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Canadian Dairy Network

Using a Parameter Space to Improve GMACE Results

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Canadian Dairy Network

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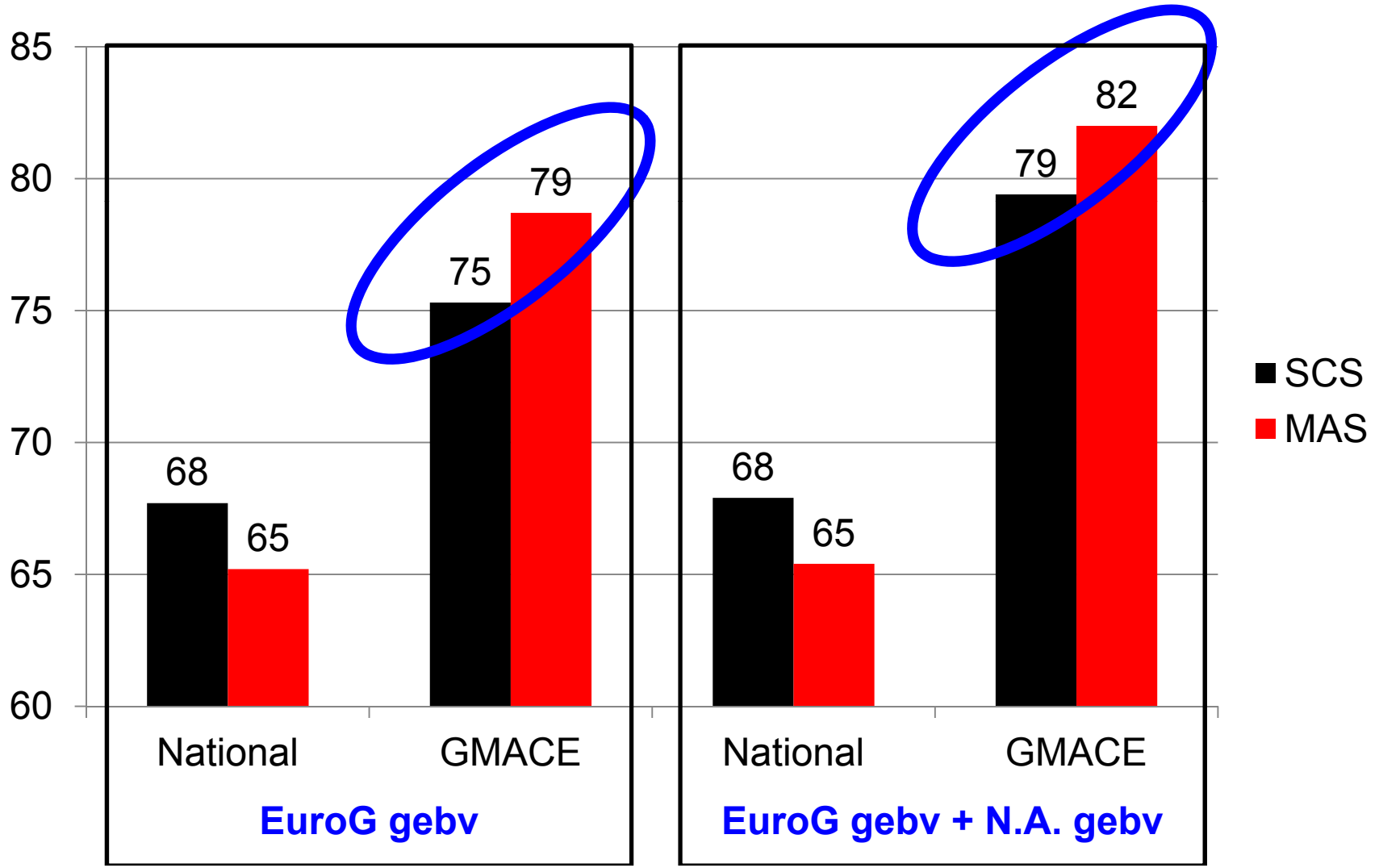
GMACE (1512)
(MAS:NLD) What's wrong?



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Introduction

- **National Reliabilities lower for MAS than SCS**
- **GMACE Reliabilities higher for MAS than SCS**
  - **Question:** Where does the extra information come from in the GMACE evaluation for MAS?
  - **1 Answer:** much lower residual correlations (r_e) were used in GMACE for MAS (**WHY?)** ... quick review of r_e :
    - **MACE**: independent daughter phenotypes by country → **$r_e = 0$**
    - **GMACE**: genomic sharing → **$r_e > 0$** (VanRaden & Sullivan, **2010**)
    - Revised definition → **lower r_e** (Sullivan & VanRaden, **2011**)
    - Predicted Reliability → **higher r_e** (Sullivan and Jakobsen, **2014**)
    - Routine GMACE service begins (Aug **2014**)

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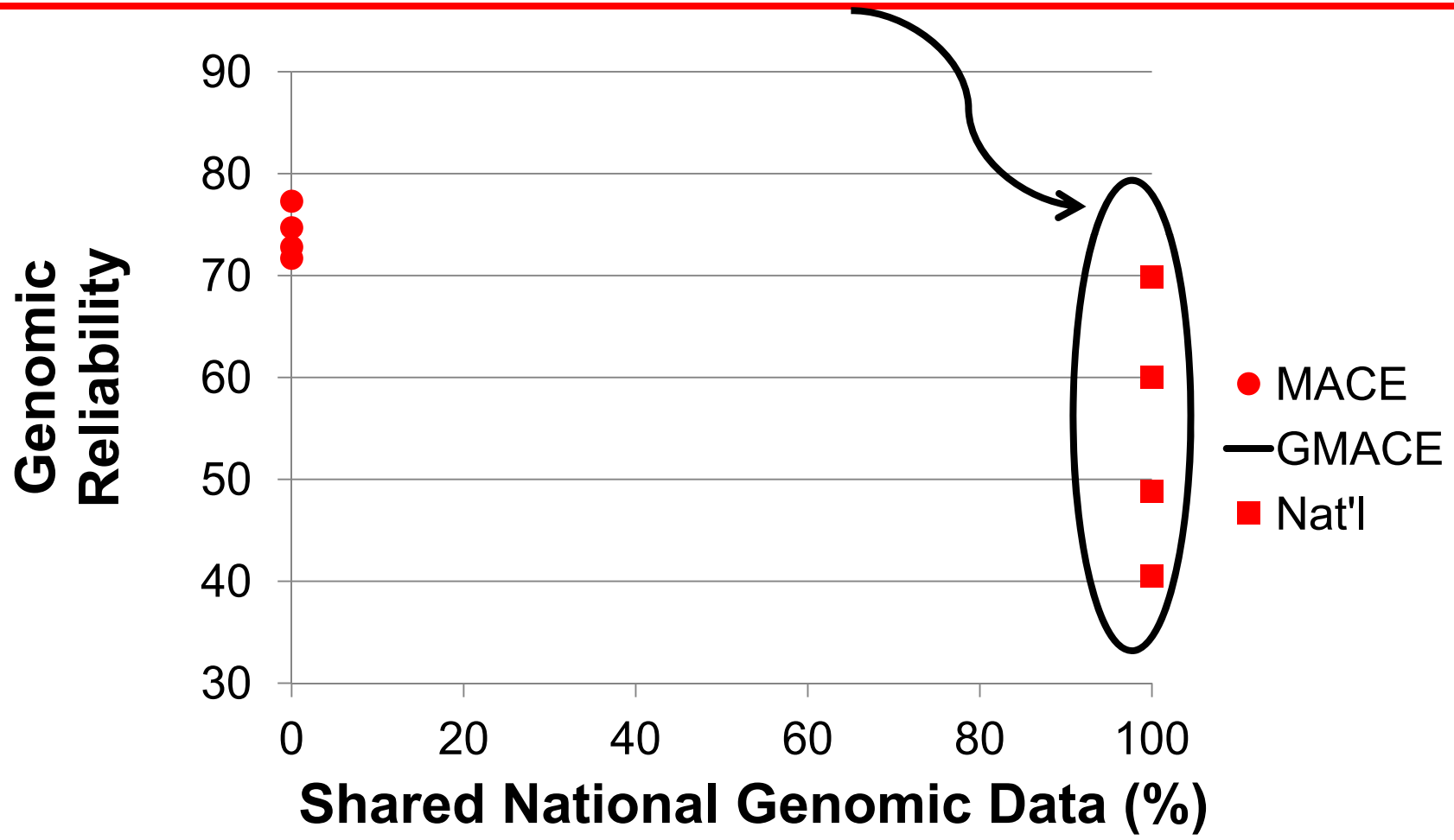
Example: 4 countries

