GMACE – PILOT #4

ADJUSTING THE NATIONAL RELIABILITY INPUT DATA

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Business Mtg (Aug 2013)

Impacts of national GREL on GMACE

"Simulate" GRELn errors:

Predict with a regression equation:

GRELn = trait + size of local reference + size of foreign reference + error

Two GMACE runs:

1. **Using as input: GRELn**
2. **Using as input: GRELn – error**

Relate change in GRELn input to changes in GMACE parameters and results

Objectives

- Predict national genomic reliabilities (N):

  N = *f(trait, reference pop'n, methods)*

- Apply GMACE using different sets of national reliability input data:
  - *National reliabilities* as provided by countries
  - *Predicted reliabilities* from *f()*

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 – Predicting Reliability

- Exponential transformation of Reliability (N) creates a linear relationship with genomic reference population size:

$$\exp(N) = \text{Trait} + b_1 L + b_2 F + M + e$$

- L = ∑Rel(EBV) ... Local bulls
- F = ∑Rel(MACE) ... Foreign bulls
- M = SNP panels used, imputations, %polygenic, SNPs evaluated, EBV-DGV blending, ...

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- P eliminates E = (M + e)... but we want to keep M and eliminate only the e portion of E.
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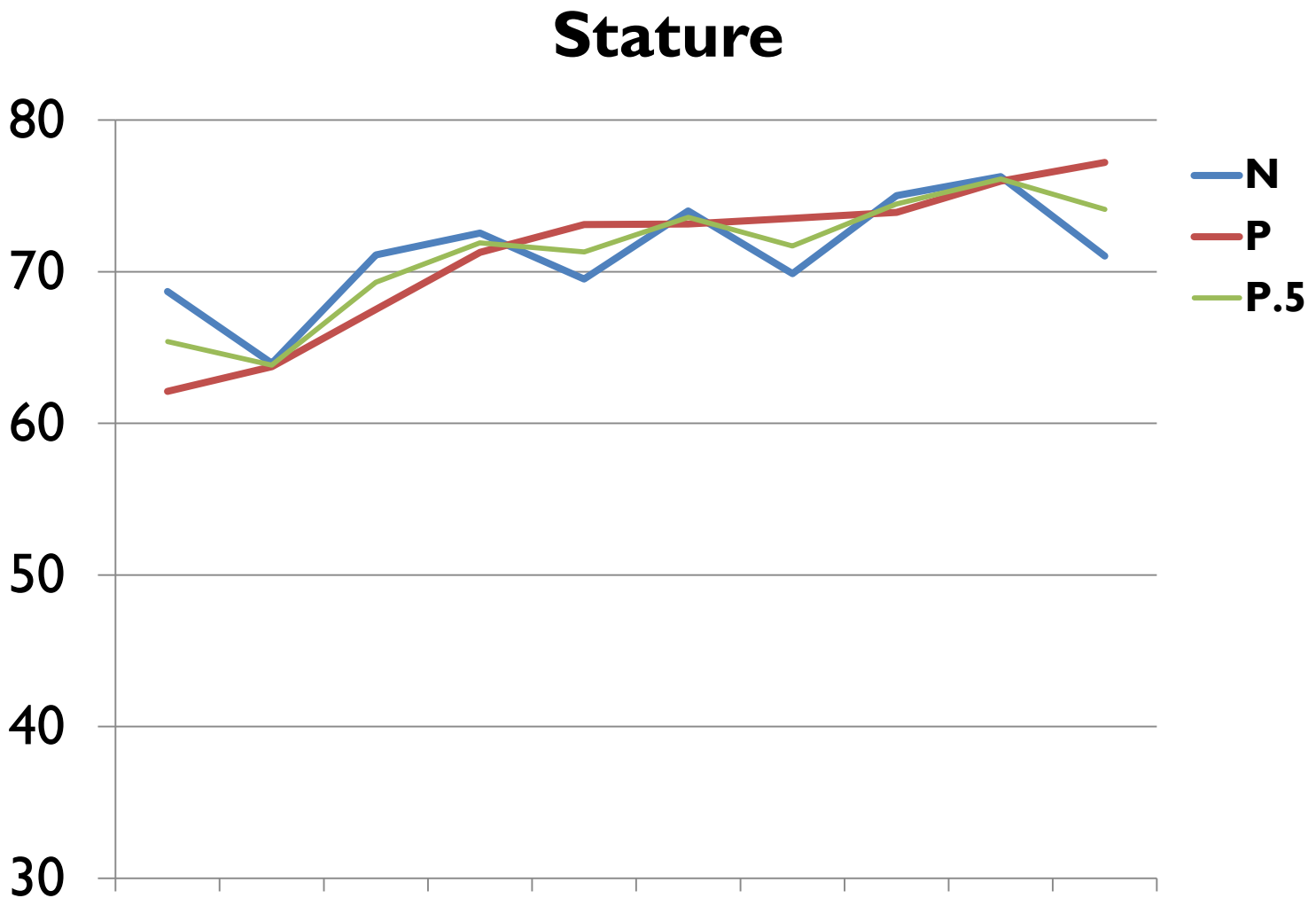
- Assuming national evaluation centres do a good job of approximating N, then we can include M by finding an (optimum?) intermediate value between P and N, for example:

