GMACE
WITHOUT VARIANCE ESTIMATION

P.G. Sullivan[1] and J.H. Jakobsen[2]

[1]CDN, Guelph, Canada

[2]Interbull Centre, Uppsala, Sweden

Introduction

- Does VR = V(gebv|PE) / V(EBV|PE) = 1.0 ?
- Need VR=1.0 to pass Interbull GEBV tests, but
  - *Are the tests powerful and comprehensive enough?*
- GMACE included a VR adjustment since 2011
  - *IF VR was not the same for all countries / traits*
  - *AND we can estimate VR well enough, then*
  - *GMACE gives better results using a VR adjustment*
- Sharing of both knowledge and data for genomic evaluations continues to grow
  - *Is VR adjustment still helpful and/or needed today?*

Objectives

- Determine if GMACE without a VR adjustment works better today than it did the last time we checked (Aug 2011)?

- Re-apply cross-validation tests:

  - ➢ *Checks how well GMACE can predict a local GEBV, when using only foreign-country GEBV as input*

Data

- December 2013 implementation run
  - GEBV from 11 evaluation centres
    - A. *[CAN, GBR, ITA, USA] ... Share genotypes*
    - B. *[DEU, DFS, FRA, NLD] ... Share genotypes*
    - C. *[AUS] [CHR] [POL]*
  - 37 of the 38 MACE traits

    Production: *Protein (pro), ...*

    Conformation: *Stature (sta), ...*

    Udder Health: *SCS, Clinical Mastitis (scs, mas)*

    Longevity: *(dlo), ...*

    Calving: *Direct Stillbirth (dsb), ...*

    Fertility: *Cow Conception 1 (cc1), ...*

    Workability: *(msp)*

Methods – GMACE

- As in Aug 2013: Apply GMACE equations to Mendelian Sampling estimates of young bulls individually, adjusting with MACE parent averages.

- G => Use Genomic variance estimates.

Approach	Average Reliability Input (X)
G	As provided by countries (N)
GP	Predicted (P)
GP.5	P*.5 + N*.5
	Individual Reliability Input
	Provided Reliability + (X-N)

Methods – GMACE

- As in Aug 2013: Apply GMACE equations to Mendelian Sampling estimates of young bulls individually, adjusting with MACE parent averages.
- M => Use MACE   variance estimates... (VR=1.0)

Approach	Average Reliability Input (X)
M	As provided by countries (N)
MP	Predicted (P)
MP.5	P*.5 + N*.5
	Individual Reliability Input
	Provided Reliability + (X-N)

Methods – Cross Validation

- *y* = national GEBV

- *x* = GMACE prediction of *y* ($\hat{y}$) using only GEBVs from foreign countries

- Goals are to:

  1. Maximize: r(y,x)

  2. Minimize: | b(y,x) – 1.0 |

     ➤ Minimize: Top Bull Bias = percentage difference between a top bull (x=μ+3σ) and the corresponding E[y | x= μ+3σ]

