

# Walloon single step genomic evaluation system integrating local and MACE EBV

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# Context

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- ❑ Walloon dairy cattle:
  - Small scale population
  - Foreign AI sires of:
    - ❖ **87%** of cows in 1<sup>st</sup> to 3<sup>rd</sup> lactation in 2012, of which:
      - ✓ 25% sired by 371 bulls born in USA
      - ✓ 16% sired by 298 bulls born in NLD
      - ✓ 16% sired by 110 bulls born in FRA
      - ✓ 15% sired by 240 bulls born in DEU
      - ✓ 12% sired by 177 bulls born in CAN
      - ✓ 16% sired by bulls born in other countries
  
- ❑ Most reliable GEBV if estimated from all available sources

# Context

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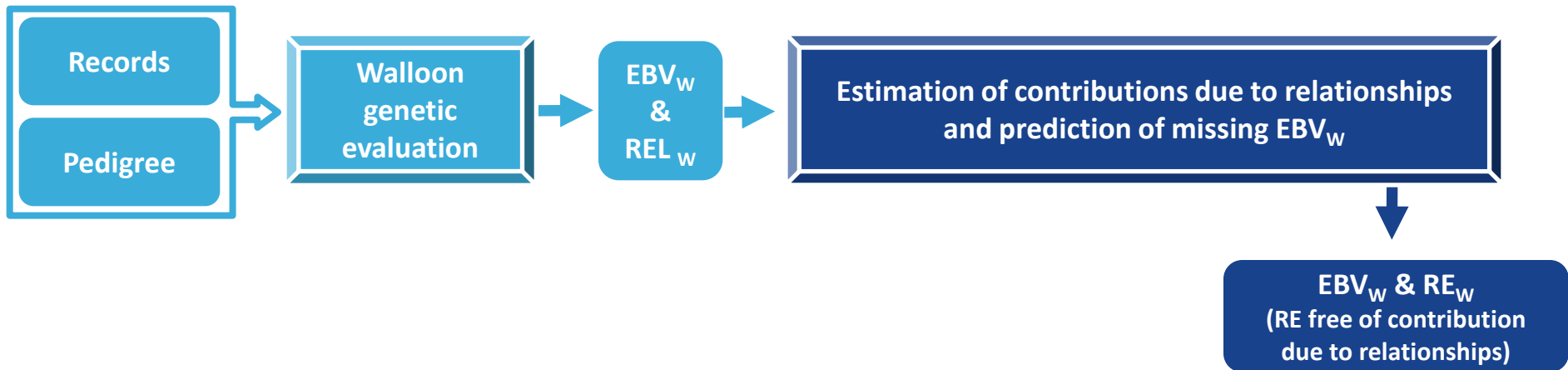
- ❑ Single-step genomic evaluation (ssGBLUP):
  - Simultaneous combination of genomic, pedigree and phenotypic information
- ❑ Current limitation
  - Only available local records used
  - External phenotypic information (*e.g.*, available as MACE EBV) not used

# Aim

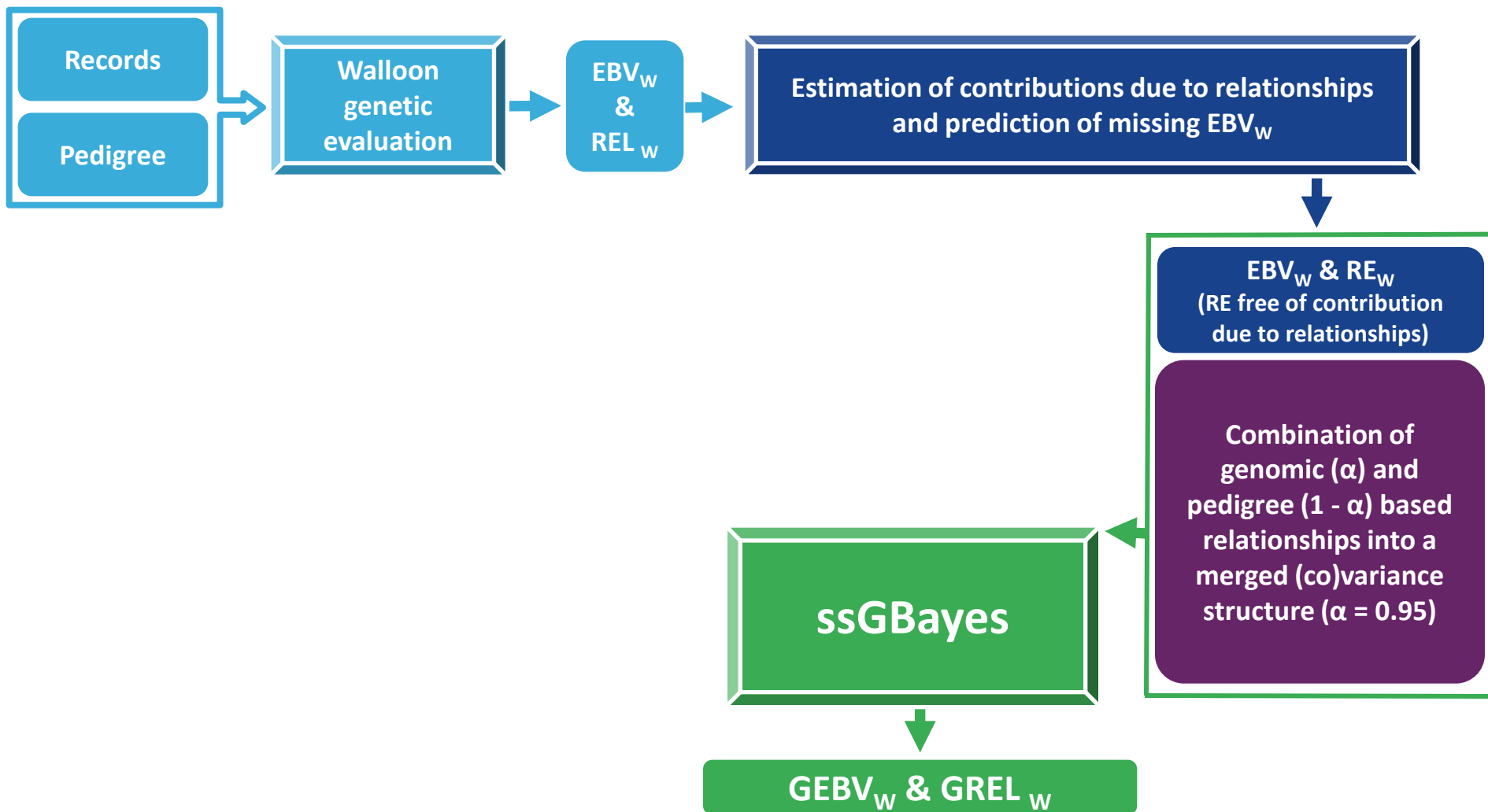
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- ❑ To develop a genomic evaluation adapted to Walloon dairy cattle
  - ➔ Needs to combine simultaneously:
    - Genotypes
    - Pedigree
    - Local information
    - Foreign information
- ❑ Local and foreign information:
  - Considered as *a priori* known external information
  - Incorporated using a Bayesian approach
  - Correct propagation of all this information without multiple considerations of contributions due to relationships and due to records
- ❑ Miming hypothetical mixed model equations and replacing pedigree information by combined pedigree and genomic information ➔ **Bayesian single step Genomic Evaluation: ssGBayes**

