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► **To cite this version:**

Laure H el ene Maugan, Thierry Tribout, Vincent Ducrocq. An approach to reduce computation time in multi-trait single-step evaluations.. 72nd Annual Meeting of the European Association of Animal Production, Aug 2021, Davos, Switzerland. hal-03336898

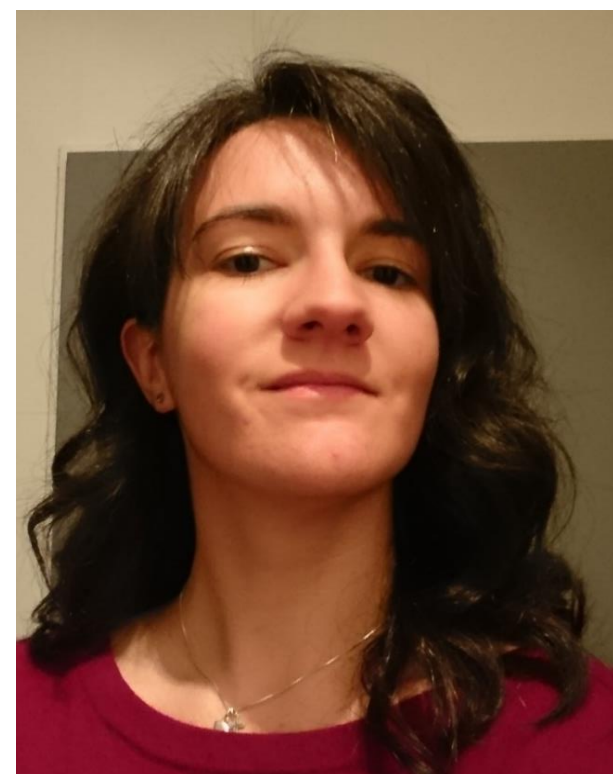
HAL Id: hal-03336898

<https://hal.science/hal-03336898>

Submitted on 9 Sep 2021

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UMR 1313 : Animal Genetics and Integrative Biology (GABI) 78350 Jouy-en-Josas France
Research team : Bovine genetics and genomics (G2B)



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

L.-H. MAUGAN¹, T. Tribout¹, V. Ducrocq¹

¹Université Paris-Saclay, INRAE, AgroParisTech, GABI, 78350, Jouy-en-Josas

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**:

- 1st step: univariate SS evaluations adapted to each trait to derive adjusted phenotypes
- 2nd 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)

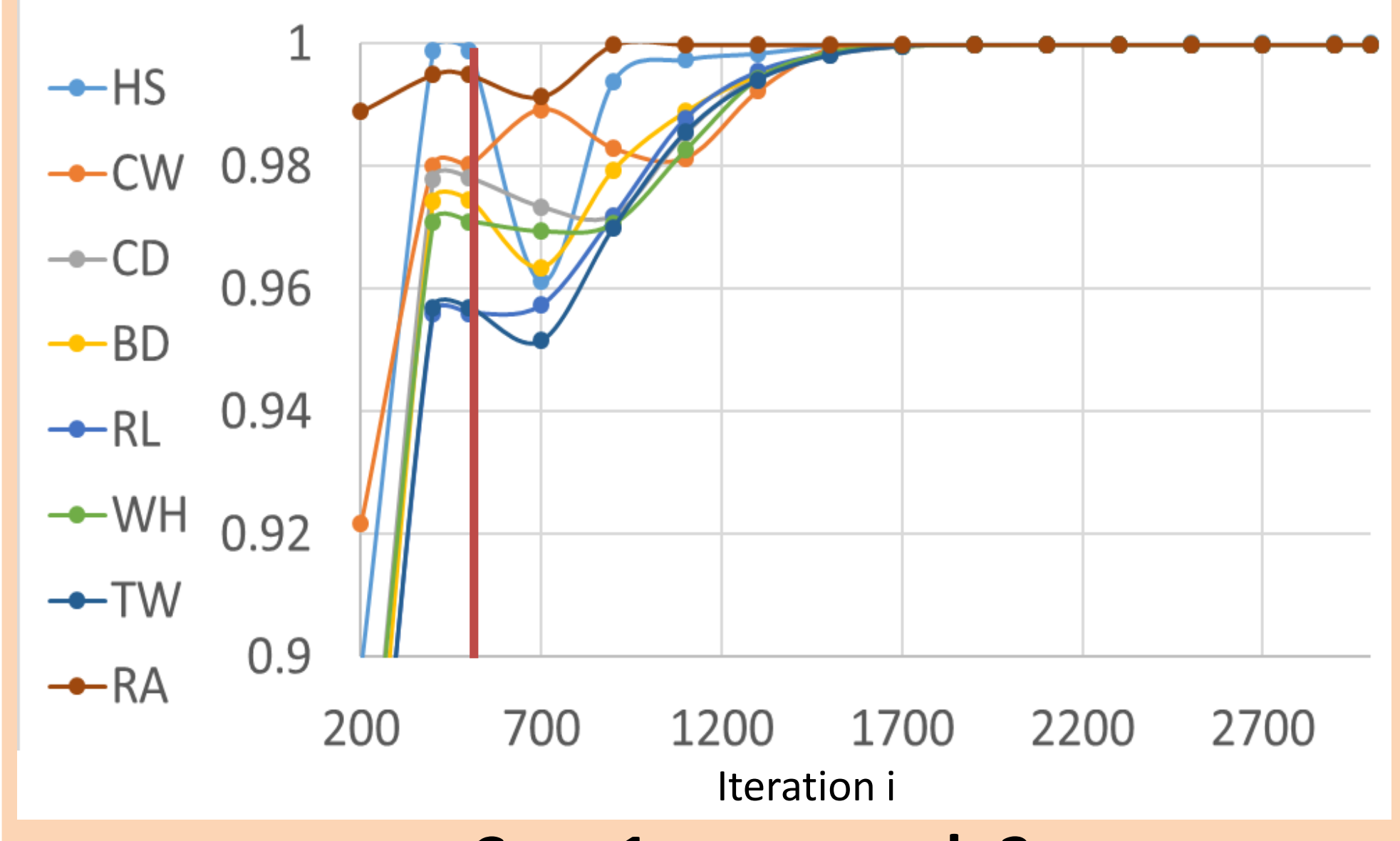
Step 2 : $y_{kj_corrected}$ for fixed effects = $\mu_{an} + a_j + e_{kj}$ (Multitrait model)