$$P.25 = 0.25 * P + 0.75 * N$$

$$P.5 = 0.50 * P + 0.50 * N$$

$$P.75 = 0.75 * P + 0.25 * N$$

National Genomic Reliabilities



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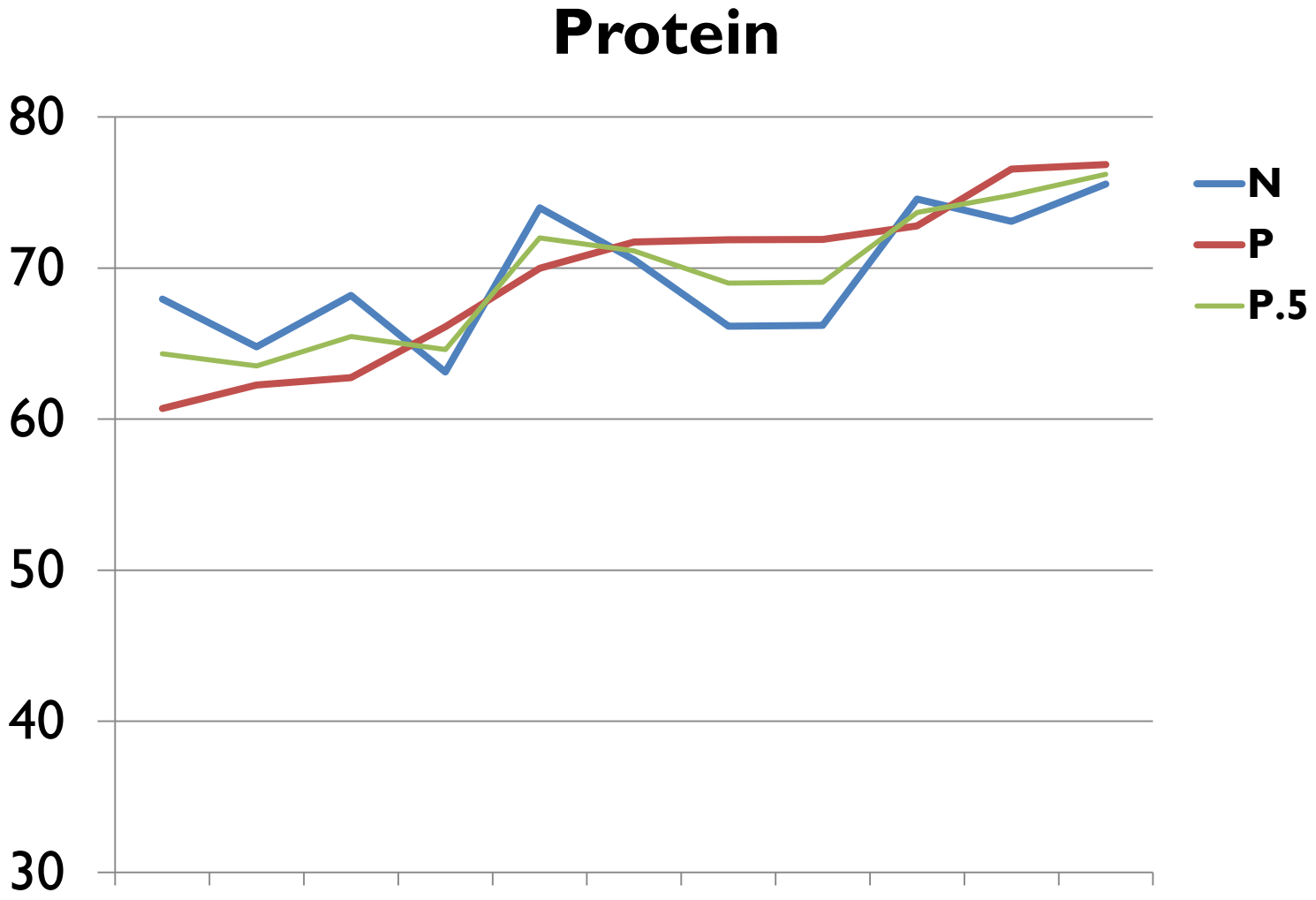

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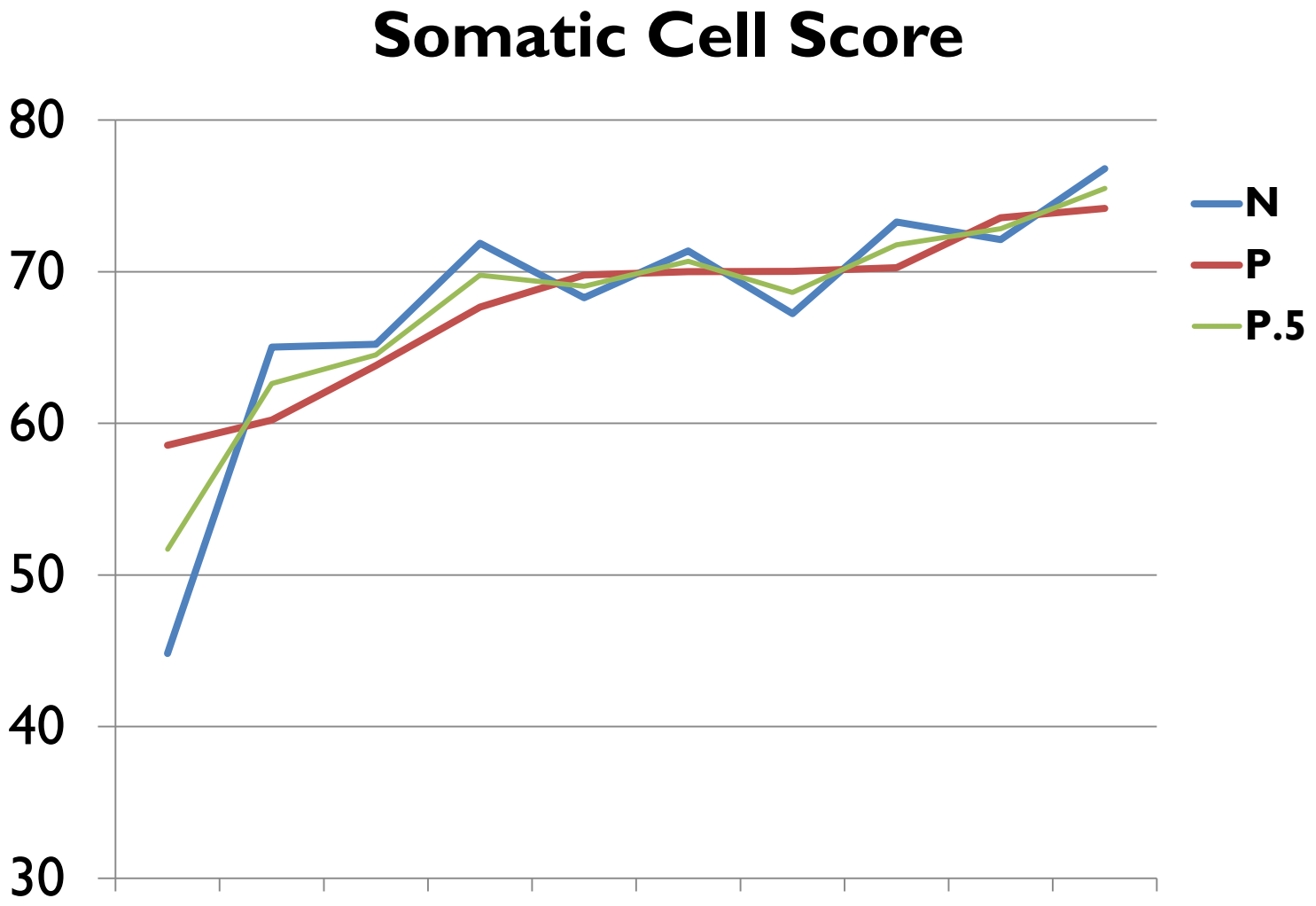

