



Robust MACE

*H. Benhajali, Z. Liu, P. Sullivan, P.M. VanRaden, G.P. Aamand,
G.de Jong, E. Mantysaari & V. Ducrocq*



A bit of history...

➤ What is Robust MACE?

=MACE (Multiple Across Country Evaluation)

Country x Birth-Year effect instead of Country effect

Inspired from *Ducrocq et al., 2003*

Benhajali et al., 2013 showed that

- Despite the trend validation tests, some discrepancies caused by ΔG biases remain
- Robust MACE can correct these discrepancies

Benhajali et al., 2014 tested the robustness of the Robust Mace model by simulating a systematic ΔG bias for one or two countries

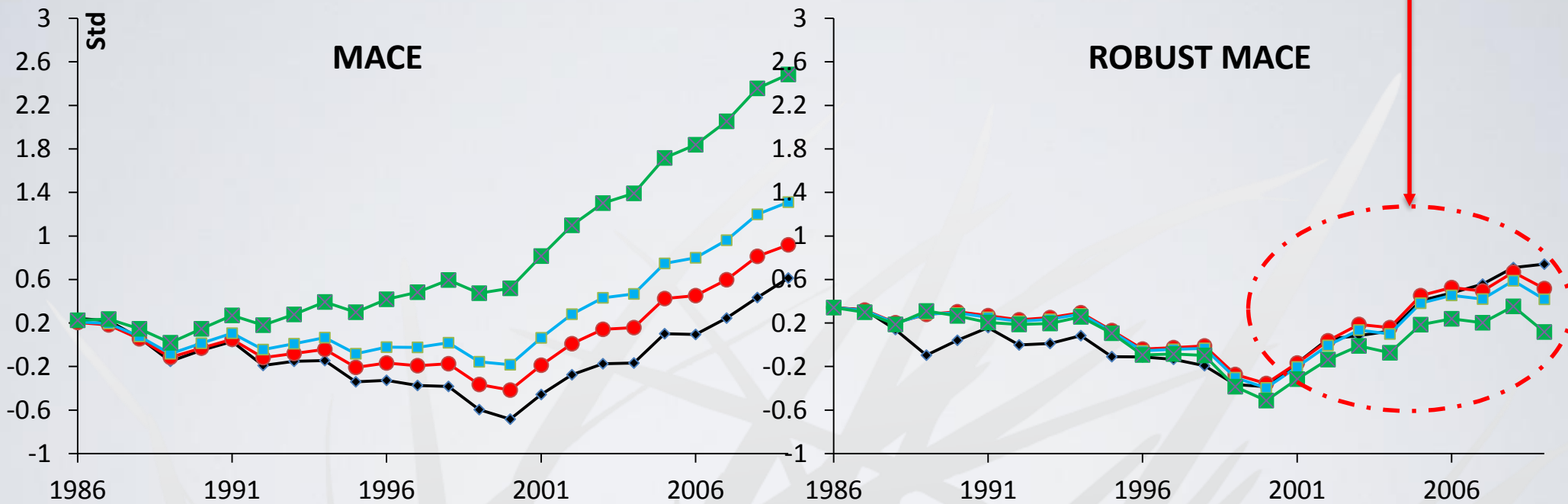


A bit of history...

FRA bulls on FRA scale

ΔG_SCS

Over-correction?

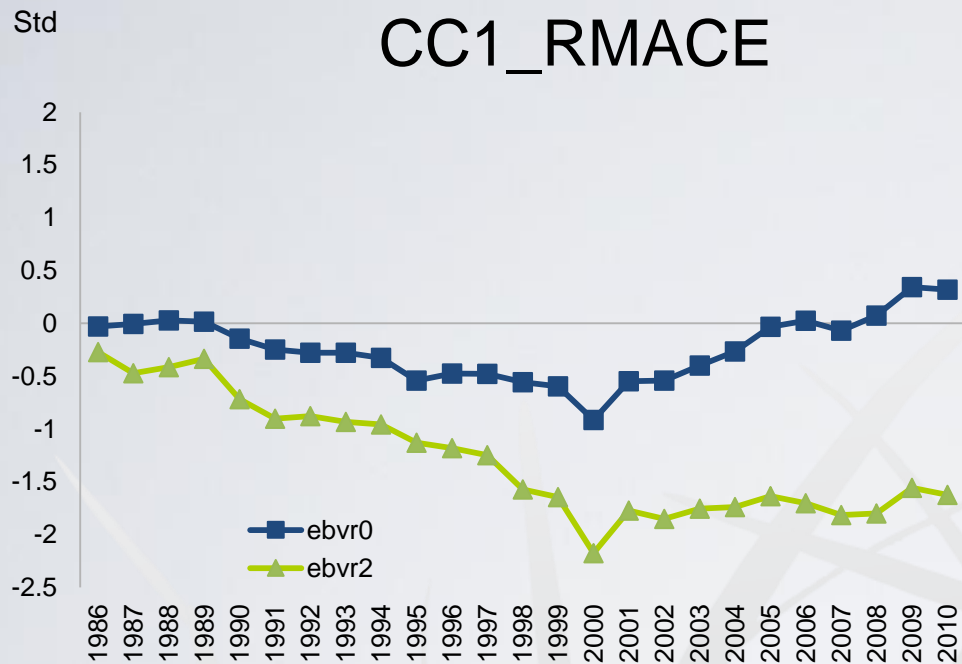


- ◆— bias= 0% STD
- bias= 2% STD
- bias= 4% STD
- ×— bias= 10% STD

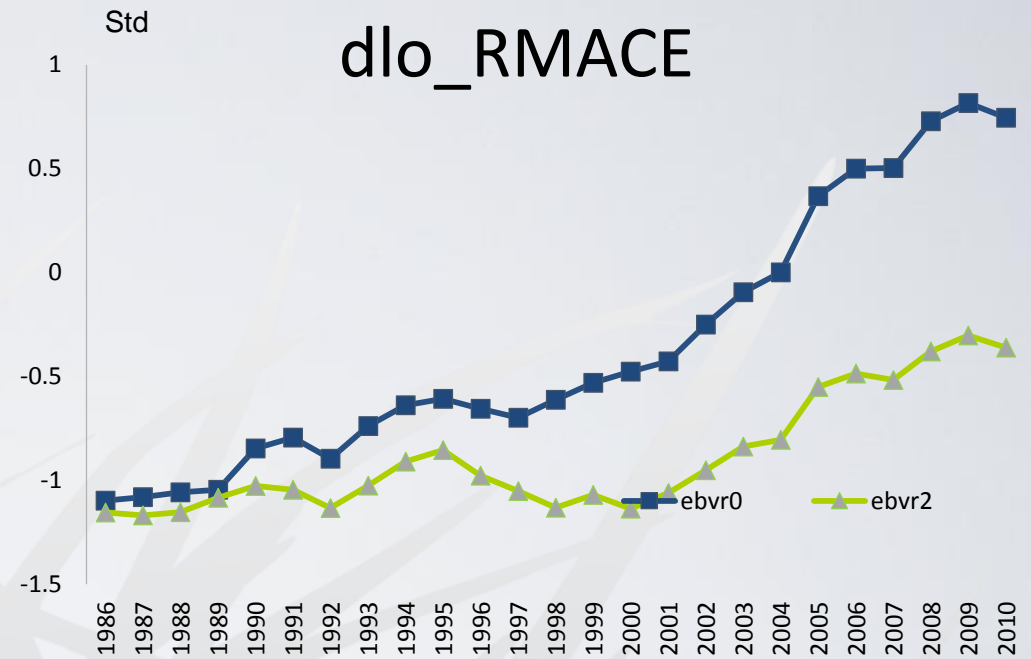
Benhajali et al., 2014



Some other Unpublished results



ebvr0: No bias, RMACE model



ebvr2:+10%FRA, RMACE model



Why is Robust MACE over-correcting the bias ?



Include the country*year effect in the de-regression model



Current study

- Change the de-regression procedure by including a country year effect in the model
- Repeat the study with 5 trait

protein(pro), somatic cells(scs), stature(sta), longevity(dlo) and fertility(cc1)



DATA

- **Data on Holstein breed from INTERBULL routine evaluation of December 2015:**
- **14 countries:**
- **AUS CAN DEU DFS ESP FRA GBR IRL ITA JPN NLD NZL POL USA**
- **5 trait: SCS, dlo, sta, pro, cc1**

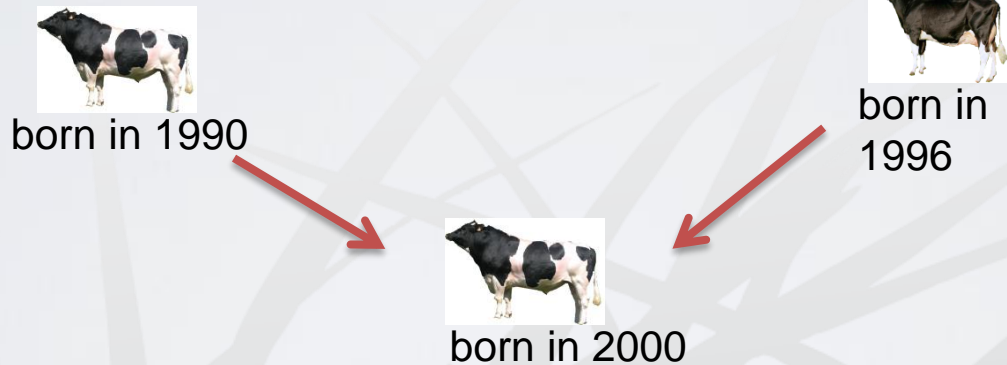


BIAS

$$\text{Bias} = (0.5(\text{BY}_{\text{bull}} - 1986) + 0.25(\text{BY}_{\text{sire}} - 1986) + 0.25(\text{BY}_{\text{dam}} - 1986)) * \text{stdg} * \mathbf{B}$$