national reliabilities differ



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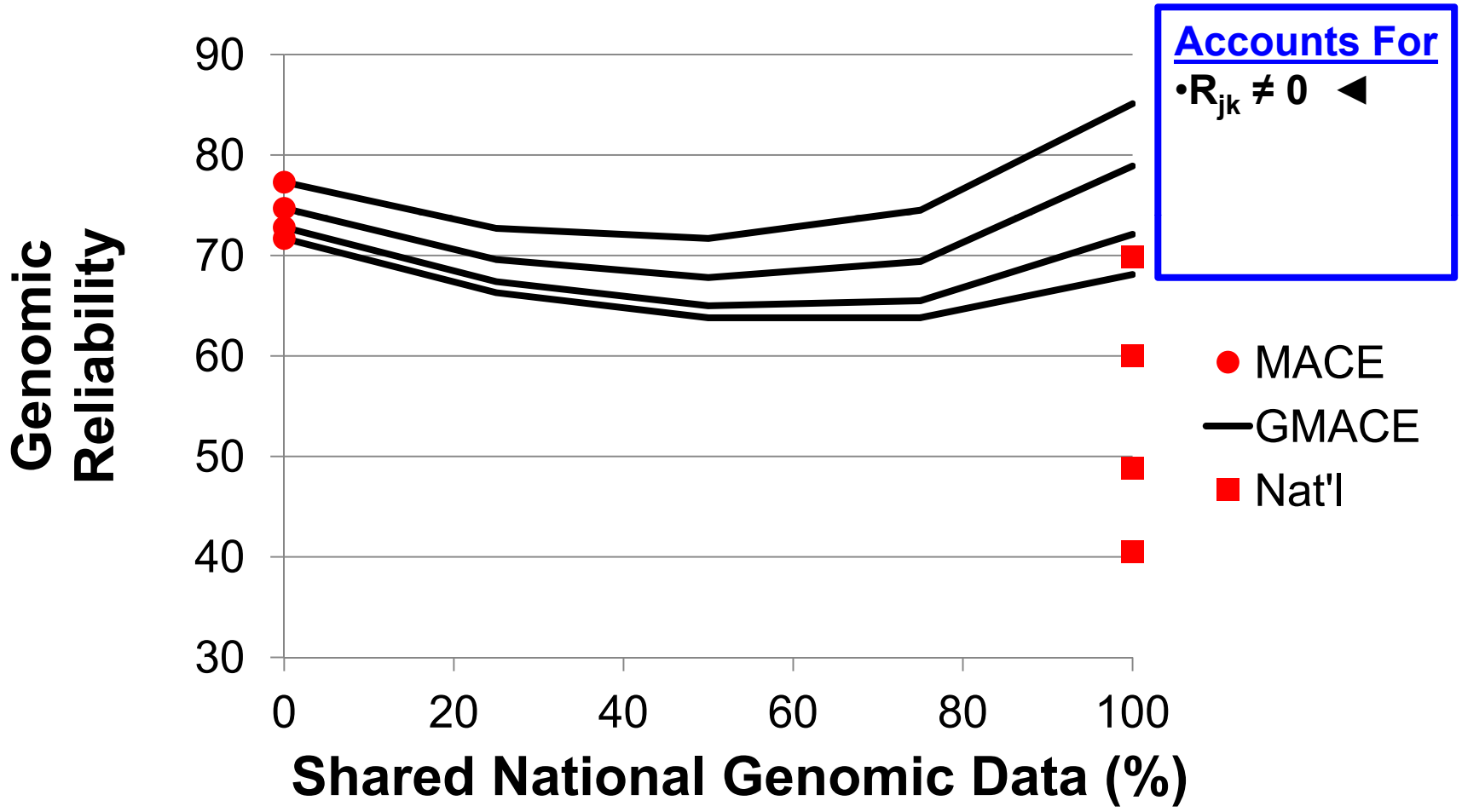
Example: 4 countries

GMACE: 2010



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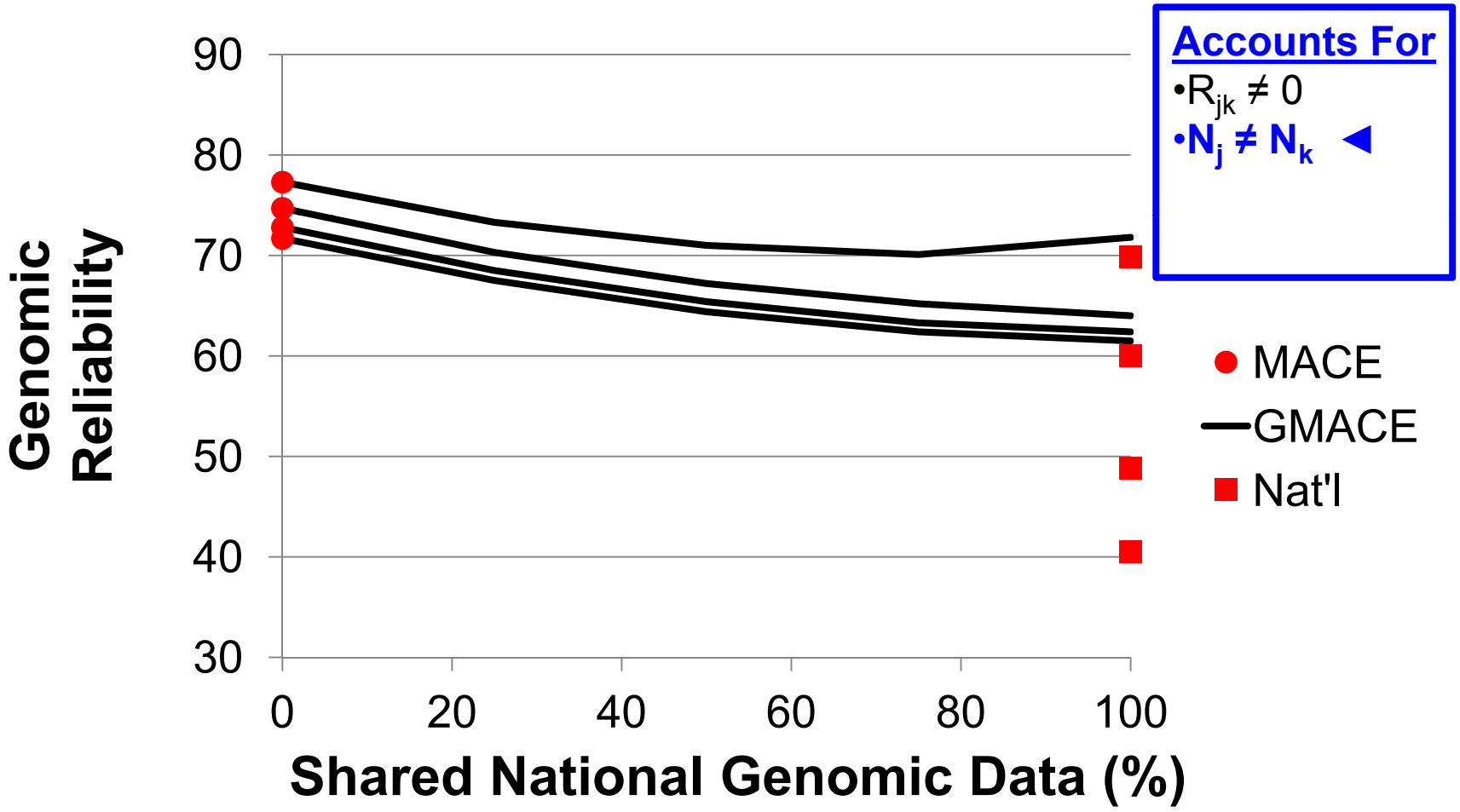
Example: 4 countries