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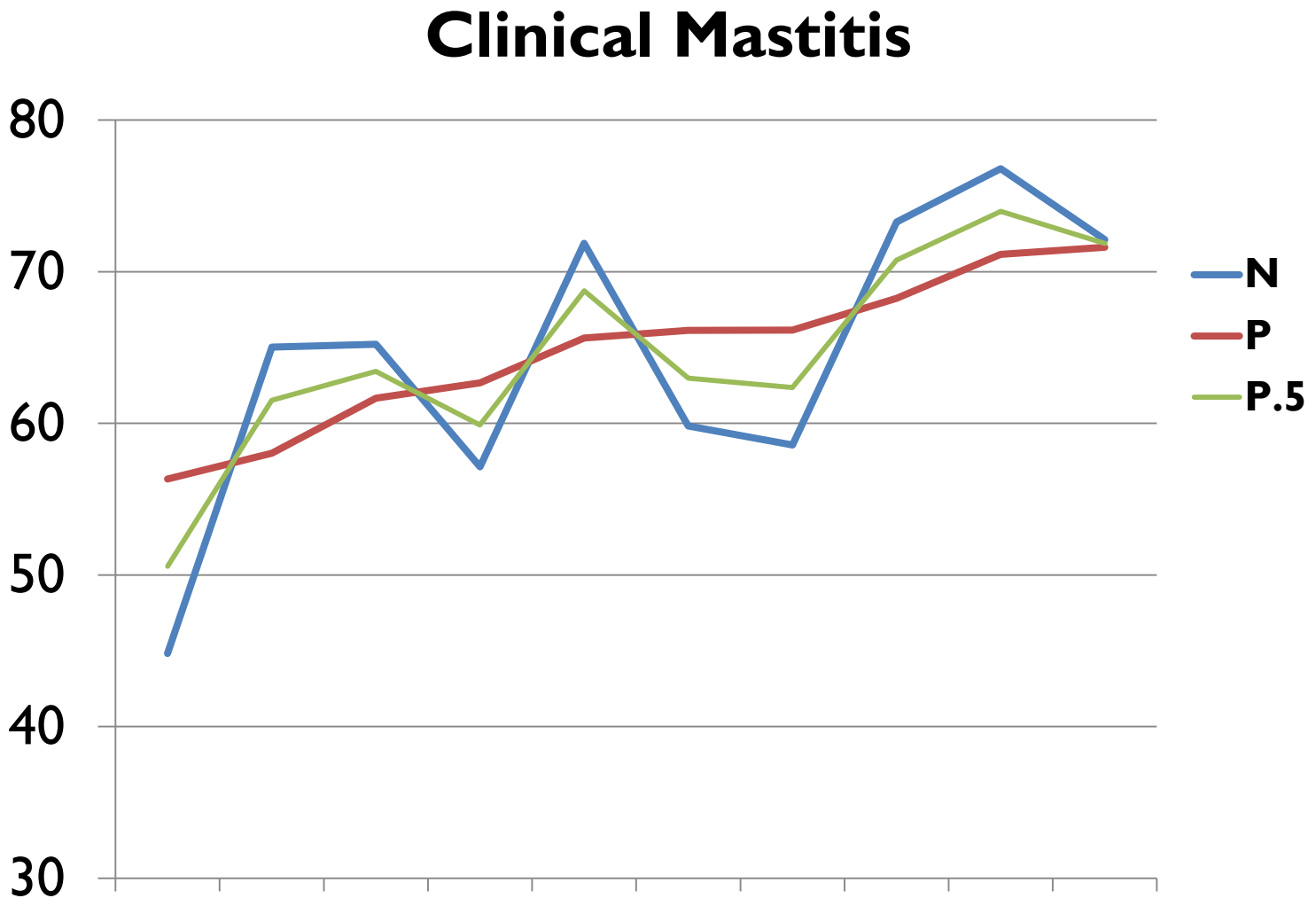

