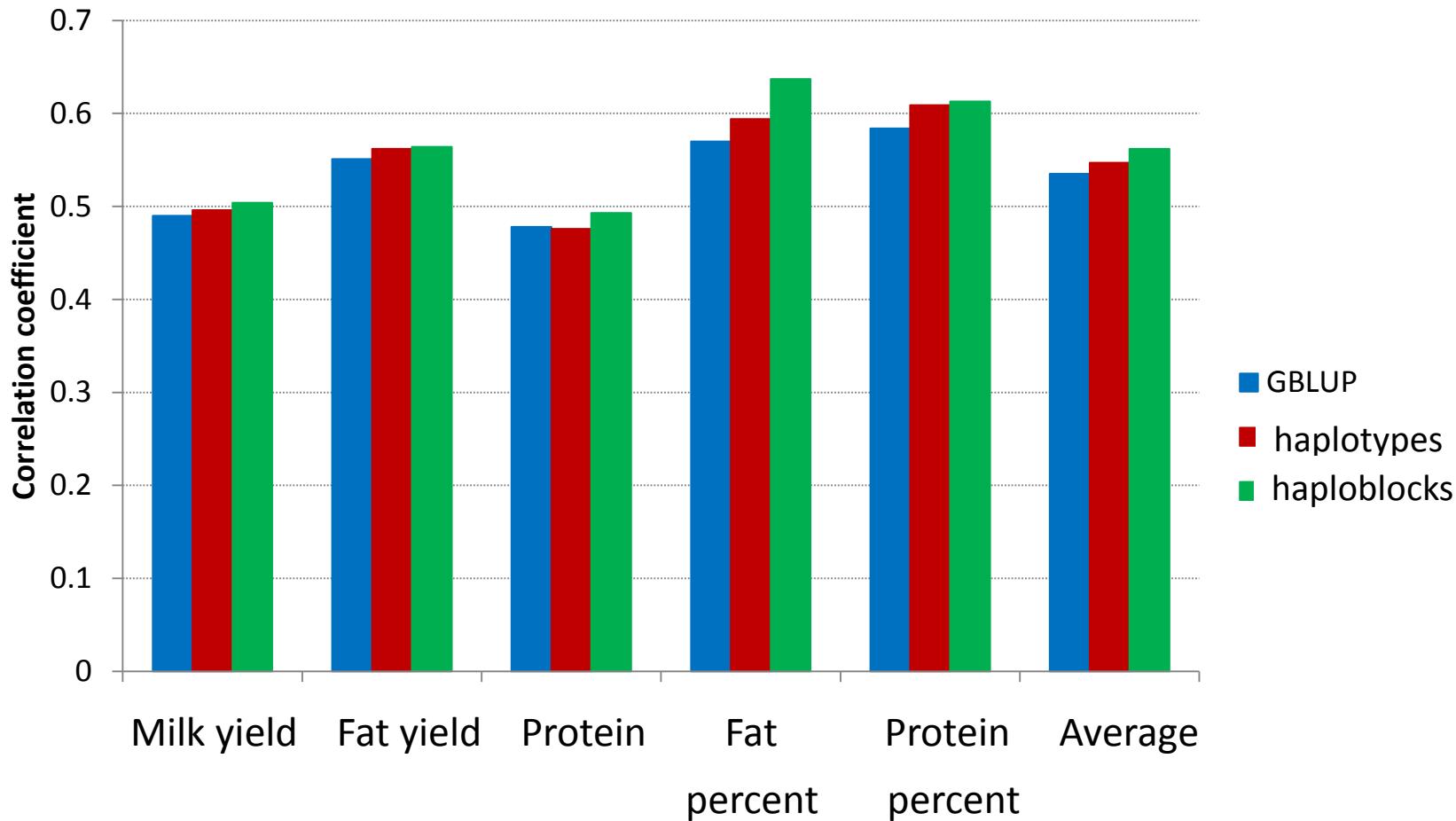
||| Haplotypes



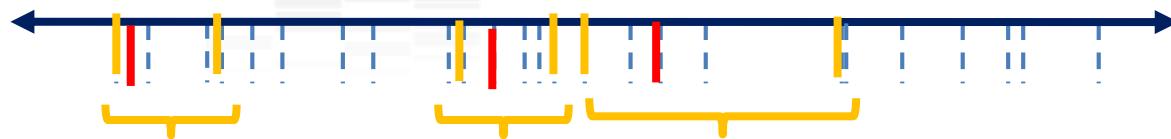
||| **Haplloblocks**  
based on LD

(Jonas et al, 2017, in press)

