Can MACE and ssGBLUP cohabitate without double-counting?

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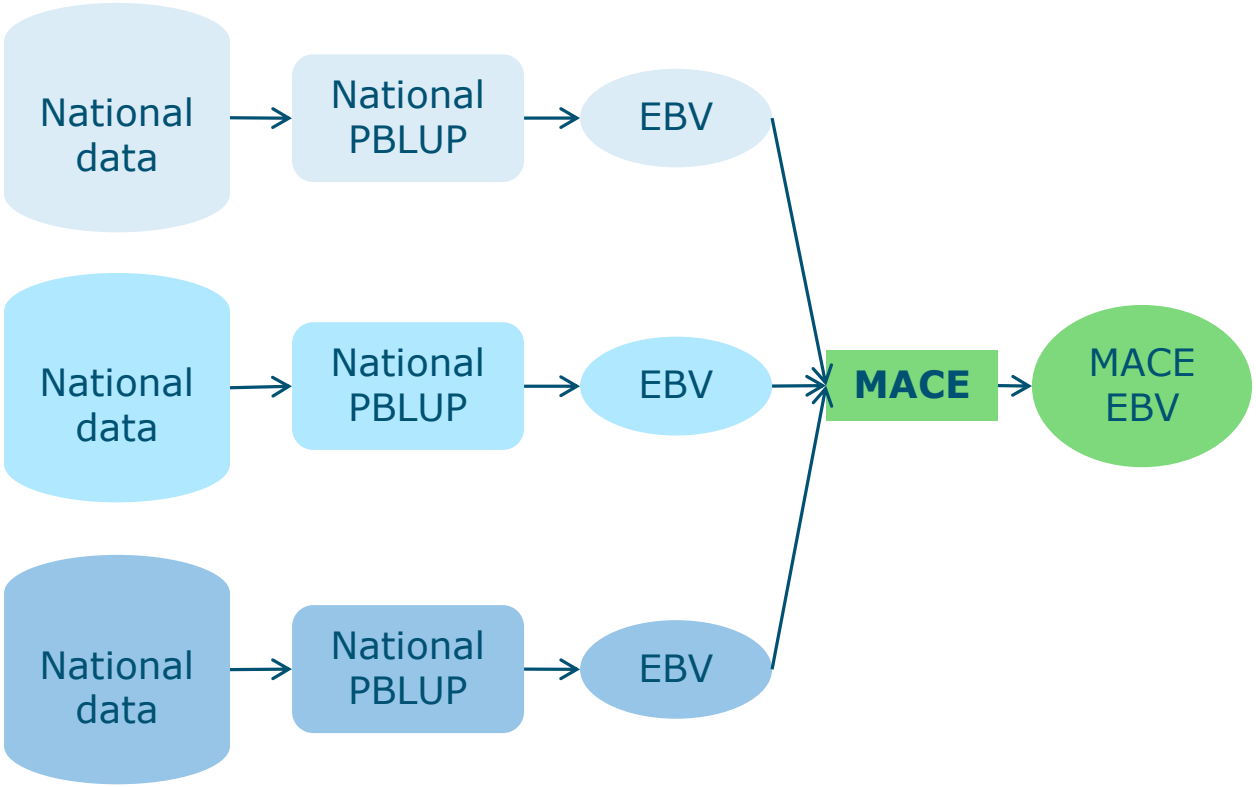
Aim