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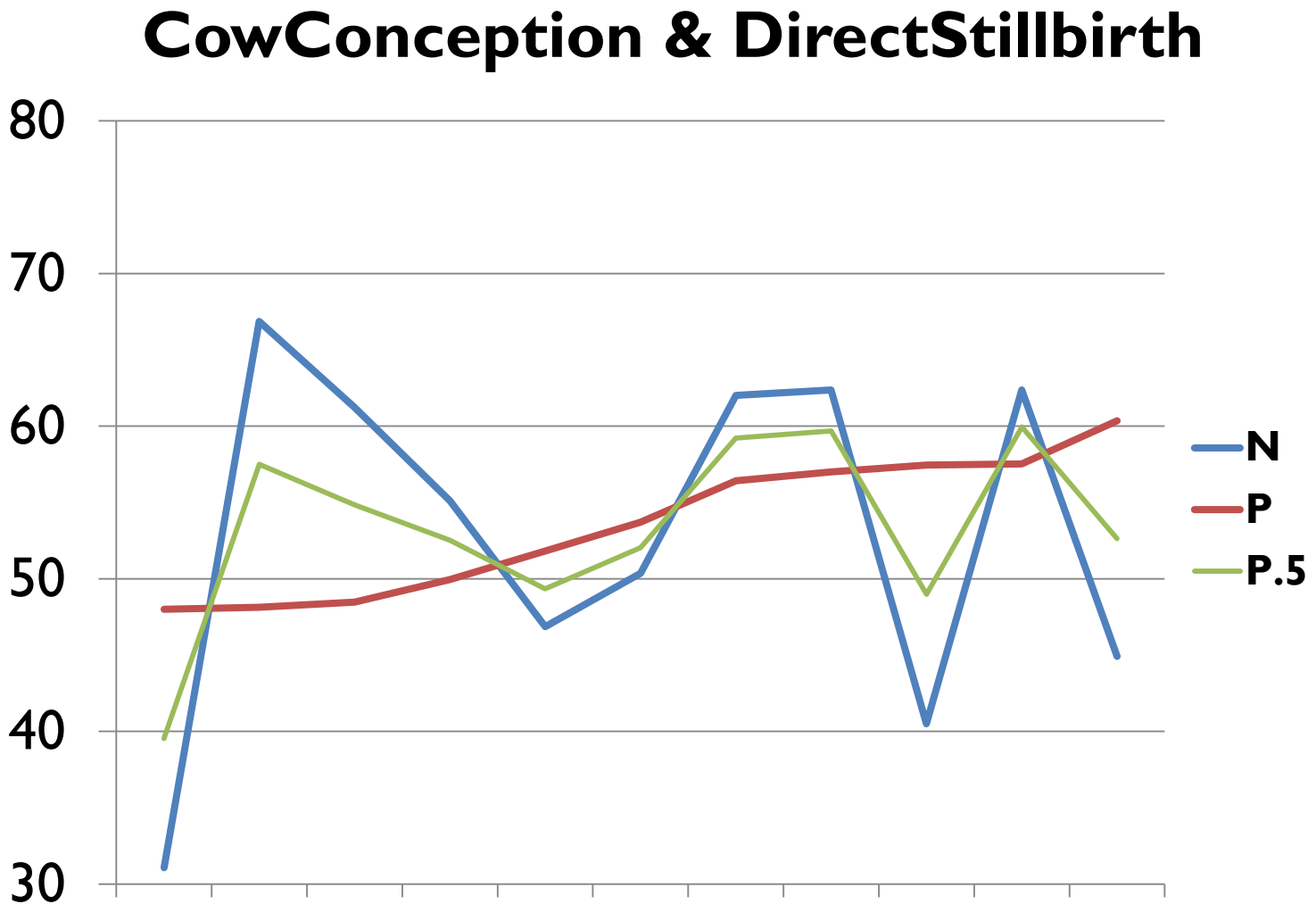
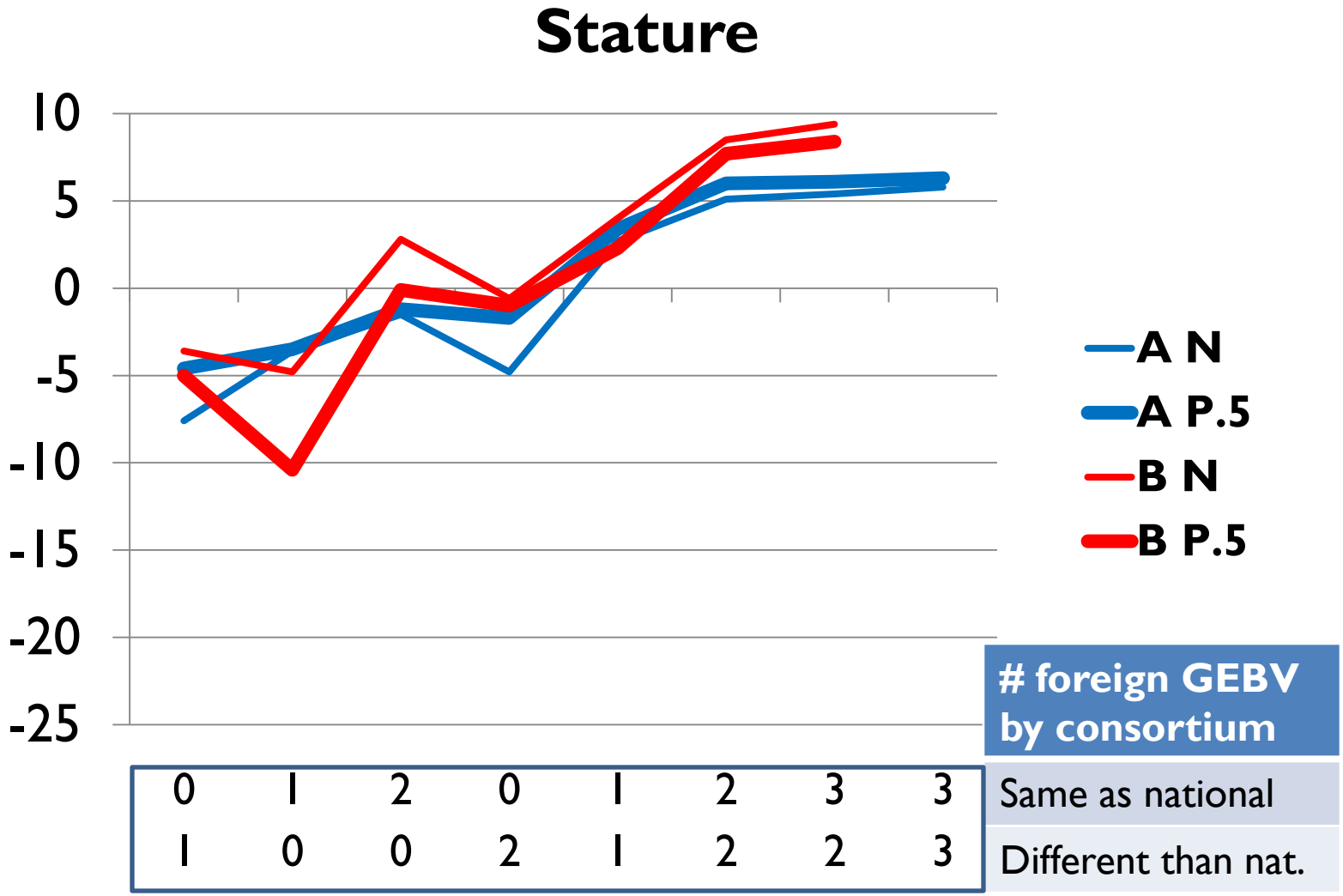