     ➤ Bias = $(\hat{y} - E(y \mid \hat{y})) / E(y \mid \hat{y})$

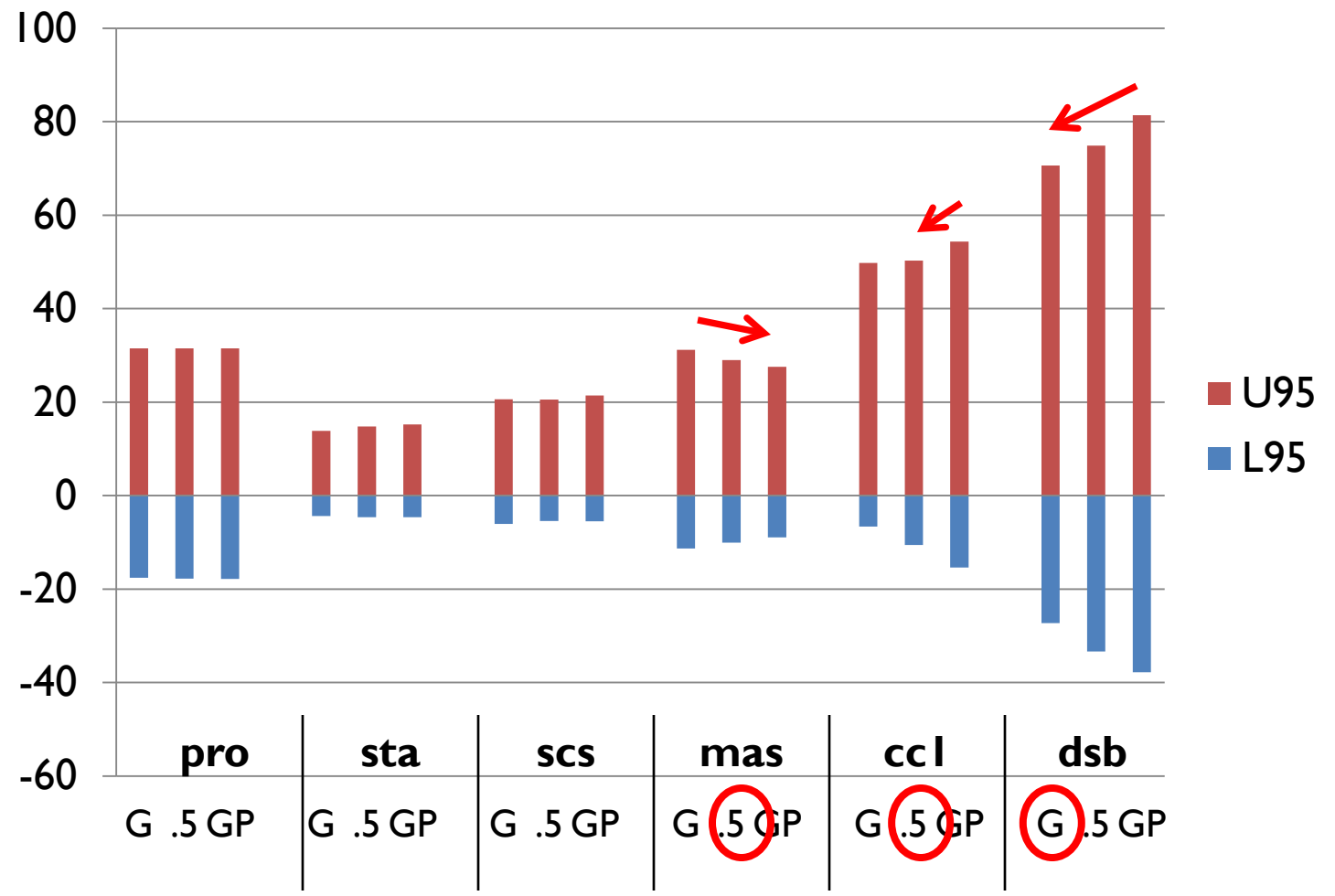# Results – Predict Reliabilities?