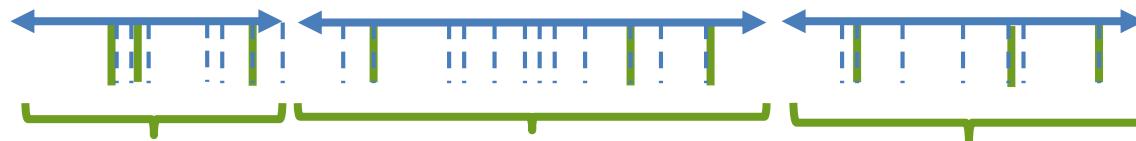
# Validation results (Montbéliarde, 5 traits)



# Can we do better → haploblocks?

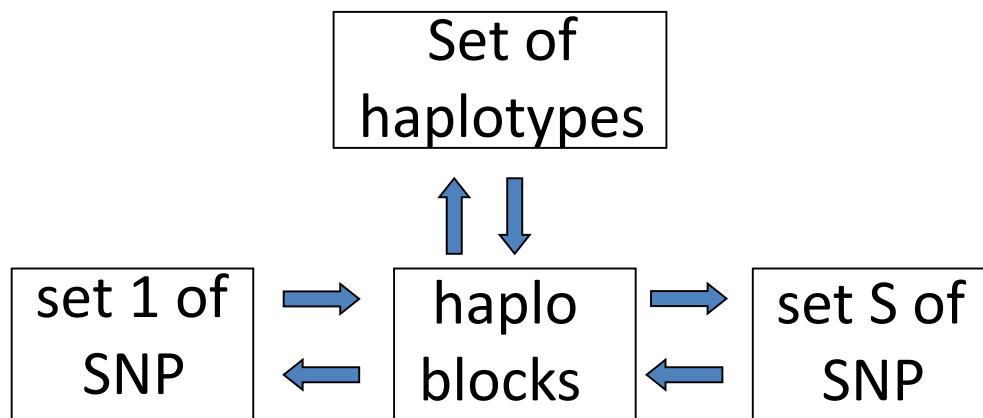


|| | Haplotypes



|| | 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 ?



