Solutions for the fixed effects, yield deviations and daughter yield deviations from a data subject to genomic selection

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NAV - Nordic Cattle Genetic Evaluation

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Challenges of genomic selection

- Genomic selection is the main source of genetic progress in dairy cattle breeding
- In theory evaluations ignoring genomic selection (= Animal Model BLUP) are biased
- Still, AMBLUP results are used as input:
  - Multi-step genomic evaluations
  - International Evaluations (i.e. MACE)

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- Genomic selection is the main source of genetic progress in dairy cattle breeding

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- Still, AMBLUP results are used as input:
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- The genomic selection is accounted in **Single-step GBLUP**

- Frequently ssGBLUP shows higher genetic trend in selected animals than the AMBLUP

  Reasons not well understood:

  - AMBLUP are often assumed to find genetic progress from well connected overlapping data

- ssGBLUP results cannot be used as input for
  - Multi-step genomic evaluations
  - MACE

Aims of this study

- After genomic selection, GEBVs from a single-step evaluation and from Animal Model BLUP (AMBLUP) are different ⬅➔ They show different trends
  - We try to disentangle the differenses
- Biased national EBVs lead into biased MACE results!
  - We test if the *Yield Deviations* from ssGBLUP are usefull in AM BLUP (or MACE)
    - ➔ could YD be used as input to MACE

Methods and material

Evaluations:

1. Animal Model BLUP run --> EBVs
2. Single step GBLUP run --> GEBVs (and YD)

3. Animal Model BLUP run using single-step yield deviations (YD)

Methods and material

Nordic Holstein 305d production data

- 16 million lactation records compiled from the October 2017 data used in the official nordic TD evaluations
- 36,400 genotyped genotyped animals

AMBLUP

- Multitrait (lactations 1-3) model for protein

- Model: Protein = Herd_Year + Calving_Year_Season*Period + Calving_Age + Animal + Residual

  ! Weights= (Number of TD)/10

- Variance parameters derived from national evaluations, for example
- $h^2_1 = 0.36$
- $h^2_2 = 0.29$
- $h^2_3 = 0.26$

EBVs from the YD

Step 1

Calculation of YD

$$\mathbf{YD}_{ss} = \mathbf{y} - \mathbf{Xb}_{ss}$$

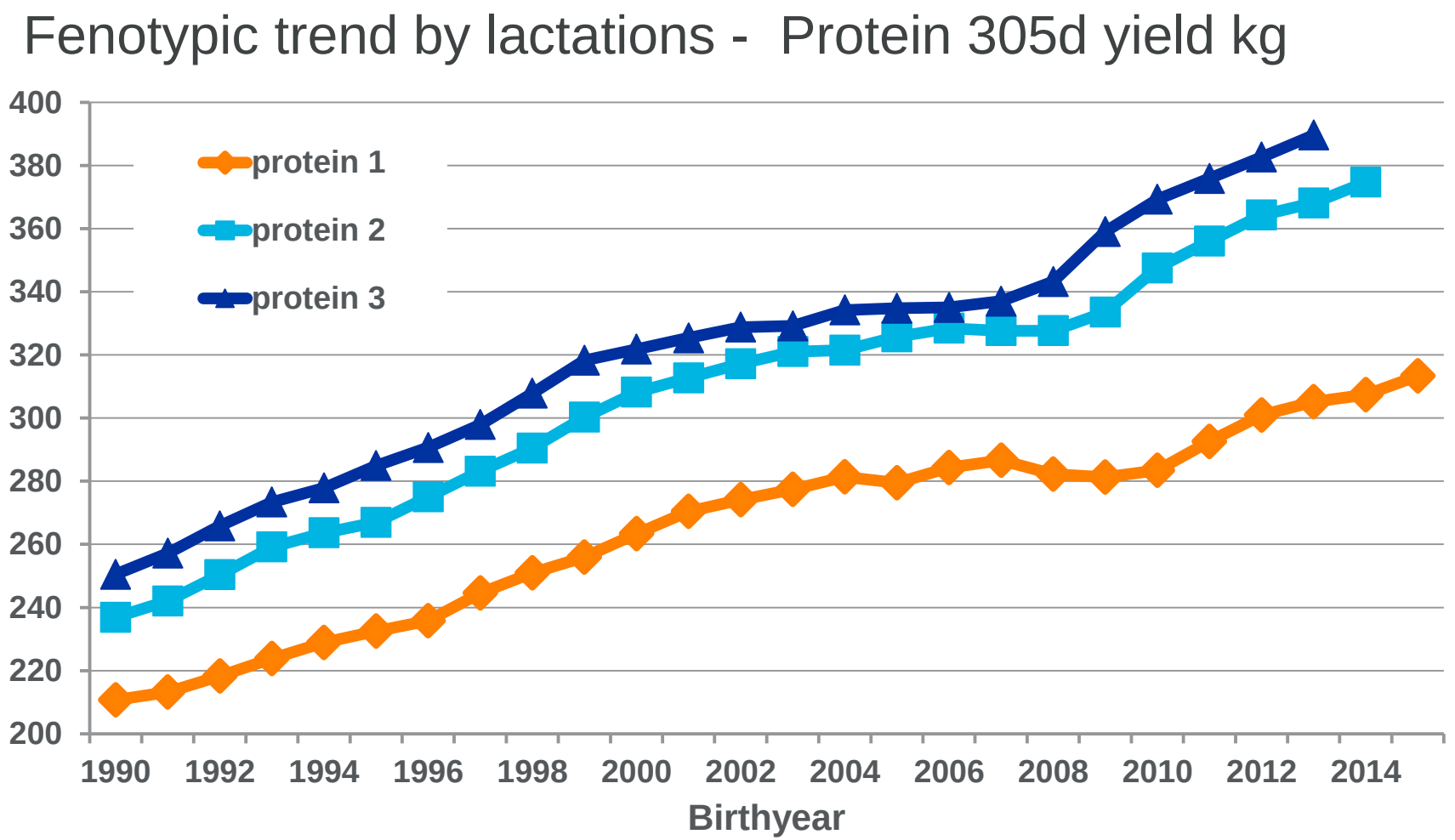
where $\mathbf{b}_{ss}$ are the solutions of fixed effects from the ssGBLUP evaluation

Step 2 (EBV_YD model)

$$\mathbf{YD}_{ss} = \mathbf{1}\mu + \mathbf{Za} + \mathbf{e},$$

where **a** is a vector of breeding values, and **Z** is a matrix relating breeding values to $\mathbf{YD}_{ss}$, and **e** is a vector of random residuals. ERC was used as a weight.