r(Y,X) pooled across countries
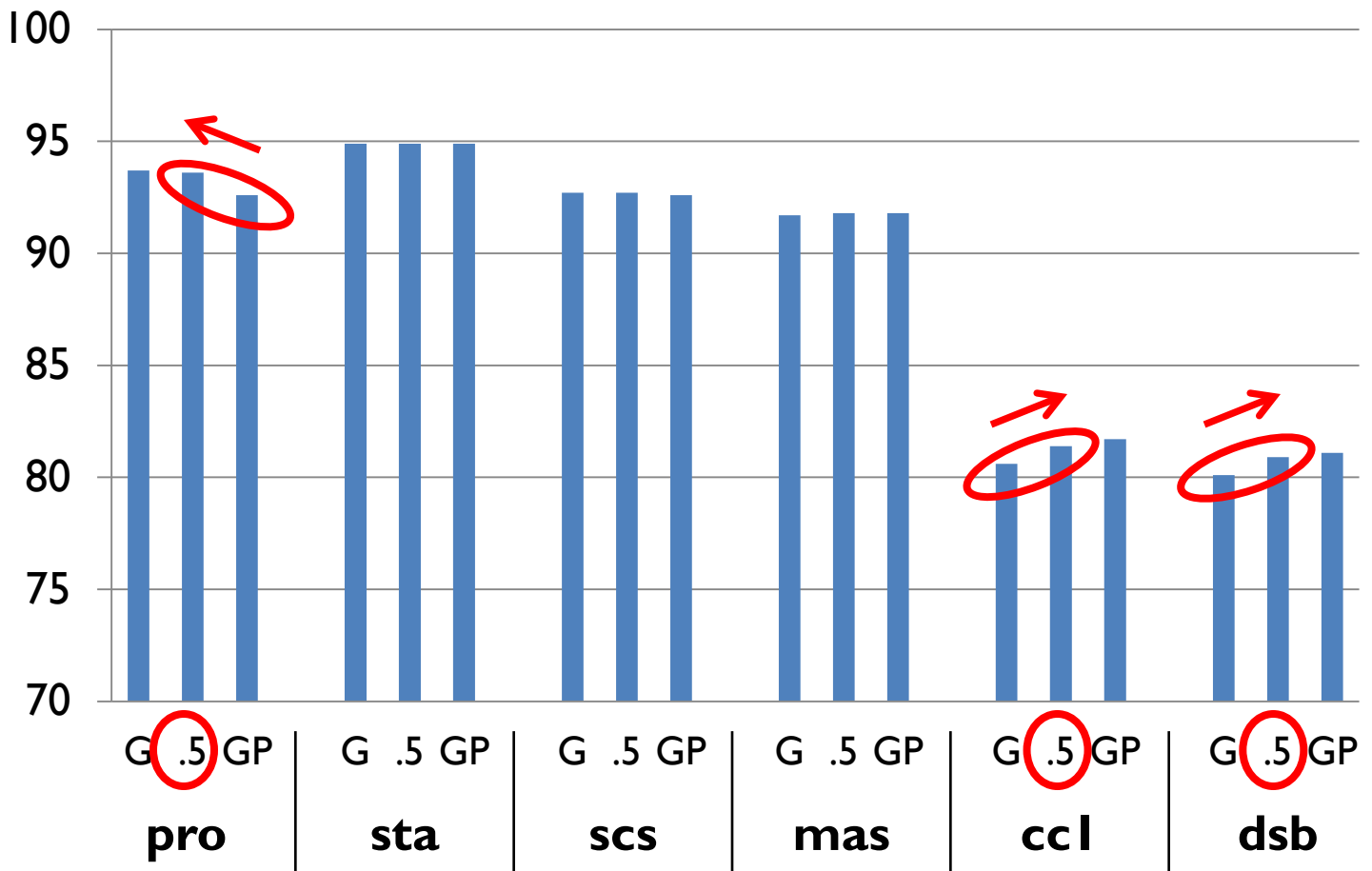
