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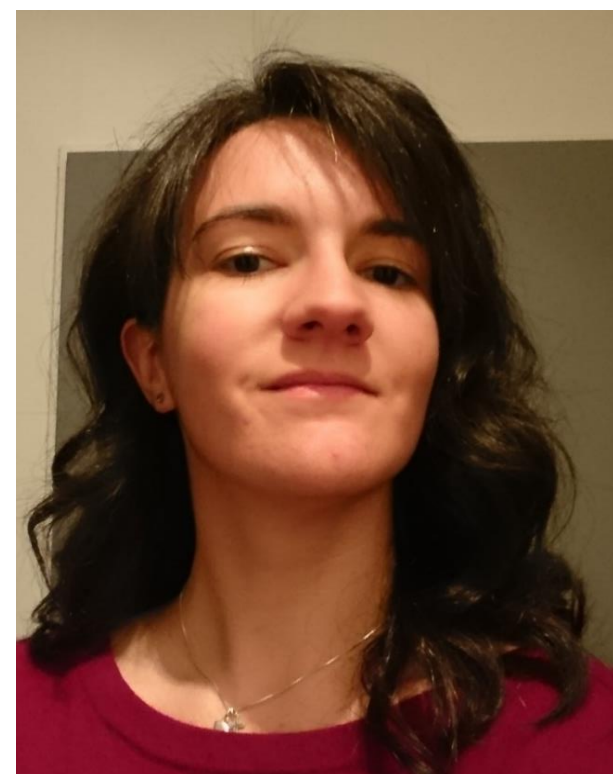
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# An approach to reduce computing time in multi-trait single-step evaluations

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### Context

- **Single-Step (SS) evaluation** = most convenient genetic evaluation, according to articles (Aguilar et al., 2010; Misztal et al., 2009; Legarra et al., 2009). SS simultaneously considers **pedigree, phenotype** and **genotype** information.
- Often: **slow convergence** (Mäntysaari et al., 2020), especially for multivariate SS for large populations. Using simplified (univariate) models is not desirable → **loss of information**

### Objective

Develop a **combined SS evaluation**:

- 1<sup>st</sup> step: univariate SS evaluations adapted to each trait to derive adjusted phenotypes
- 2<sup>nd</sup> step: multivariate SS evaluation on adjusted phenotypes with a unique simplified model

Combined polygenic evaluations are used since 2001 in France, for computation of Total Merit Indices (Ducrocq et al., 2001).

### Hypotheses

**Improved accuracy** for less heritable traits, proper **correction** for selection on correlated traits, **decrease in computing time**.  
 The **reference solutions** are GEBV obtained after 3000 iterations calculated with a Multitrait SS evaluation.

## Material and Methods

### Data

1,618,843 animals with performances for 8 correlated type traits (Montbéliarde breed).

Trait	Height at sacrum (HS)	Chest width (CW)	Chest depth (CD)	Body depth (BD)	Rump length (RL)	Width at hips (WH)	Width at thurl (TW)	Rump angle (RA)
Case 1	No missing records							
Case 2	Records missing for ¾ oldest animals		Records missing for ½ oldest animals		Records missing for ¼ oldest animals		No missing records	
Case 3	Records missing for ¾ youngest animals		Records missing for ½ youngest animals		Records missing for ¼ youngest animals		No missing records	

### Model

**Approach 1 : Standard Multitrait Single-Step approach**

$$y_{kj} = \sum_{k=1}^3 b_k + a_j + e_{kj}$$

$y_{kj}$ : animal performance;  $b_k$ : fixed effects (calving age, lactation stage and herd x day x classifier);  $a_j$ : additive genetic effect of animal j;  $e_{kj}$ : residual

