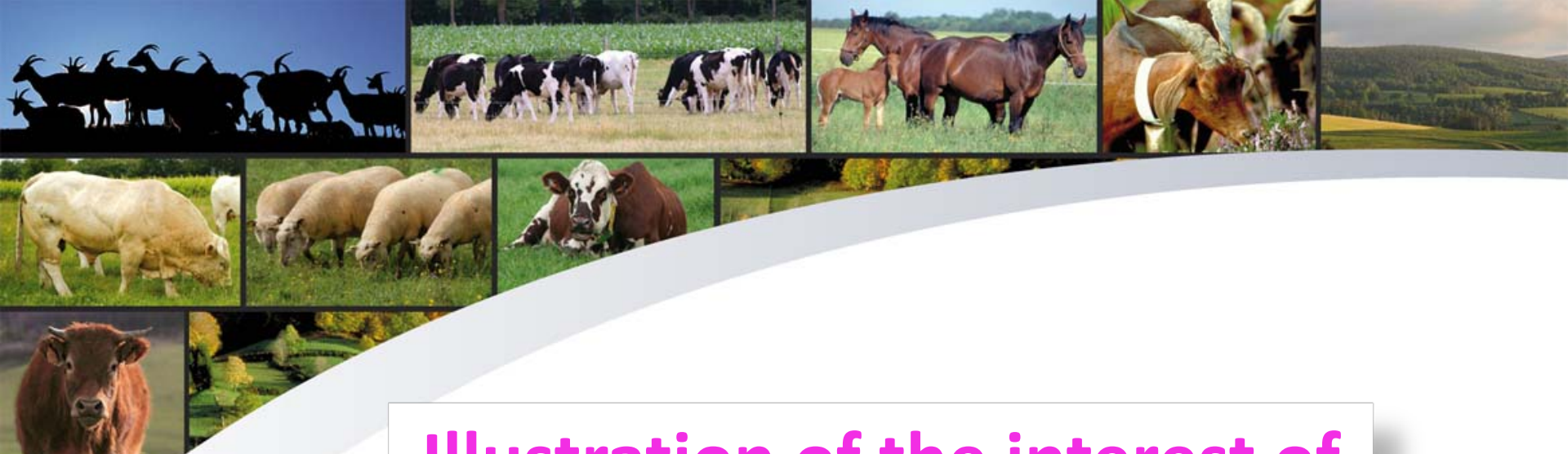


Illustration of the interest of Robust MACE

H. Benhajali, V. Palucci, S. Mattalia, H. Jorjani & V. Ducrocq

INTRODUCTION

- **What is Robust MACE?**

  =MACE (Multiple Across Country Evaluation)

Country x Birth-Year effect instead of Country effect

Inspired from *Ducrocq et al., 2003*

- **Why?**

- Despite the trend validation tests, some discrepancies caused by ΔG biases remain.

- Robust MACE can correct these discrepancies (*Benhajali et al., 2013*)

AIM OF STUDY

Test the robustness of the Robust Mace model by simulating a systematic ΔG bias for:

- ❑ **One country**
- ❑ **Two countries (opposite directions)**

DATA

- Data on Holstein breed from INTERBULL routine evaluation of:
  - December 2013:
- 14 countries:

AUS CAN DEU DFS ESP FRA GBR IRL ITA JPN NLD NZL POL USA

- 1 trait: SCS
- Same within country sire variances and genetic correlations as in December 2013 routine evaluation.

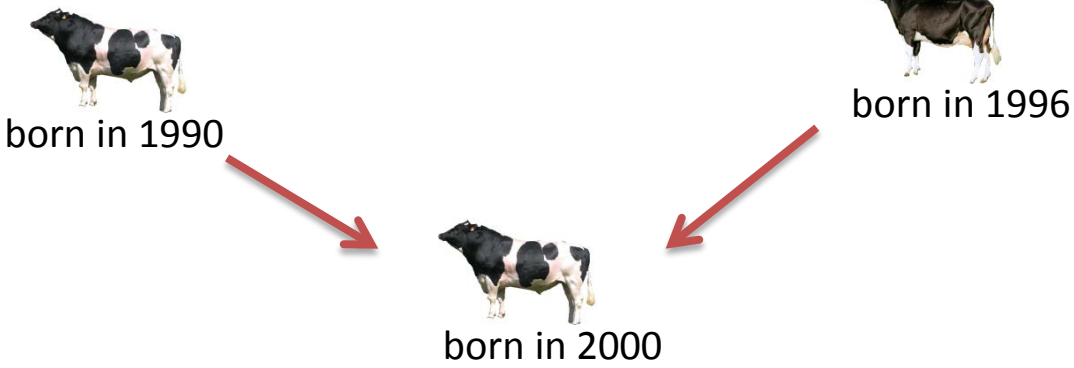
METHODS

❑ Bias

Bias= (**0.5**(BY_{bull}-1986)+**0.25**(BY_{sire}-1986)+**0.25**(BY_{dam}-1986))*stdg*B