Different levels of bias: $\mathbf{B} = 0\%, 10\%, -10\%$

Example:



$$\text{Bias} = (0,5 * 14 + 0,25 * 4 + 0,25 * 10) * \mathbf{B} * \text{stdg} = 10,5 * \mathbf{B} * \text{stdg}$$



BIAS

$$\text{Bias} = (0.5(\text{BY}_{\text{bull}} - 1986) + 0.25(\text{BY}_{\text{sire}} - 1986) + 0.25(\text{BY}_{\text{dam}} - 1986)) * \text{stdg} * \mathbf{B}$$

Different levels of bias: $\mathbf{B} = 0\%, 10\%, -10\%$

Systematic biases were simulated in only one country (FRA) or two countries (FRA and NLD)



1. FRA_+10
2. NLD_-10



RUNS

6 Data sets



6 runs/trait

1. Regular data for all the countries

2. Regular data for all the other countries + **FRA_+10**

3. Regular data for all the other countries + **FRA_+10+ NLD_-10**



3 MACE

3 R_MACE



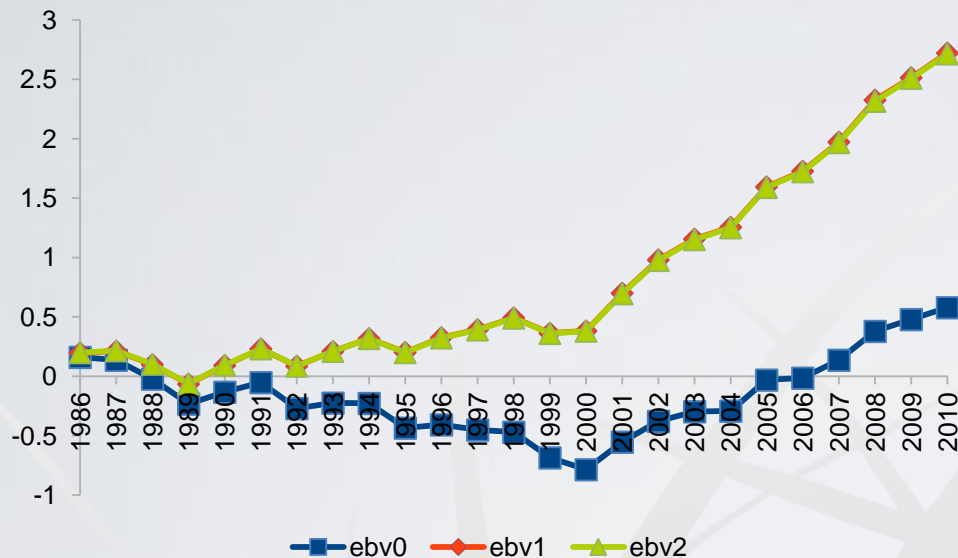
NEW RESULTS



ΔG SCS: FRA BULLS/FRA scale

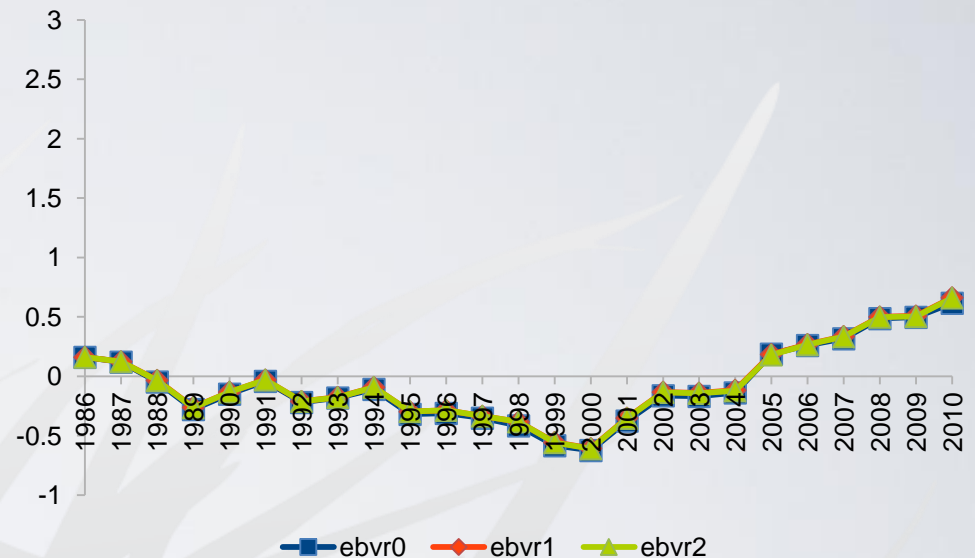
Std

MACE



Std

RMACE



ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

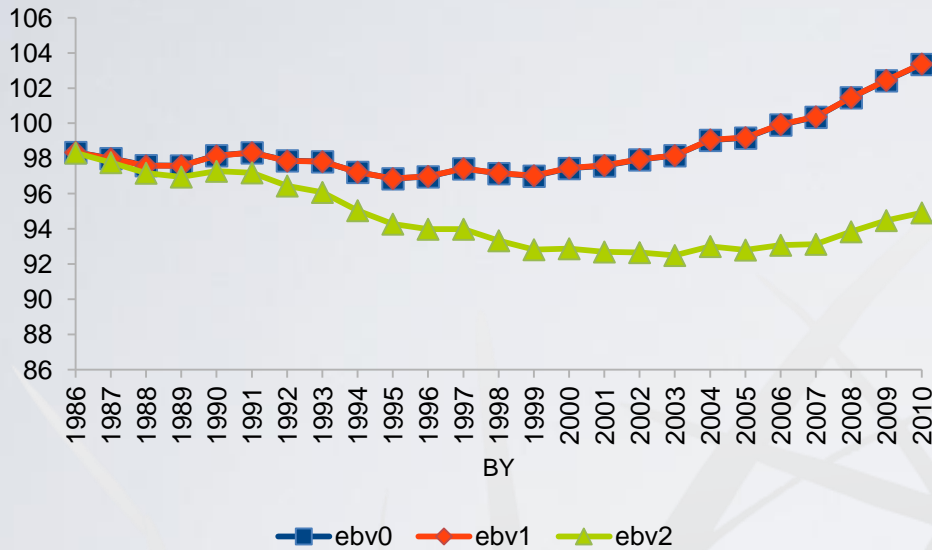
ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG SCS: NLD BULLS/NLD scale