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

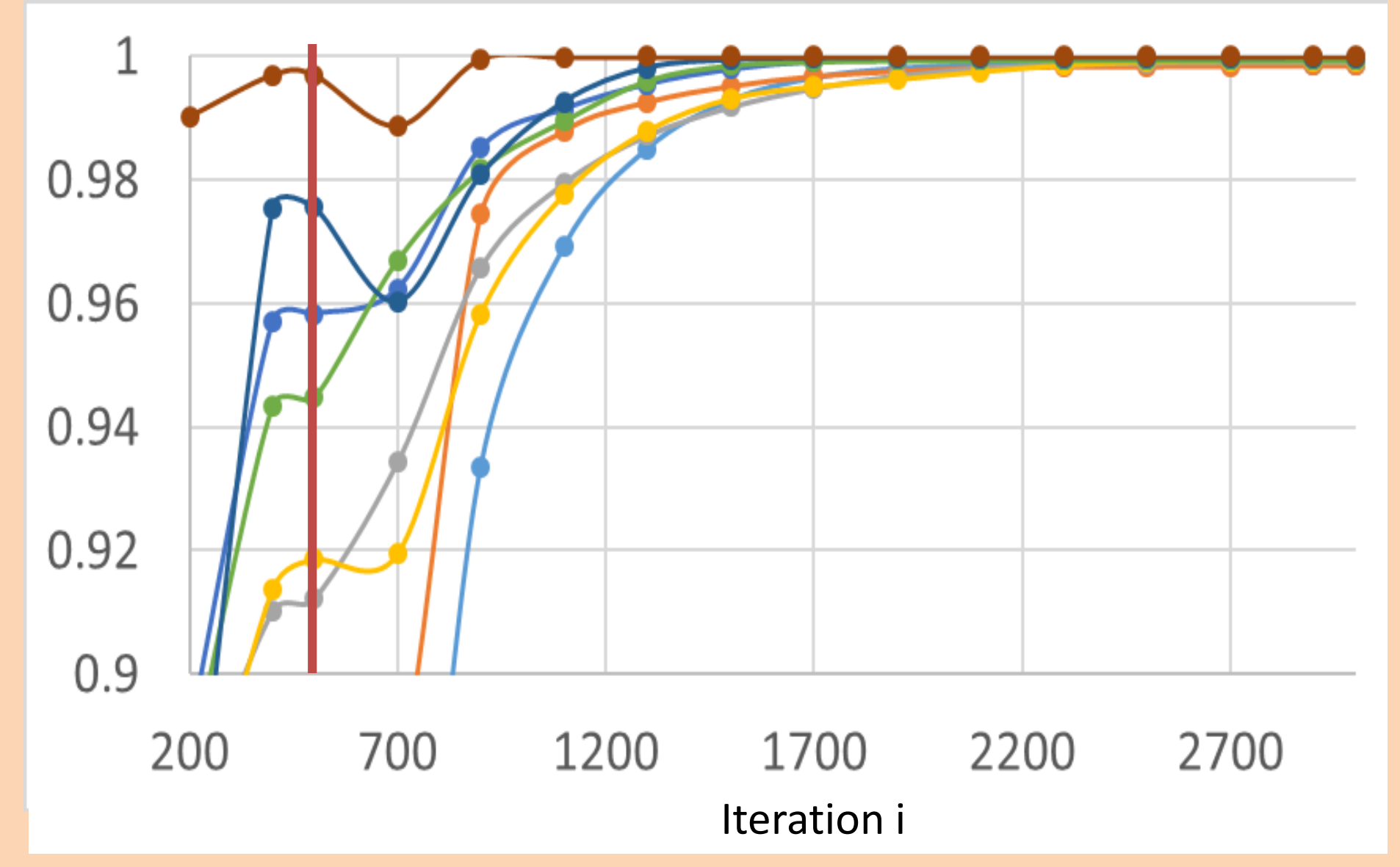
Software to calculate (G)EBVs