Investigation of possible double-counting within MACE

if the MACE input comes from

national ssGBLUP integrating MACE information

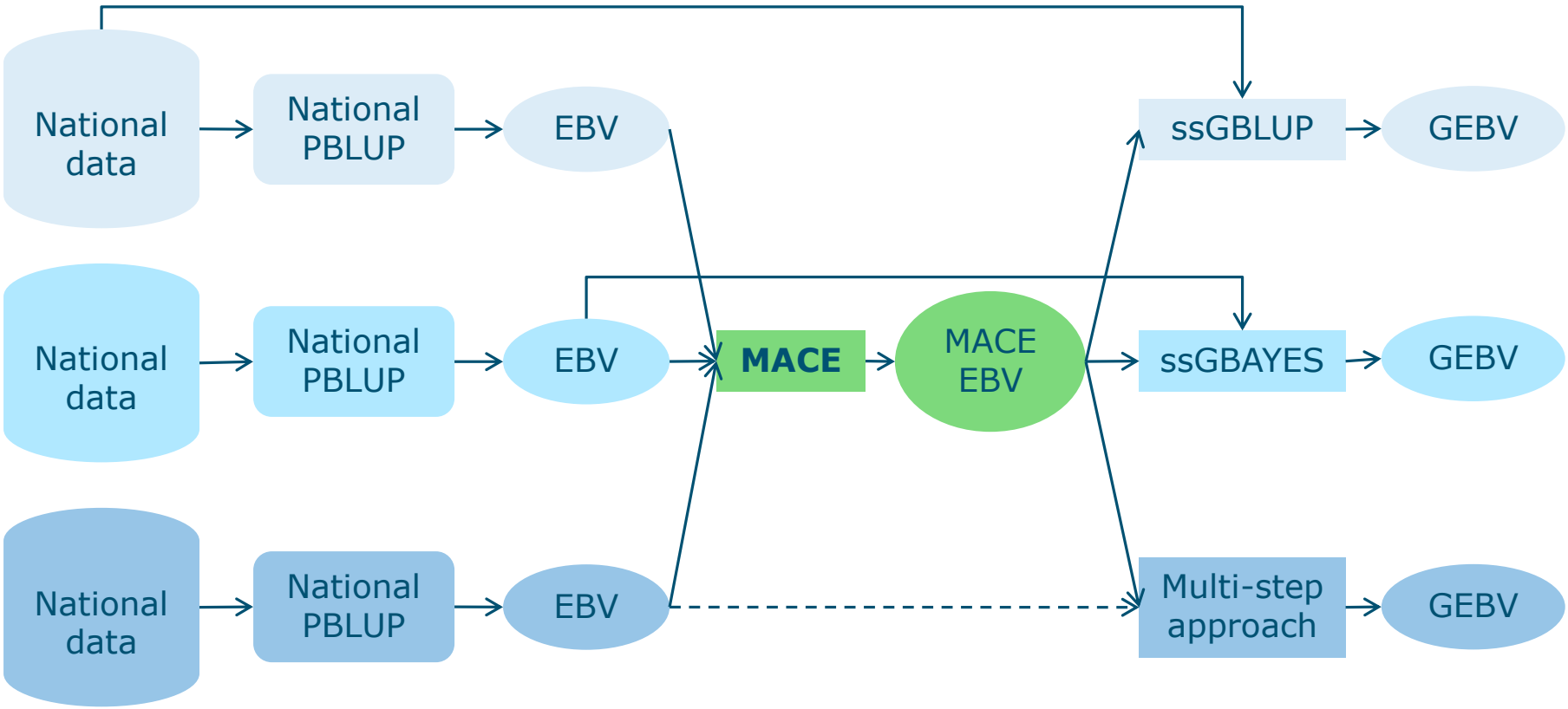
Current situation



MACE requires DRP and EDC

➔Deregression of national EBV

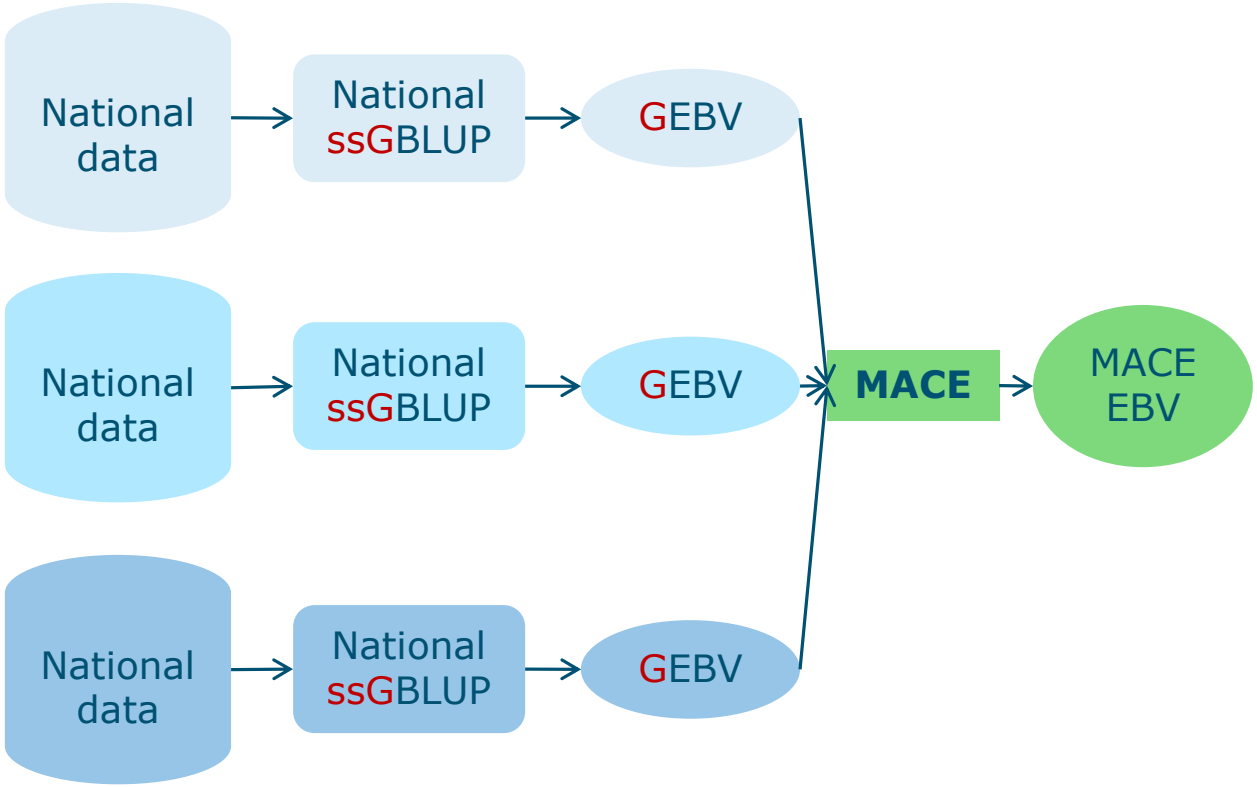
Current situation + genomic evaluation



- Genomic (pre-)selection
- MACE: no (obvious?) double-counting

Pribyl et al., 2012; Vandenplas et al., 2014; VanRaden et al., 2009

What happens with national ssGBLUP?



➔Double-counting of (pedigree-)genomic information

- Importance of the deregression of national GEBV

Avoiding double-counting of genomic info

Solutions?

1. MACE
    - EDC without pedigree-genomic information
    - Deregression of GEBV by mimicking a ssGBLUP
        - $\mathbf{H}^{-1}$ for all (genotyped) bulls
        - EDC = Amount of information coming from

          -own records

          -relatives (national daughters)

          ➔no pedigree-genomic information

EDC without pedigree-genomic info

Different estimation approaches

a. Current approach
    1. Estimation of REL based on own performance
    2. Combination of sources of information

b. Solving $diag\left(\left(\mathbf{EDC} + \mathbf{H}^{-1}\lambda\right)^{-1}\right) = \mathbf{PEV}$