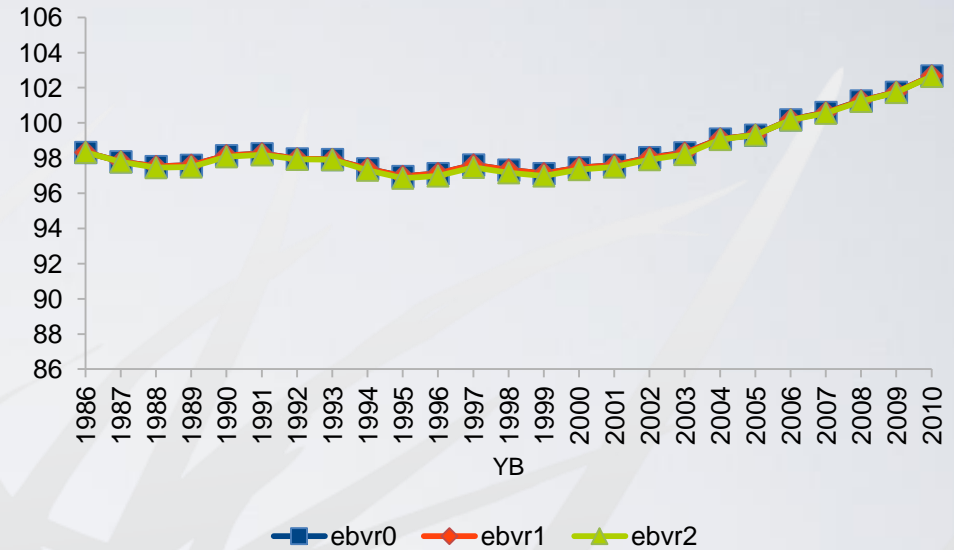
Std

MACE



Std

RMACE

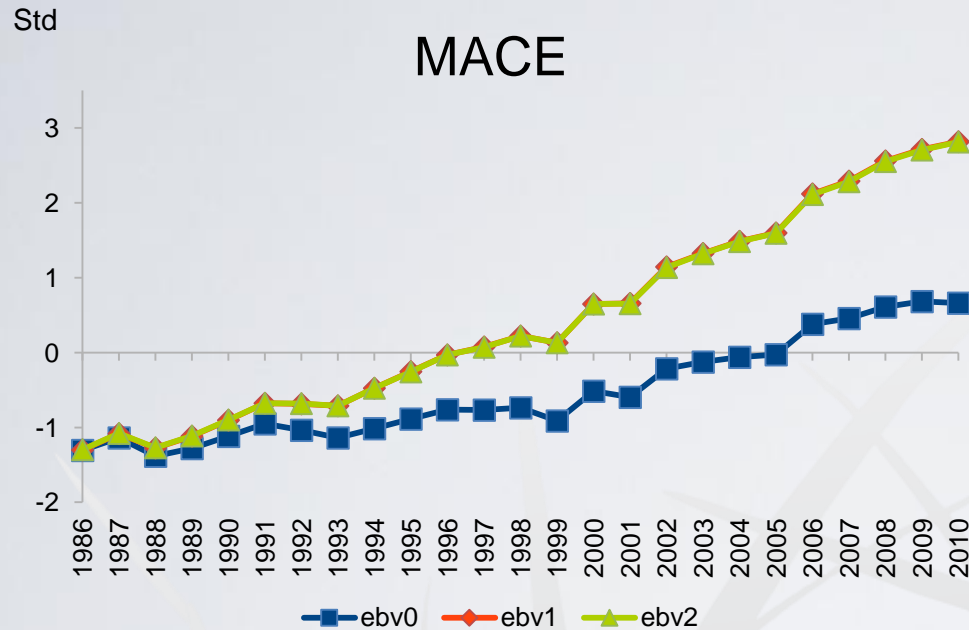


ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

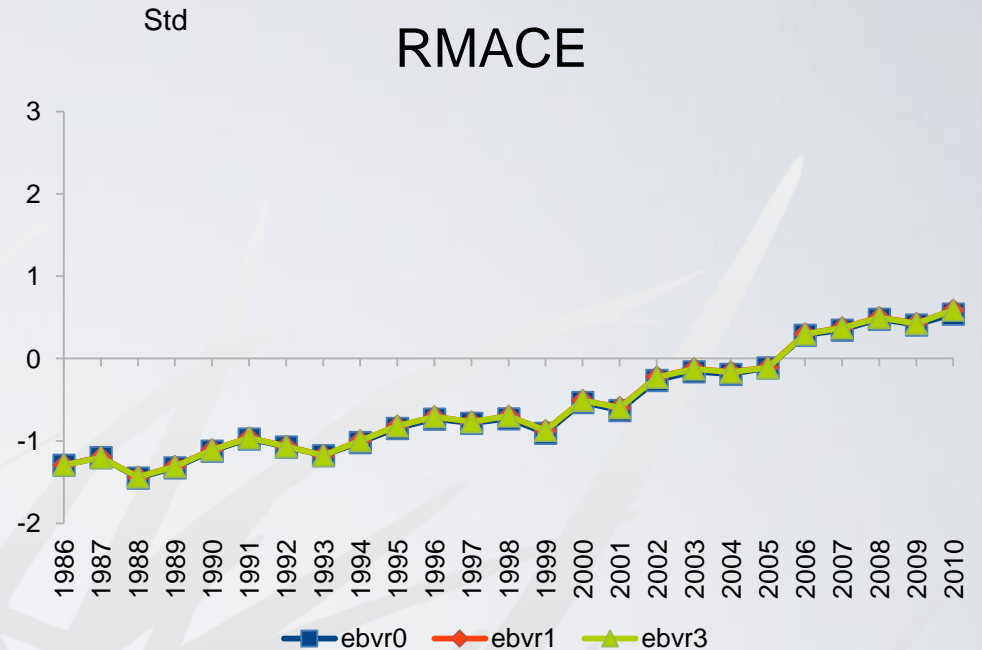
ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG STA: FRA BULLS/FRA scale



ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model



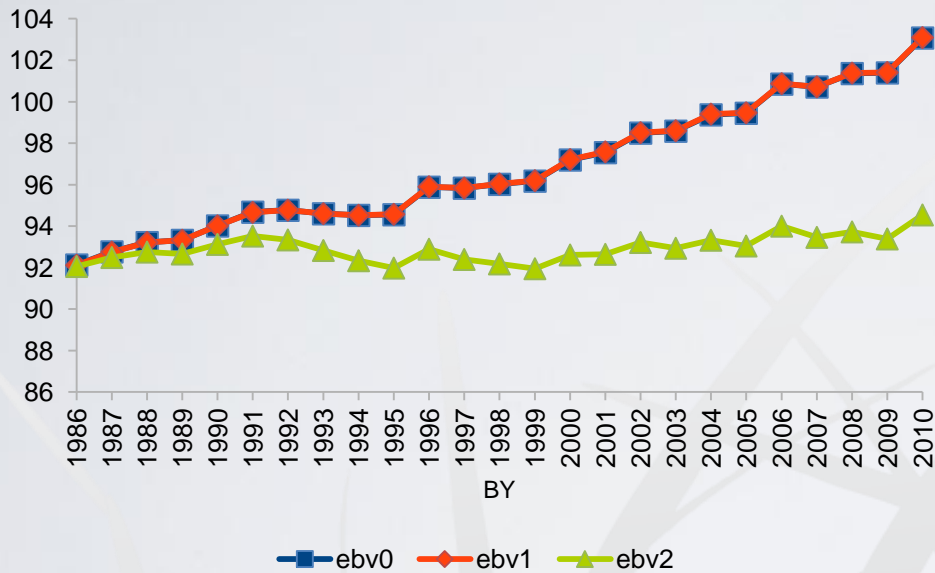
ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG STA: NLD BULLS/NLD scale