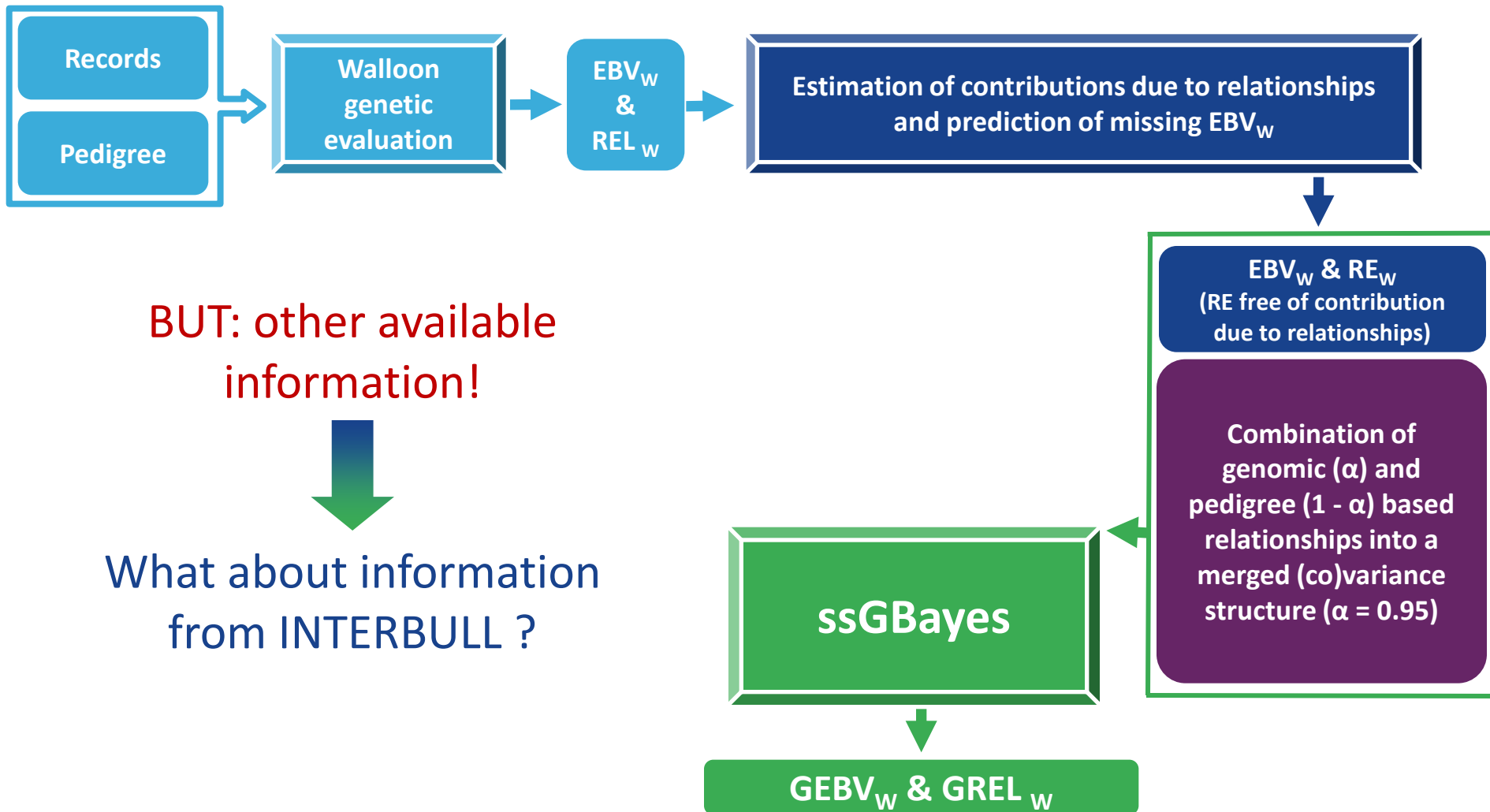
# Methods



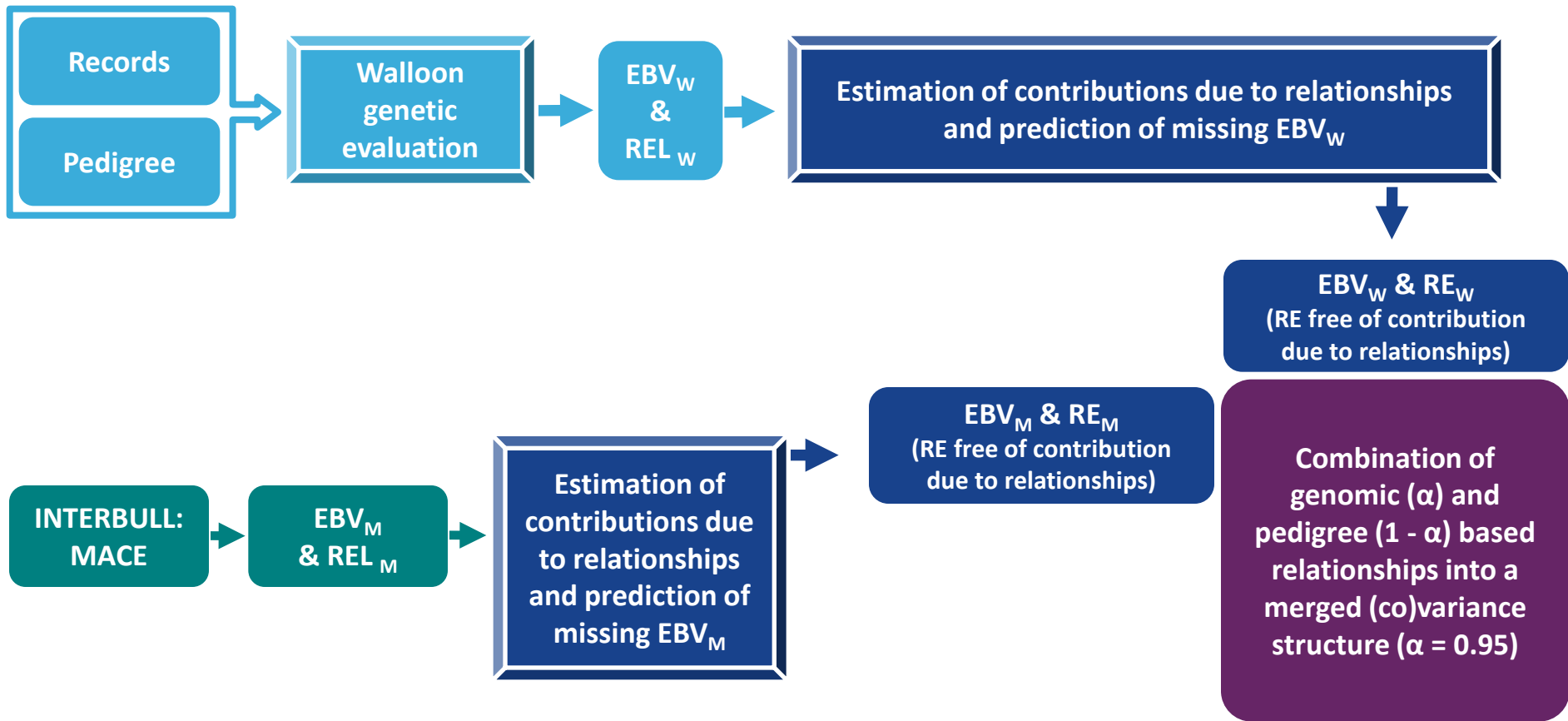