Reliability Difference (foreign GMACE – national)



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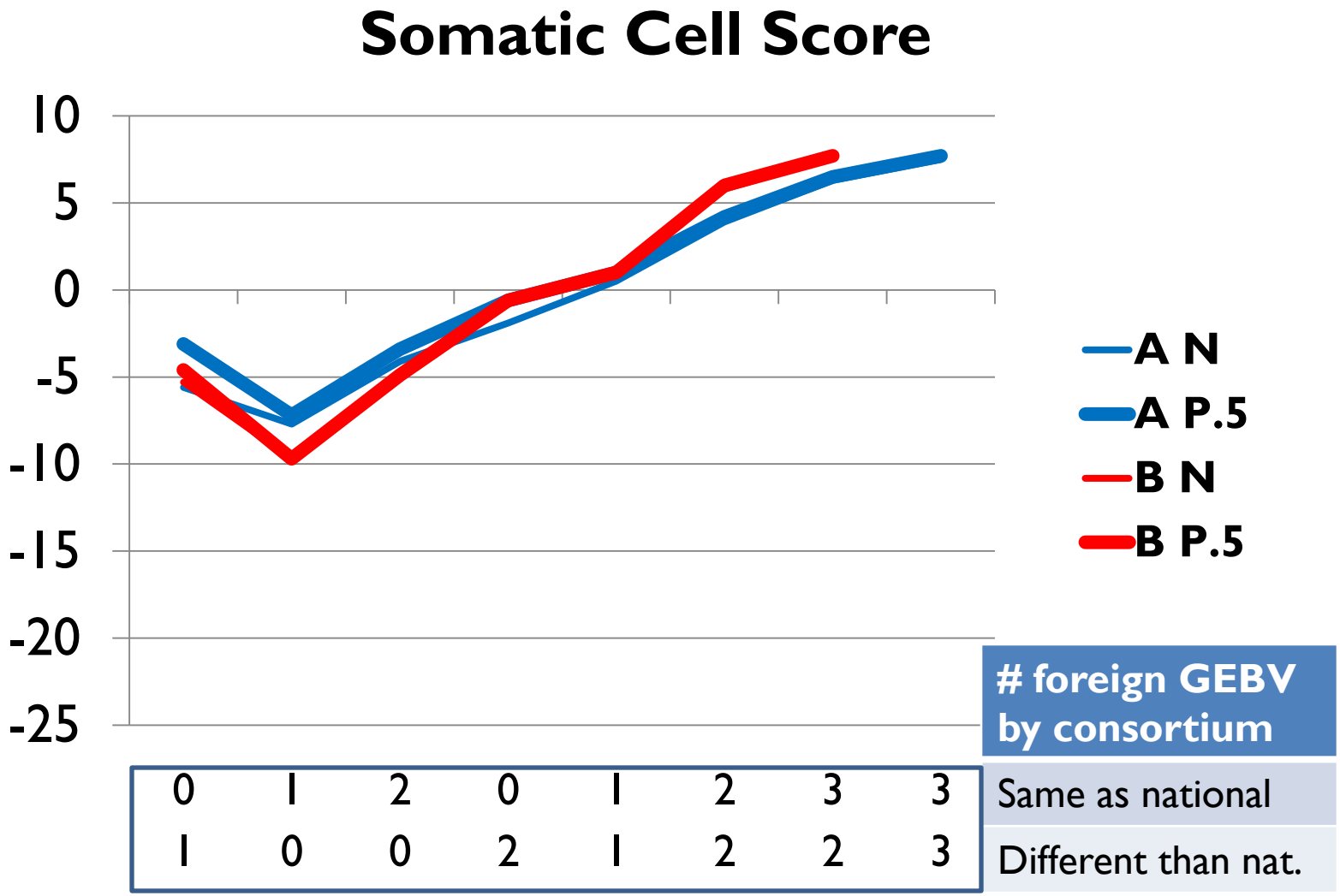