Std

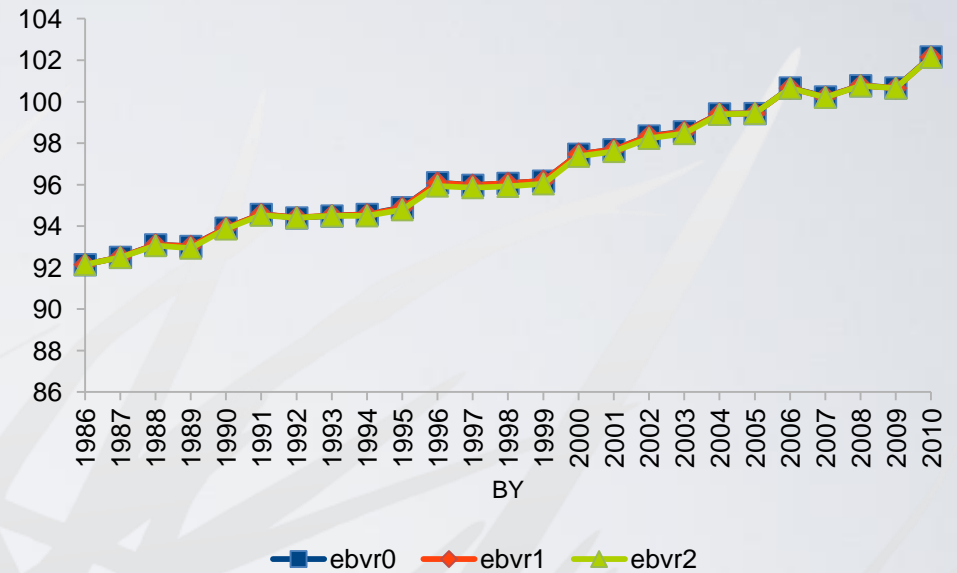
MACE



ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

Std

RMACE

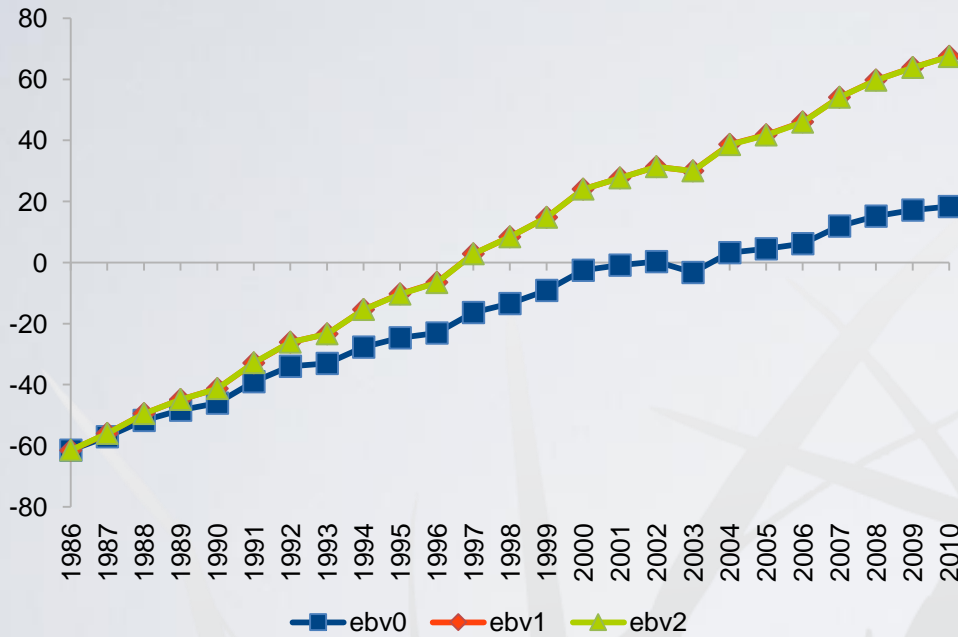


ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



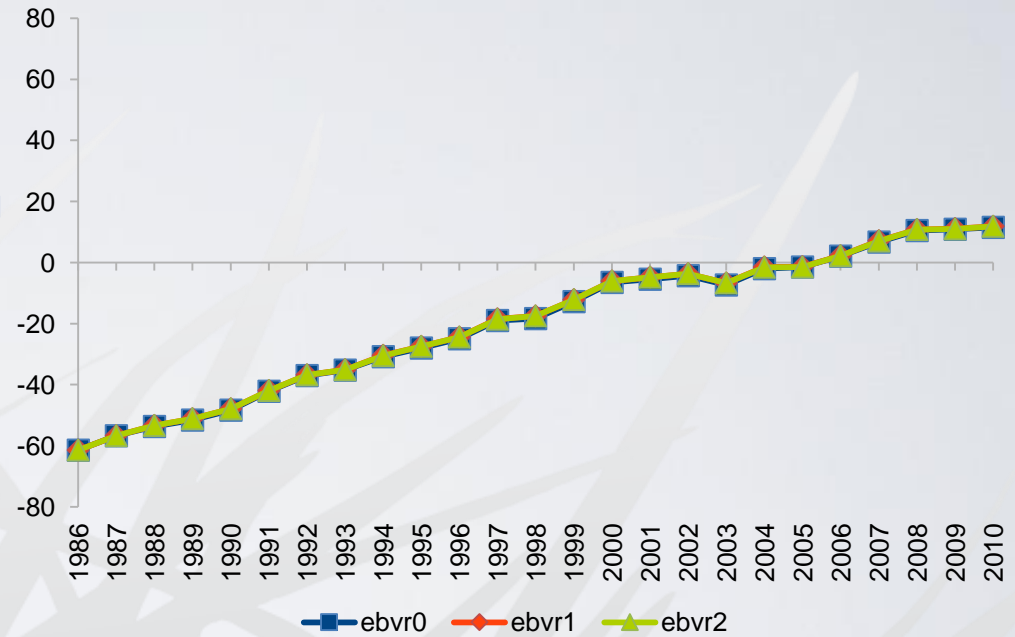
ΔG PRO: FRA BULLS/FRA scale

MACE



ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

RMACE

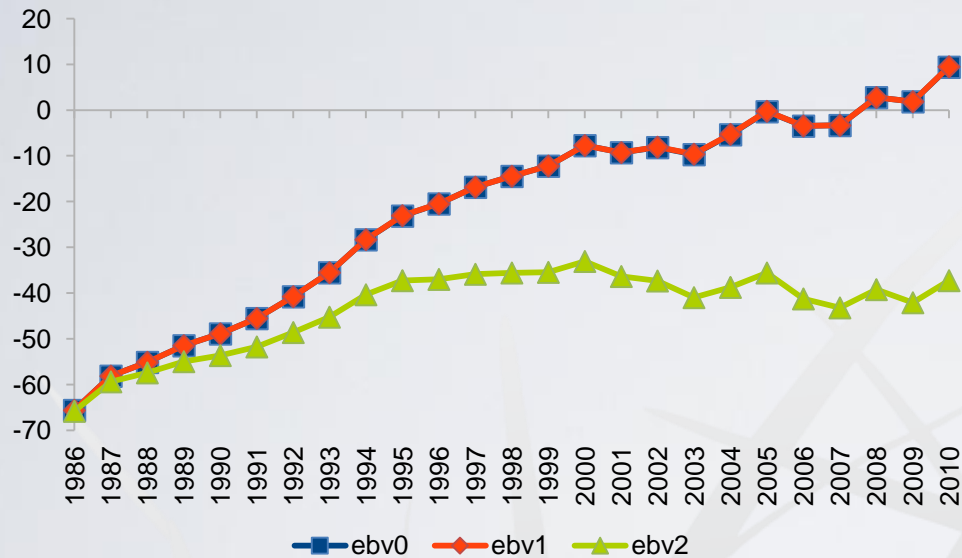


ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



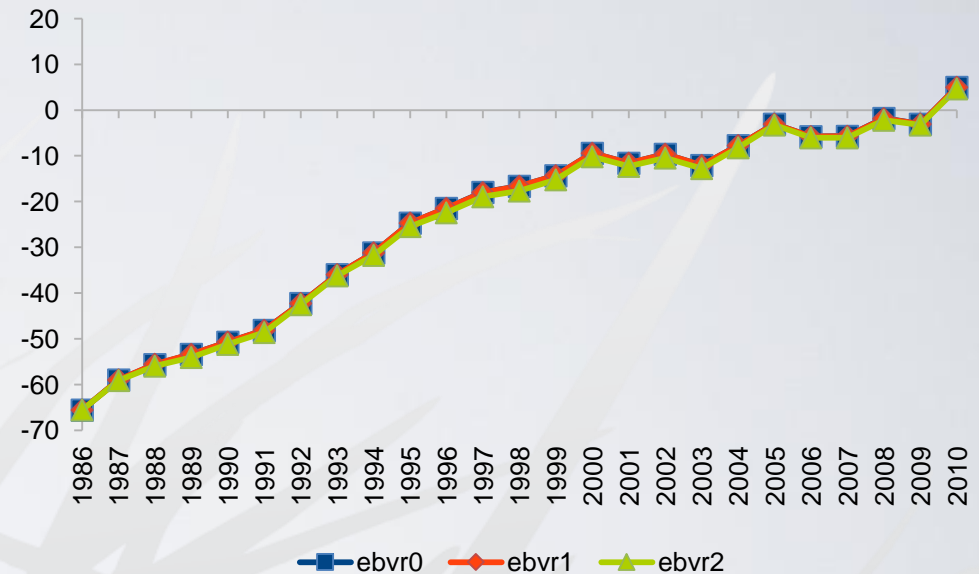
ΔG PRO: NLD BULLS/NLD scale

MACE



ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

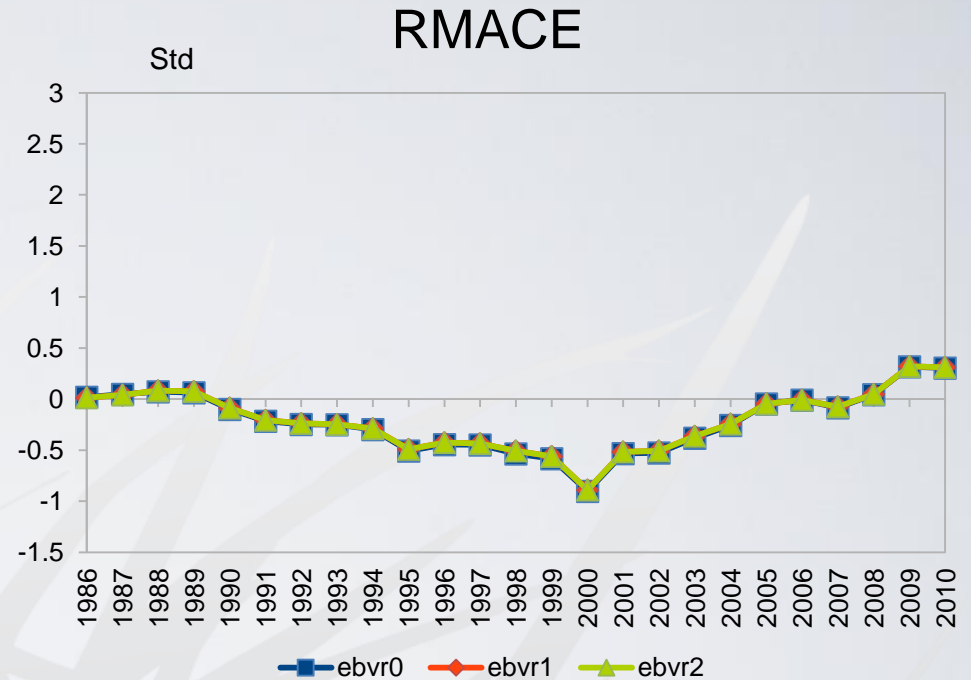
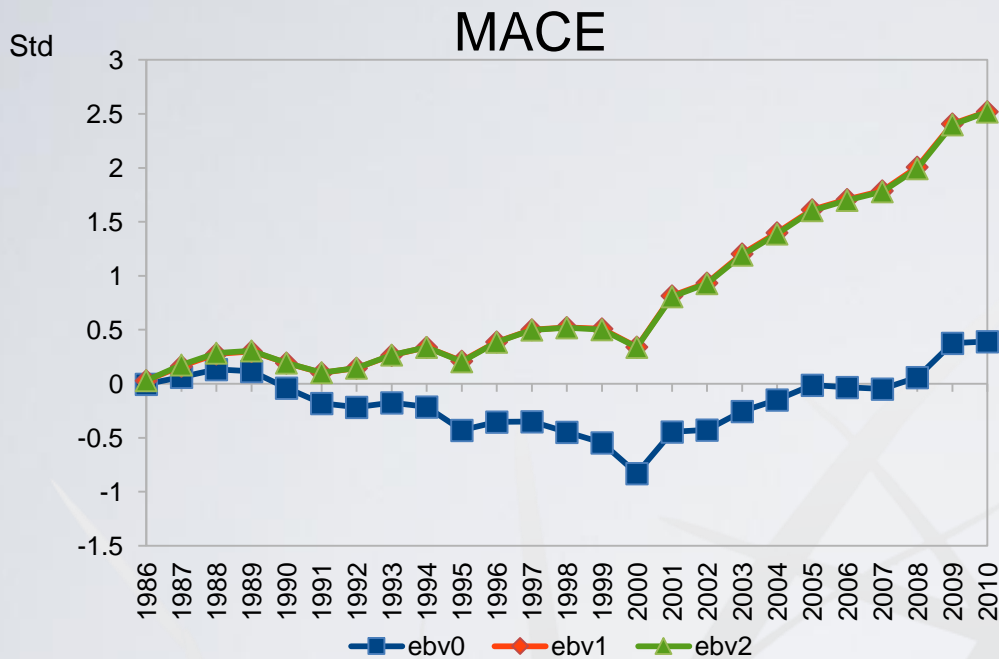
RMACE



ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG CC1: FRA BULLS/FRA scale

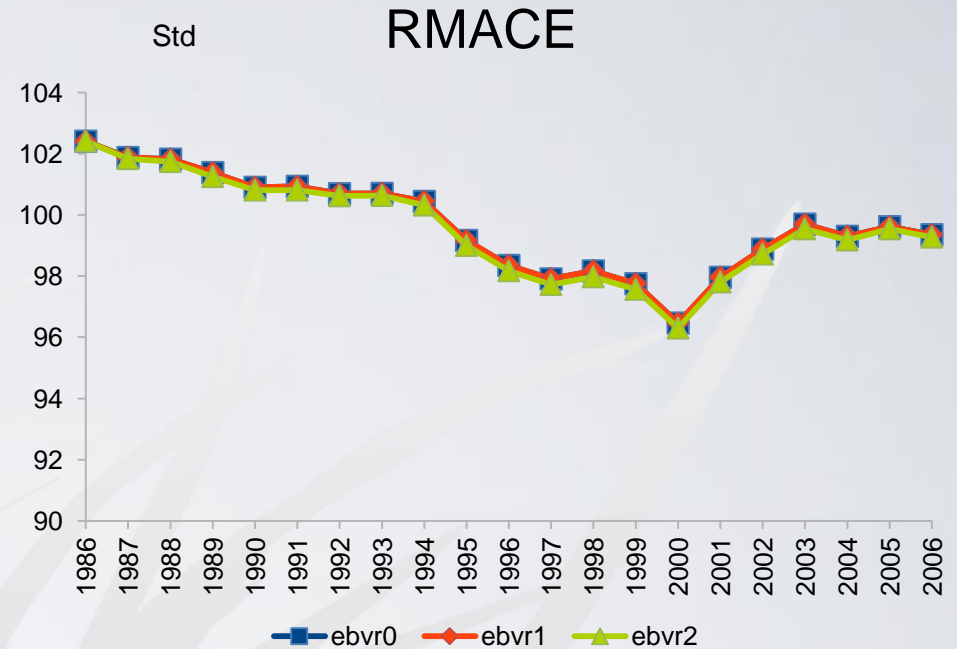
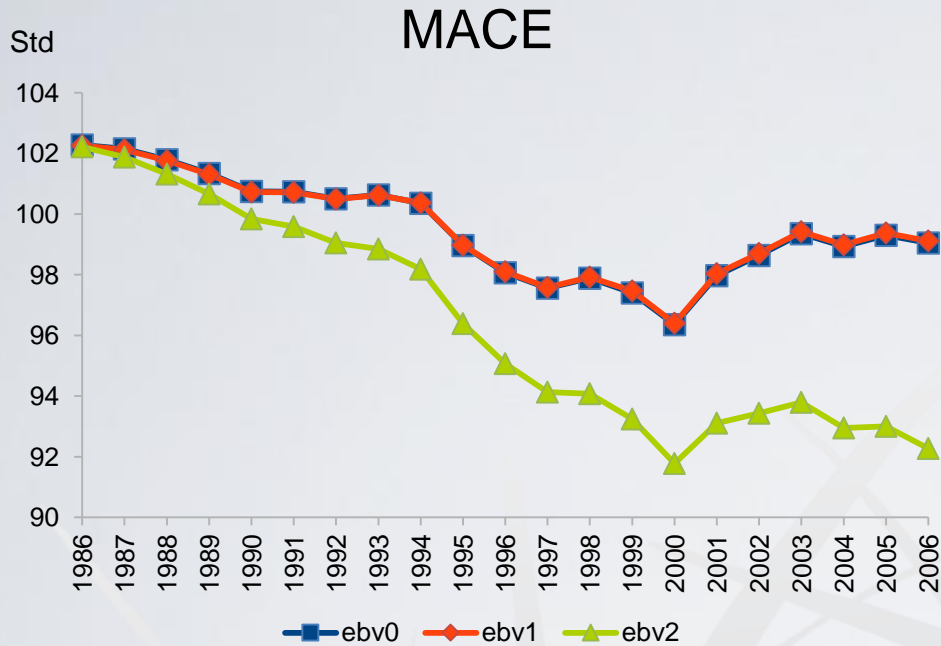


ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG CC1: NLD BULLS/NLD scale

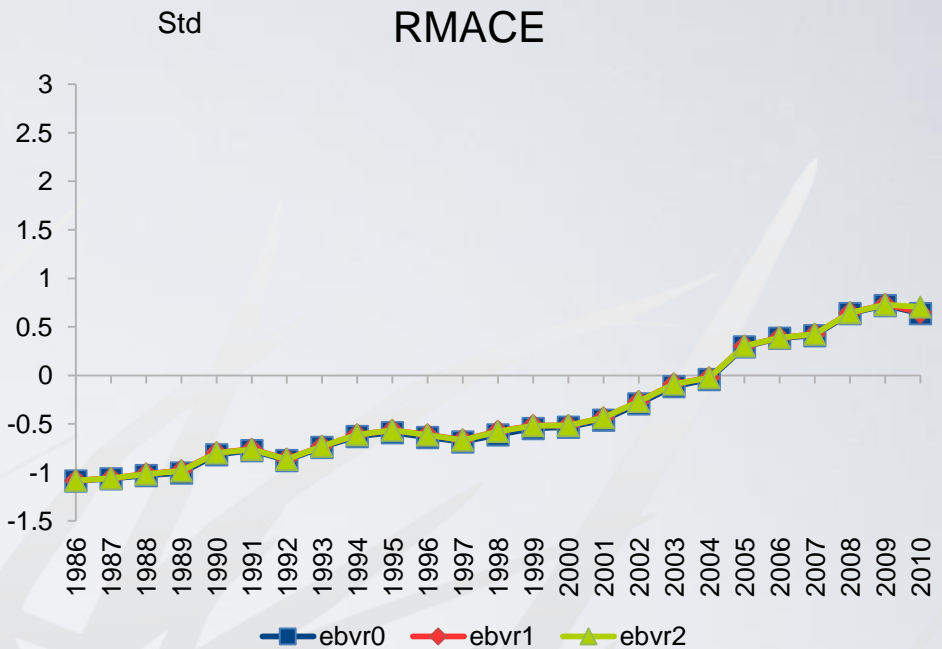
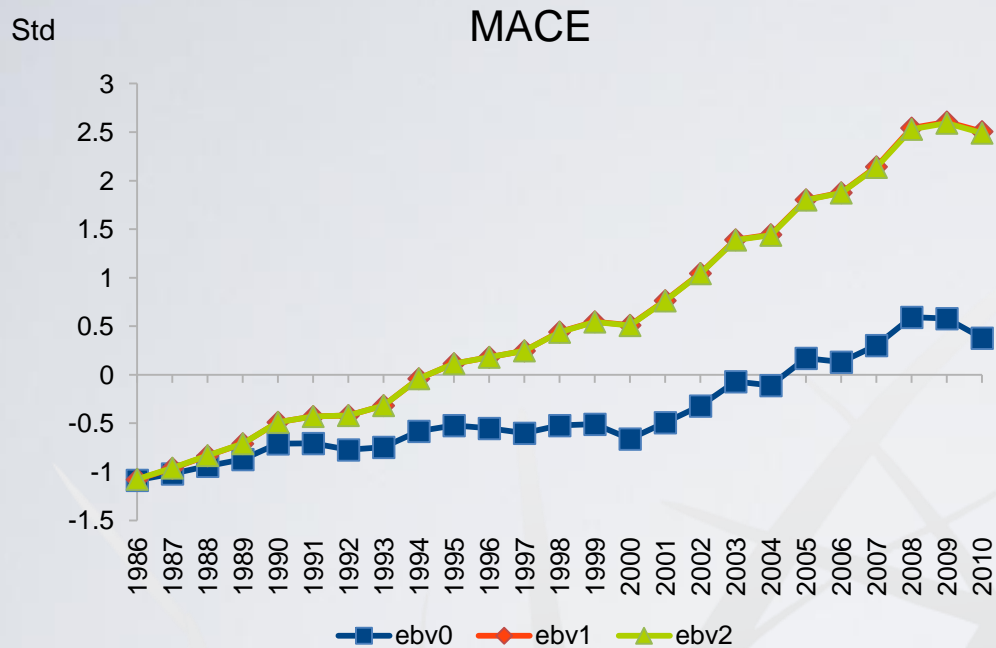


ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



ΔG dlo: FRA BULLS/FRA scale



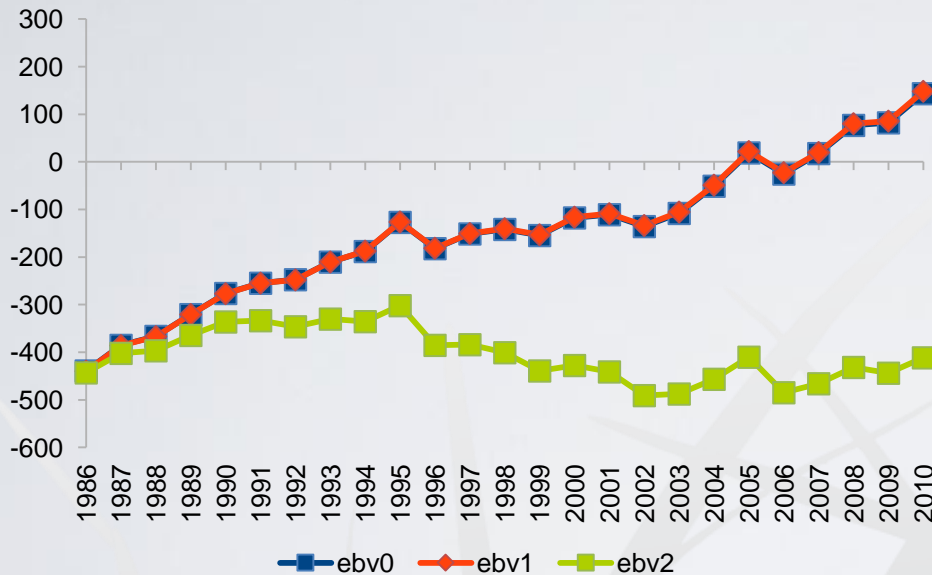
ebv0: No bias, MACE model
 ebv1: +10%FRA, MACE model
 ebv2: +10%FRA, -10%NLD, MACE model

ebvr0: No bias, RMACE model
 ebvr1: +10%FRA, RMACE model
 ebvr2: +10%FRA, -10%NLD, RMACE model



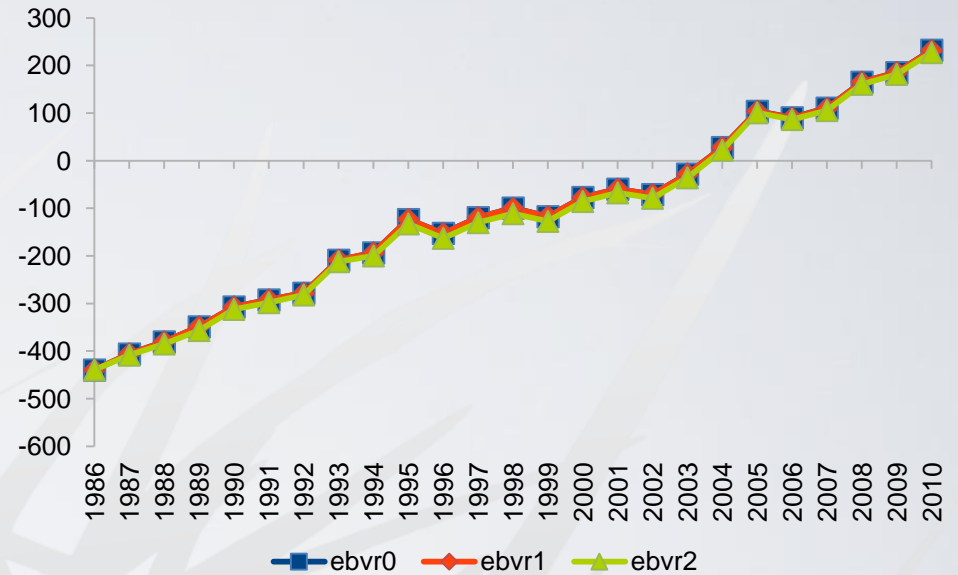
ΔG dlo: NLD BULLS/NLD scale

MACE



ebv0: No bias, MACE model
 ebv1:+10%FRA, MACE model
 ebv2:+10%FRA, -10%NLD, MACE model

RMACE



ebvr0: No bias, RMACE model
 ebvr1:+10%FRA, RMACE model
 ebvr2:+10%FRA, -10%NLD, RMACE model

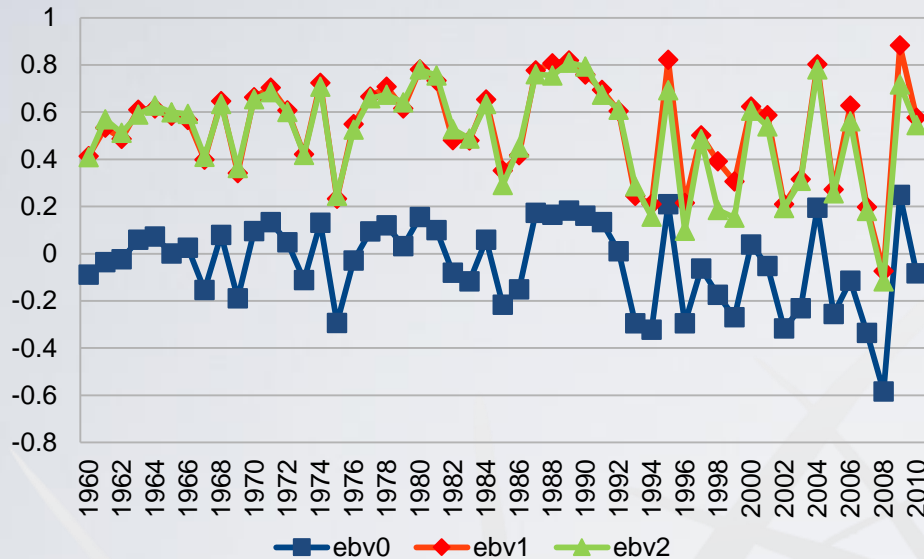


What about genetic groups?

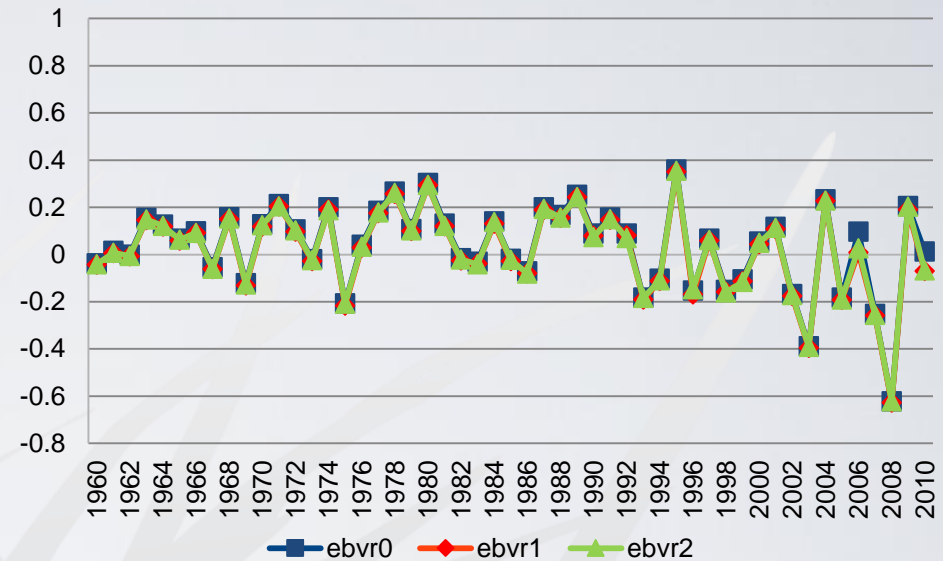


ΔG SCS: GRP_DAM/FRA scale

MACE



RMACE



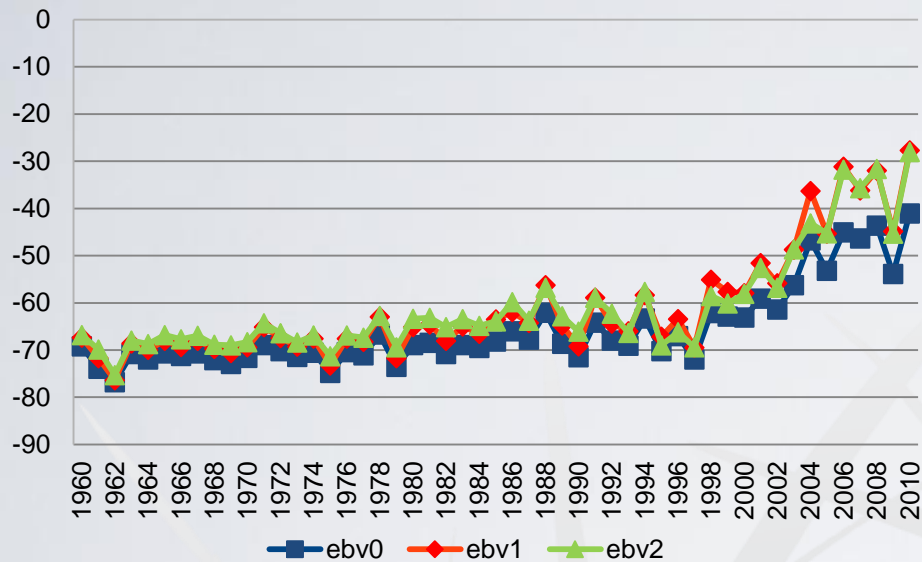
ebv0: No bias, MACE model
ebv1:+10%FRA, MACE model
ebv2:+10%FRA, -10%NLD, MACE model

ebvr0: No bias, RMACE model
ebvr1:+10%FRA, RMACE model
ebvr2:+10%FRA, -10%NLD, RMACE model