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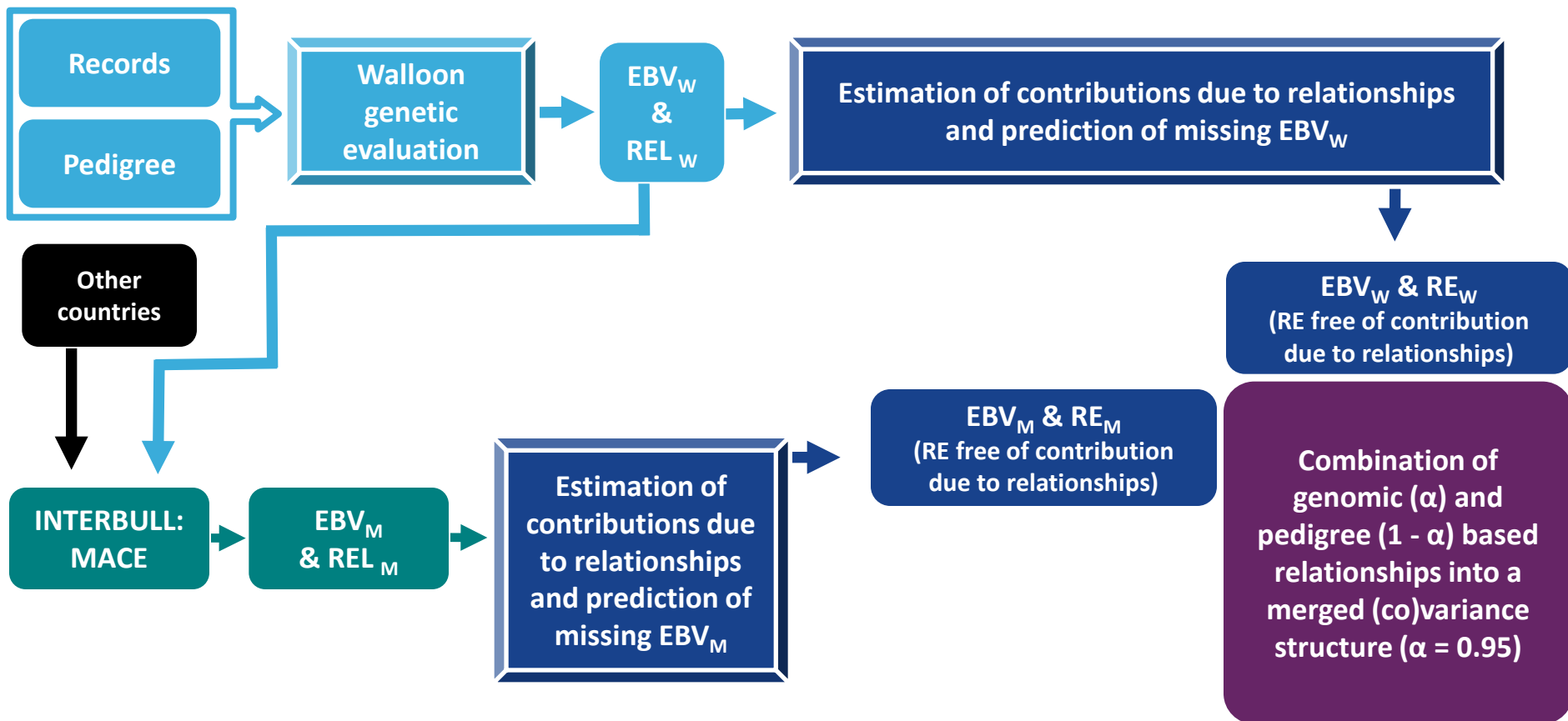