Different levels of bias: B= 0%, 2%, 4% ,10%, -2%, -4% ,-10%

Example:



Bias= (0,5*14 +0,25*4+ 0,25*10)*B*stdg= 10,5*B*stdg

METHODS

❑ Bias

Bias= (**0.5**(BY_{bull}-1986)+**0.25**(BY_{sire}-1986)+**0.25**(BY_{dam}-1986)) ***B***stdg

Different levels of bias: **B**= 0%, 2%, 4% ,10%, -2%, -4% ,-10%

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

1. FRA_+2
2. FRA_+4
3. FRA_+10

1. NLD_-2
2. NLD_-4
3. NLD_-10

METHODS

7 Data sets → **14 runs**

1. Regular data for all the countries

2. Regular data for all the other countries + FRA_+2
3. Regular data for all the other countries + FRA_+4
4. Regular data for all the other countries + FRA_+10

5. Regular data for all the other countries + FRA_+2 + NLD_-2
6. Regular data for all the other countries + FRA_+4 + NLD_-4
7. Regular data for all the other countries + FRA_+10+ NLD_-10

→ **7 MACE**

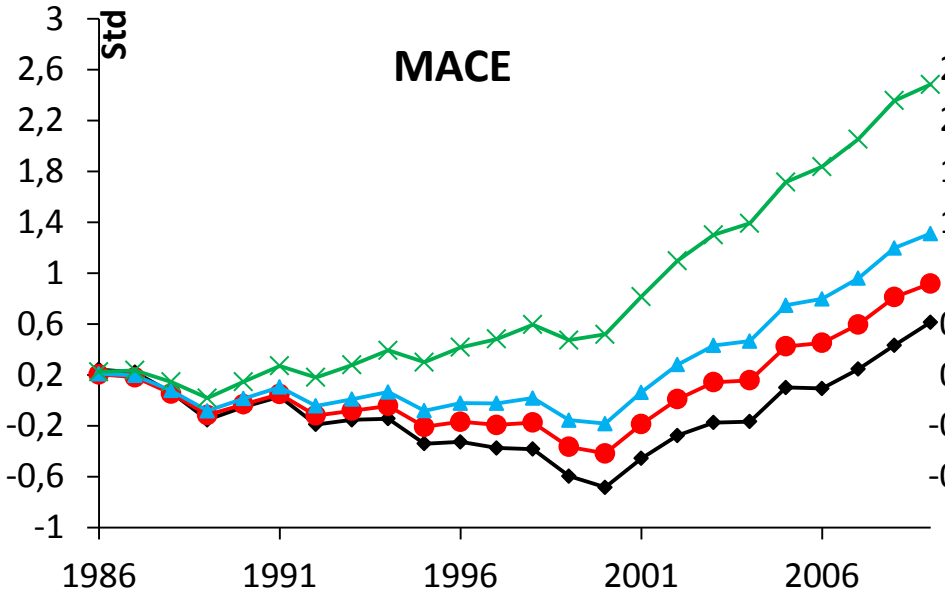
→ **7 R_MACE**

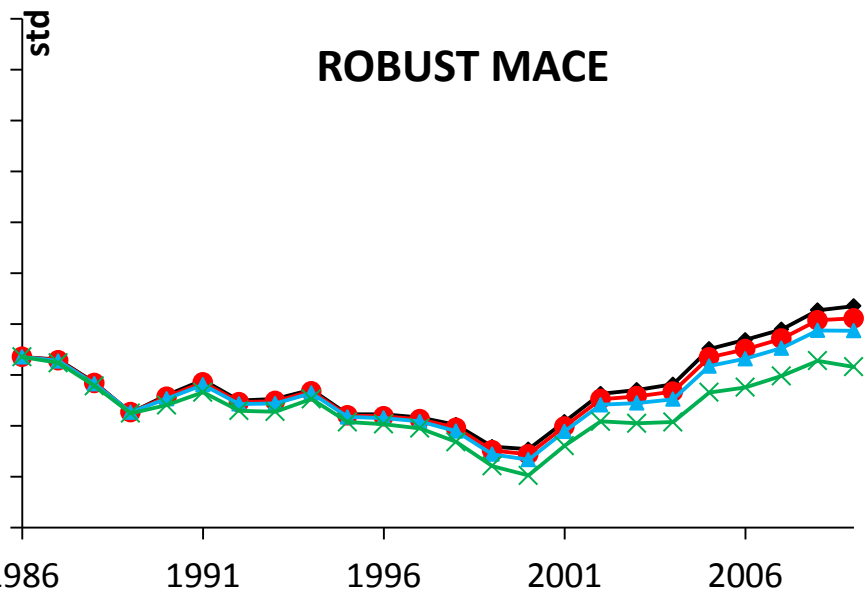
RESULTS

CASE N°1

- BIASES WERE CREATED FOR ONLY ONE COUNTRY: FRANCE

ΔG SCS: FRA BULLS



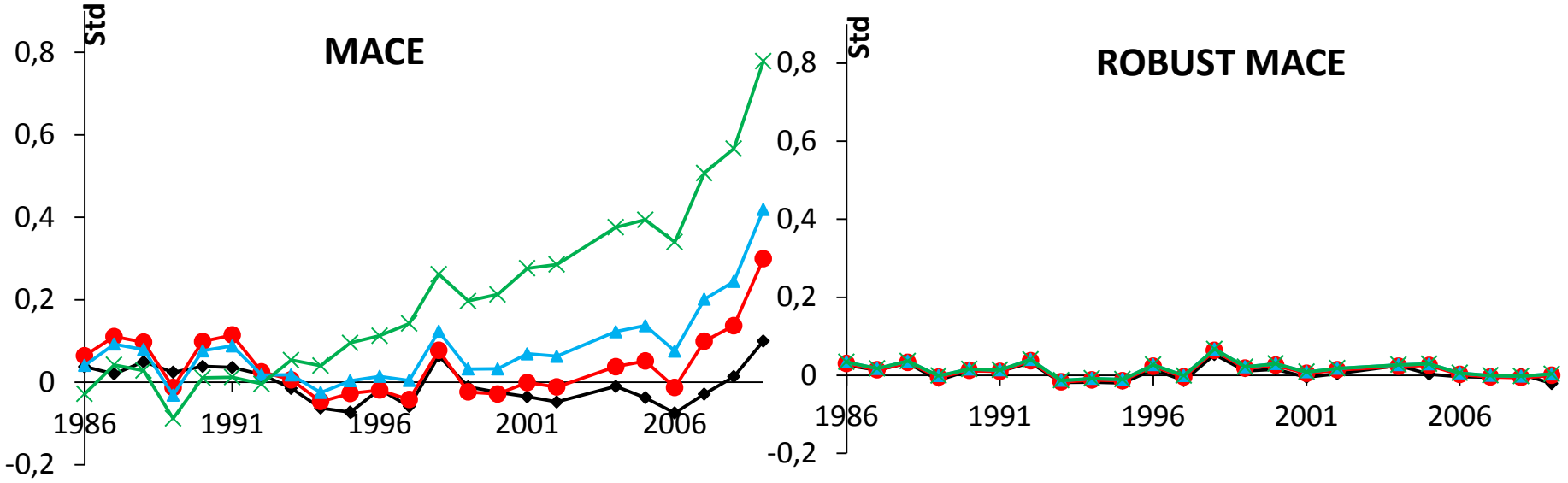


FRA scale

bias= 0% STD
bias= 2% STD
bias= 4% STD
bias= 10% STD

RESULTS

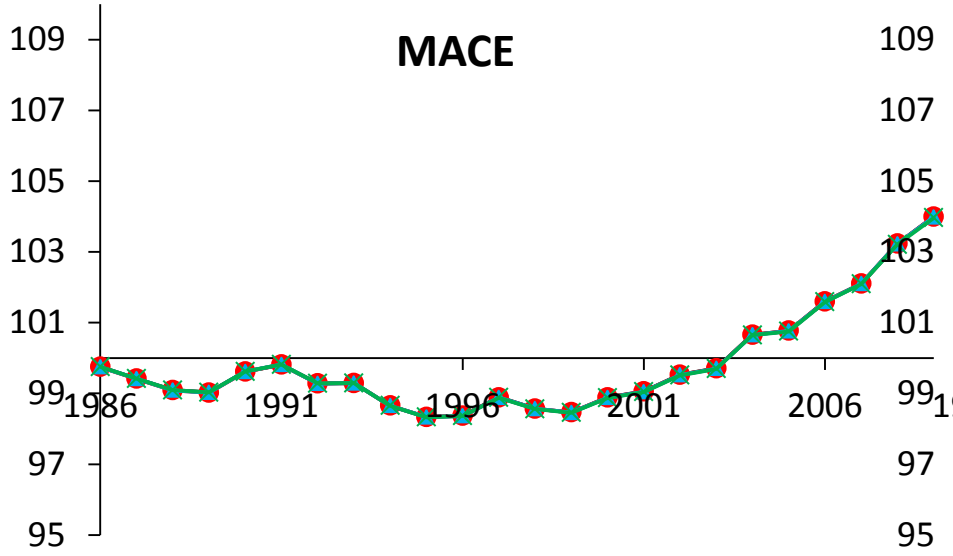
Mendelian samplings estimates: FRA bulls