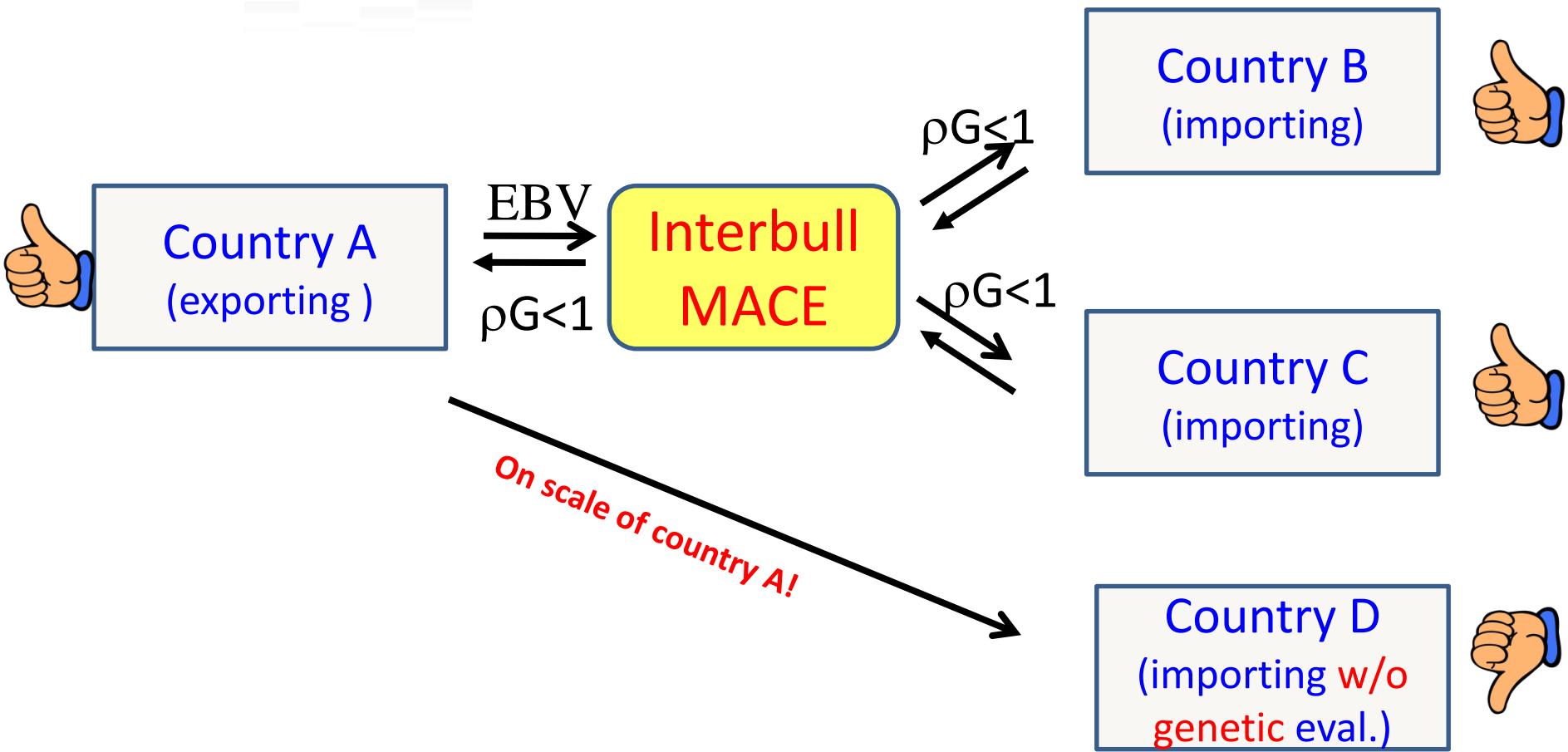
- ❖ Benefit to all: higher reliability of SNP effects  
higher reliability of GEBV for both sexes
- ❖ Open new horizons for understanding what we do  
(detection and use of causal variants, source of GxE,  
multibreed genomic evaluation,... )



Will it be enough ?