EDC to be estimated

Pedigree-genomic relationship matrix between (genotyped) bulls

Prediction error variances from national ssGBLUP

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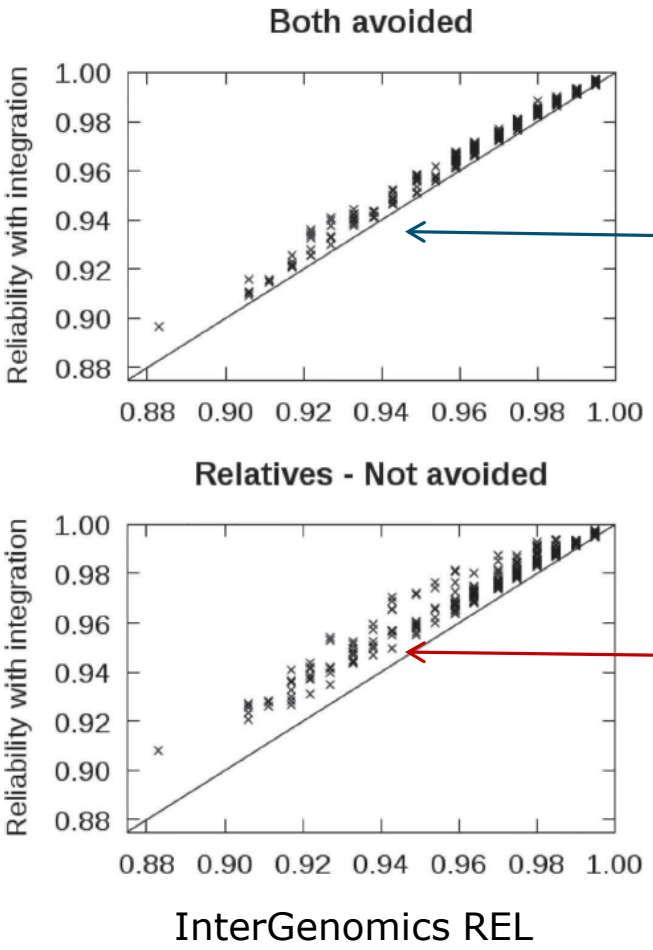
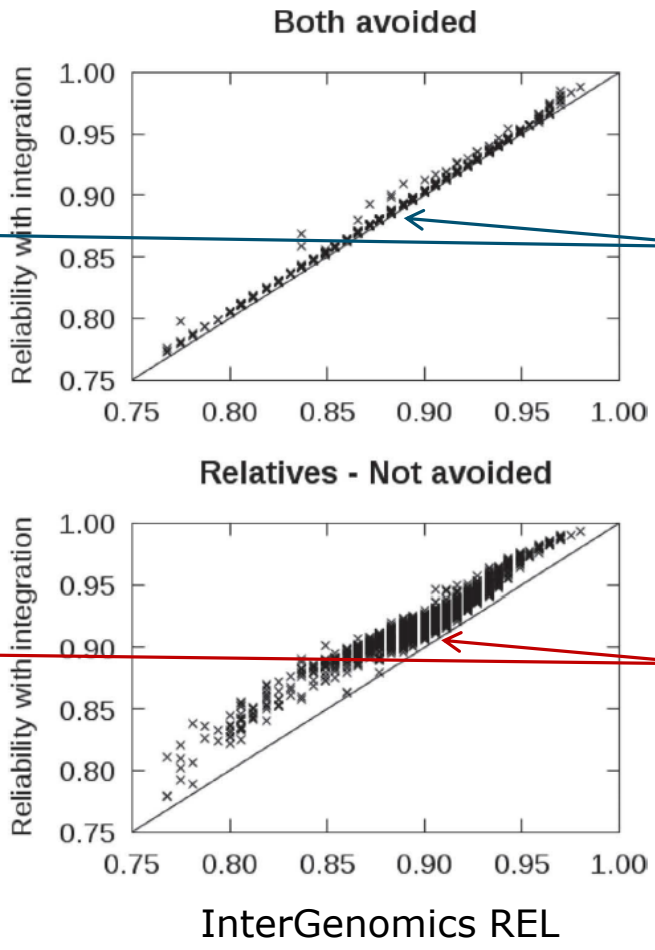
Fikse and Banos, 2001; Vandenplas et al., 2017

Slovenian ssGBLUP integrating IG GEBV

Internally used bulls



Internally unused bulls



Double-counting (mostly) **avoided**

Overestimation due to double-counting of pedigree-genomic information

Vandenplas et al., 2017

Avoiding double-counting of genomic info

Solutions?

1. MACE
    - EDC without pedigree-genomic information
    - Deregression of GEBV by mimicking a ssGBLUP

2. MACE ➔ GMACE
    - EDC with genomic information
    - Deregression of GEBV by mimicking a BLUP
        - $\mathbf{A}^{-1}$ for all (genotyped) bulls