Look for the data



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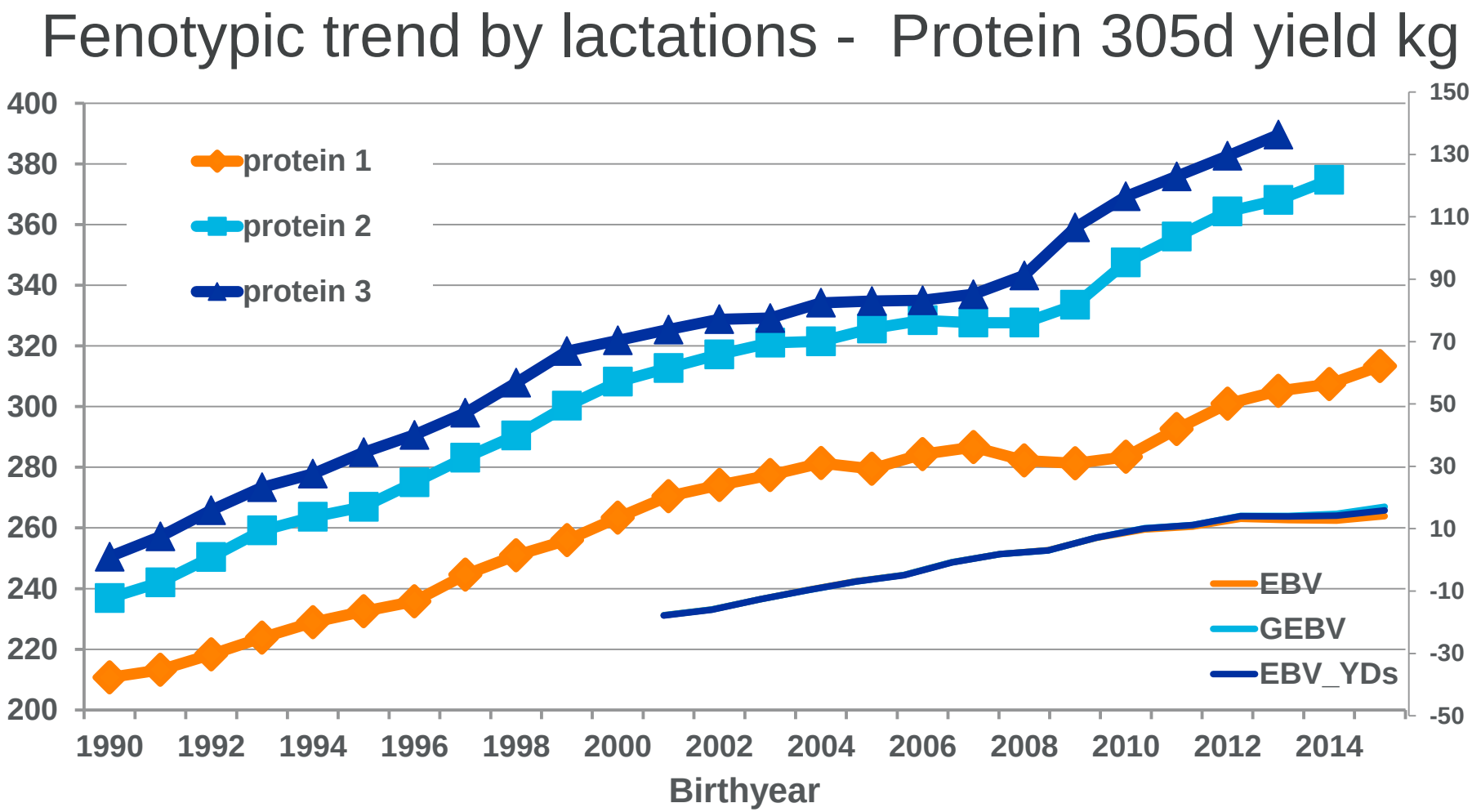

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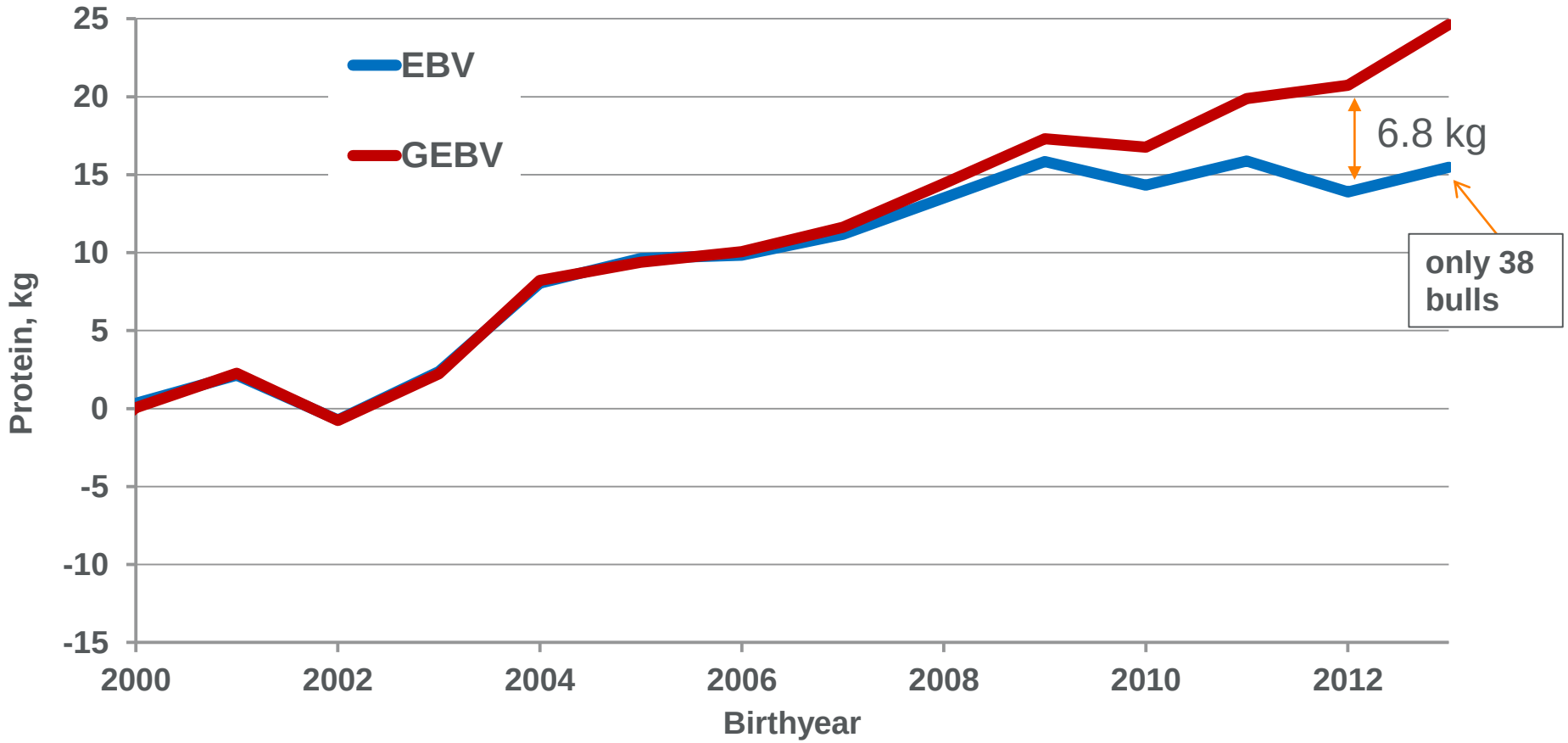
Genetic trend with AMBLUP and ssGBLUP