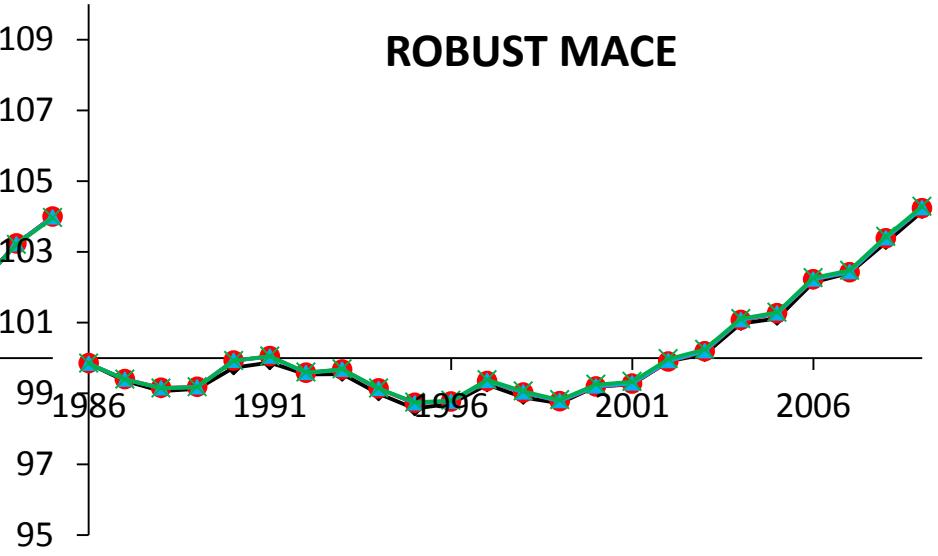


FRA scale

bias= 0% STD
bias= 2% STD
bias= 4% STD
bias= 10% STD

ΔG SCS: NLD BULLS

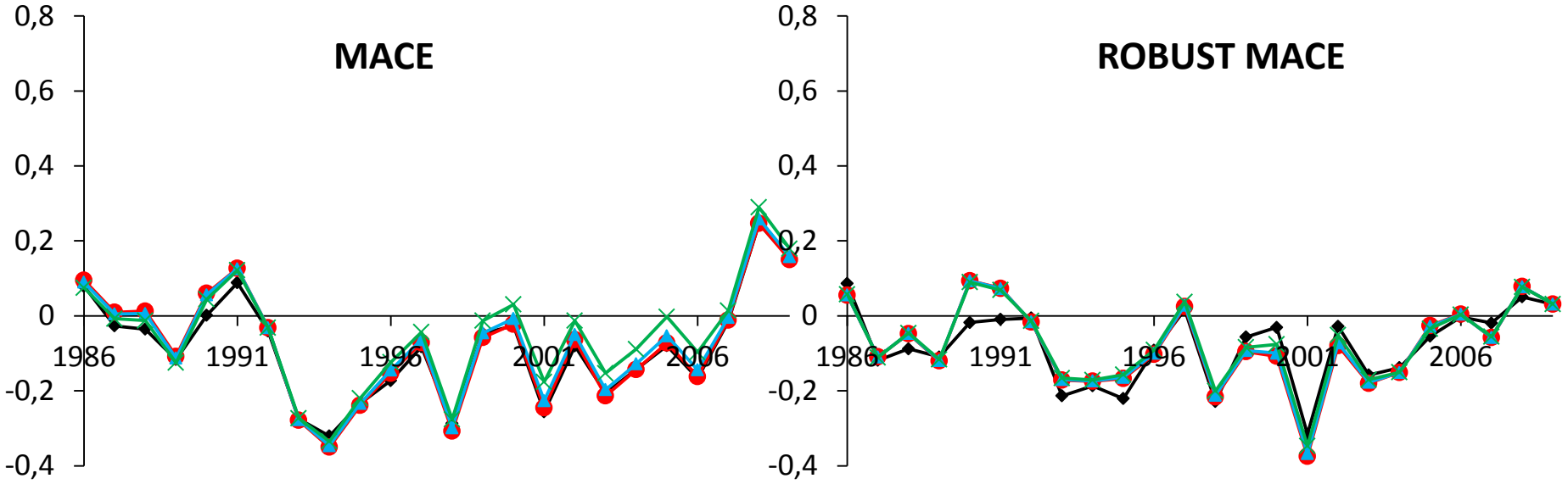




NLD scale

bias= 0% STD