GMACE: 2011



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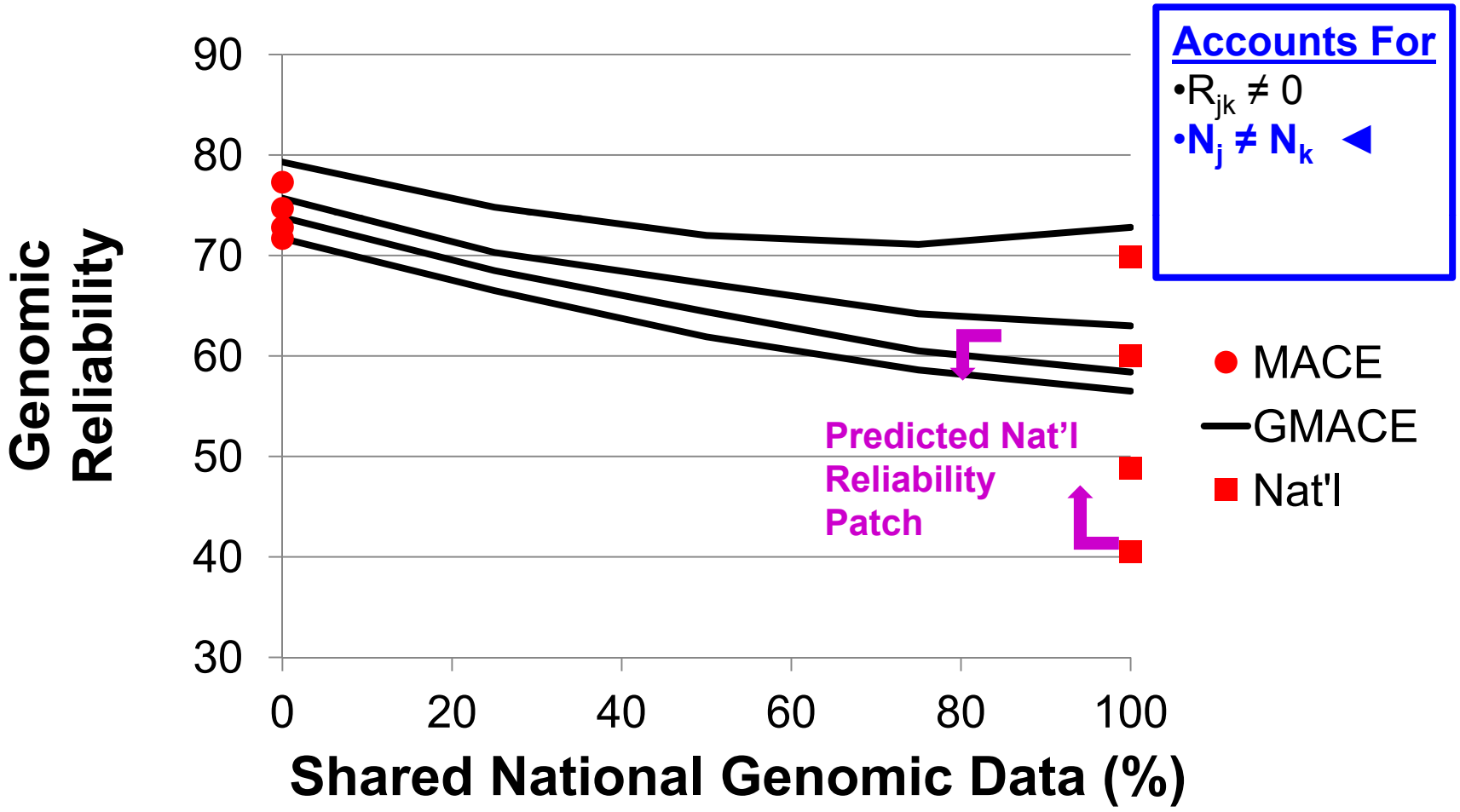
Example: 4 countries

Interbull GMACE: 2014



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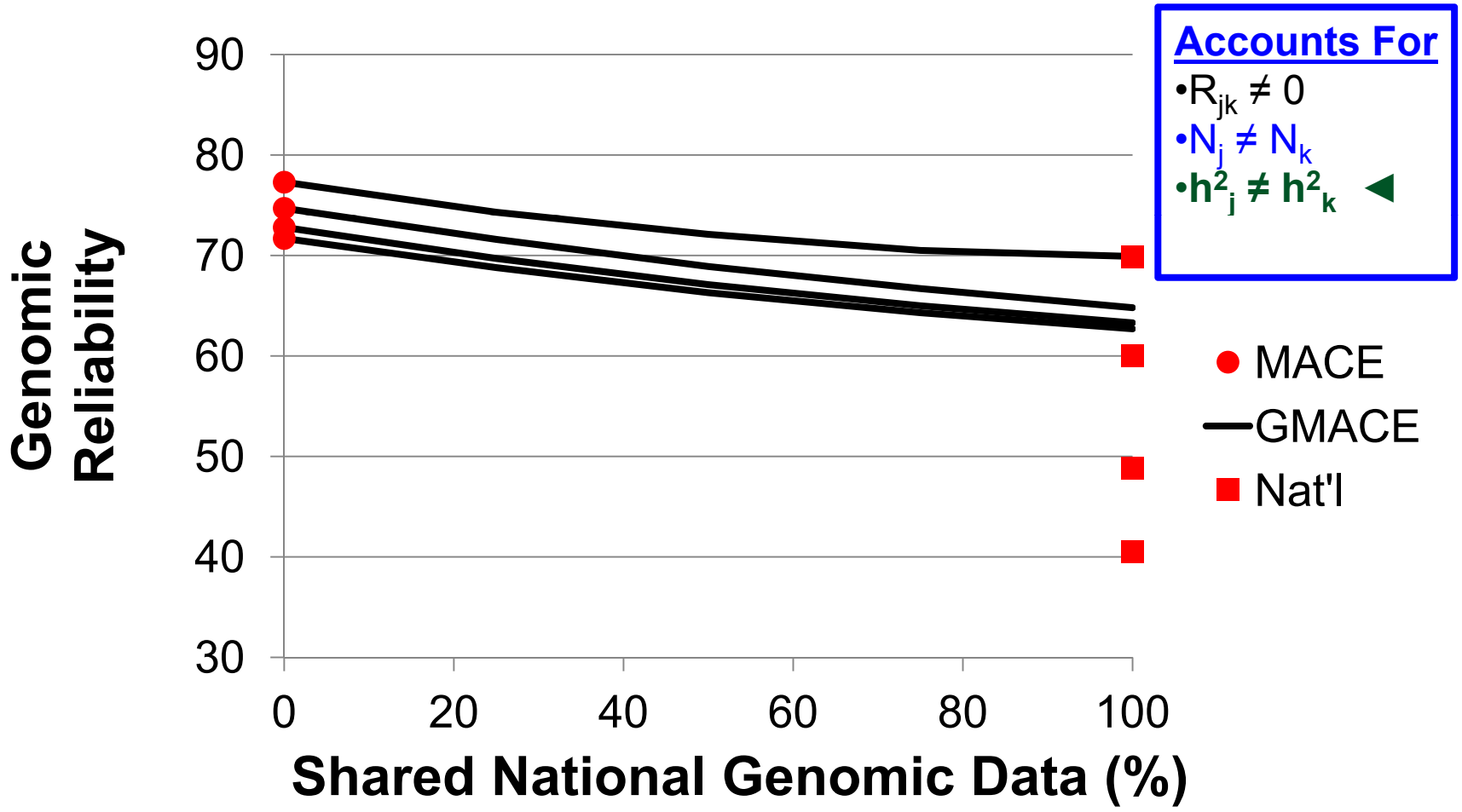
Example: 4 countries