Nordic genotyped AI-bulls with at least 20 daughters



Year	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013
N:o bulls	274	263	297	258	317	341	385	301	271	240	212	171	170	38

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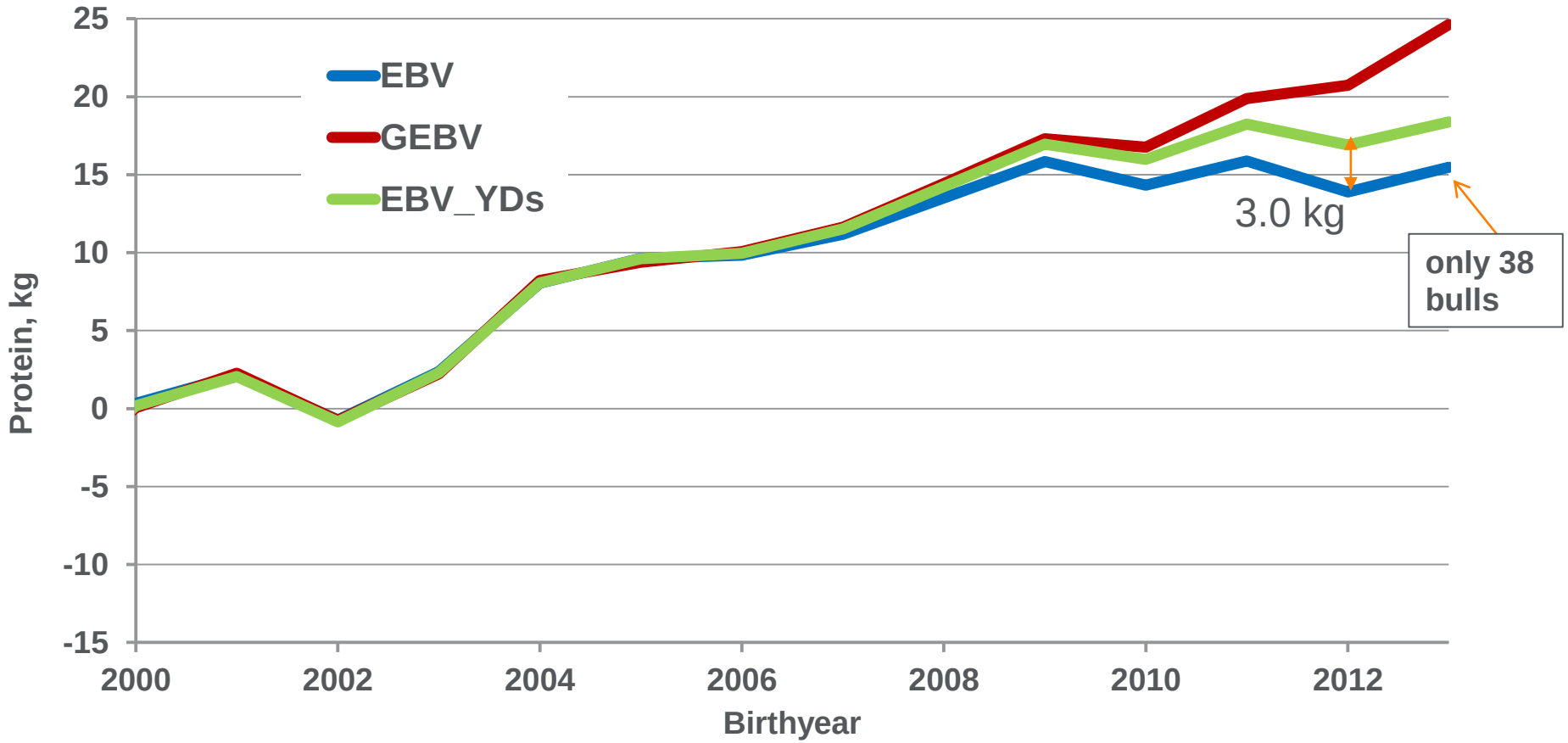