# Methods

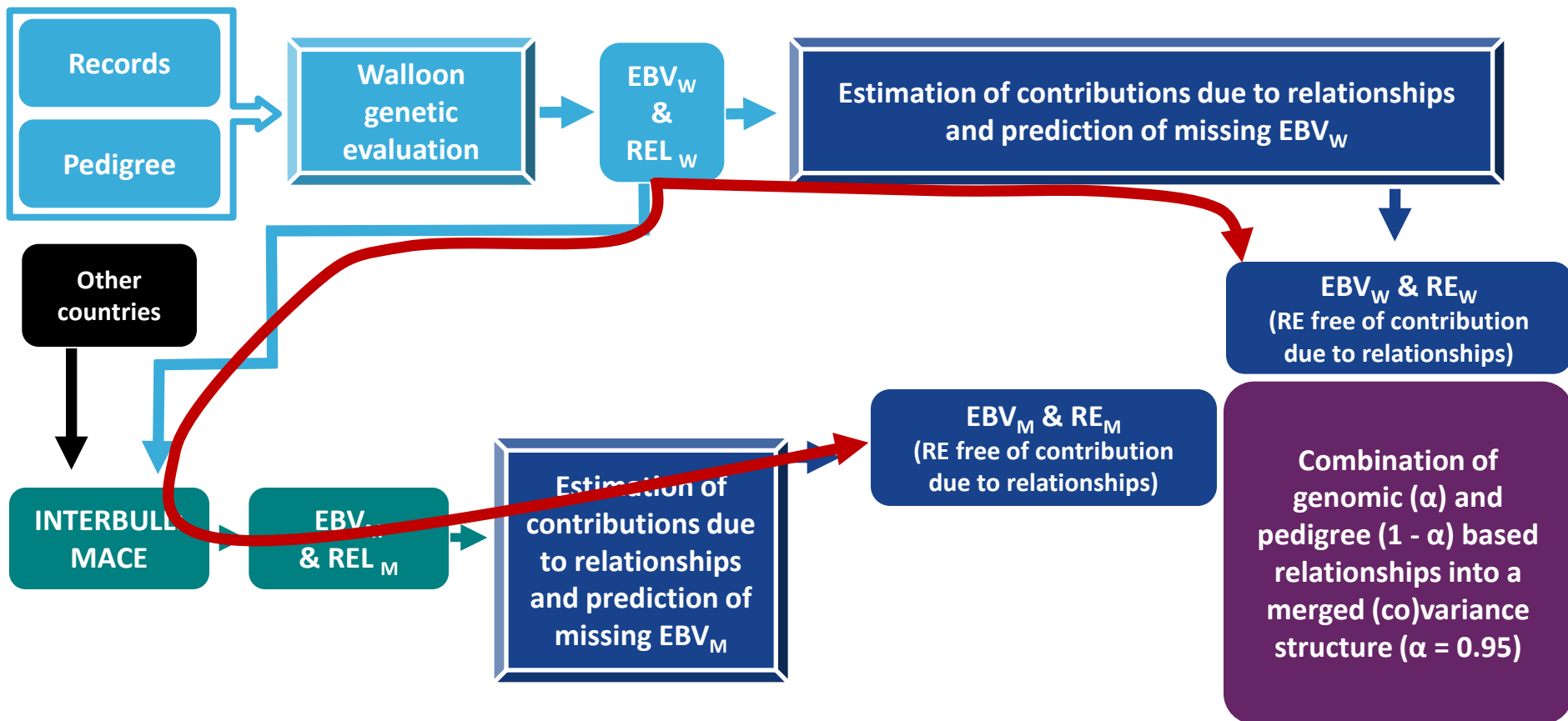




# Methods

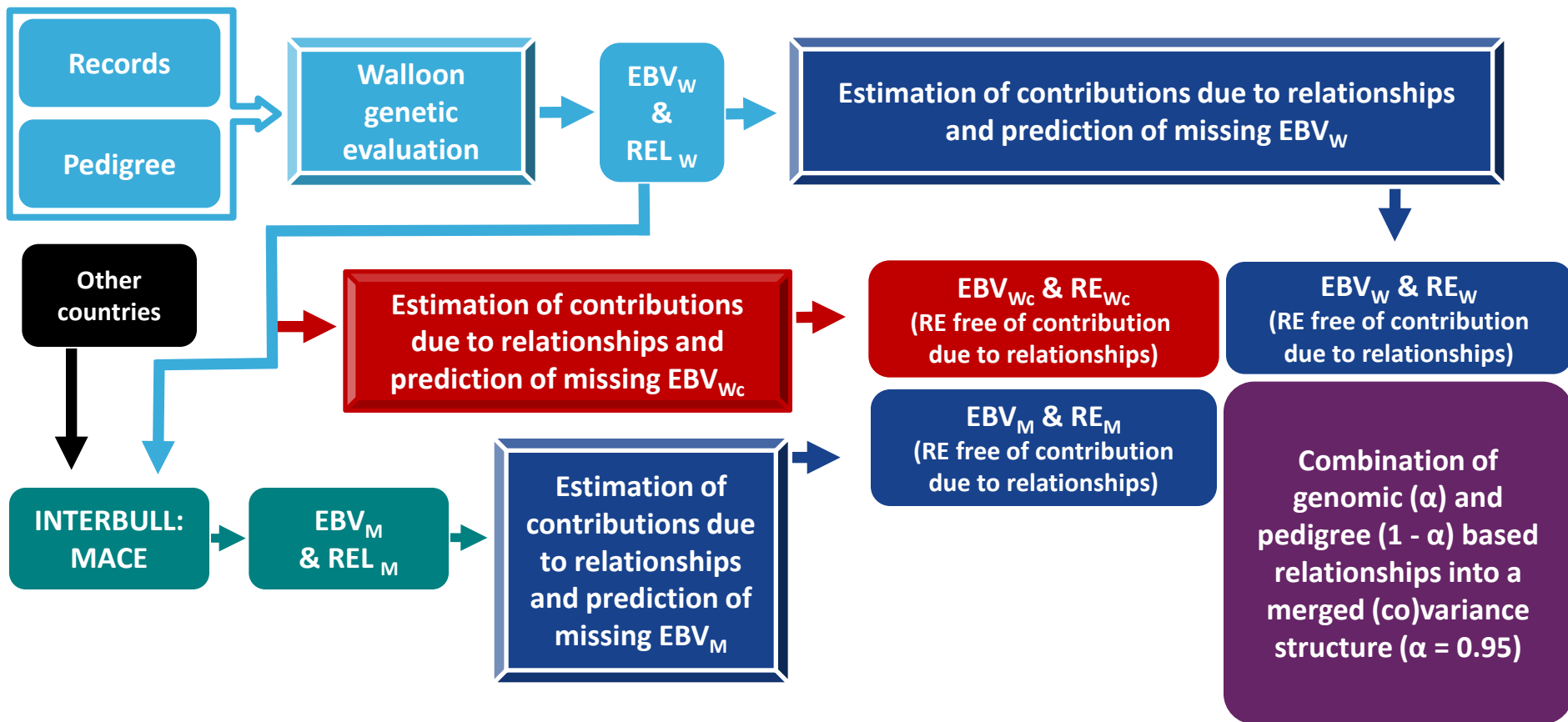