VanRaden and Sullivan, 2010

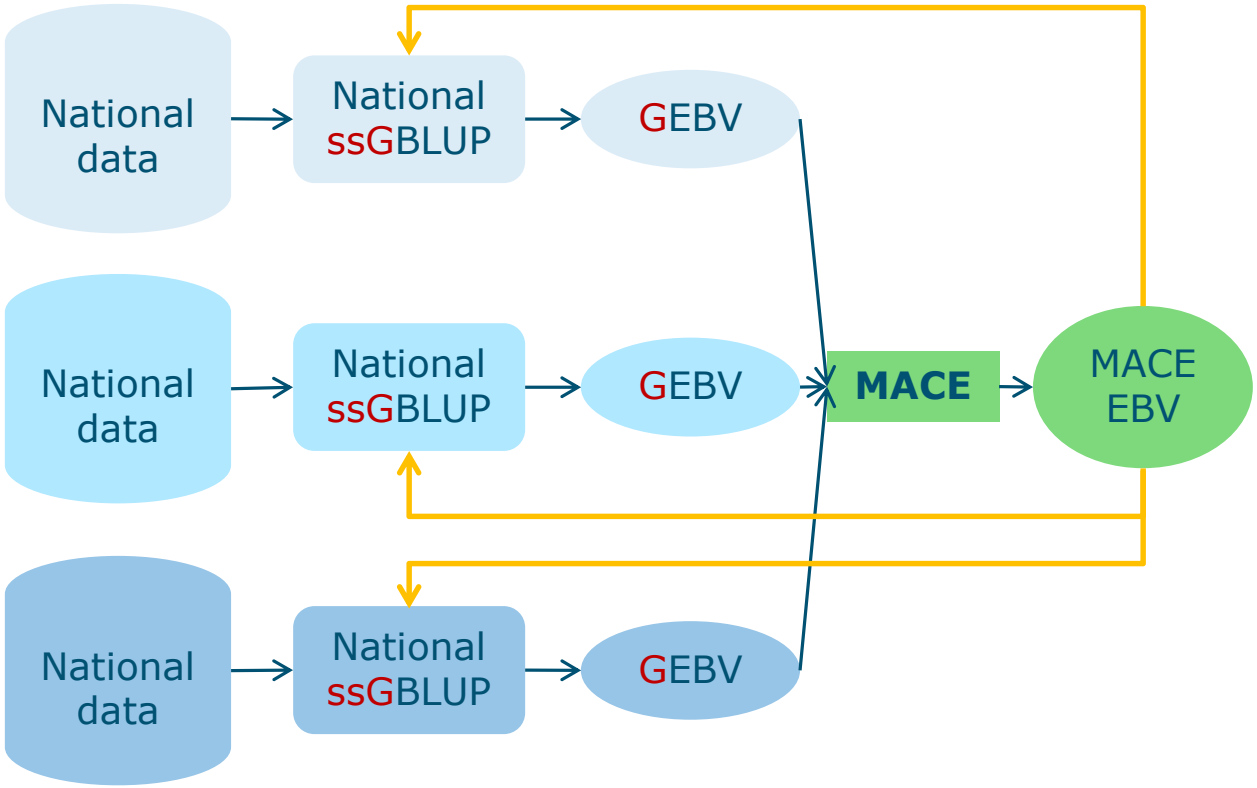
Double-counting: pedigree-genomic info

- Impact of double-counting (e.g., Fikse and Banos, 2001; Vandenplas et al., 2014; Calus et al., 2016)
  - EBV: low
  - REL: overestimation
    - Especially for animals with low REL (cows, young bulls)