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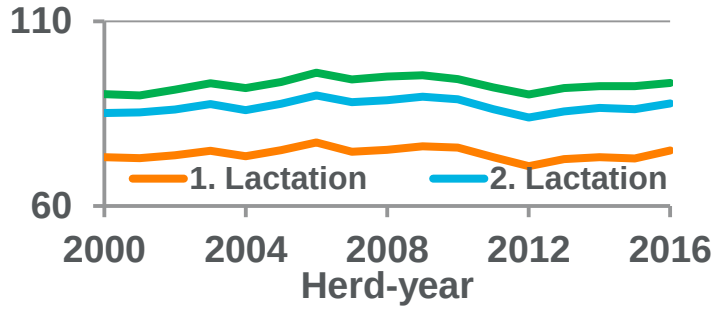
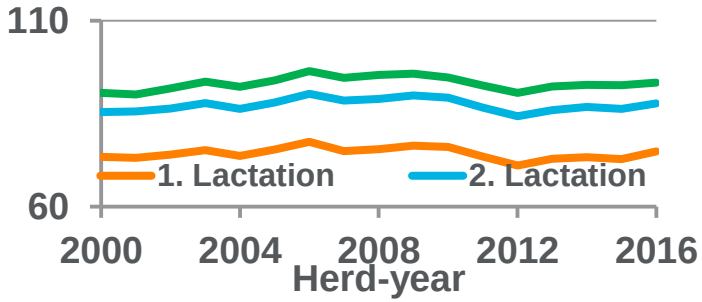
How different were the fixed effect solutions?

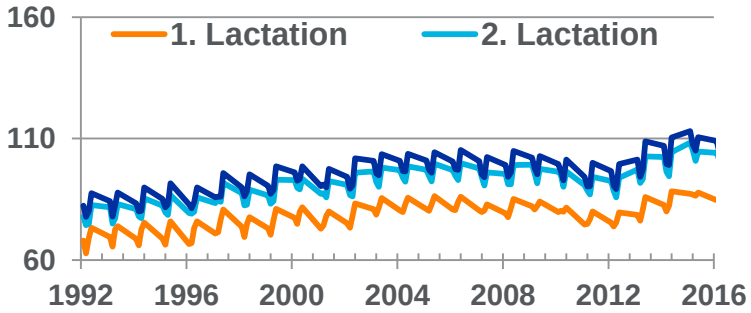
Animal model

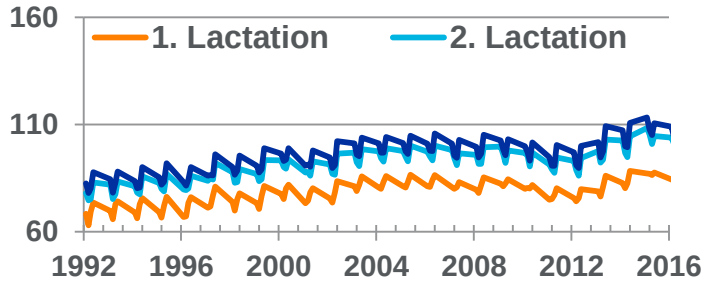
Herd-year means



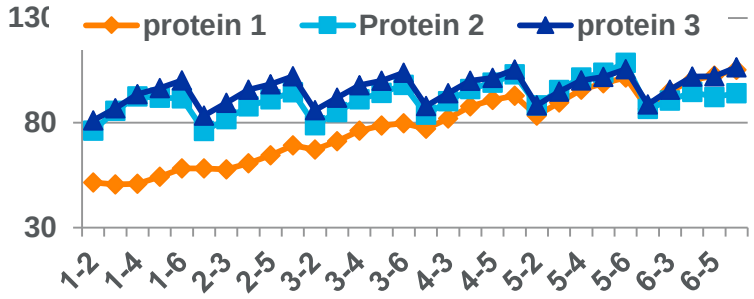


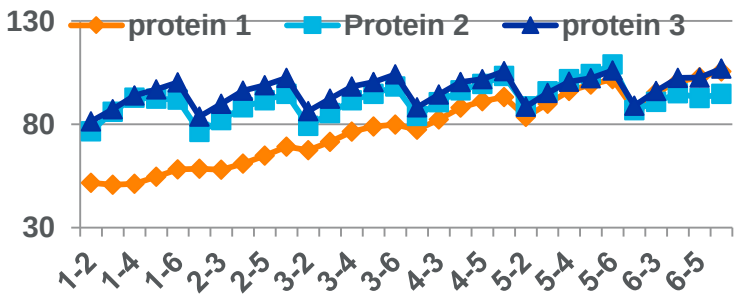
Calving-year-season effect





Effect of Calving age





SSGBLUP

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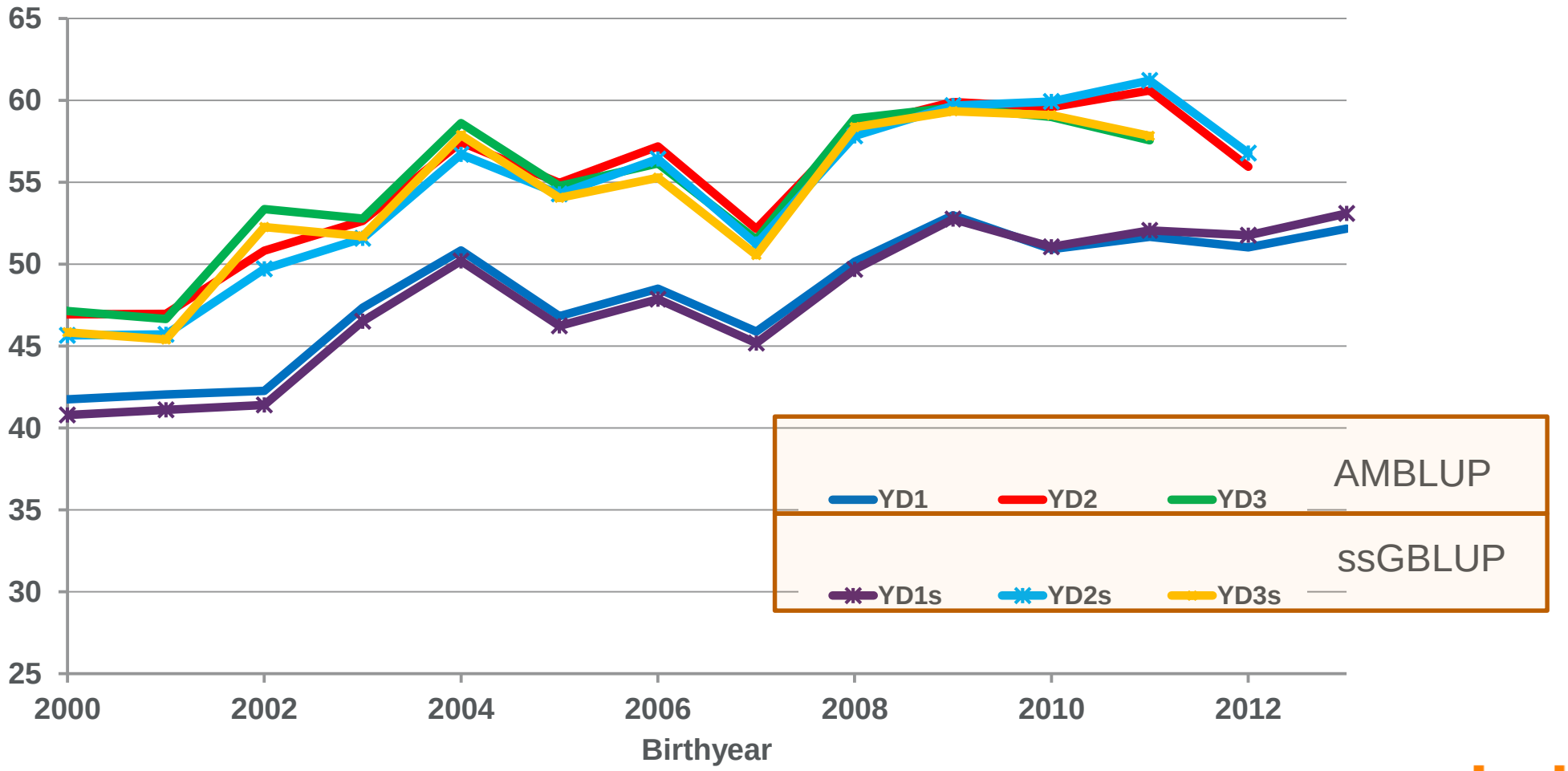
Protein YD trend of daughters of AI-bulls by birthyear of bull (lactations 1-3)