GMACE: 2017



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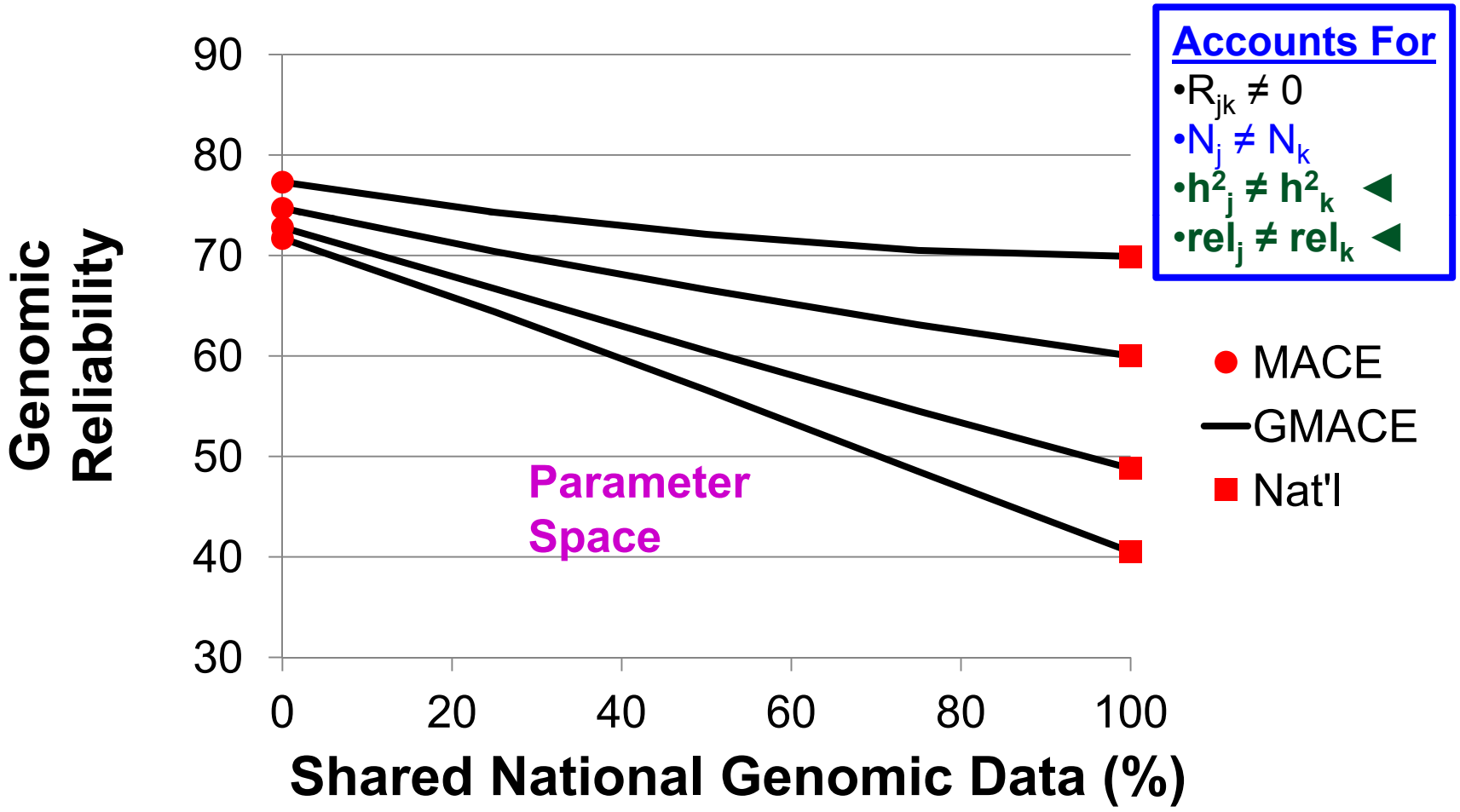
Example: 4 countries

New GMACE: 2017



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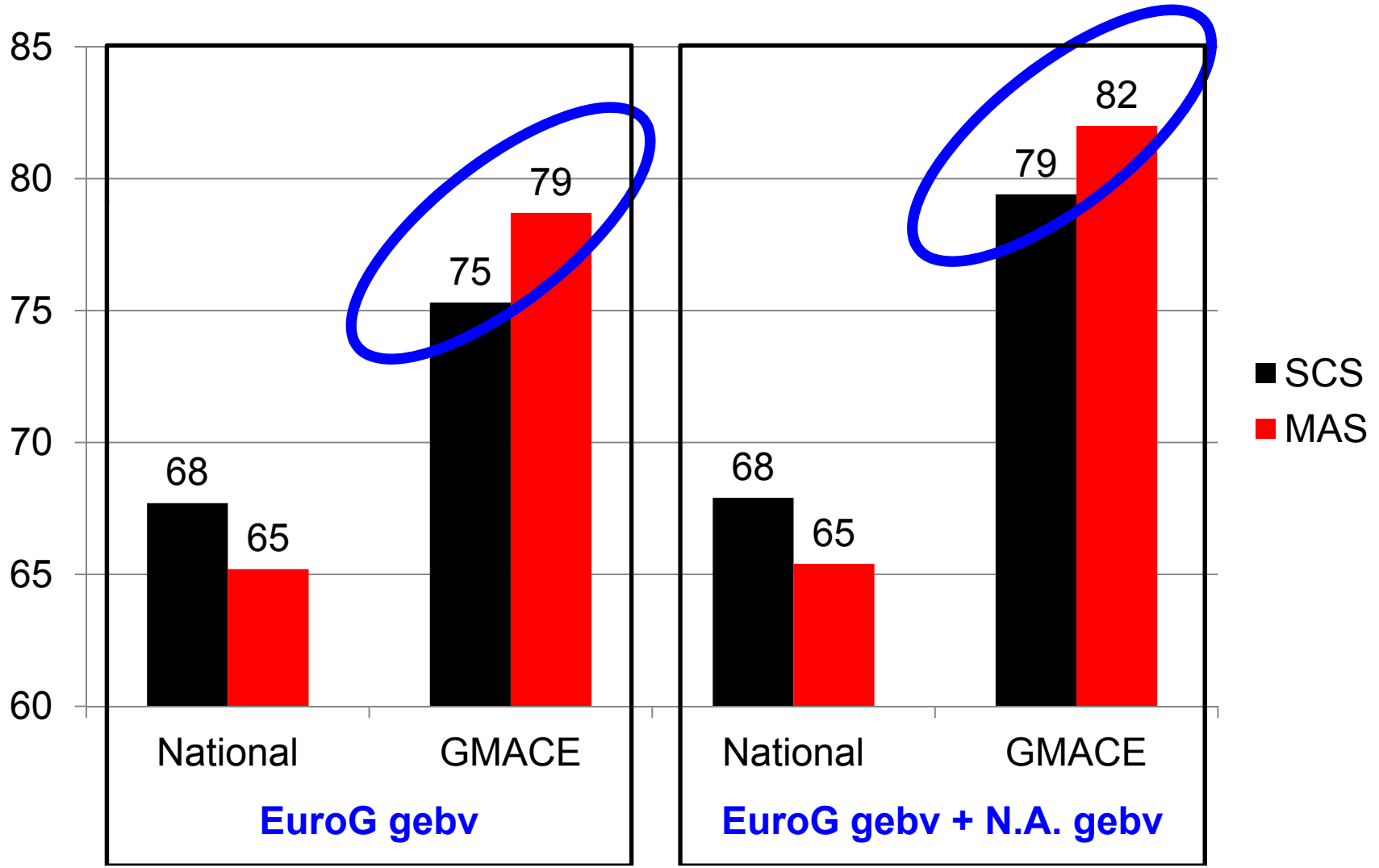
GMACE (1512)
(MAS:NLD) What's wrong?