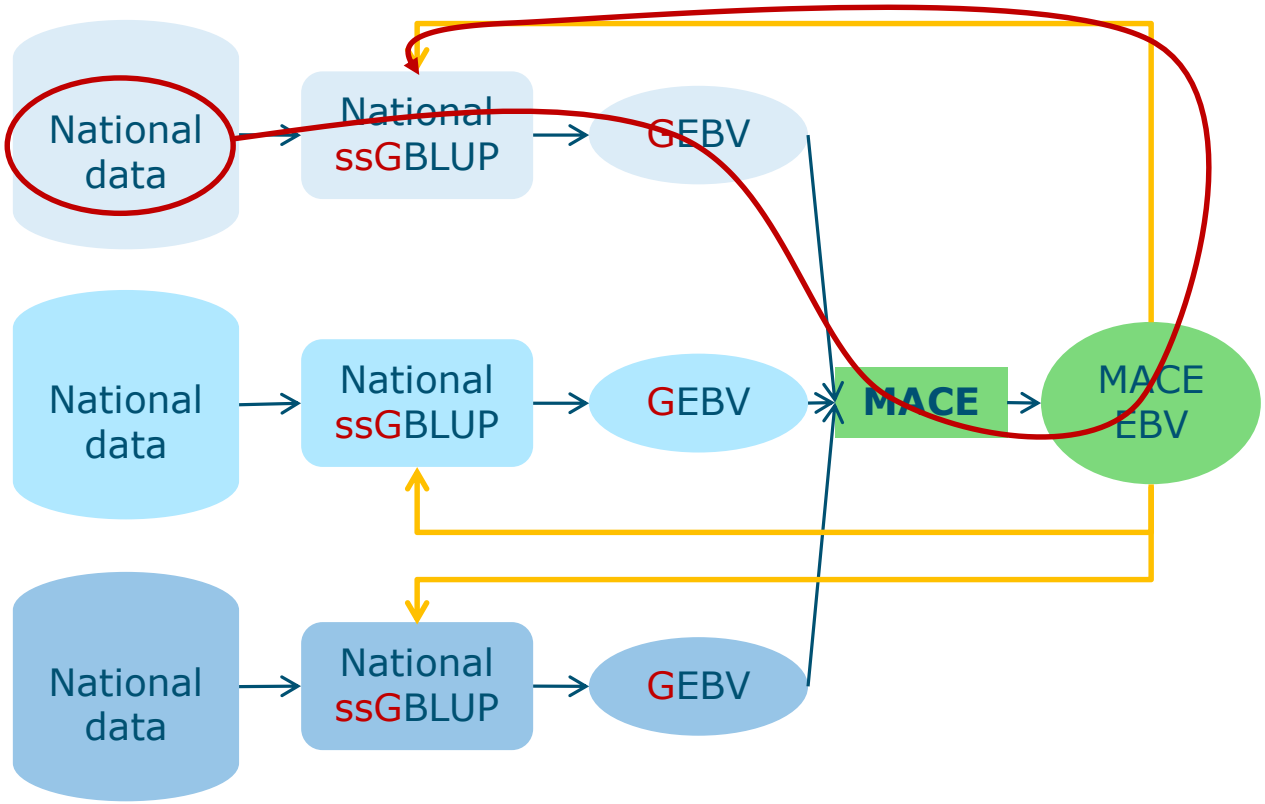
- Solutions exist

  ➔ Must be tested (in the context of ssGBLUP)

What happens with ssGBLUP+MACE?

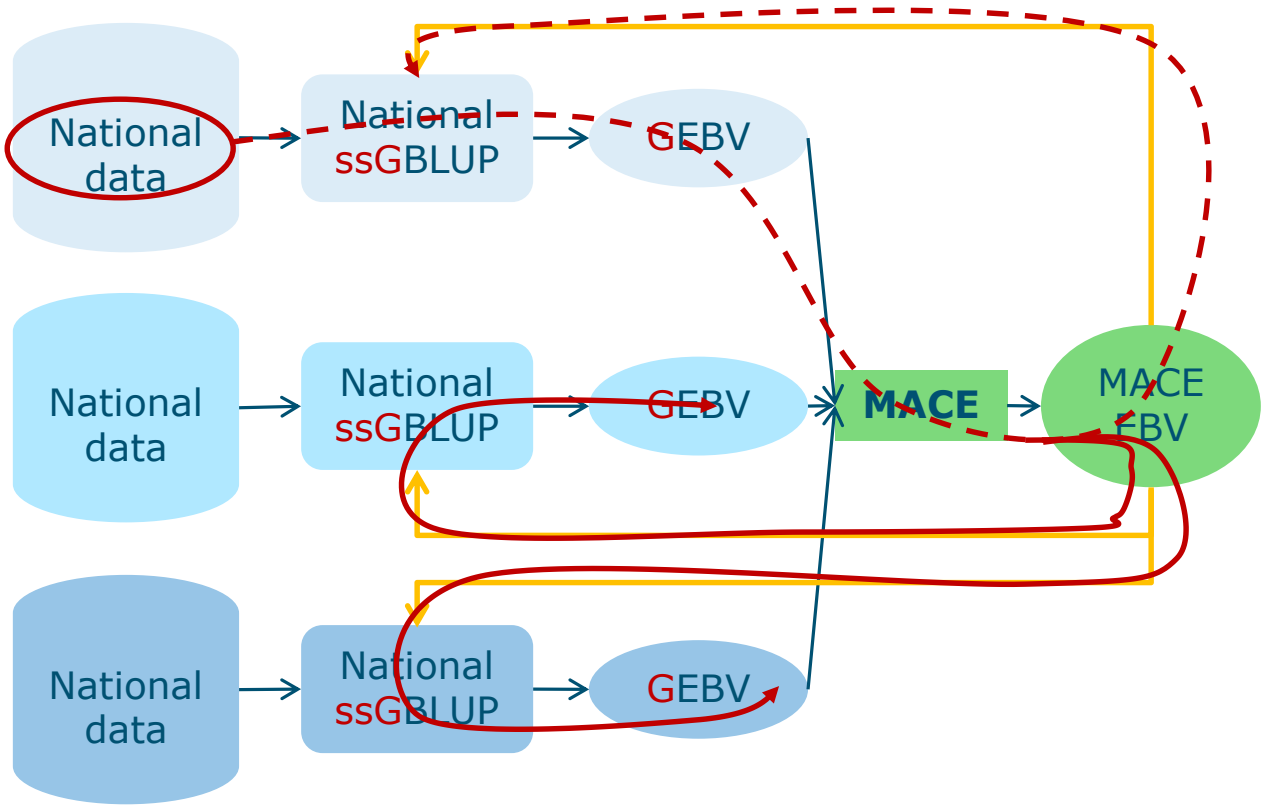


What happens with ssGBLUP+MACE?