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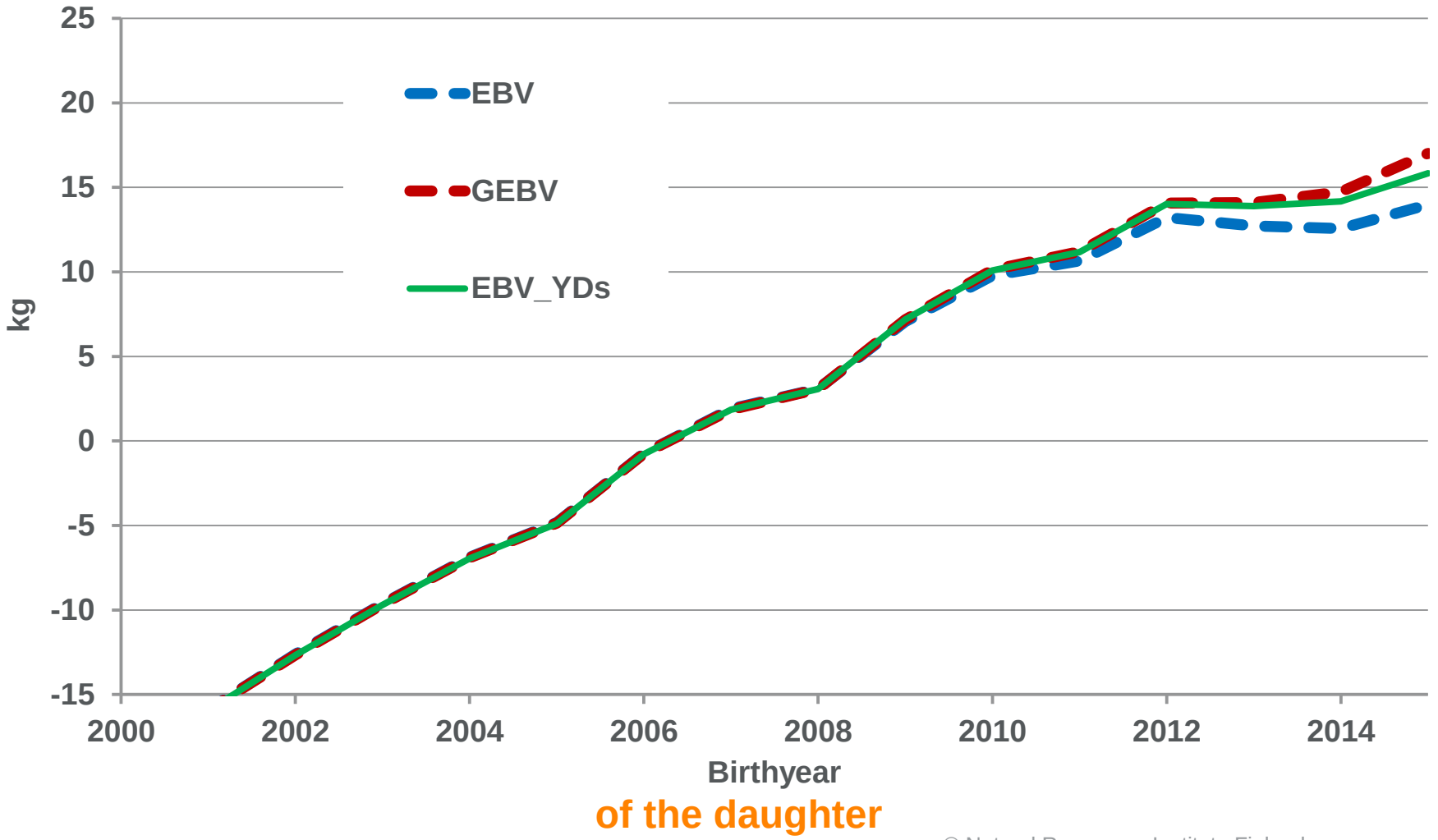
Protein trend with different models - daughters of genotyped bulls