**Approach 2 : Combined Single-Step approach**

**Step 1 :**  $y_{kj} = \sum_{k=1}^3 b_k + a_j + e_{kj}$  (**8 Univariate models**)

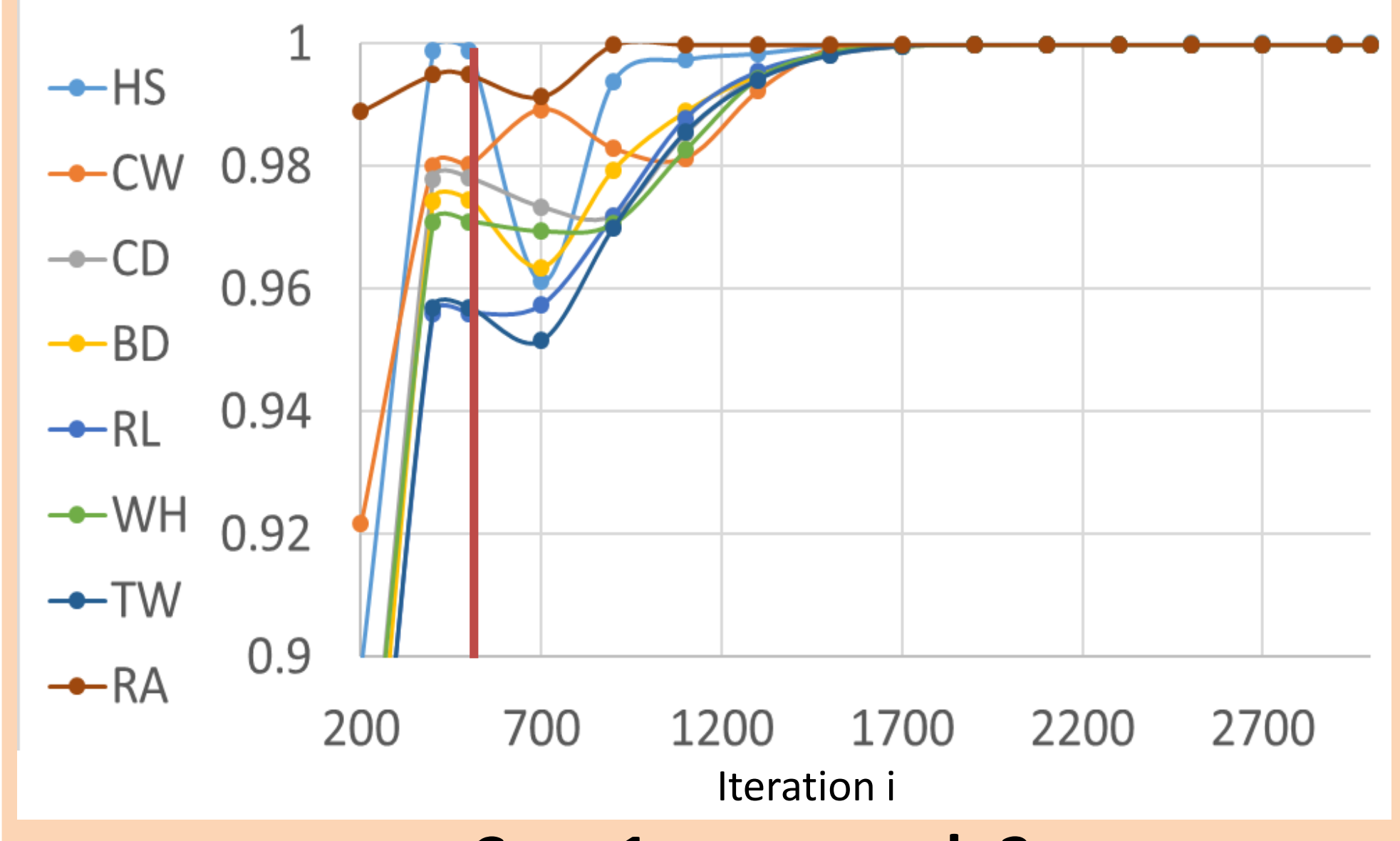
**Step 2 :**  $y_{kj\_corrected \text{ for fixed effects}} = \mu_{an} + a_j + e_{kj}$  (**Multitrait model**)

$y_{kj\_corrected \text{ for fixed effects}}$ : animal performance corrected for fixed effects of step 1;  $\mu_{year}$ : a year effect;  $a_j$ : additive genetic effect of animal j;  $e_{kj}$ : residual