- Double-counting of own national information "solved"

What happens with ssGBLUP+MACE?



- Double-counting of own national information "solved"
- Double-counting of "foreign" information at MACE level

Double-counting: foreign information

- Double-counting at MACE level
  - BUT specific to each national evaluation!
- DRP + EDC from national ssGBLUP+MACE
  - Free of pedigree-genomic information
  - Includes
    - National information
    - Foreign information provided by other ssGBLUP+MACE

Avoiding double-counting of foreign info

1. Residual covariances (~GMACE)?

2. Deregression of foreign information

   ➔Subtraction of foreign information from the total amount of information used in ssGBLUP+MACE

3. Others?

National evaluation + external info

- External info = EBV+REL from joint evaluation (national + foreign data)
  - Amount of internal information: ~46%

Correlation	External	Internal
Joint - Internal	**0.57** (0.13)	**0.93** (0.02)
Joint – (Internal + ext. info)	**0.96** (0.02)	**0.98** (0.00)
Joint - (Internal + ext. info. – int. info)	**>0.99** (0.00)	**>0.99** (0.00)

➔Double-counting avoided

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Vandenplas et al., 2014

Walloon evaluation + MACE info

- MACE includes Walloon information ➔double-counting
- Ref.: MACE EBV

Milk yield	Corr.	Regr. coef.	REL
Walloon	0.89	0.87	0.74 (0.22)
Walloon+MACE	**0.99**	**0.98**	**0.91** (0.05)
Walloon+MACE -Walloon	**0.99**	**>0.99**	**0.90** (0.06)

➔Low impact

➔To be evaluated per national evaluation, type of animals,...

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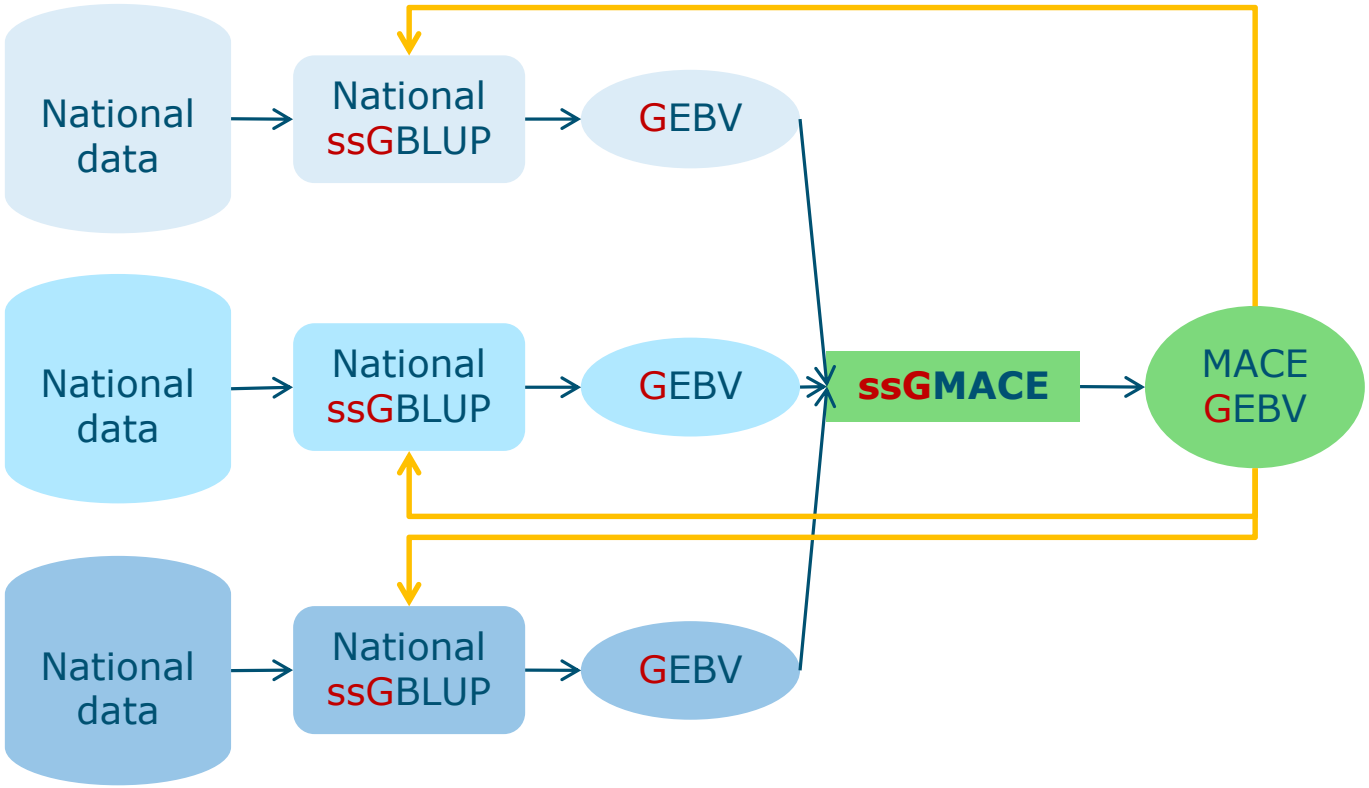
Vandenplas et al., 2014