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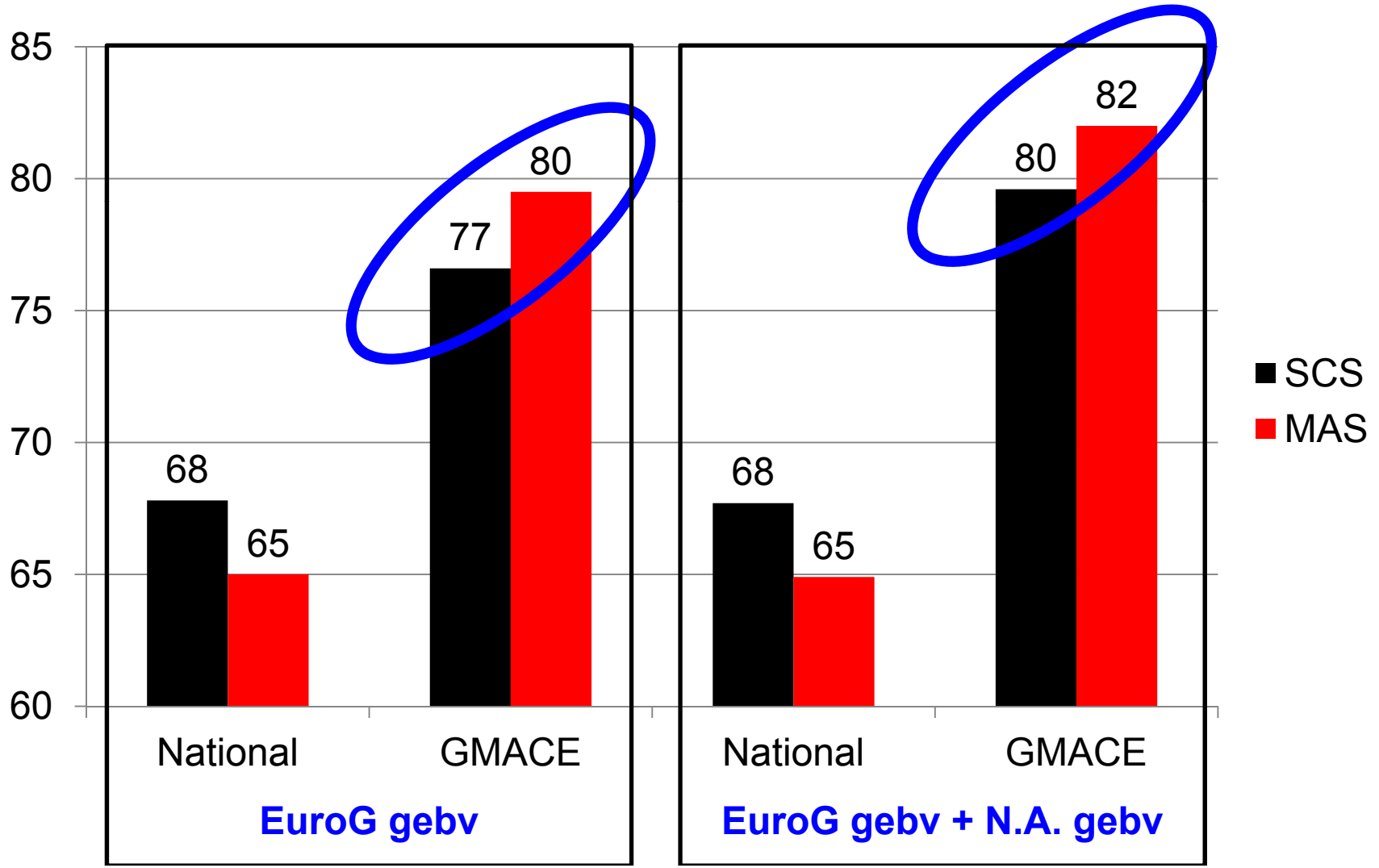
GMACE (1609)
(MAS:NLD) What's wrong?



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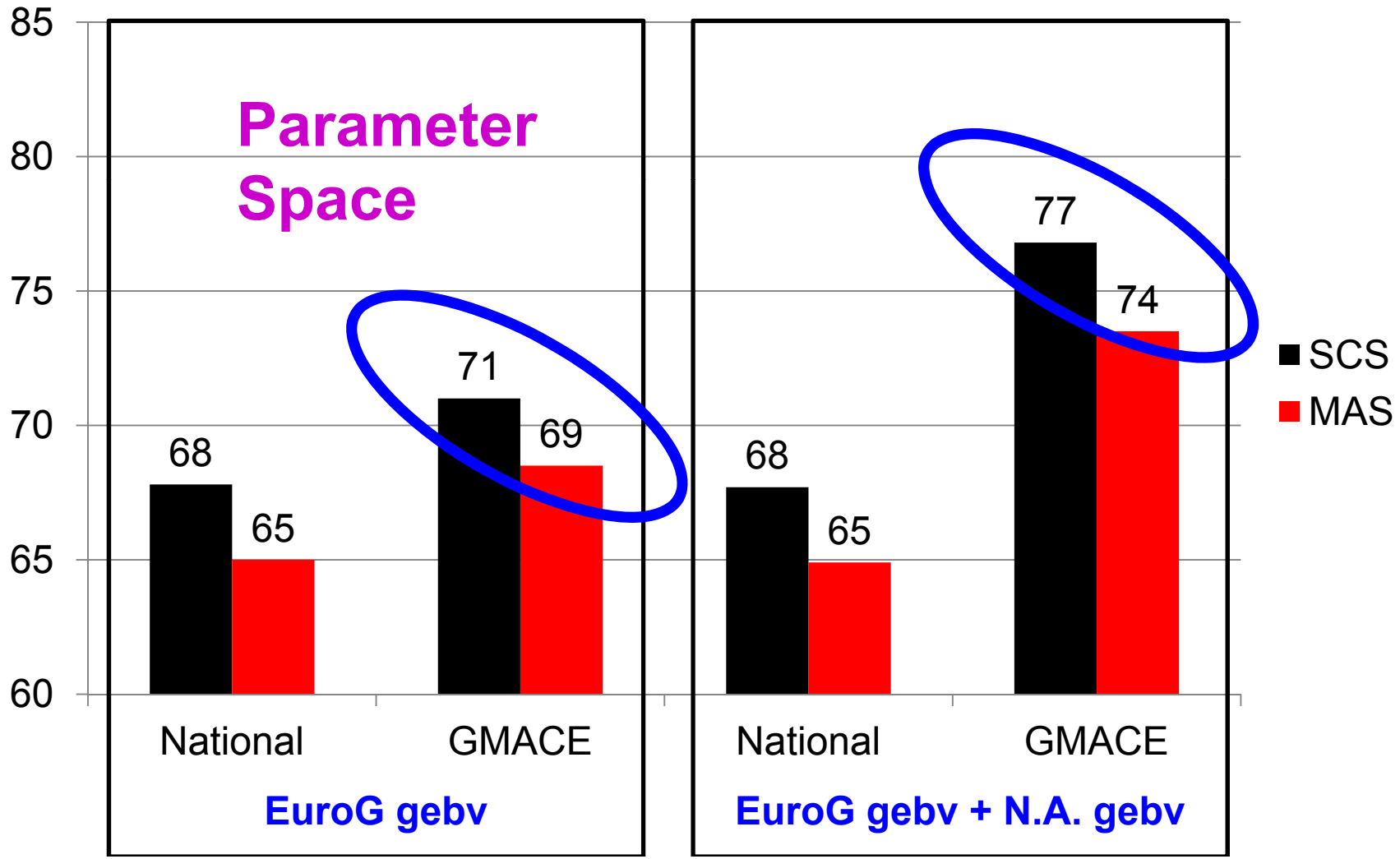
New GMACE (1609) (MAS:NLD) Much Better