# Methods

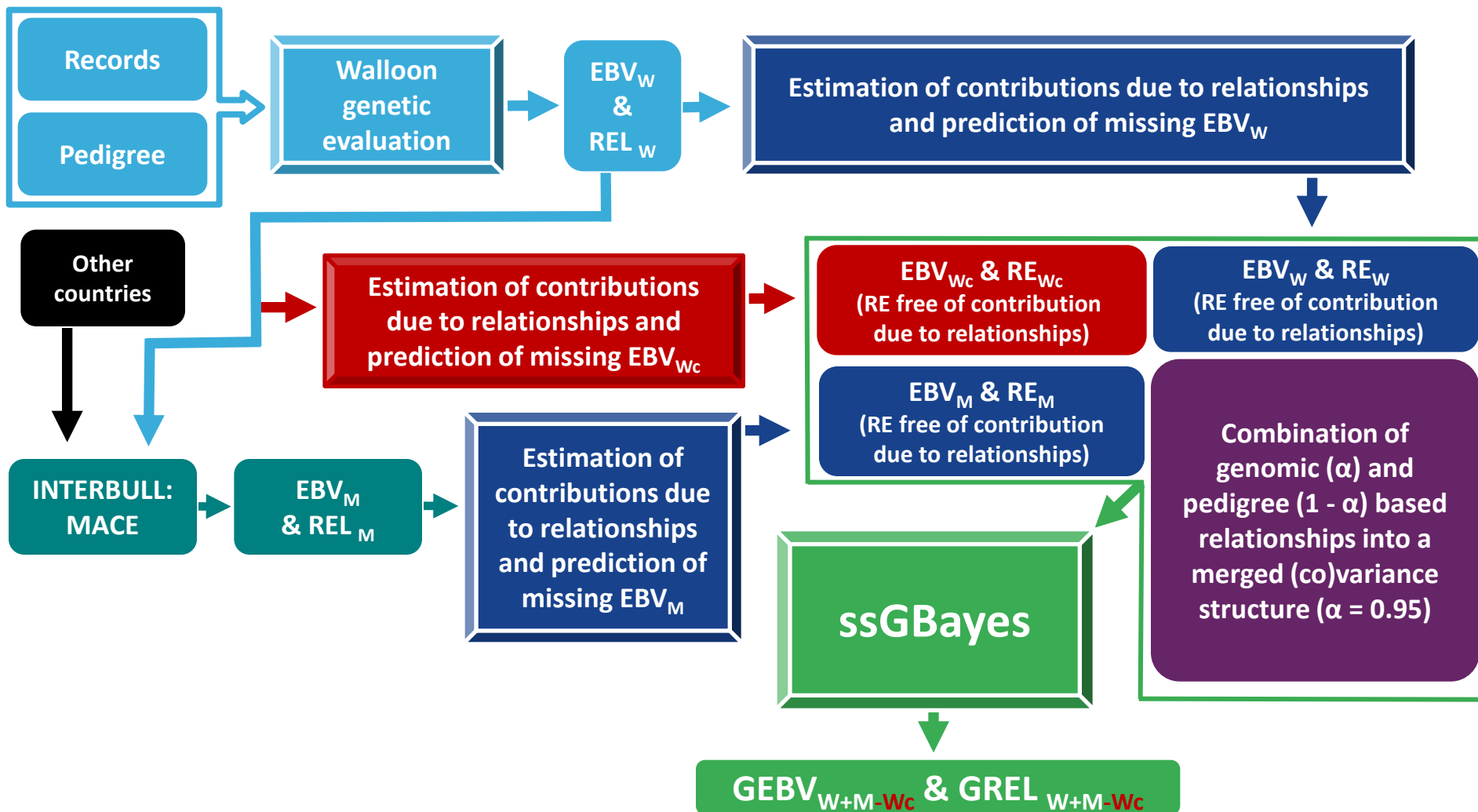


Double counting of information!!