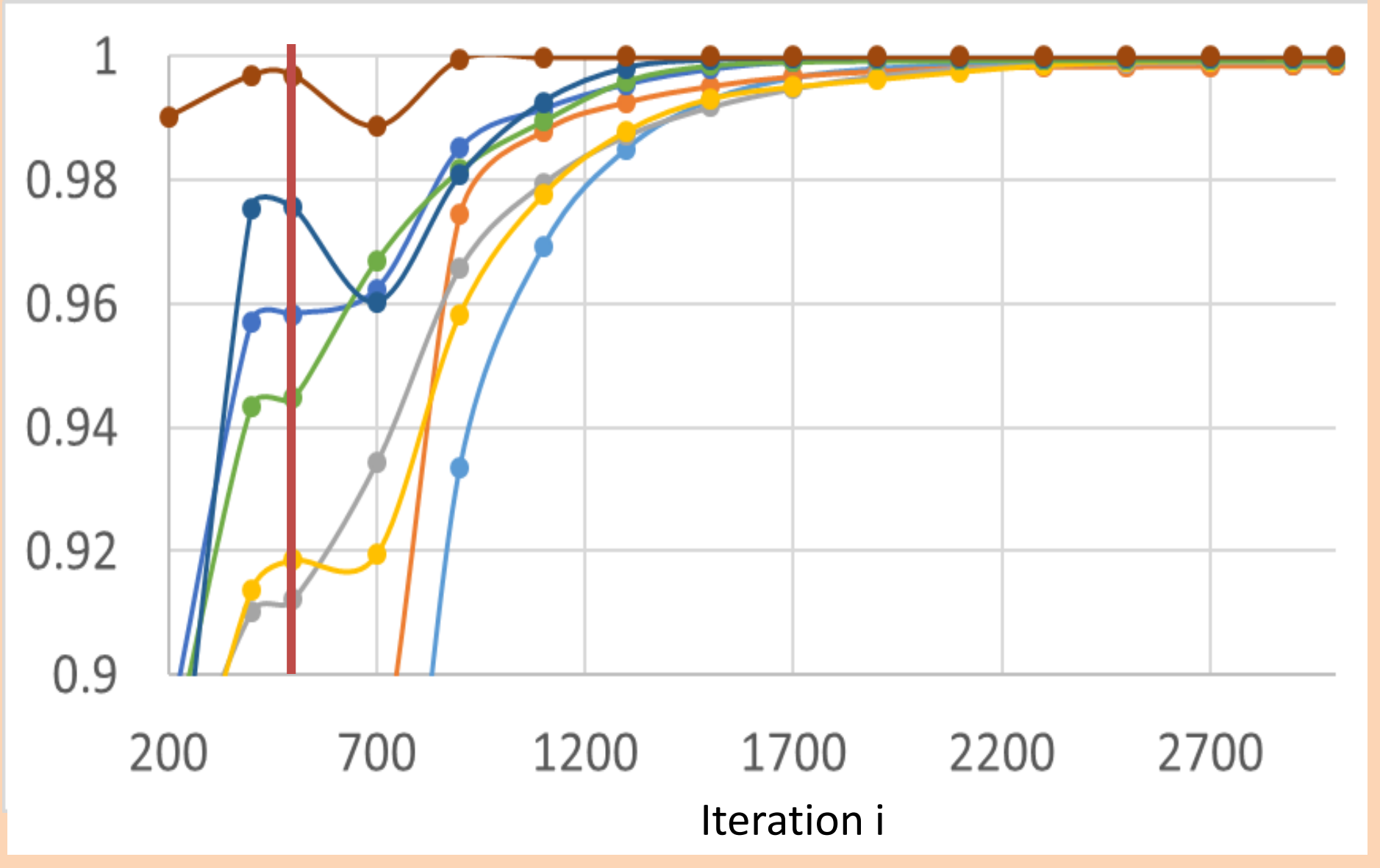
### Software to calculate (G)EBVs

HSSGBLUP developed at INRAE (Tribout et al., 2020)