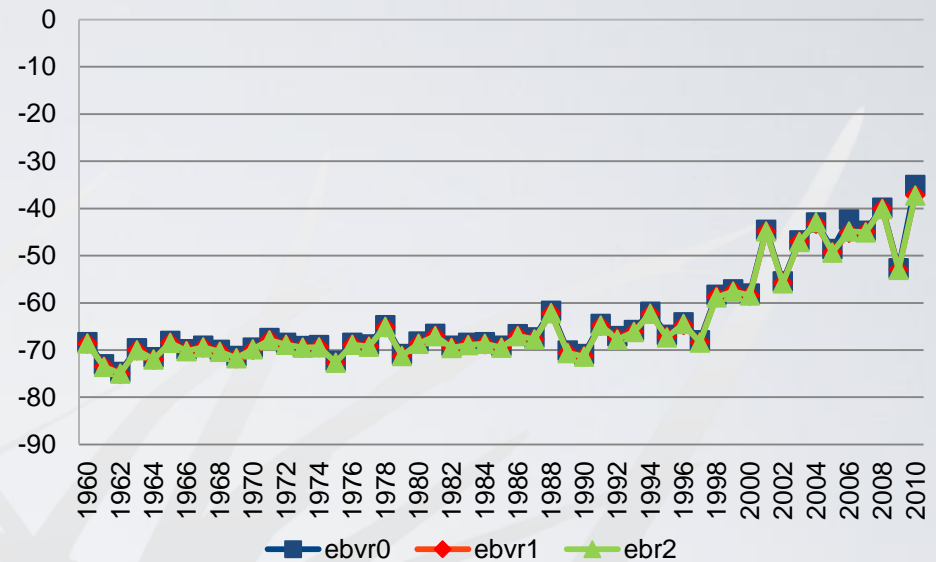
ΔG PRO: GRP_DAM/FRA scale

MACE



ebv0: No bias, MACE model
ebv1: +10%FRA, MACE model
ebv2: +10%FRA, -10%NLD, MACE model

RMACE

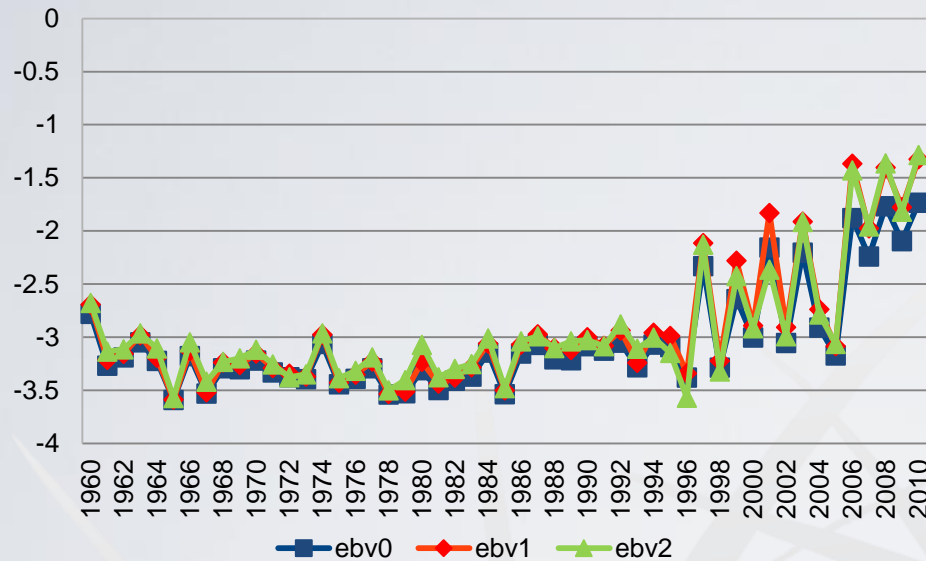


ebvr0: No bias, RMACE model
ebvr1: +10%FRA, RMACE model
ebvr2: +10%FRA, -10%NLD, RMACE model



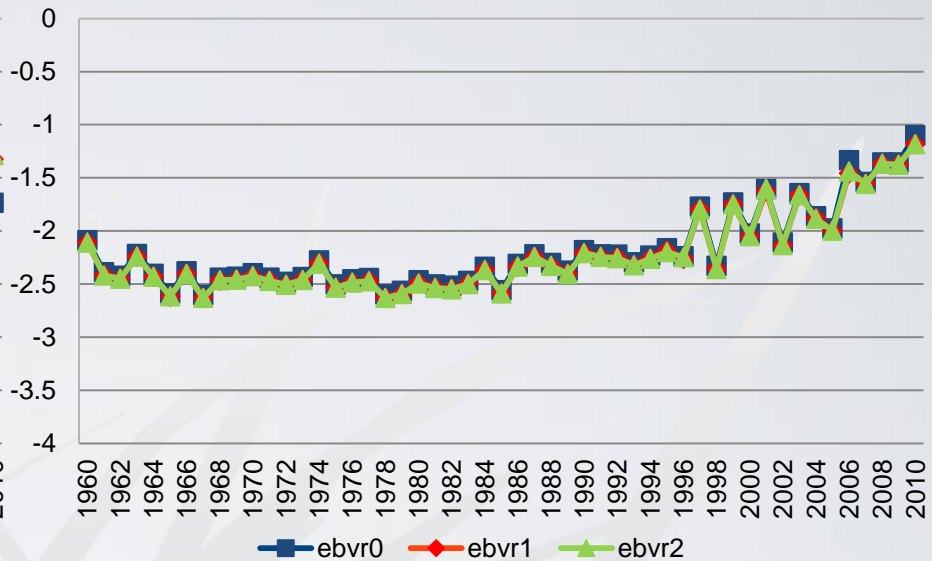
ΔG STA: GRP_DAM/FRA scale

MACE



ebv0: No bias, MACE model
ebv1: +10%FRA, MACE model
ebv2: +10%FRA, -10%NLD, MACE model

RMACE

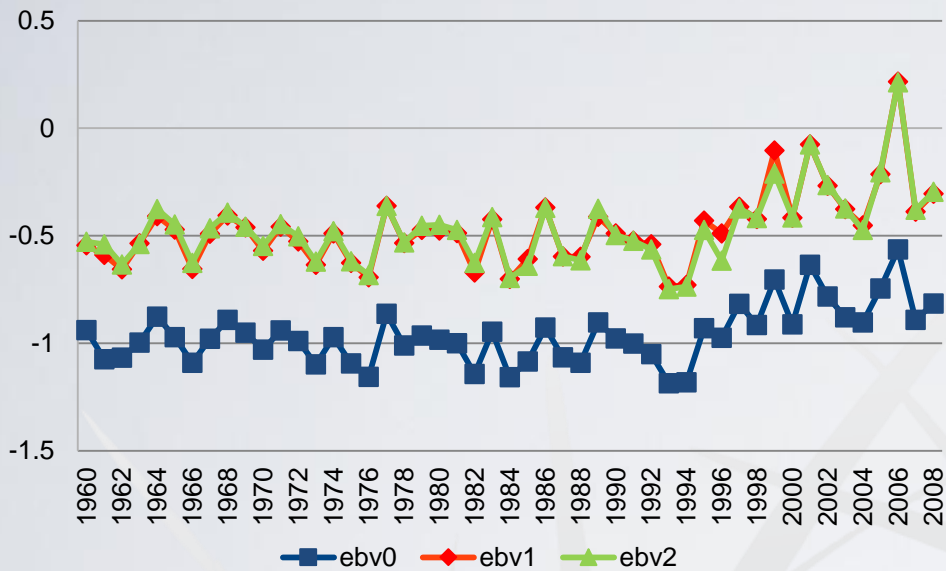


ebvr0: No bias, RMACE model
ebvr1: +10%FRA, RMACE model
ebvr2: +10%FRA, -10%NLD, RMACE model



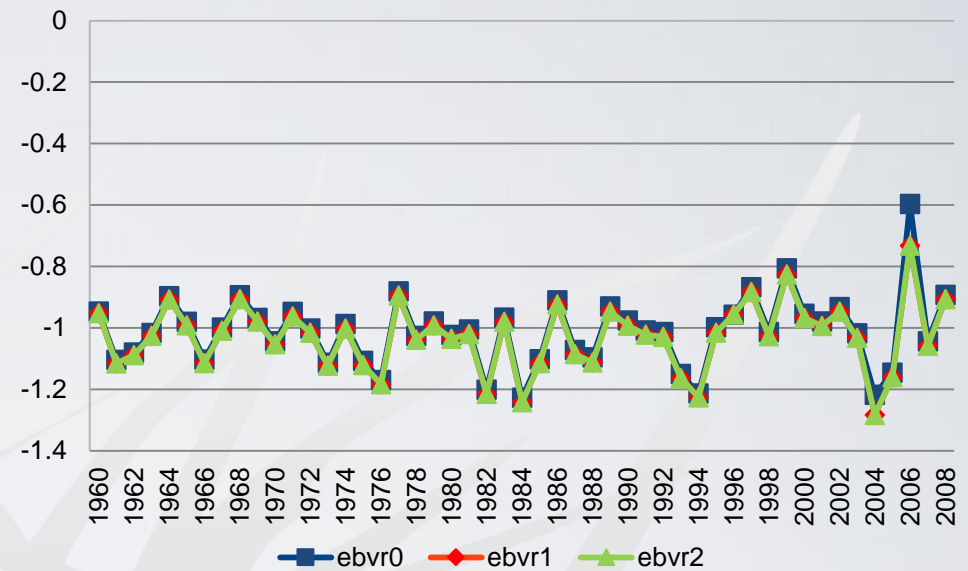
ΔG dlo: GRP_DAM/FRA scale

MACE



ebv0: No bias, MACE model
 ebv1:+10%FRA, MACE model
 ebv2:+10%FRA, -10%NLD, MACE model