bias= 2% STD
bias= 4% STD
bias= 10% STD

Mendelian samplings estimates: NLD bulls



RESULTS

CASE N°2

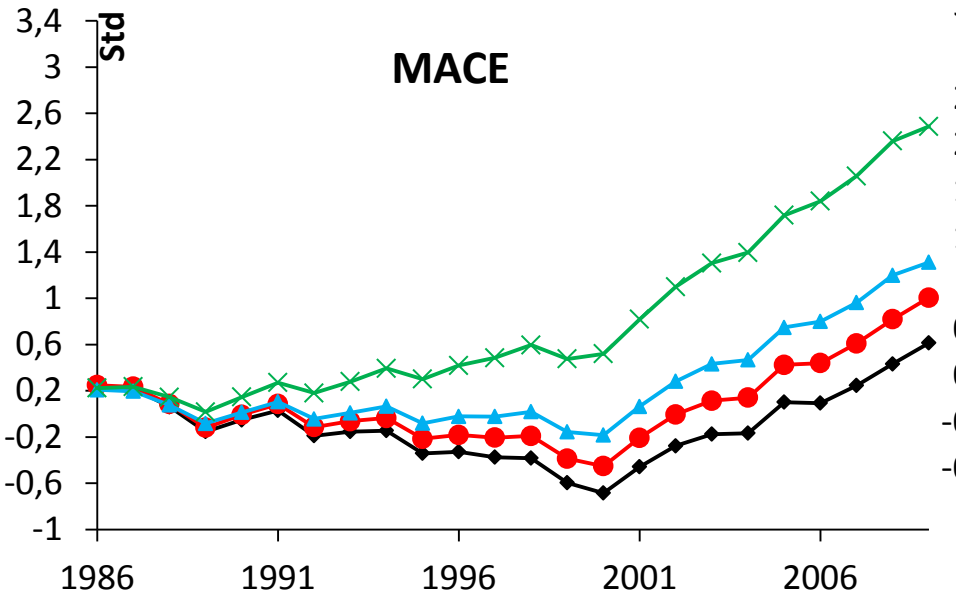
- **BIASES WERE CREATED FOR TWO COUNTRIES:**