ssGMACE?

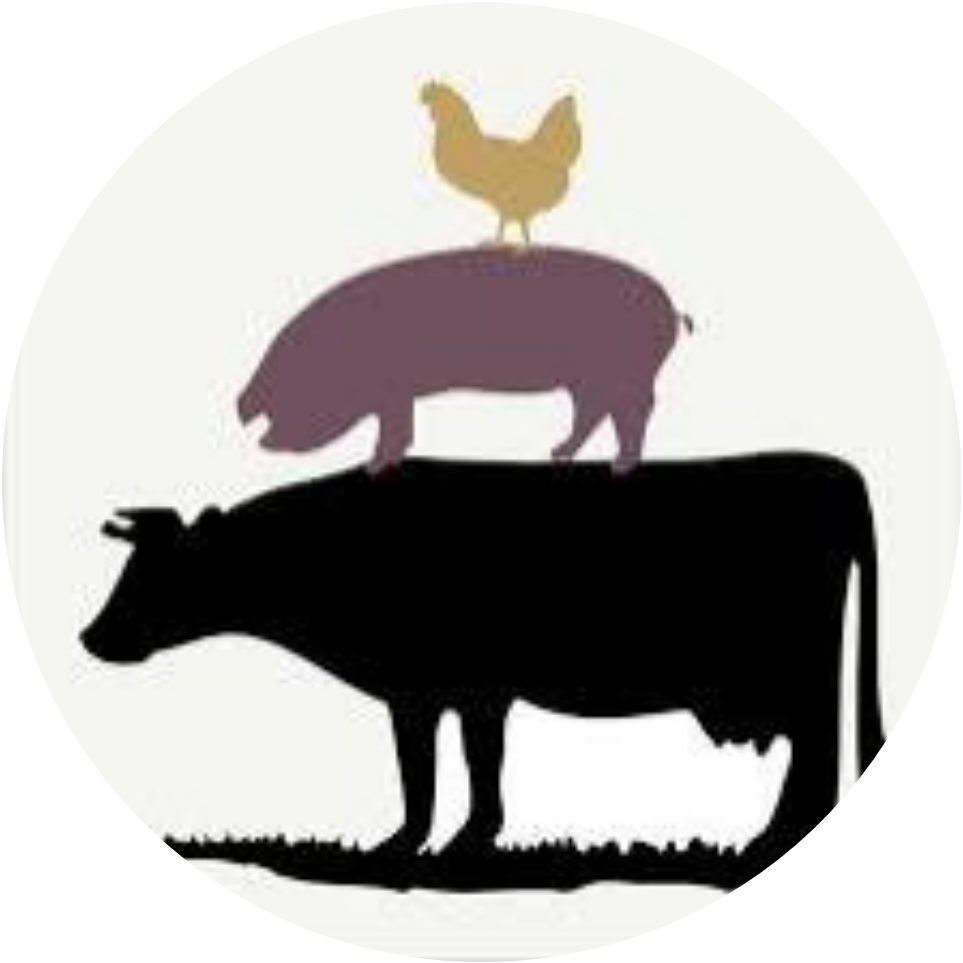


➔MACE using a pedigree-genomic relationship matrix?

Conclusions

- Double-counting can be avoided (theoretically?)
  - Pedigree-genomic information
  - Foreign information
- Solutions exist!
  - ➔Must be tested
  - ➔In practice, many approximations at several stages
- Impact of double-counting may differ among countries

Questions?



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