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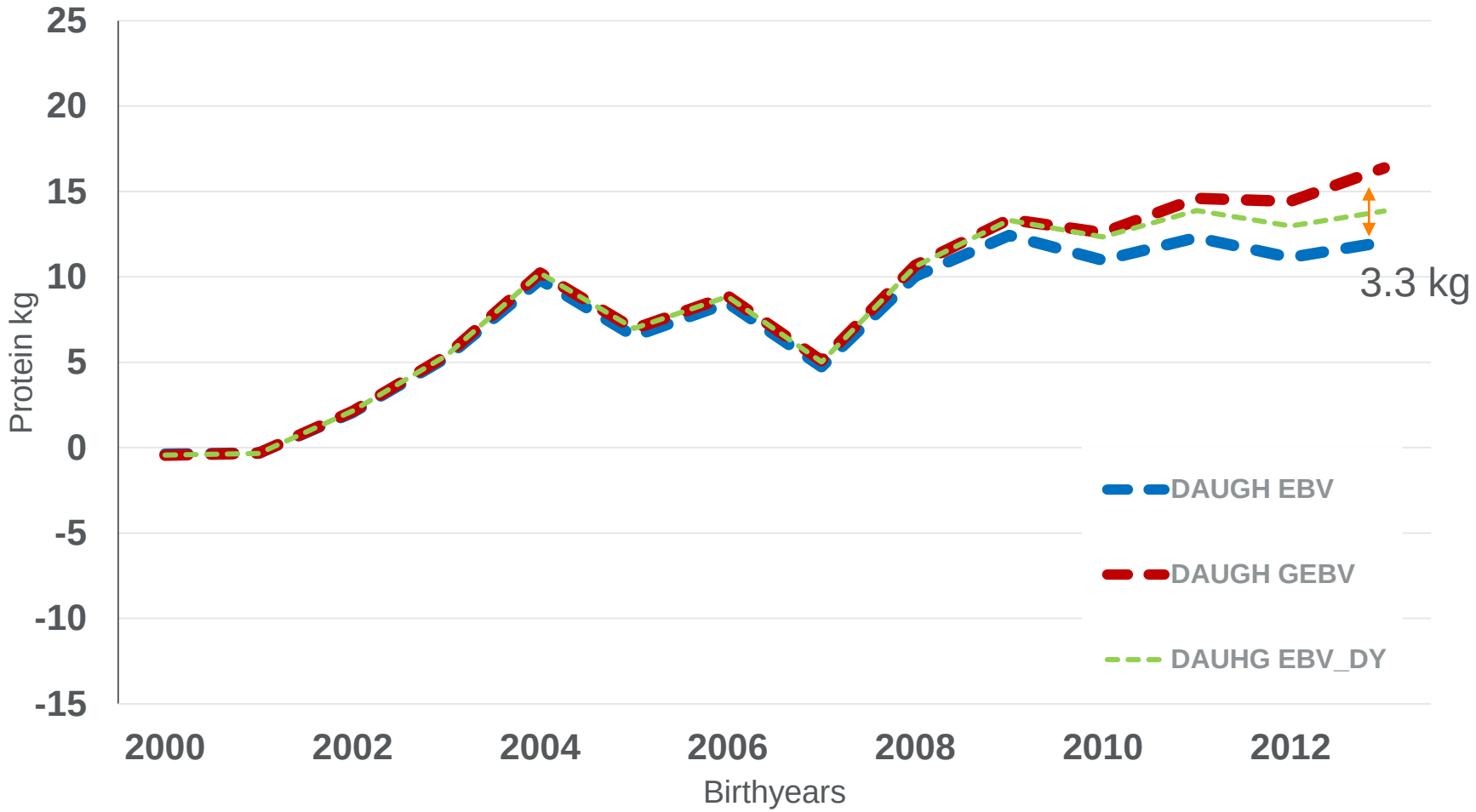
Genetic trend with AMBLUP and ssGBLUP

Daughters of genotyped bulls (> 20 daughters)



of the bulls

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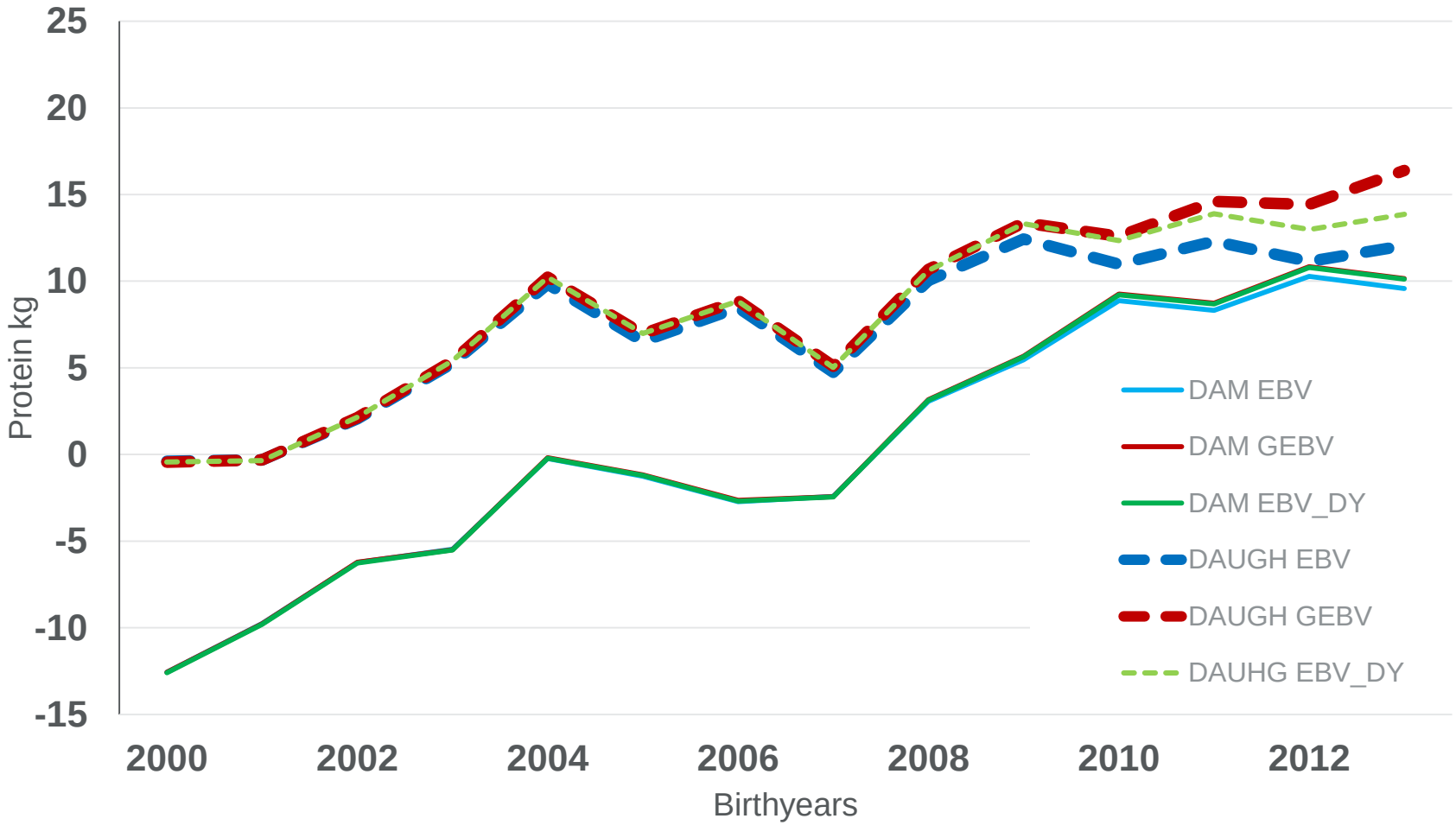
Genetic trend with AMBLUP and ssGBLUP