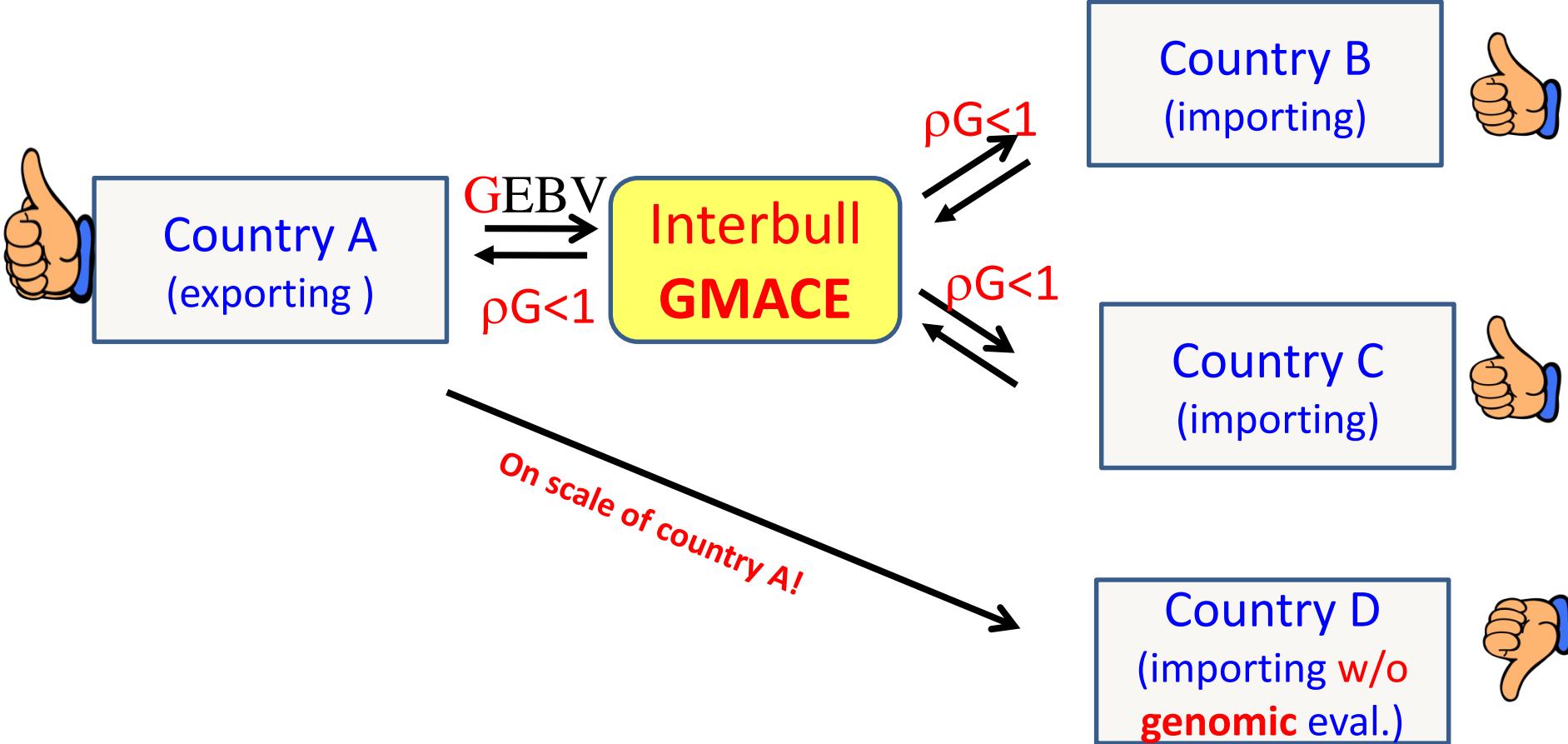


# International genetic evaluations

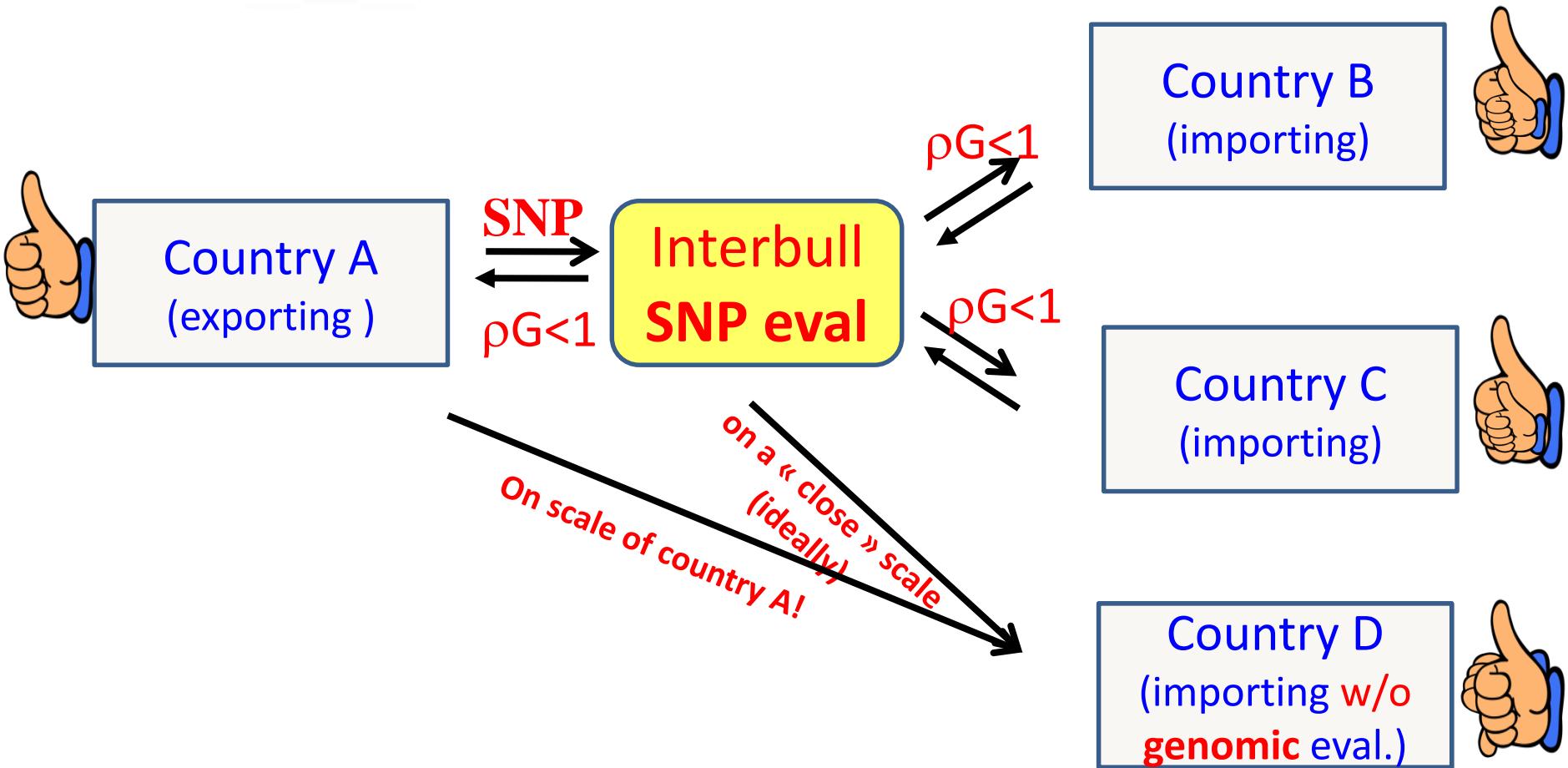


# International genomic evaluations

Initially    Now ...



# International SNP evaluations



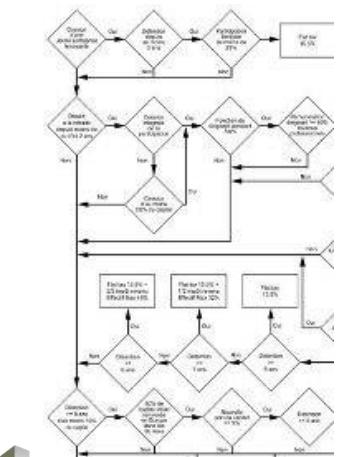


# Summary

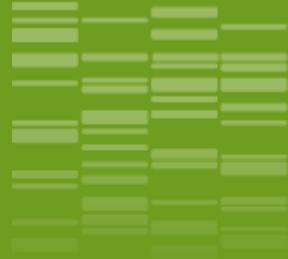
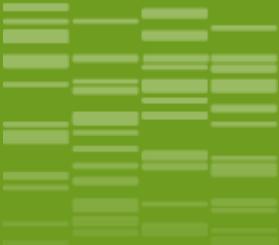
- Challenge 1 : redundant information
- Challenge 2: national genomic evaluations differing from GBLUP or with different sets of SNP
- Challenge 3: inclusion of a « residual polygenic » effect
- Challenge 4: Interbull chores and monitoring
- Challenge 5: acceptability ...

# Summary

- Opportunity 1: added reliability for all (incl. females)
  - Opportunity 2: end of the Interbull « white elephant » ?  
("Rube Goldberg 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, ...)



# THE FUTURE IS EXCITING



# Some opportunities and challenges regarding SNP international evaluations



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