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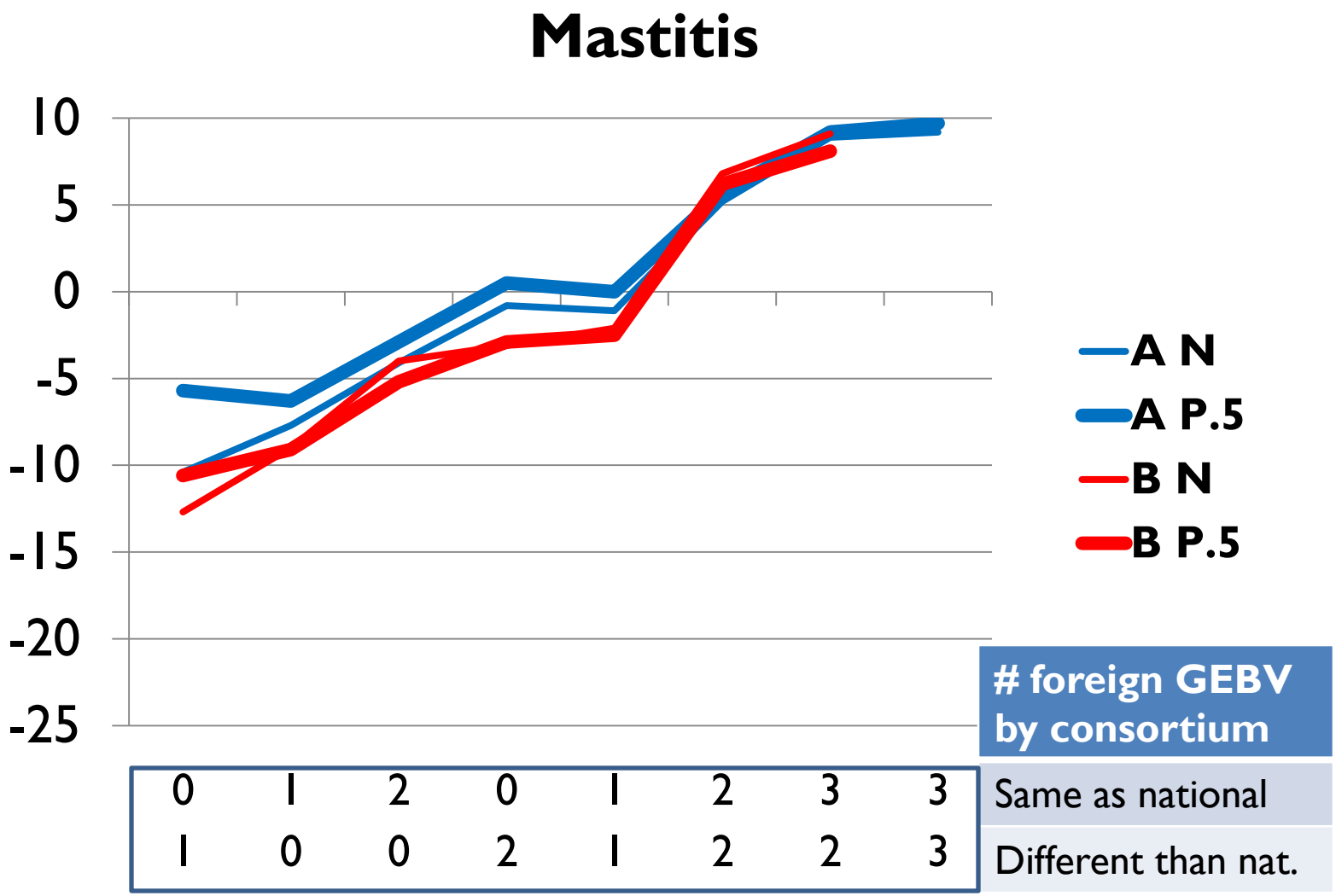