Mates and daughters of bulls (> 20 daughters)



of the bulls

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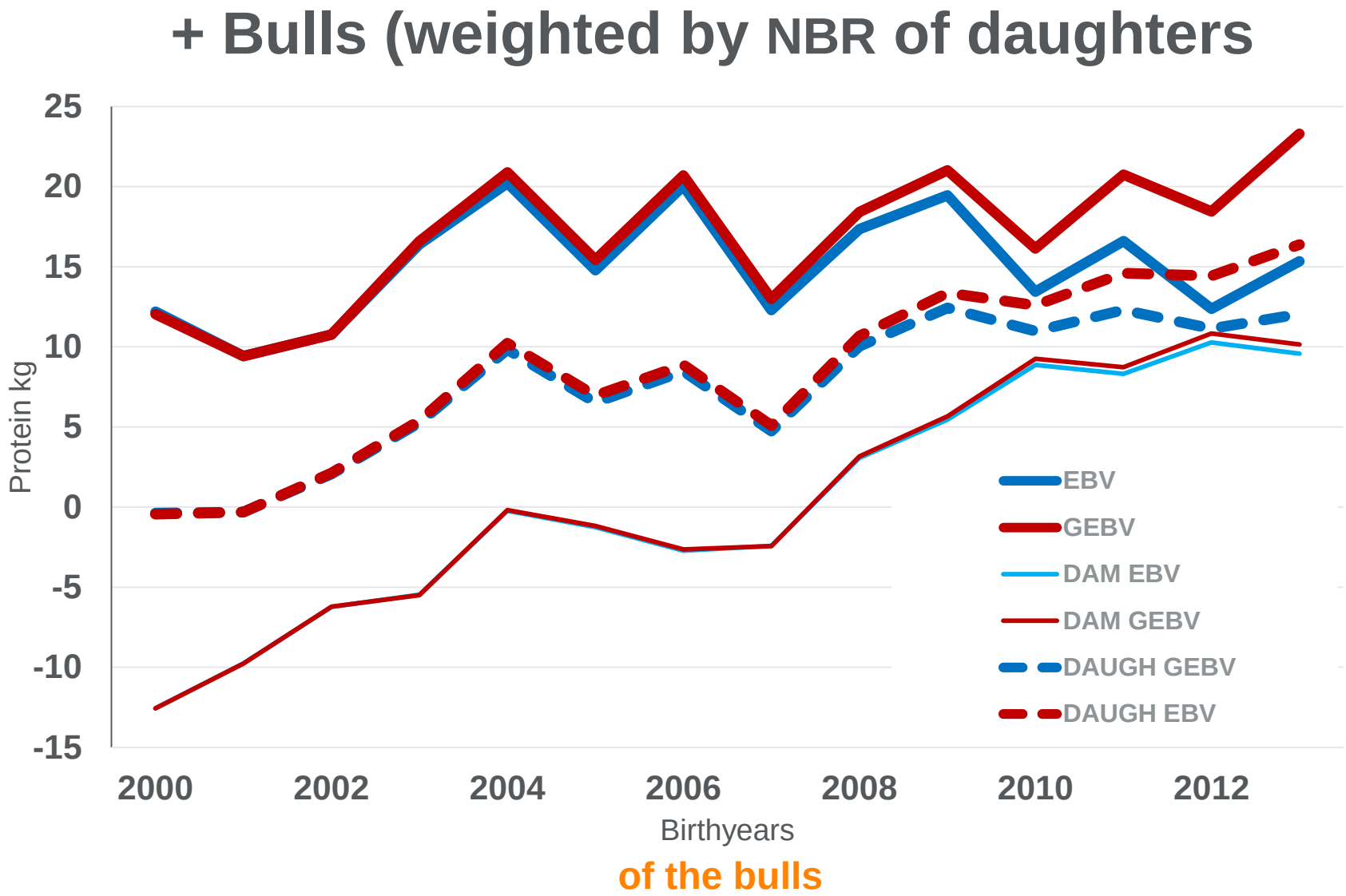

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What is the explanation of large differences in bull BV trends estimated with AMBLUP and ssGBLUP?

- To small extend explanation is the differences in environmental trend estimates (i.e. in solutions of fixed effects)