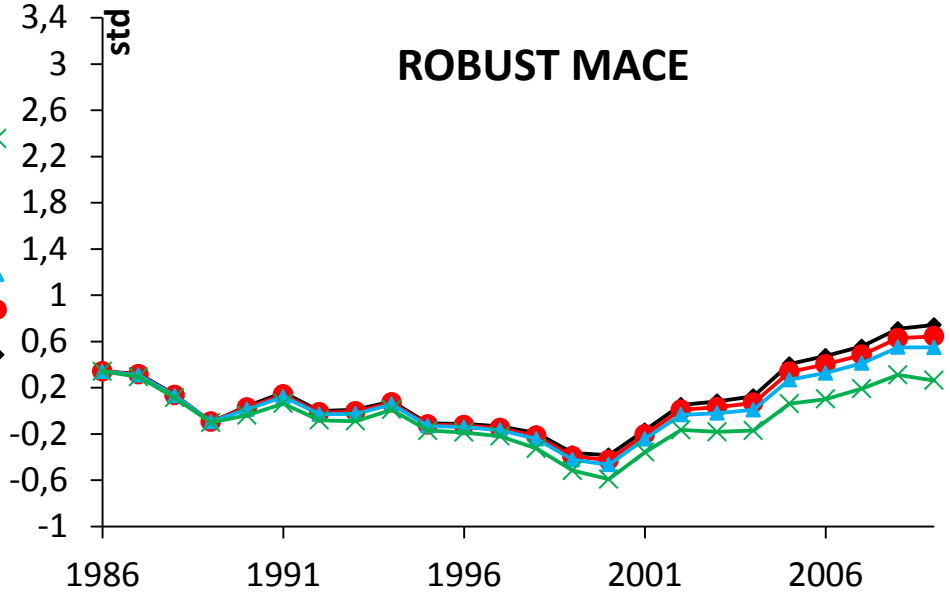
  FRANCE: +

  NETHERLANDS: -

RESULTS

ΔG SCS: FRA BULLS





FRA scale

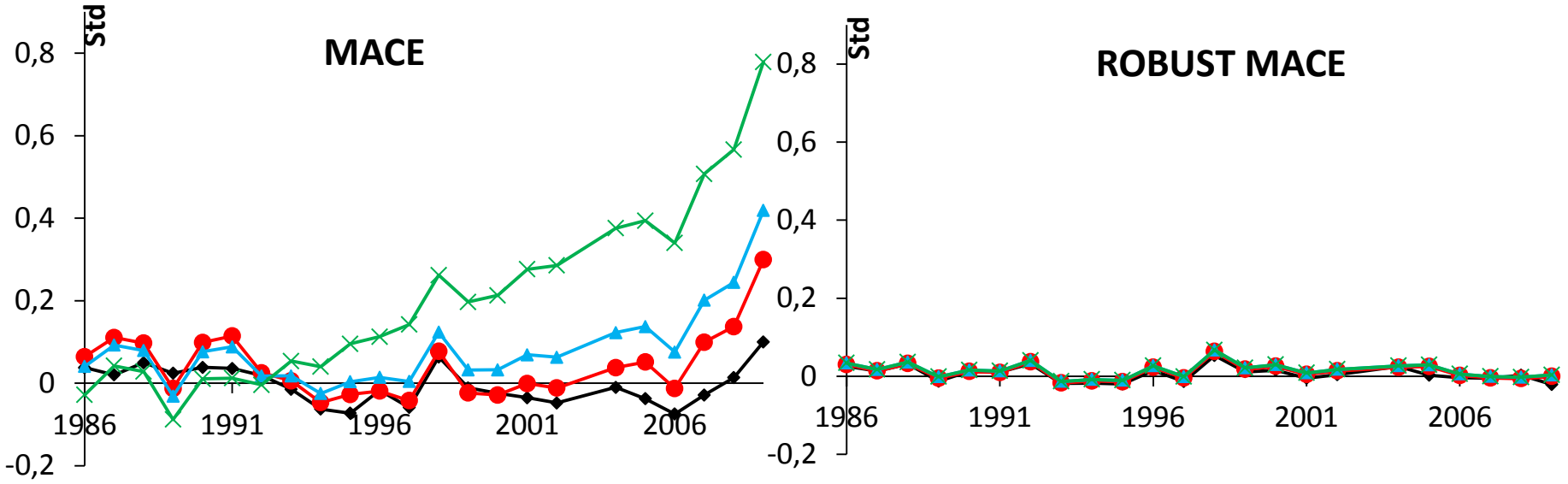
Bias=0%

Bias=+2%FRA -2%NLD

Bias= +4%FRA-4%NLD

Bias=+10%FRA-10%NLD

Mendelian samplings estimates: FRA bulls

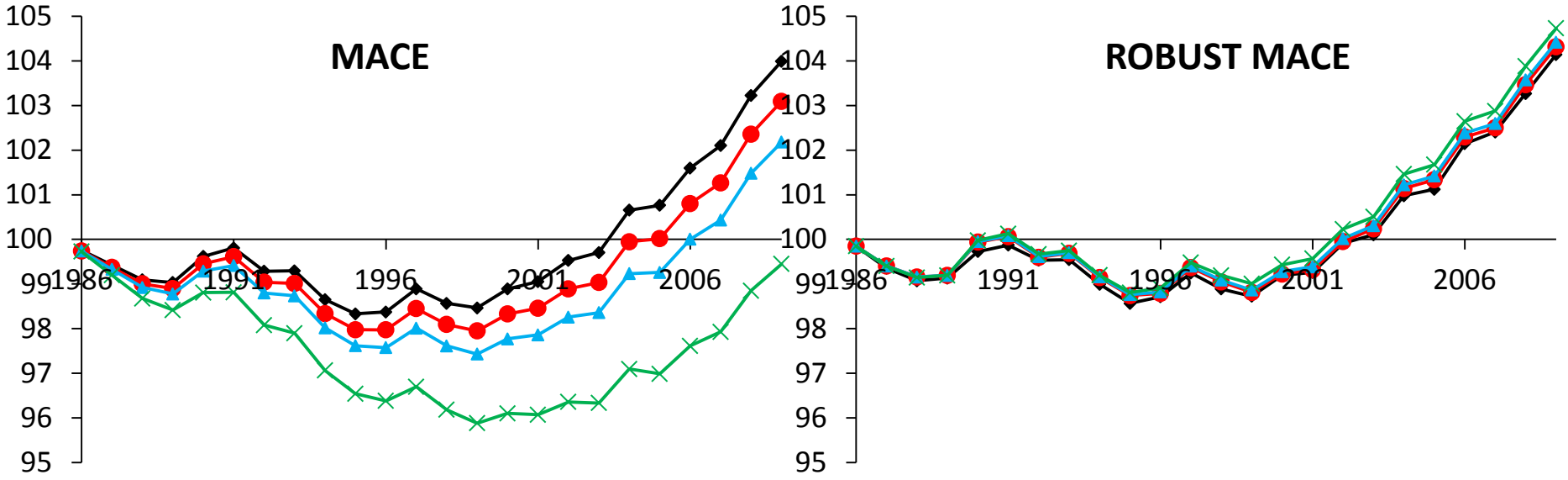


FRA scale

bias= 0% STD
bias= 2% STD