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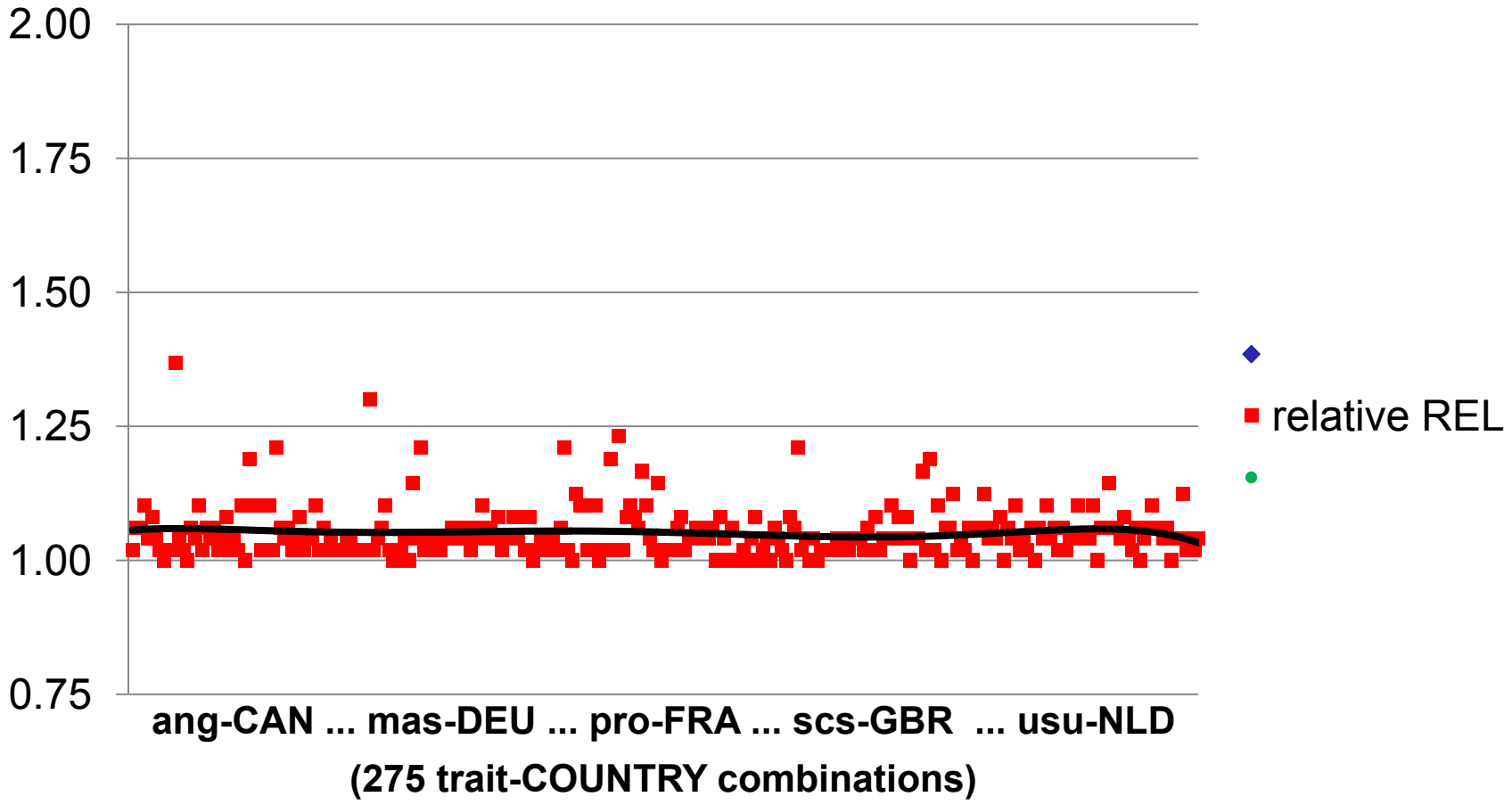
Interbull GMACE (1609)
(GEBV from 1 Consortium)



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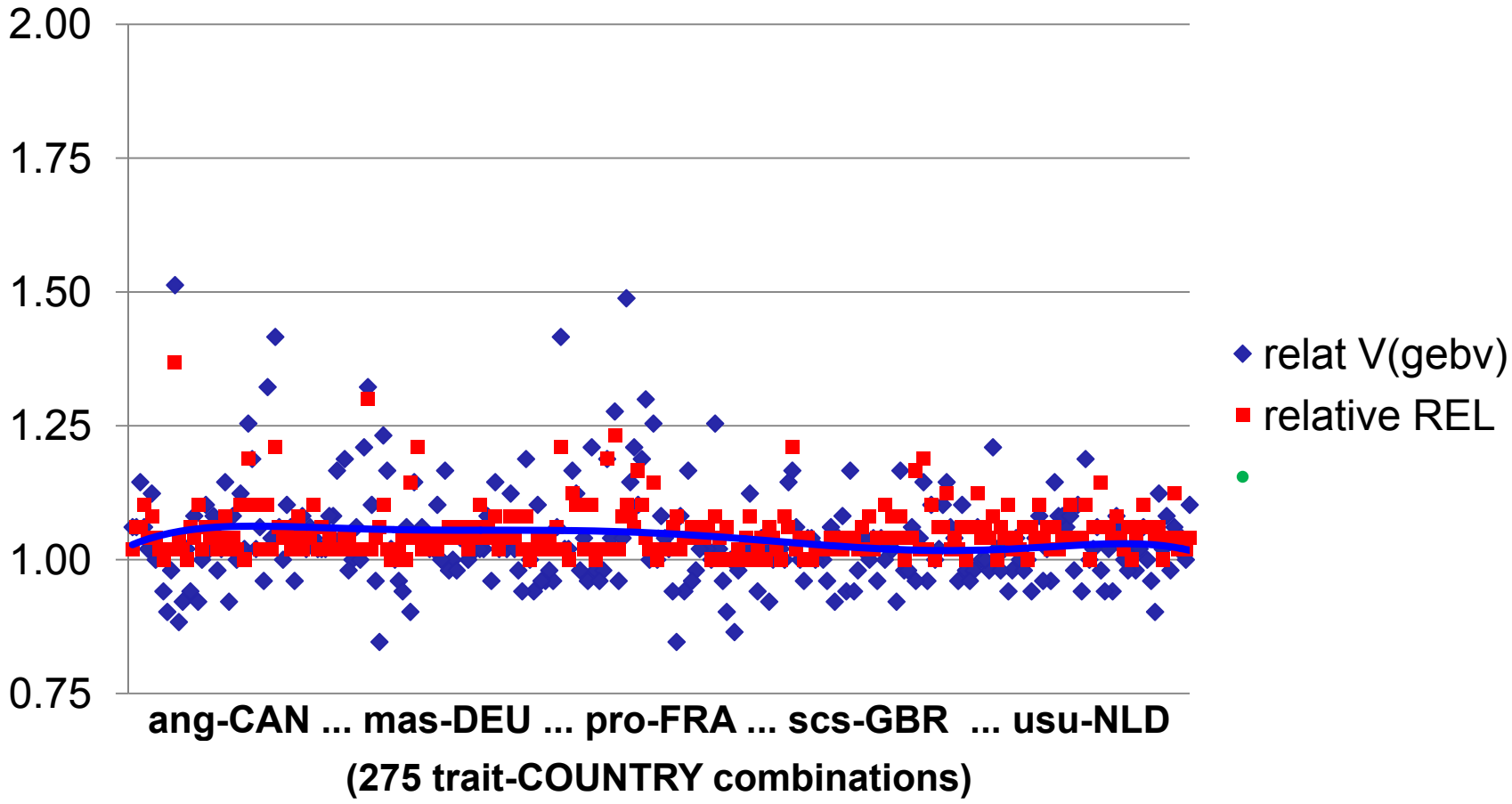