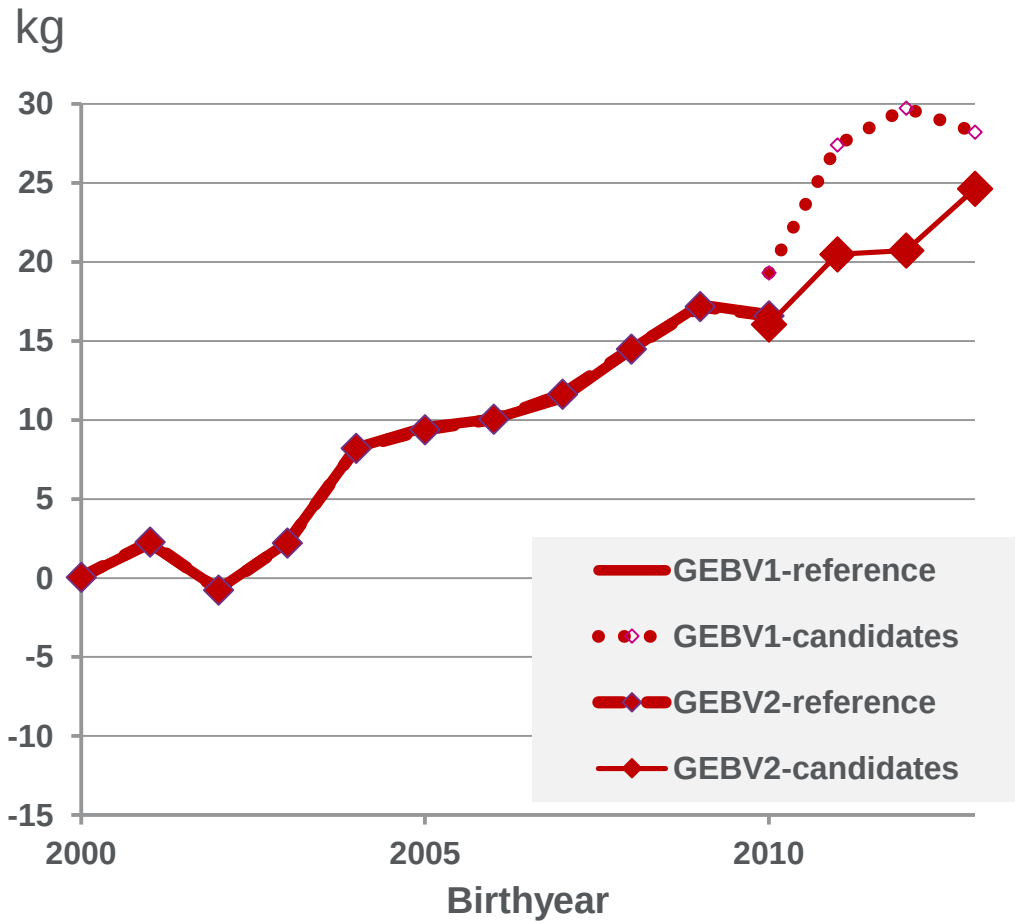
- It is not the level of estimates of BVs of mates
- [We also verified that] the residuals do not show big differences

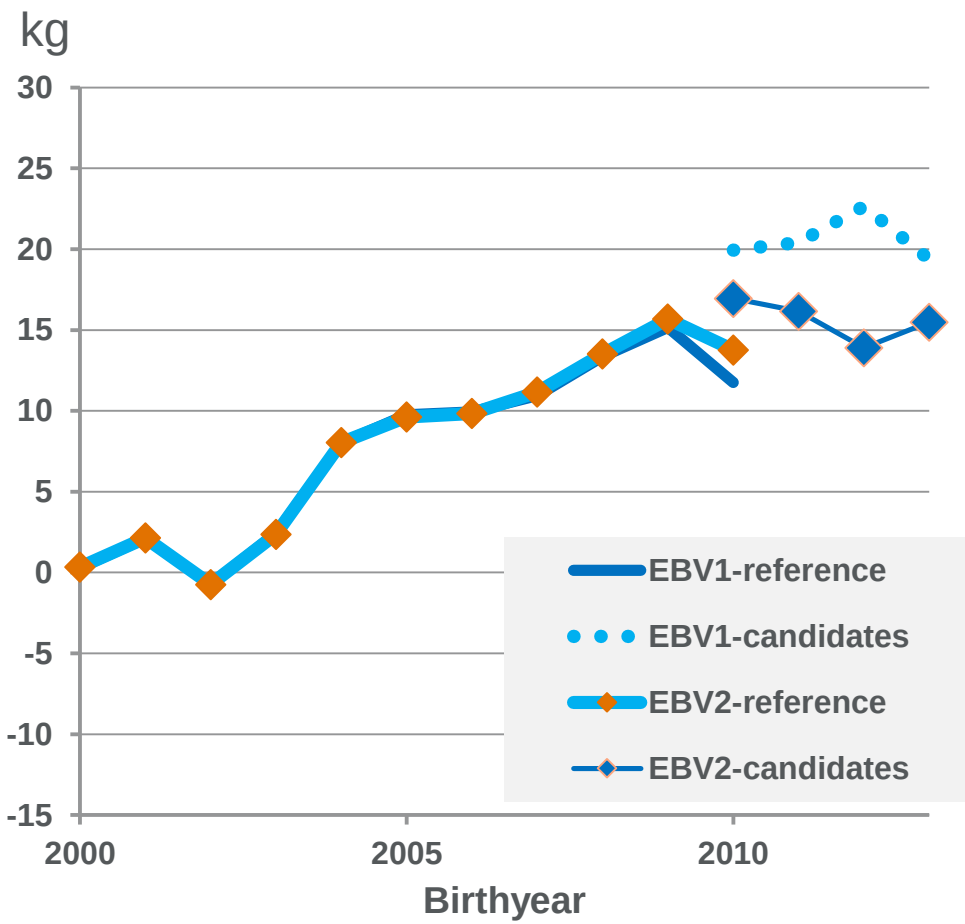
- Possible explanation could be in the ”expectations” of young bulls
  - For the AMBLUP the expectation is parent average
  - For the ssBLUP the expectation is DNA based breeding value estimate

  - To find the expectations we deleted the daughter data of the youngest bulls

Recuced (10/2017) vs. Full data evaluations (12/2014)
Bull protein GEBV and EBV birthyear averages

(G)EBV1 reduced
(G)EBV2 recent





Candidate:
ERC1 == 0
ERC2 >= 3.

Note:

Reference:	189			
Candidates	5	106	170	38

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Conclusions

1. Animal Model BLUP predicted the genomic selected bulls born 2012 almost 7 kg lower than ssGBLUP
2. The simple presumption: ”genetic trend slides to environment solutions” was not correct
   - AMBLUP with fixed effects from ssGBLUP do not match with ssGBLUP
3. Both, the Parent average EBV, and the first GEBV are over-estimated
   - GEBV actually drops more but still remains higher
   - PA drops slightly less but it still drops to lower level
4. YD from from ssGBLUP are not much different from YD from AM BLUP
   - It seems possible to us YD as input for SNP BLUP
   - But maybe it would not help MACE ?

Thank you!