# Methods



# Methods



# Methods

- Combination of genotype, pedigree, local and foreign information  
→ **ssGBayes**

$$\left( \mathbf{H}^{-1} + \Lambda_W + \Lambda_M - \Lambda_{Wc} \right) \hat{\mathbf{a}} = \mathbf{D}_W^{-1} \hat{\mathbf{u}}_W + \mathbf{D}_M^{-1} \hat{\mathbf{u}}_M - \mathbf{D}_{Wc}^{-1} \hat{\mathbf{u}}_{Wc}$$

- $\mathbf{H}$  : Combined genomic ( $\alpha$ ) and pedigree ( $1 - \alpha$ ) based relationships into a merged (co)variance structure ( $\alpha = 0.95$ )
- $\hat{\mathbf{a}}$  :  $\text{GEBV}_{W+M-Wc}$
- $\hat{\mathbf{u}}_W, \hat{\mathbf{u}}_M$  and  $\hat{\mathbf{u}}_{Wc}$  : Available and predicted  $\text{EBV}_W, \text{EBV}_M$  and  $\text{EBV}_{Wc}$
- $\mathbf{D}_W, \mathbf{D}_M$  and  $\mathbf{D}_{Wc}$  : Prediction error (co)variance matrix of  $\hat{\mathbf{u}}_W, \hat{\mathbf{u}}_M$  and  $\hat{\mathbf{u}}_{Wc}$

# Methods

- Combination of genotype, pedigree, local and foreign information  
→ **ssGBayes**

$$\left( H^{-1} + \Lambda_W + \Lambda_M - \Lambda_{Wc} \right) \hat{a} = D_W^{-1} \hat{u}_W + D_M^{-1} \hat{u}_M - D_{Wc}^{-1} \hat{u}_{Wc}$$

Least square part of LHS of hypothetical BLUP of Walloon information

Least square part of LHS of hypothetical BLUP of foreign information free of Walloon information

RHS of hypothetical BLUP of Walloon information

RHS of hypothetical BLUP of foreign information free of Walloon information

For more information about the theory behind this equation, see presentation of Vandenplas *et al.* at EAAP meeting, session 34, Wednesday 28<sup>th</sup> PM

# Data

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- ❑ 1,903 genotyped animals
  - 1,378 bulls and 525 cows
  - 38,604 SNP after editing
- ❑ 6-generations extracted pedigree: 16,234 animals
- ❑ Traits: milk, fat and protein yields, SCS, longevity, stature and udder support
- ❑ Walloon EBV ( $EBV_W$ )
- ❑ MACE EBV ( $EBV_M$ )
- ❑ Bulls with Walloon EBV contributing to MACE ( $EBV_{Wc}$ )

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- ❑ Traits: milk, fat and protein yields, SCS, longevity, stature and udder support *e.g.:* MILK
- ❑ Walloon EBV ( $EBV_W$ ) 12,046
- ❑ MACE EBV ( $EBV_M$ ) 1,981
- ❑ Bulls with Walloon EBV contributing to MACE ( $EBV_{Wc}$ ) 601
  
- ❑ Reliabilities (REL) for all GEBV obtained through inversion of left-hand side



# Results: Milk yield

- Average REL (SD) associated to  $EBV_W$ ,  $GEBV_W$  and  $GEBV_{W+M-Wc}$  for genotyped bulls

Class of $REL_W$	N	$EBV_W^1$	$GEBV_W^2$
< 0.50	647	0.25 (0.12)	0.44 (0.09)

<sup>1</sup> REL obtained from Walloon polygenic evaluation

<sup>2</sup> REL obtained from Walloon genomic evaluation using only  $EBV_W$

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< 0.50	647	0.25 (0.12)	0.44 (0.09)	0.80 (0.09)

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Class of $REL_W$	N	$EBV_W$ <sup>1</sup>	$GEBV_W$ <sup>2</sup>	No. of publishable GEBV	$GEBV_{W+M-Wc}$ <sup>3</sup>	No. of publishable GEBV
< 0.50	647	0.25 (0.12)	0.44 (0.09)	194	0.80 (0.09)	628

<sup>1</sup> REL obtained from Walloon polygenic evaluation

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< 0.50	647	0.25 (0.12)	0.44 (0.09)	194	0.80 (0.09)	628
0.50 – 0.74	173	0.63 (0.07)	0.69 (0.06)	173	0.87 (0.05)	173

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< 0.50	647	0.25 (0.12)	0.44 (0.09)	194	0.80 (0.09)	628
0.50 – 0.74	173	0.63 (0.07)	0.69 (0.06)	173	0.87 (0.05)	173
≥ 0.75	390	0.90 (0.07)	0.91 (0.06)	390	0.94 (0.04)	390

<sup>1</sup> REL obtained from Walloon polygenic evaluation

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<sup>3</sup> REL obtained from Walloon genomic evaluation using  $EBV_W$ ,  $EBV_M$  and  $EBV_{Wc}$

# Results: All traits

- Average REL (SD) associated to  $EBV_W$ ,  $GEBV_W$  and  $GEBV_{W+M-Wc}$  for genotyped bulls

Traits	REL <sub>W</sub> < 0.50			
	N	EBV <sub>W</sub> <sup>1</sup>	GEBV <sub>W</sub> <sup>2</sup>	GEBV <sub>W+M-Wc</sub> <sup>3</sup>
Milk yield	647	0.25 (0.12)	0.44 (0.09)	0.80 (0.09)
Fat yield	642	0.26 (0.12)	0.45 (0.09)	0.80 (0.09)
Protein yield	644	0.26 (0.12)	0.44 (0.09)	0.80 (0.09)
SCS	682	0.25 (0.12)	0.43 (0.09)	0.84 (0.12)
Longevity	889	0.23 (0.12)	0.36 (0.09)	0.51 (0.09)
Stature	632	0.28 (0.10)	0.46 (0.08)	0.82 (0.13)
Udder support	699	0.28 (0.10)	0.43 (0.08)	0.71 (0.14)