Results – Predict Reliabilities?
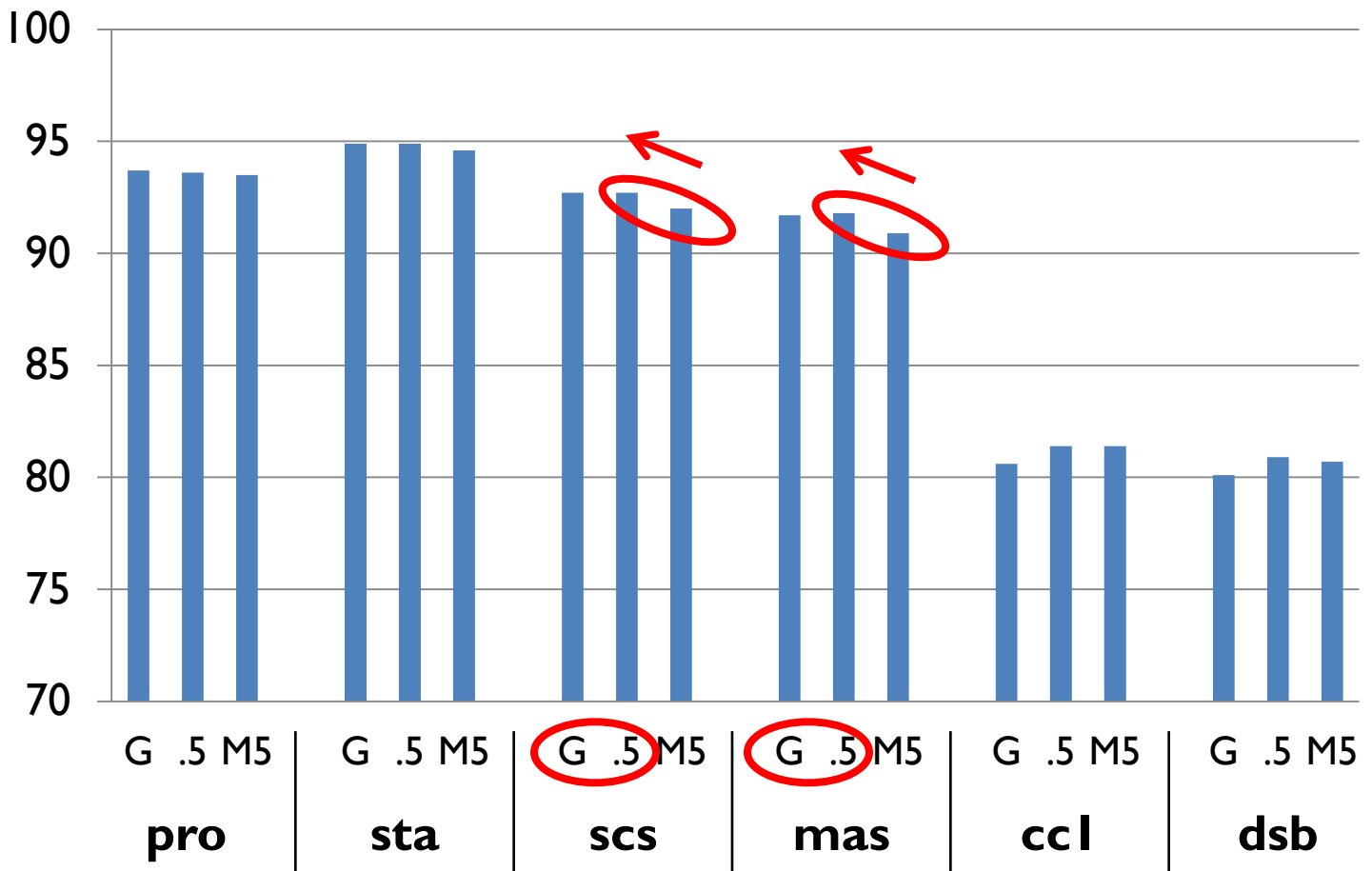