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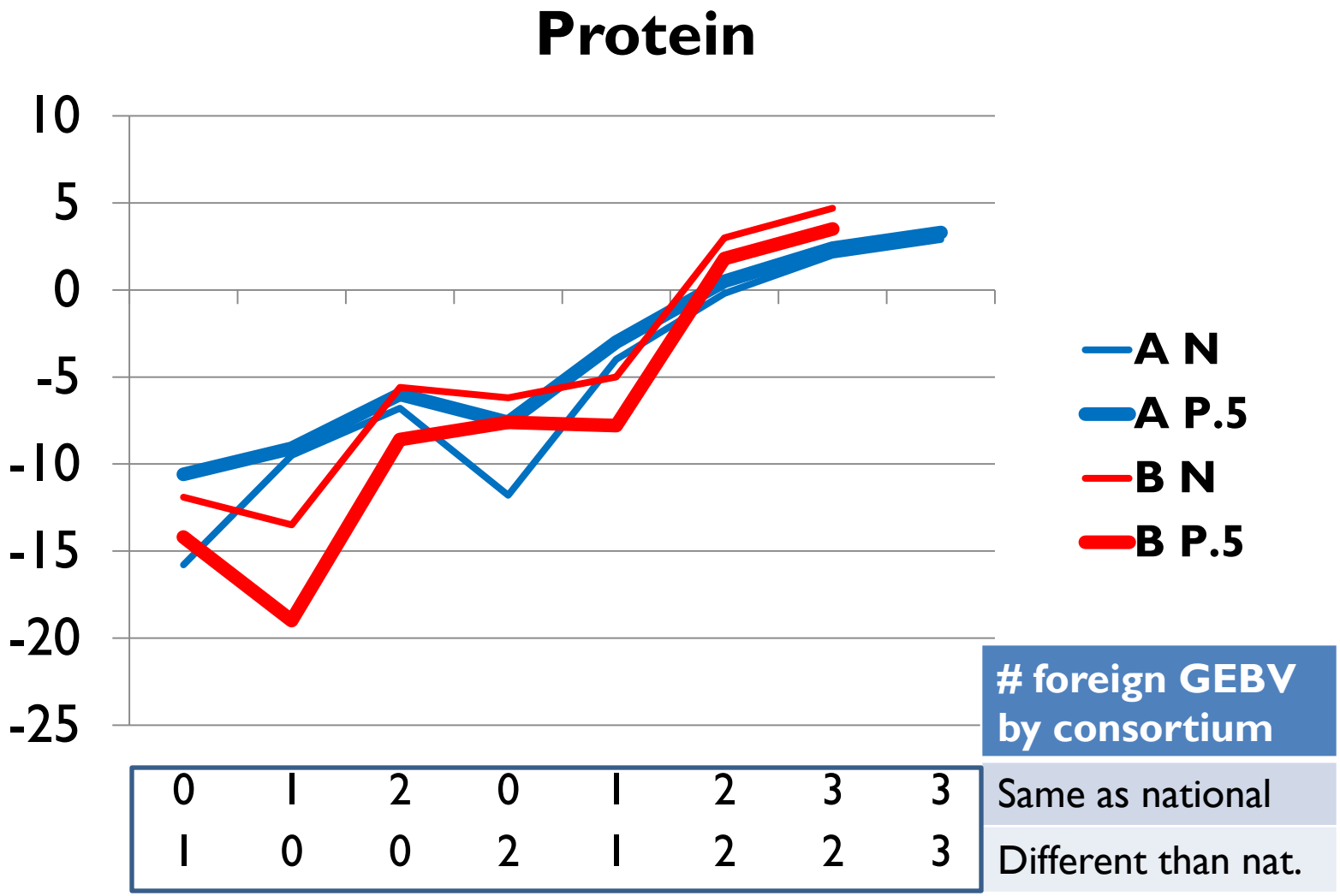

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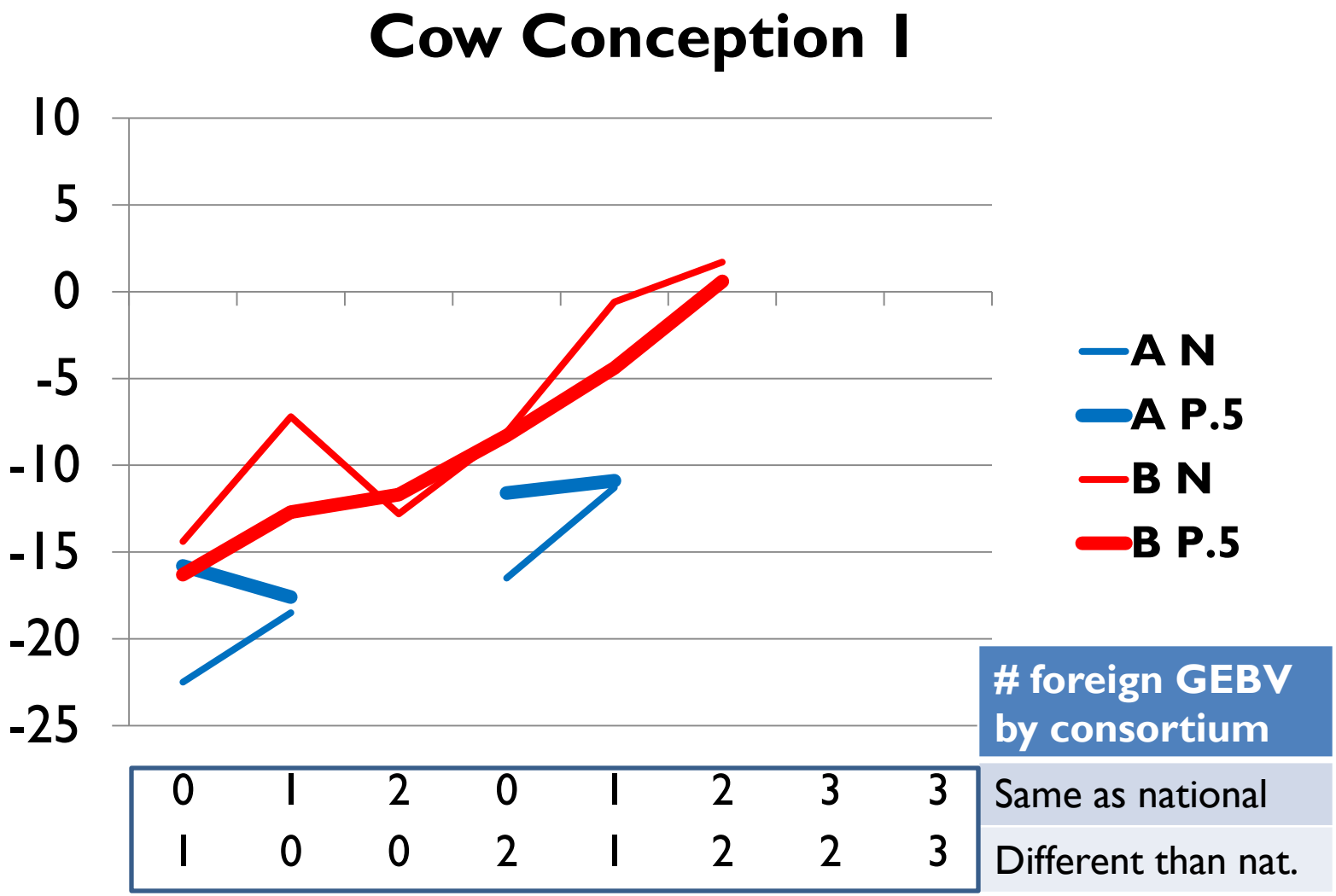