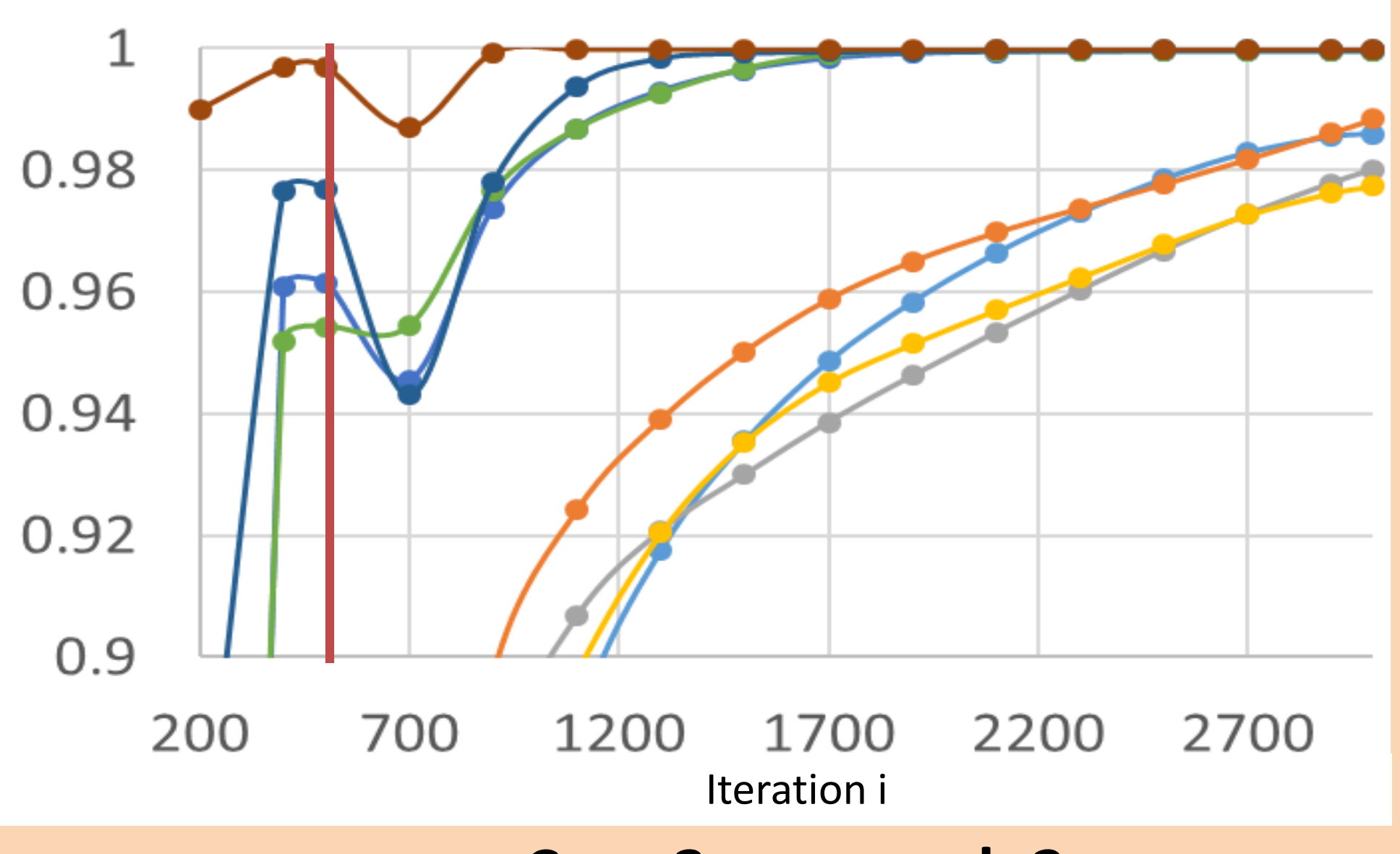
## Results and Discussion



Case 1 – approach 2



Case 2 - approach 2

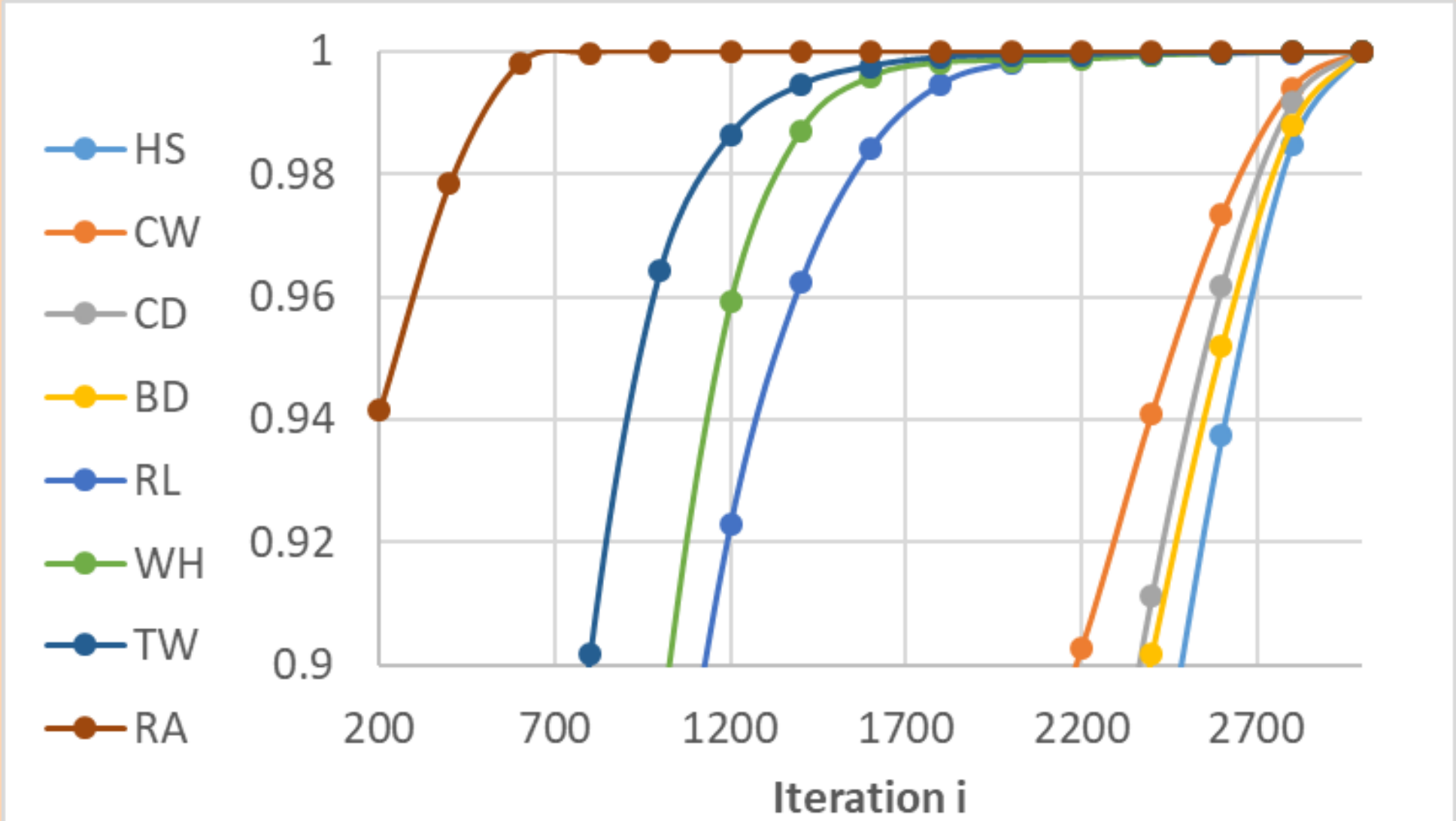


Case 3- approach 2

Correlations between GEBVs compared to final GEBVs (iteration 3000 - approach 1) for each case

(points below 0.9 are not shown, red vertical lines show start of step 2 for Approach 2 = iteration 500)

Approach 2 requires fewer iterations to converge compared with Approach 1:  
 Case 1: **1700** iterations; Case 2: **2300** iterations; Case 3 : no convergence for all traits → no convergence for Approach 1 and/or different correlation and heritability between traits



Case 3- approach 1 (points below 0.90 are not shown)

### Conclusion

- Combined Single-Step approach converges faster than a standard Multitrait approach → it decreases computing times by **reducing number of iterations required**
- Single-Step evaluation in two steps increases **modelling flexibility**