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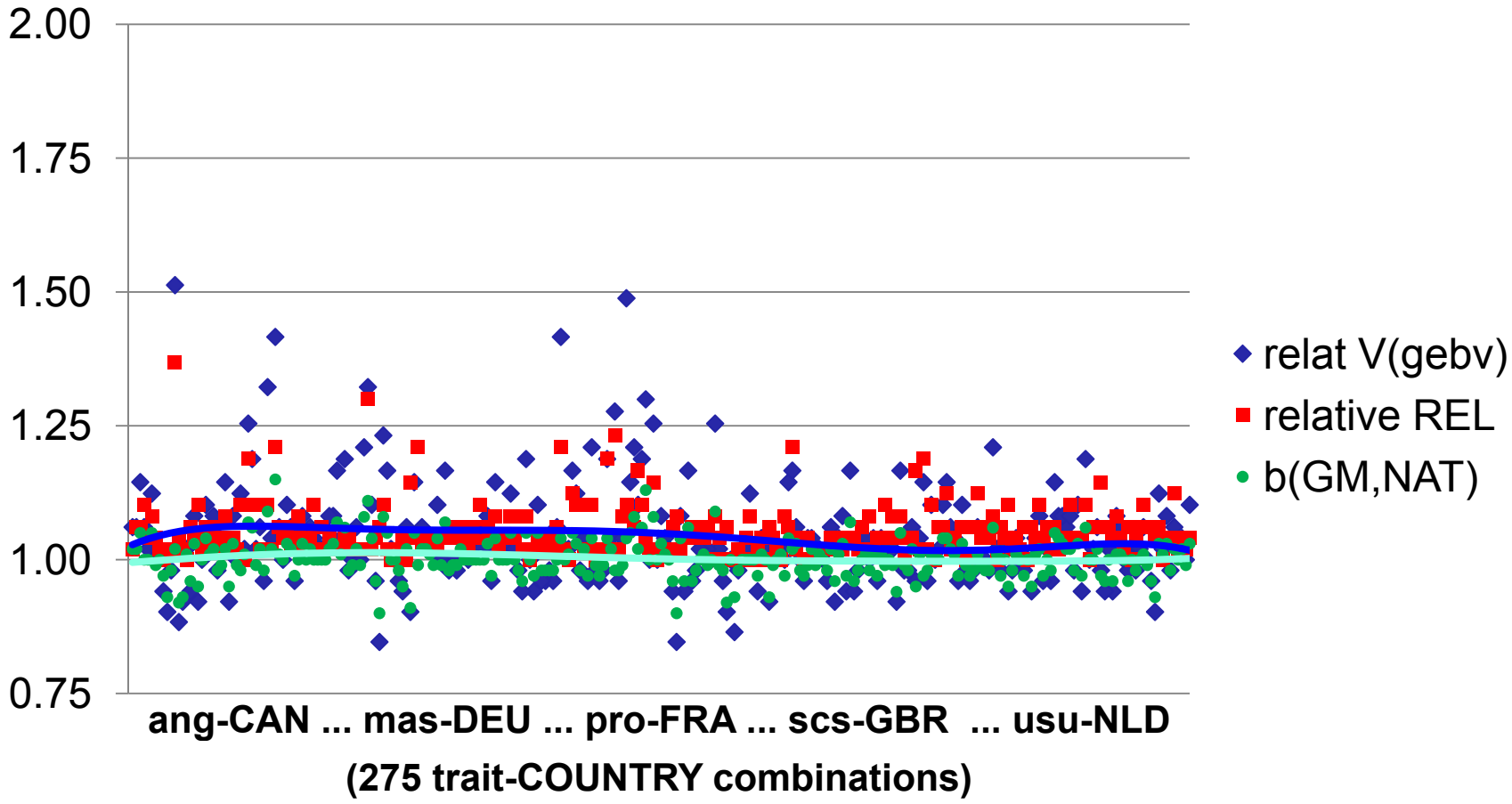

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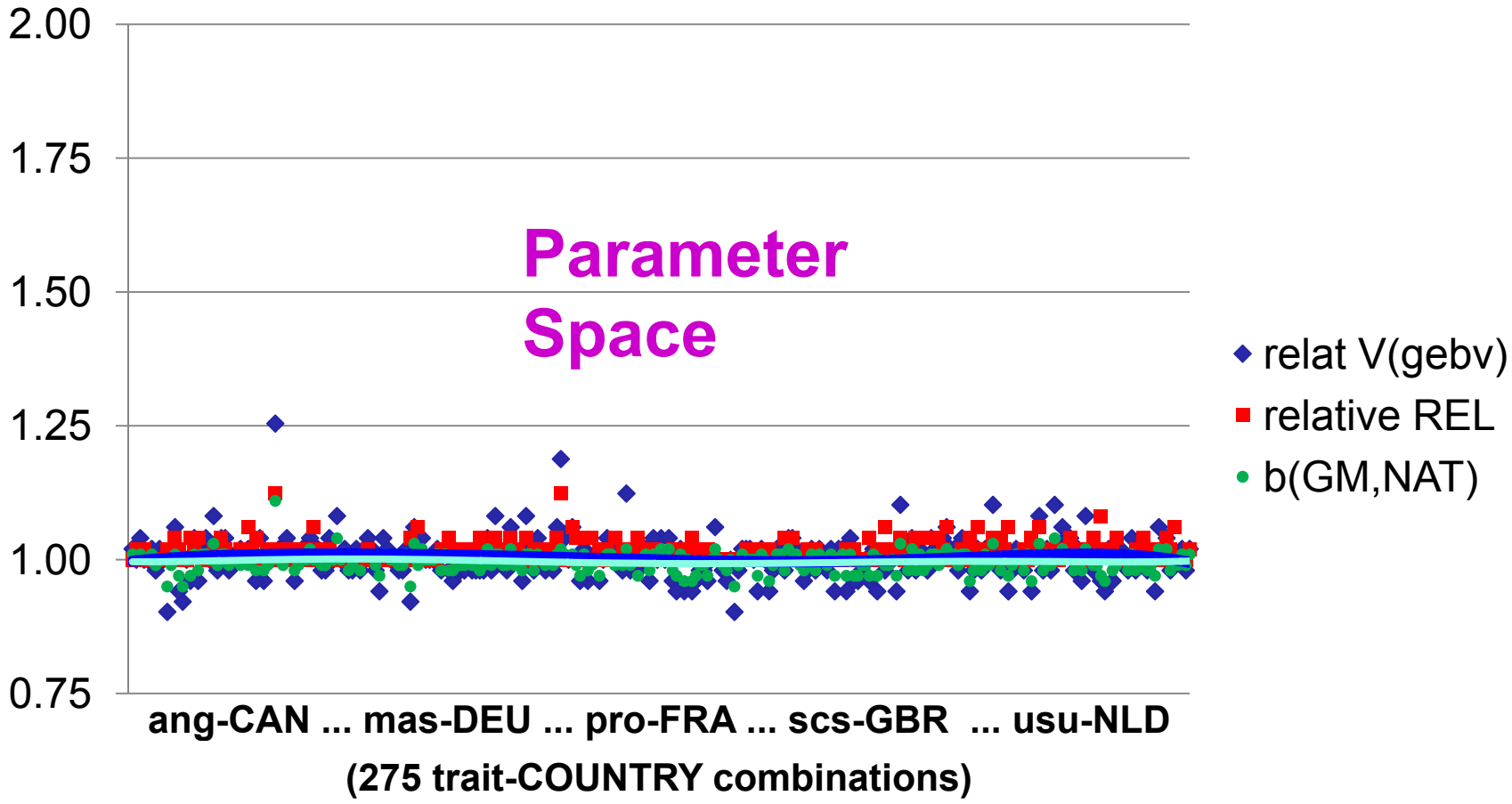
New GMACE (1609)
(GEBV from 1 Consortium)