RMACE

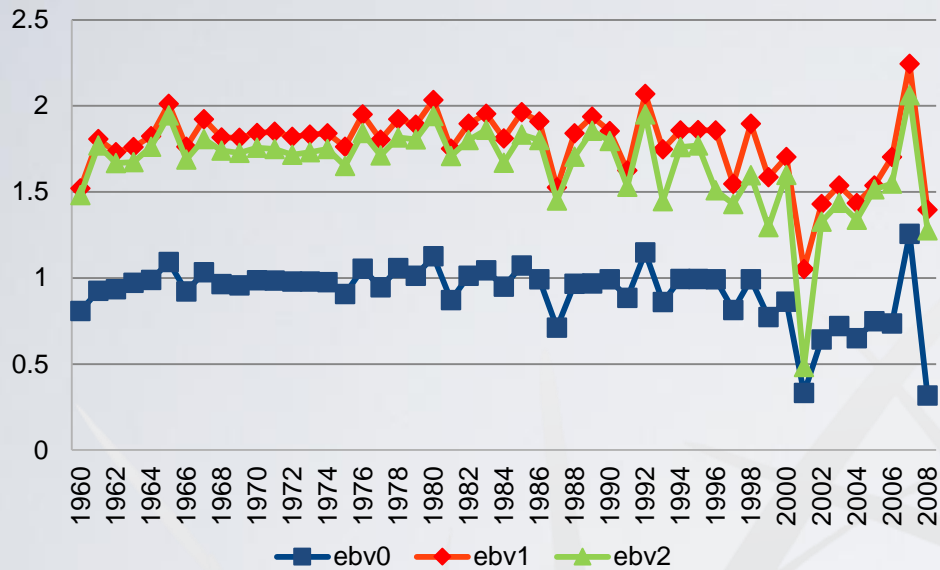


ebvr0: No bias, RMACE model
 ebvr1:+10%FRA, RMACE model
 ebvr2:+10%FRA, -10%NLD, RMACE model



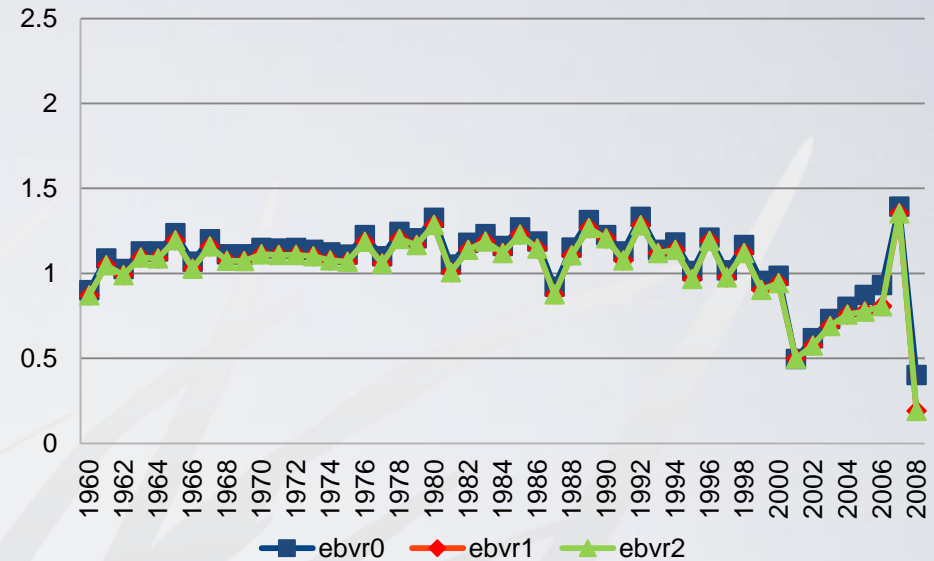
ΔG CC1: GRP_DAM/FRA scale

MACE



ebv0: No bias, MACE model
 ebv1:+10%FRA, MACE model
 ebv2:+10%FRA, -10%NLD, MACE model

RMACE



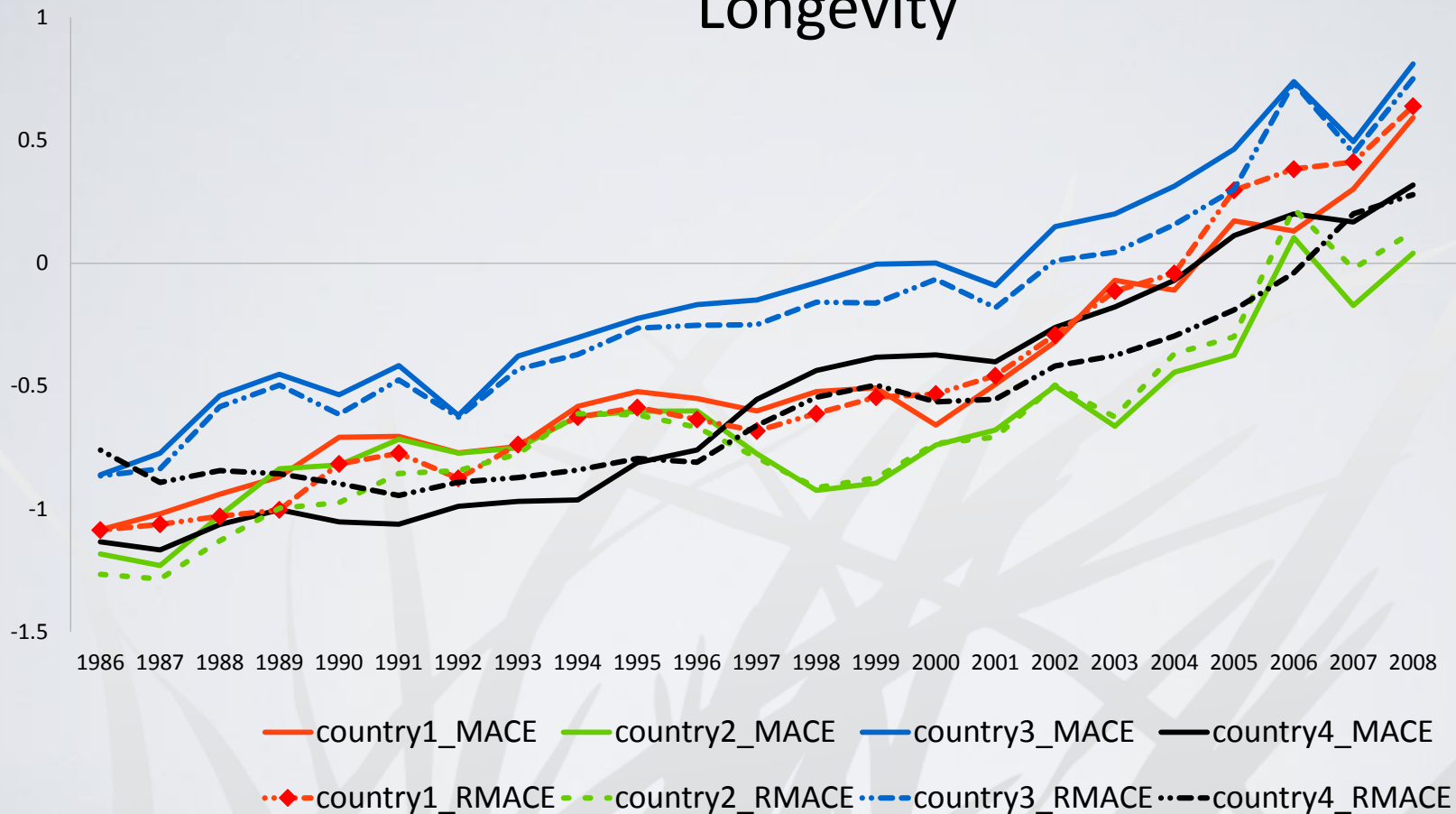
ebvr0: No bias, RMACE model
 ebvr1:+10%FRA, RMACE model
 ebvr2:+10%FRA, -10%NLD, RMACE model



MACE v.s. RMACE

current situation

Longevity





Next challenges

- Which model is better?
- Extend to all countries/breeds, effect on small populations
- Effect on correlations?



CONCLUSION

ROBUST MACE

- Does not need any new data from countries
- Ability to detect (using the country*year solutions) and correct for the discrepancies on national genetic trends
- With more consistent ΔG , It is expected to improve genetic correlations between countries (to be verified)



THANK YOU!



COUNTRY*YEAR SOLUTIONS

Scs/Regular data