95% C.I. For Top Bull Bias

Conclusions – Reliabilities

- ***GP.5 slightly better*** than G and GP
  - *Maximum r(y,x) across all traits*
  - *Minimum TopBias across all traits*
- Recommend changing from G to GP.5, but noting ***small impacts*** of this change on GMACE results
  - *better estimates of VR with better reliabilities*
- Is GMACE too sensitive to VR estimates?
  - *Consider MP.5 as alternative to GP.5*
  - *Should we estimate and adjust for VR ≠ 1.0?*
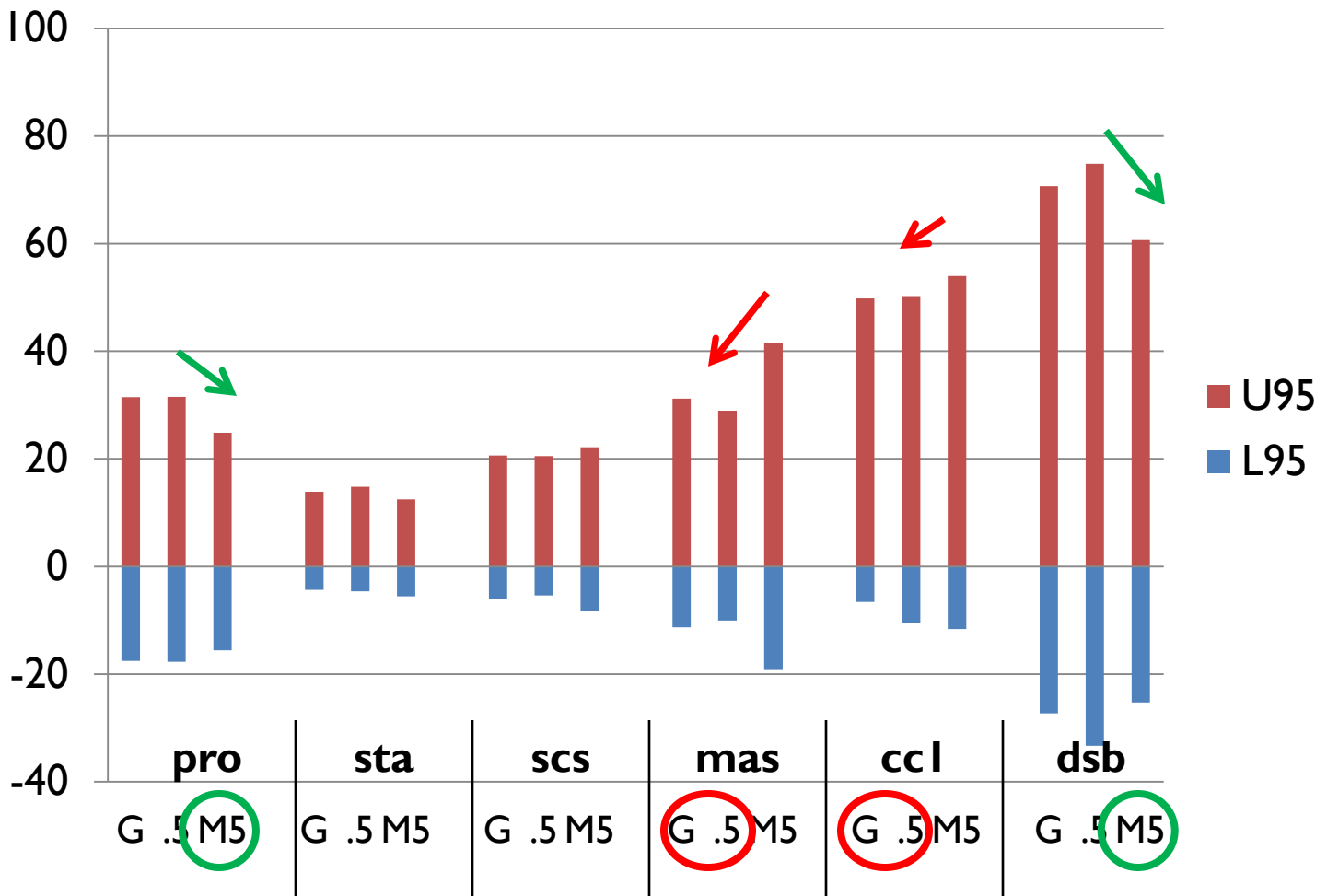
Results – Estimate VR?

r(Y,X) pooled across countries

Results – Estimate VR?


95% C.I. For Top Bull Bias

Conclusions – Estimating VR

- Across all traits, *GP.5 similar to MP.5*, based on current cross-validation results
  - ➢ *MP.5 preferred for some traits*
  - ➢ *GP.5 preferred for some traits*
- *MP.5 is easier* to apply and understand
- Member countries reviewed GP.5 and MP.5 results and preferred MP.5
  - ➢ *MP.5 was chosen as official Interbull method, starting with the Feb 2014 test run*

Acknowledgements

GMACE working group
National evaluation centers
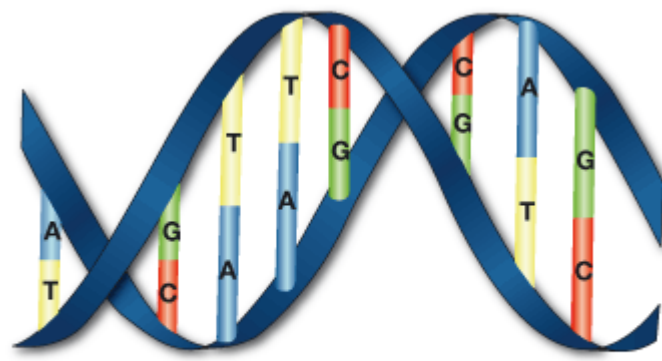
Thymine (Yellow) = T   Guanine (Green) = G
Adenine (Blue) = A   Cytosine (Red) = C