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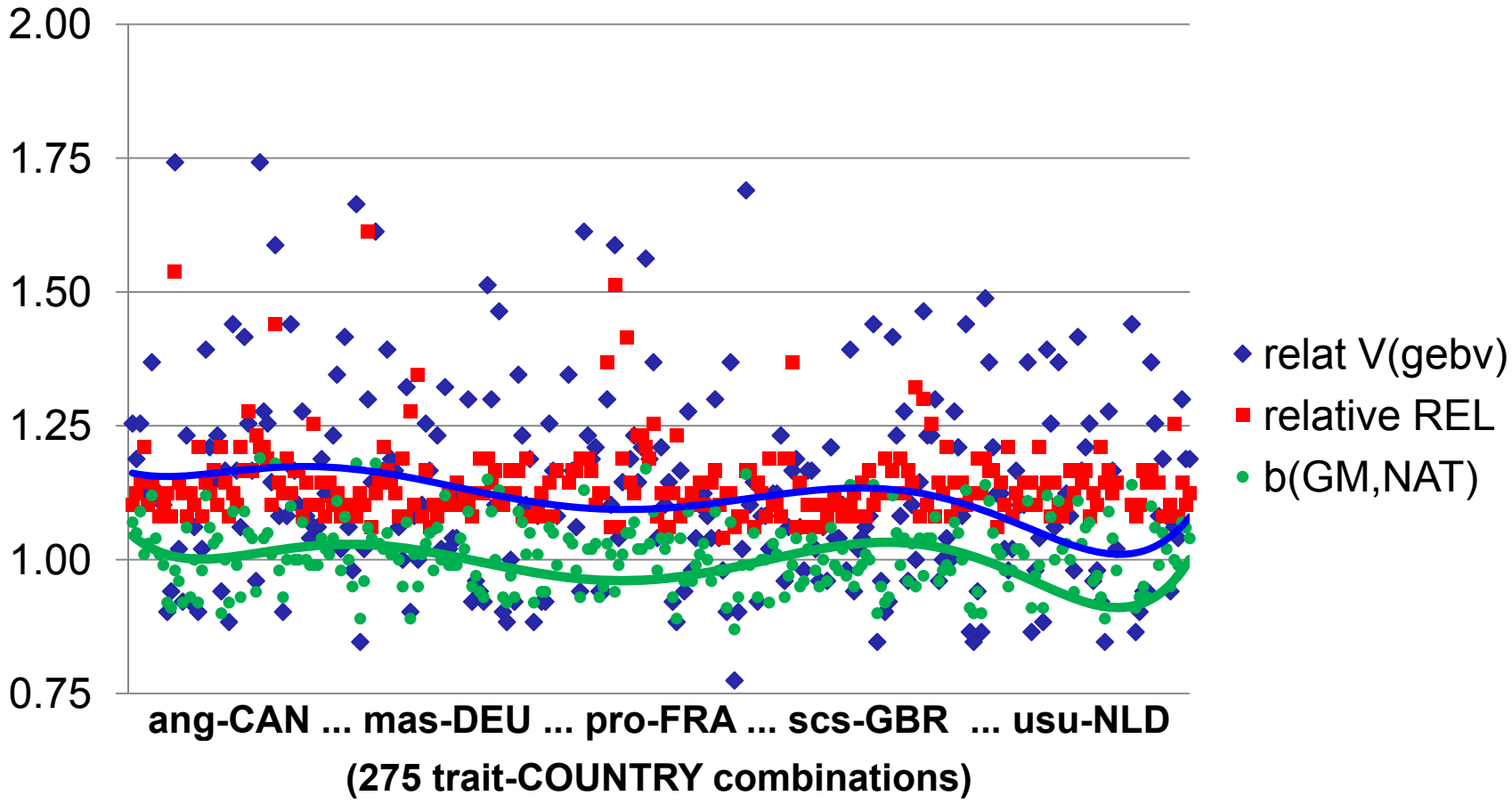
Interbull GMACE (1609)
(GEBV from 2 Consortia)



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New GMACE (1609)
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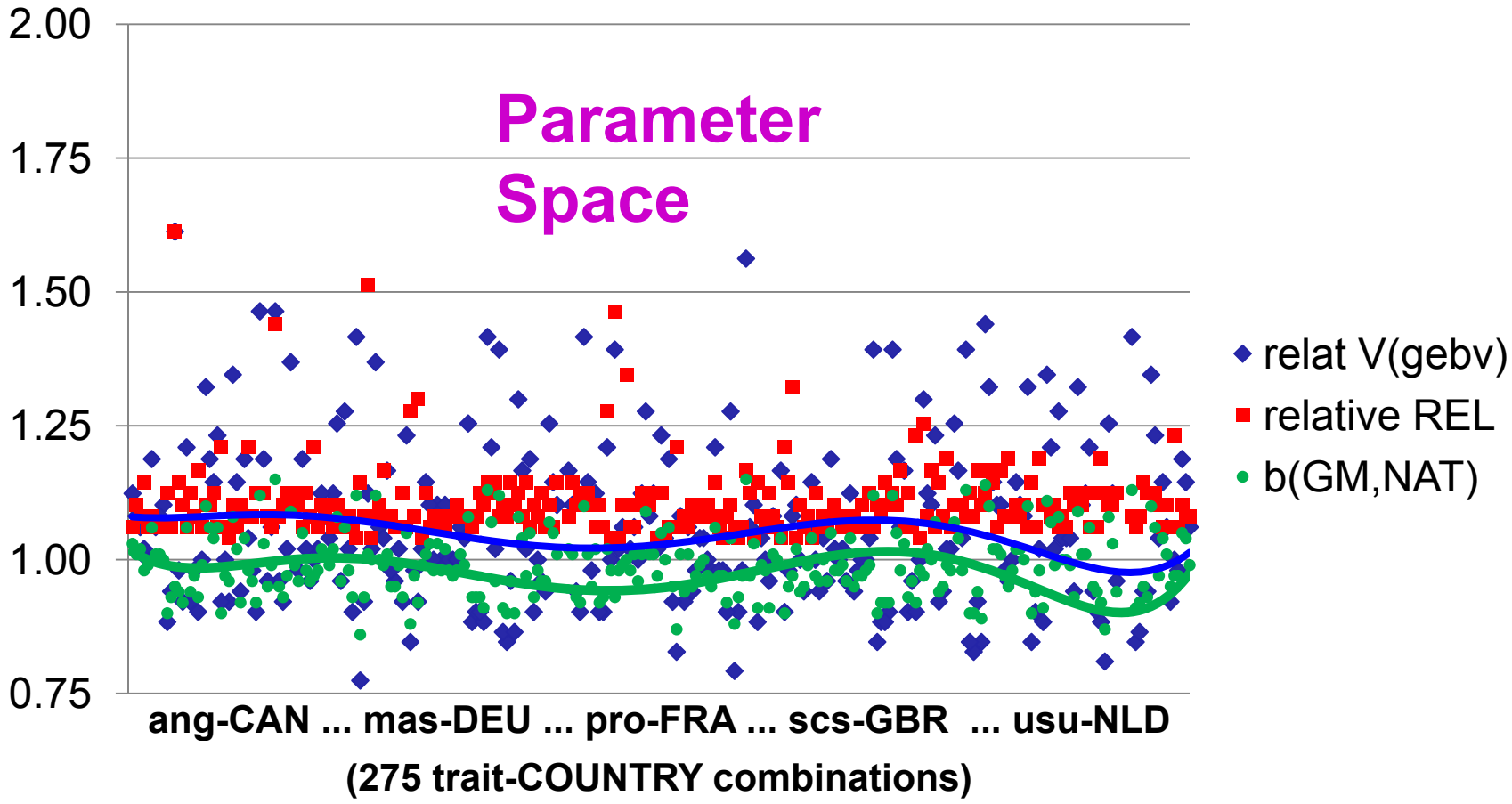

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Summary

- **Valid Concerns about GMACE for MAS**
  - **reliabilities inflated → V(gebv) inflated**
- **Solution:**

1. **Choose residual correlations that perfectly align GMACE of highest reliability country with:**
   - National reliability if countries share all genotypes
   - MACE if no genomic data are shared (r_e=0)
2. **Need to impose a parameter space to extend this same alignment to all lower-reliability countries**

- **Approach works much better and eliminates the need for predicted reliability patch**

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Summary

- **GMACE results will become:**
  - **Much more consistent across all traits,**
  - **Aligned perfectly between MACE and all National, based on level of genomic data sharing,**
  - **Alignment no longer disrupted by variation in trait heritabilities or national reliabilities**
- **Increases from national Reliab'y & V(gebv):**
  - **Zero for bulls with GEBV from 1 country**
  - **Nearly zero if multiple GEBV from 1 consortium**
  - **Notably greater than zero, but less than before if GEBV from 2 consortia**

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Recommendation

- **New methodology and results were reviewed by ITC during Aug/Sep 2016**
  - Recommendation to **implement the new GMACE model as soon as possible**
- **Next steps**
  - Update/test Interbull systems for routine and test runs
  - Use the new model for January 2017 GMACE test run
  - **Implementation for April 2017 GMACE routine run**

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Acknowledgements

- **Gerben deJong (NLD)**
  - Clear questions and helpful discussions
- **Interbull Centre staff**
  - Hossein, Haifa and Carl
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