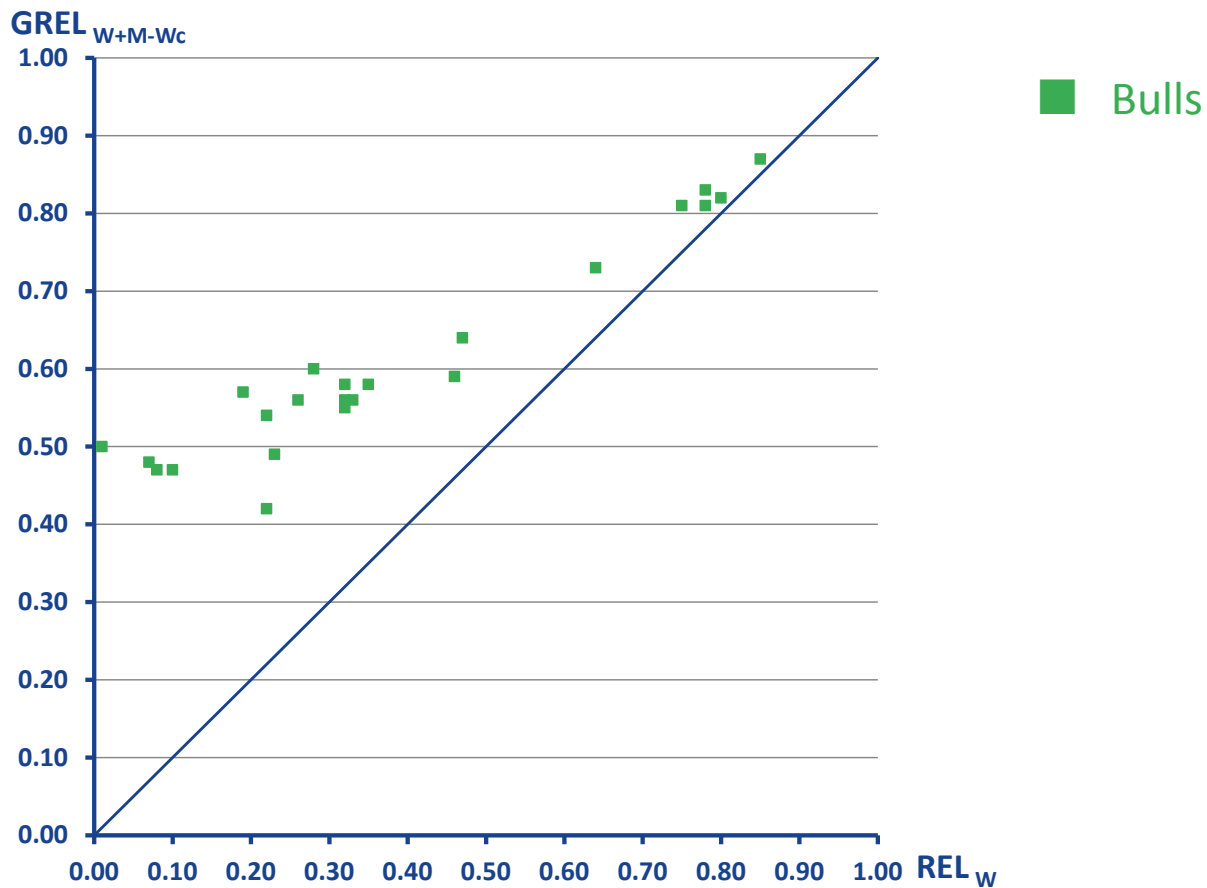
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<sup>2</sup> REL obtained from Walloon genomic evaluation using only  $EBV_W$

<sup>3</sup> REL obtained from Walloon genomic evaluation using  $EBV_W$ ,  $EBV_M$  and  $EBV_{Wc}$

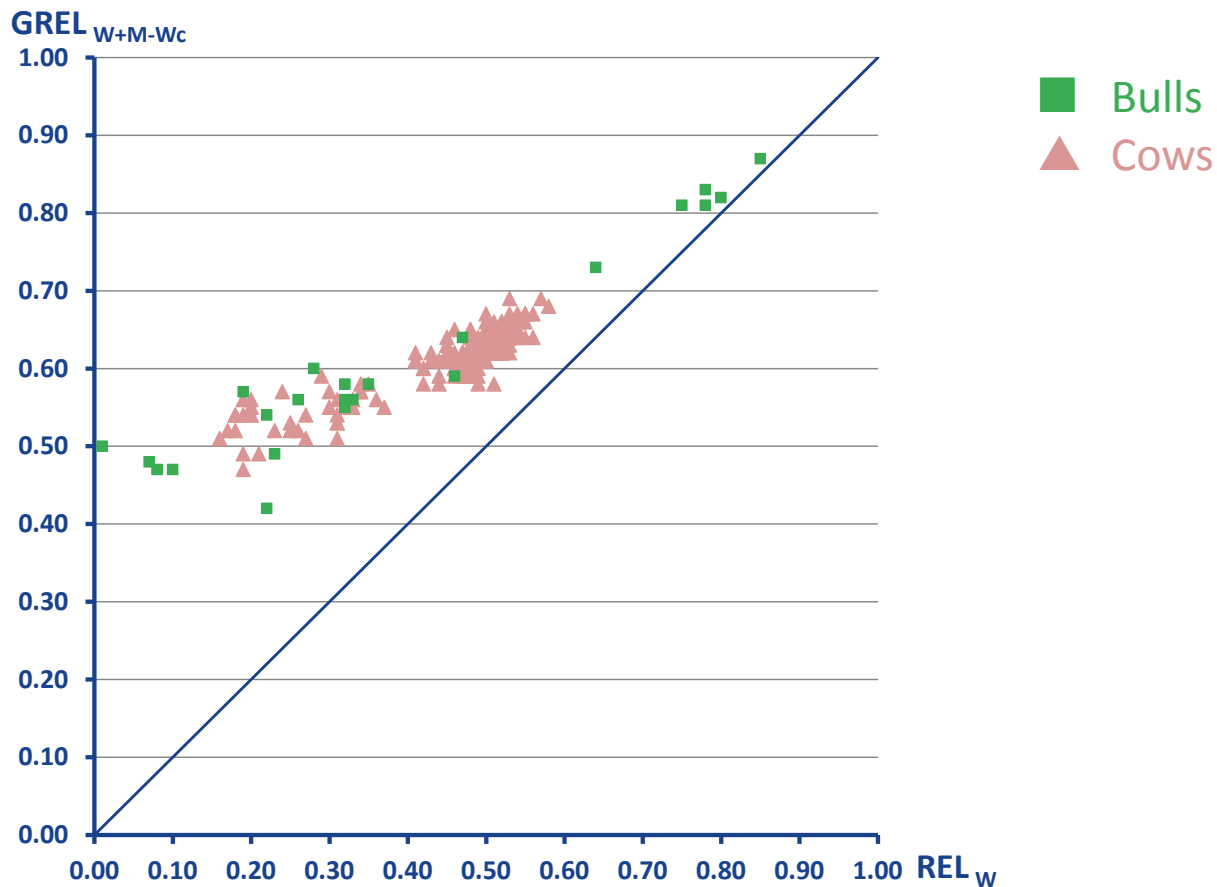
# Results: Milk yield

- Increase of REL for genotyped animals without MACE results and sired by genotyped bulls with MACE results