bias= 4% STD
bias= 10% STD

RESULTS

ΔG SCS: NLD BULLS



NLD scale

Bias=0%

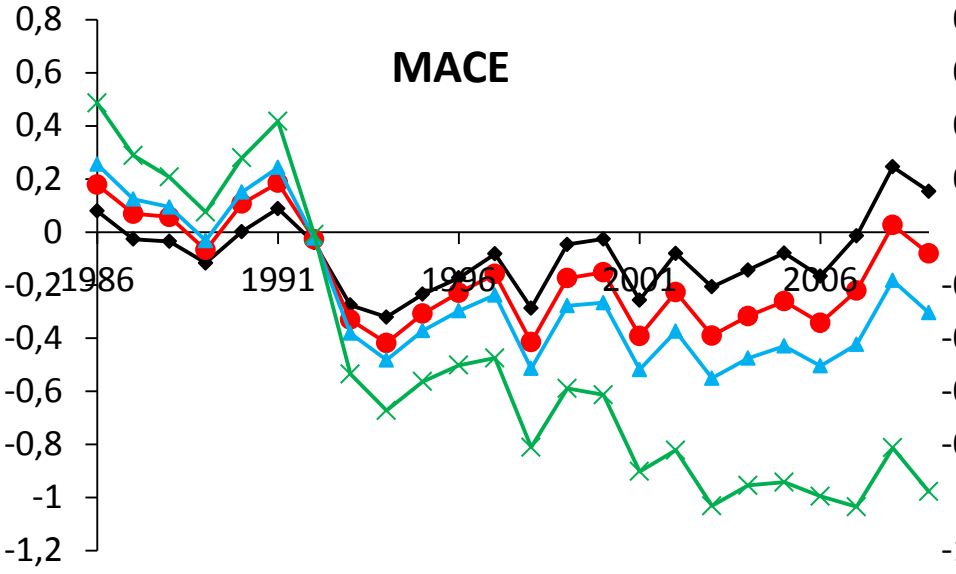
Bias=+2%FRA -2%NLD

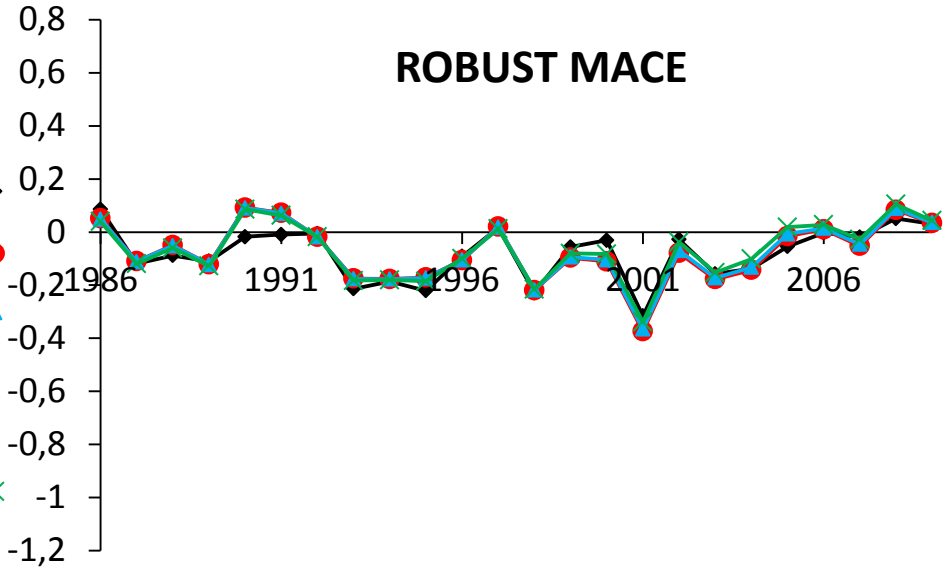
Bias= +4%FRA-4%NLD

Bias=+10%FRA-10%NLD

RESULTS

Mendelian samplings estimates: NLD bulls





NLD scale

Bias=0%

Bias=+2%FRA -2%NLD

Bias= +4%FRA-4%NLD