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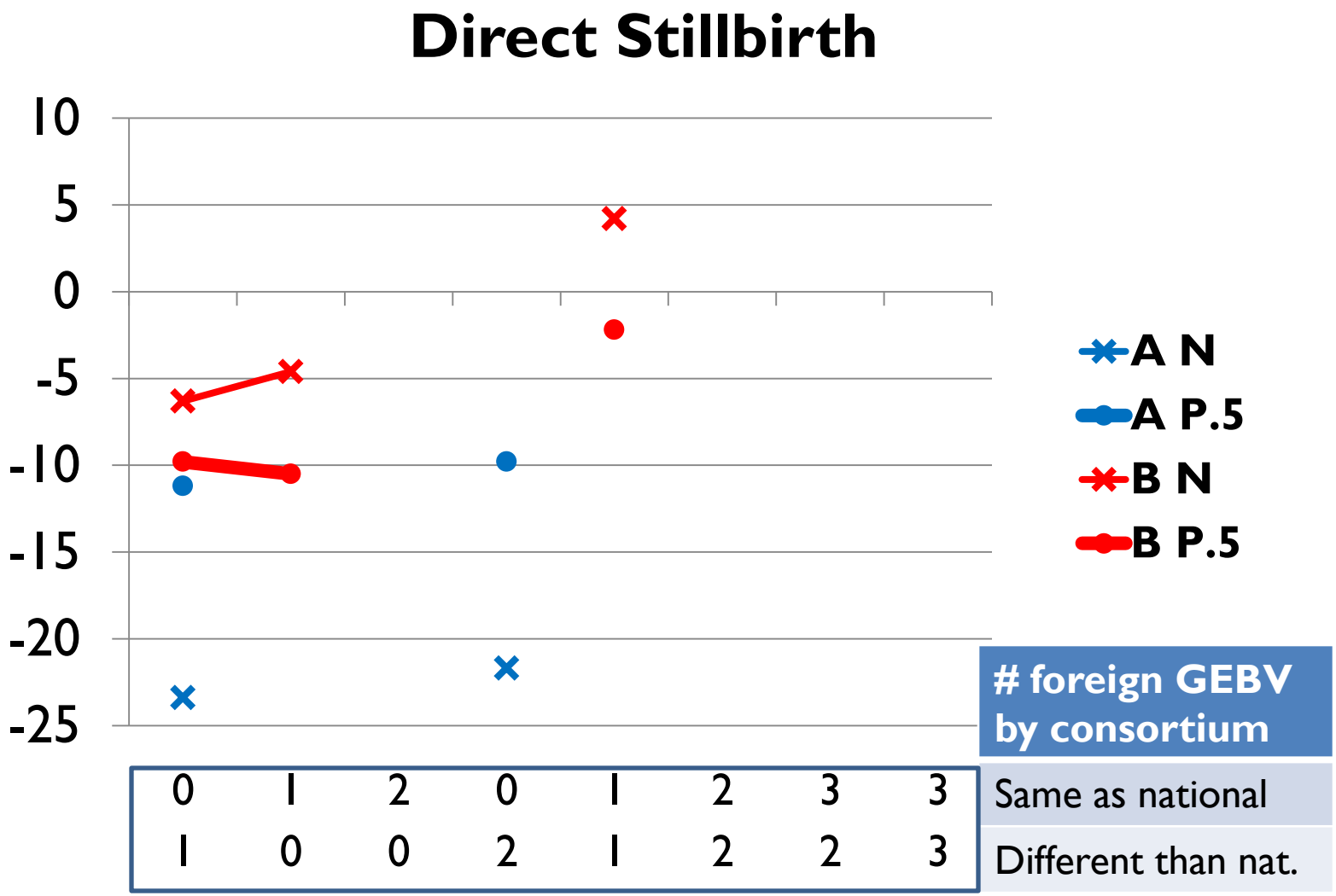
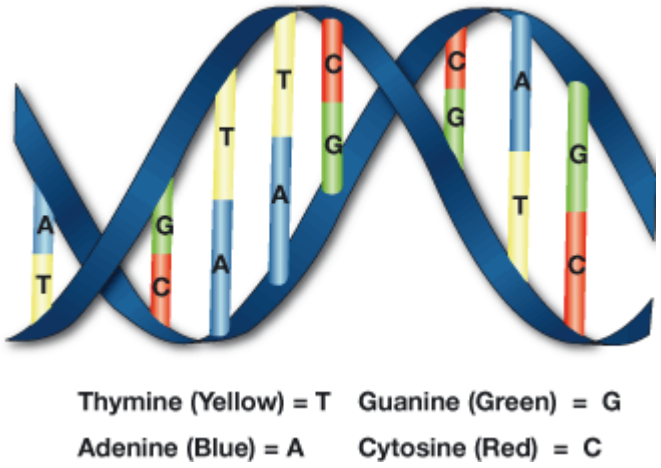


Observations

- **Re-genotyping foreign bulls locally**
  - *National genomic reliability will be higher than GMACE reliability for bulls with GEBV in only 1 or 2 foreign countries (on average)*
  - *GMACE reliability will be higher than national if bulls have GEBV in many foreign countries*
- **After the bull is genotyped locally**
  - *GMACE reliability will increase and always be equal or higher than the national reliability*
- **Same pattern with P.5 versus N**

Acknowledgements

GMACE working group

National evaluation centers