# Results: Milk yield

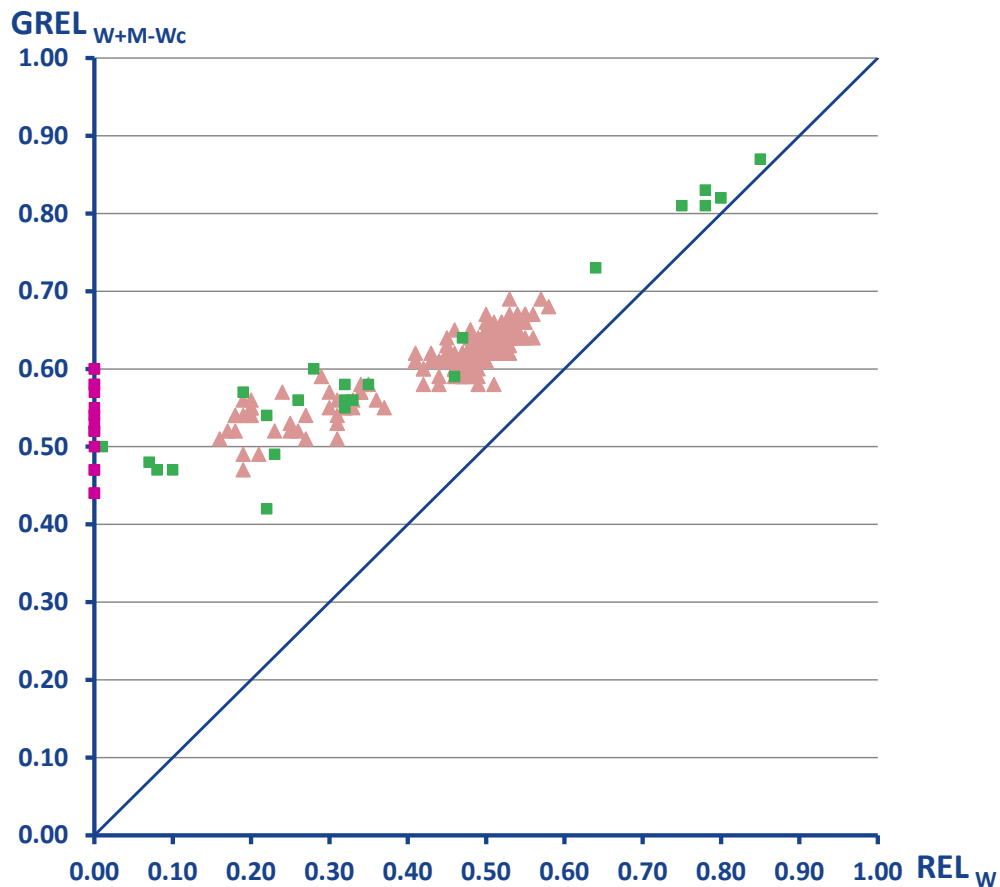
- Increase of REL for genotyped animals without MACE results and sired by genotyped bulls with MACE results





# Results: Milk yield

- Increase of REL for genotyped animals without MACE results and sired by genotyped bulls with MACE results



- Bulls
- ▲ Cows
- 17 bulls not yet included in national polygenic evaluation



$GEBV_{W+M-Wc}$  publishable  
for 14 young bulls

# Results: All traits

- Average REL (SD) associated to  $GEV_{W+M-Wc}$  for genotyped bulls without MACE result and sired by genotyped bulls with MACE result

Traits	0.01 ≤ REL <sub>w</sub> ≤ 0.24		
	N	GEV <sub>W+M-Wc</sub> <sup>1</sup>	No. of publishable GEV
Milk yield	8	0.49 (0.05)	3
Fat yield	8	0.49 (0.05)	4
Protein yield	8	0.49 (0.05)	3
SCS	9	0.52 (0.05)	8
Longevity	14	0.37 (0.06)	8
Stature	21	0.51 (0.04)	14
Udder support	21	0.46 (0.05)	14

<sup>1</sup> REL obtained from Walloon genomic evaluation using  $EBV_W$ ,  $EBV_M$  and  $EBV_{Wc}$

# Results: All traits

- Average REL (SD) associated to  $GEV_{W+M-Wc}$  for genotyped bulls without MACE result, **not yet included in national polygenic evaluation** and sired by genotyped bulls with MACE result

Traits	Missing REL <sub>W</sub> → new young bulls		
	N	$GEV_{W+M-Wc}^1$	No. of publishable $GEV$
Milk yield	17	0.53 (0.05)	13
Fat yield	17	0.53 (0.06)	13
Protein yield	17	0.53 (0.05)	13
SCS	20	0.54 (0.05)	19
Longevity	23	0.38 (0.05)	18
Stature	21	0.54 (0.06)	15
Udder support	21	0.47 (0.07)	15

<sup>1</sup> REL obtained from Walloon genomic evaluation using  $EBV_W$ ,  $EBV_M$  and  $EBV_{Wc}$

# Conclusion

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- ❑ Bayesian approach integrates well MACE results into ssBLUP
  - ➔ Recovers indirectly large amount of phenotypic information
- ❑ Correct propagation of all available information
- ❑ Double counting of contributions due to relationships and own records avoided
- ❑ More accurate prediction for genotyped animals
- ❑ Increase of publishable GEBV number

# Thank you for your attention



Wallonie



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  - Service Public de Wallonie (SPW – DGO3, Belgium) through project D31-1274 **DairySNP**
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  - Animal Science Department, University of Ljubljana, Slovenia



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