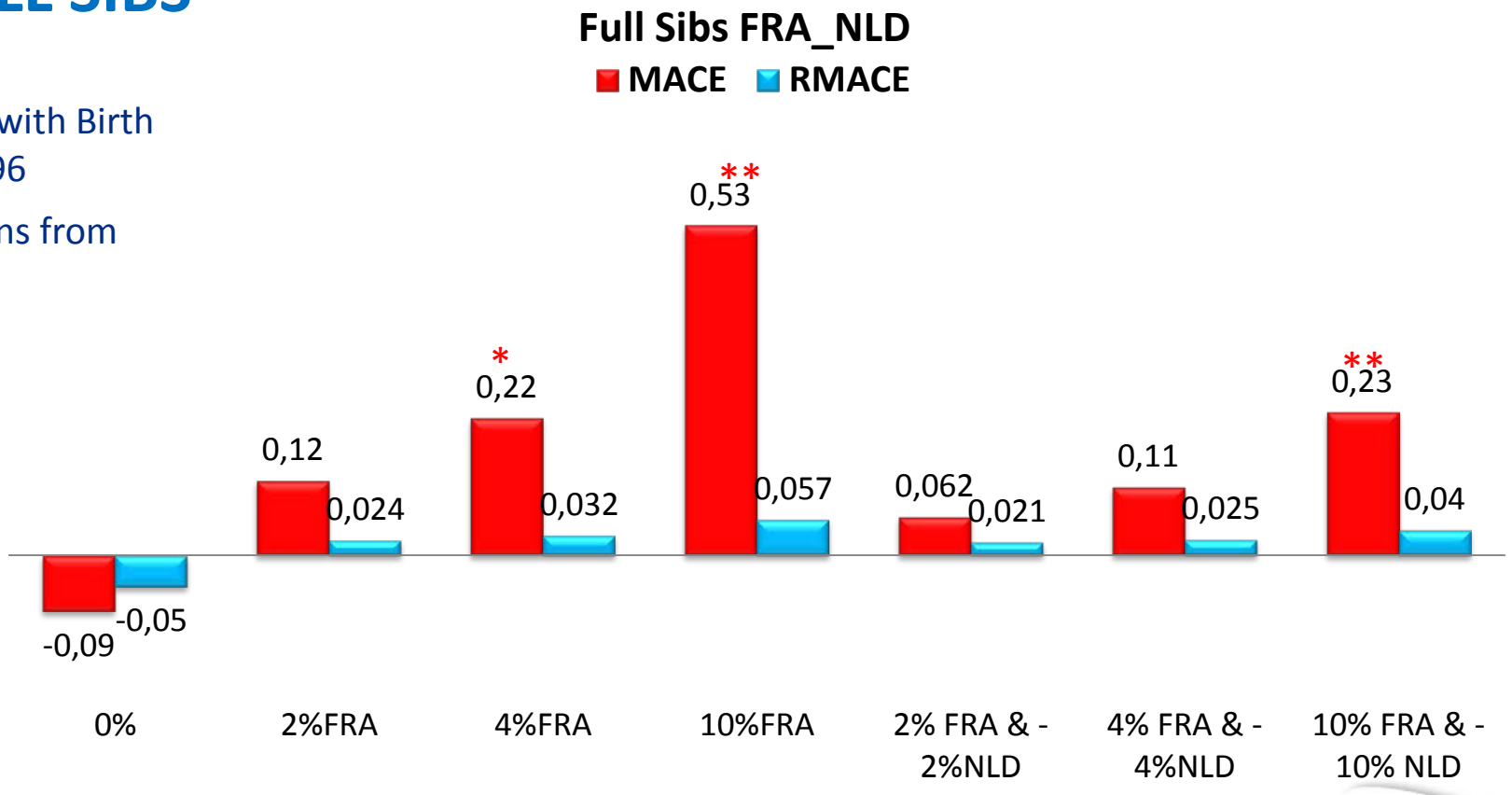
Bias=+10%FRA-10%NLD

RESULTS

FULL SIBS

-All bulls with Birth Year >1996

-Deviations from NLD



CONCLUSION

ROBUST MACE

- Easy to implement, does not need any new data
- Ability to detect (using fixed 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)
- Trend validation tests are still important

Thanks to