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

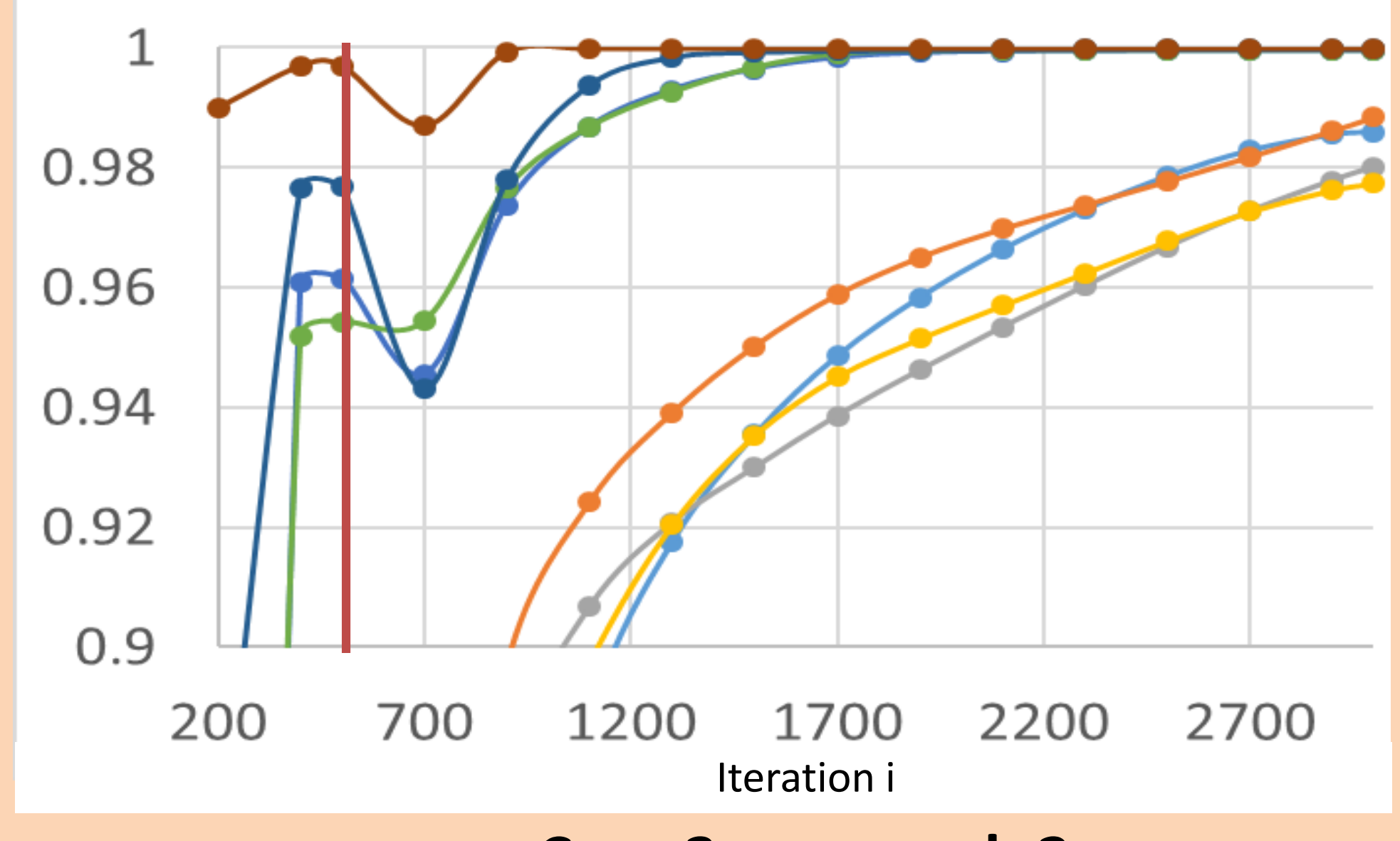
Results and Discussion



Case 1 – approach 2



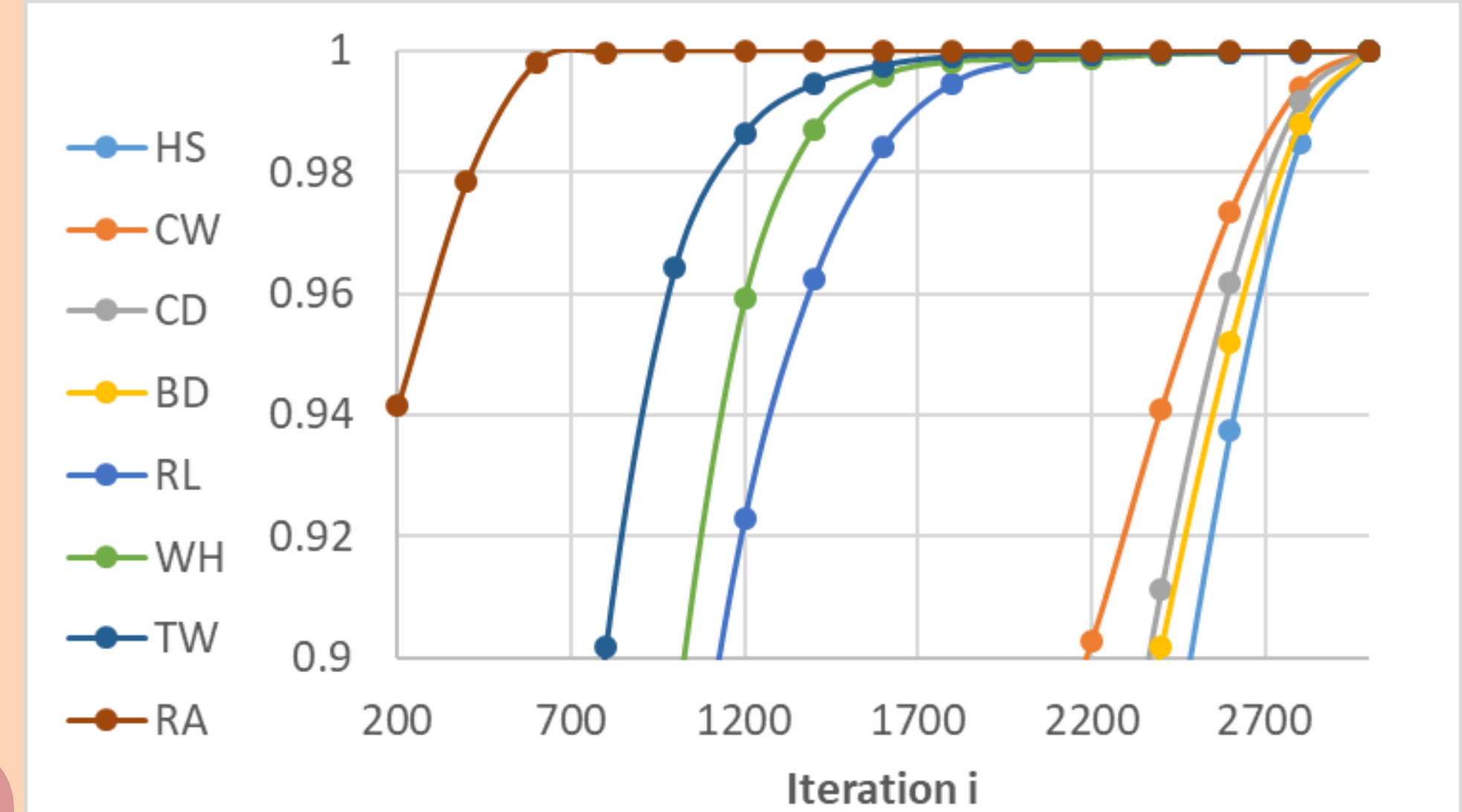
Case 2 - approach 2



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**