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MS test software:
Applications to Canadian data

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Introduction

- **Use of the software**
  - Flexibility and ease of use
  - Pre-processing requirements
  - Information / results generated
  - Post-processing opportunities
- **Impacts of ignoring genotypes in EBV calculation (i.e. GPS bias) on validation results**

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Use of the software

Flexibility and ease of use

- **Easy to use**
- **Flexible to different breeds, traits, population size, with suitable guidance in the documentation**
- **Documentation is efficient, being very helpful but not longer than necessary**
- **Runs efficiently... ~ 1 hour for all breeds and traits**

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Use of the software

pre-processing requirements

- Need to create input files for each breed
- Can have 1 file with all traits OR by groups of traits OR separate files for each trait
- Input data file(s) include for each animal: pedigree, ebv (E) and reliabilities (R):

an sire dam E_a E_s E_d R_a R_s R_d

- Input parameter file specifies the name of data file to use, which traits within the file should be tested, and the range of years to include in the test

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Use of the software

Information / results generated

- **Output information is divided among multiple files**

  ***.out, *.dat, *.summary, <console>**

- **Provides yearly estimates of: genetic variance, average MS, PEV(MS)**
- **Tests for years with outlier variance**
  - Outlier if H0 rejected for a given year
- **Tests for non-zero trend in variance**
  - H0 rejected if BOTH statistical AND practical tests are FAILS
- **Warnings and good guidance if insufficient data**

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Use of the software

Post-processing opportunities

- **Approximate PEV(MS) provided in the output, which is otherwise difficult to obtain without this software**
- **The subset of provided bulls actually used for the test (e.g. PEV is low enough) are identified**
- **User can modify input data to test impacts on validation test results**
  - Improve understanding of current EBV
  - Develop better EBV systems
- **Genomic Selection**
  - Test years prior to GPS (e.g. Bulls born 1998-2008)
  - Modify EBVs to see impact of GPS ★

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Genomic Selection for positive Mend. Sampling

- Selection intensity for genomic young bulls has increased dramatically... 1 in 20 (5%) chosen for use in AI
- Positive within-family deviations for important traits at the time of GPS selection (i.e. before AI use) ... $MS_{GPS}>0$ for 70-100% of GPS bulls (CAN,NLD,DFS data)
- After AI, the MS deviations from EBV (ignoring genotypes) of these same bulls are regressed strongly towards 0 ... $MS_{EBV}>0$ ~> 50%
- MS_{GPS} is very high, while MS_{EBV} is much closer to zero
- Recent trends in EBV are much lower due to this downward bias of MS for GPS bulls (b_{EBV} ~50% * b_{GEBV})

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Future EBV will not be biased by Genomic PreSelection (GPS)

- **Genetic evaluation centres will develop methodology to reduce/eliminate GPS bias in EBV of dairy cattle**
- **Corrections to remove GPS bias will likely increase %MS>0 ~> 100% and will increase b_{EBV} ~> b_{GEBV}**
- **How will this affect results from Interbull Validation test 4, which tests the following hypothesis?**

H0: For each year, MS ~ N(0,V_0)

- **Since GPS creates truncated distribution of MS, so H0 is dramatically unrealistic... Accepting H0 means:**
  1. GPS effects are small, or power of the test is weak.
  2. EBV are biased / do not reflect the true effects of GPS

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What might future EBV look like if NOT biased by GPS?

- Consider changes that would increase b_{EBV} ~> $2*b_{EBV}$ and increase %MS>0 from 50% ~> 100%, while not changing the EBV of very best GPS bulls (e.g. 3 st. Deviation above the average of birth year cohorts)

$$Top_0 = a + b_{EBV} * yr + 3\sigma_e$$

$$b_{EBV} *= 1.25, 1.50, 1.75, 2.00$$

$$Top_1 = a + b_{EBV} * yr + 3\sigma_1$$

Solve for σ_1, such that $Top_1 = Top_0$

Scale EBV-E(EBV) by σ_1 / σ_e

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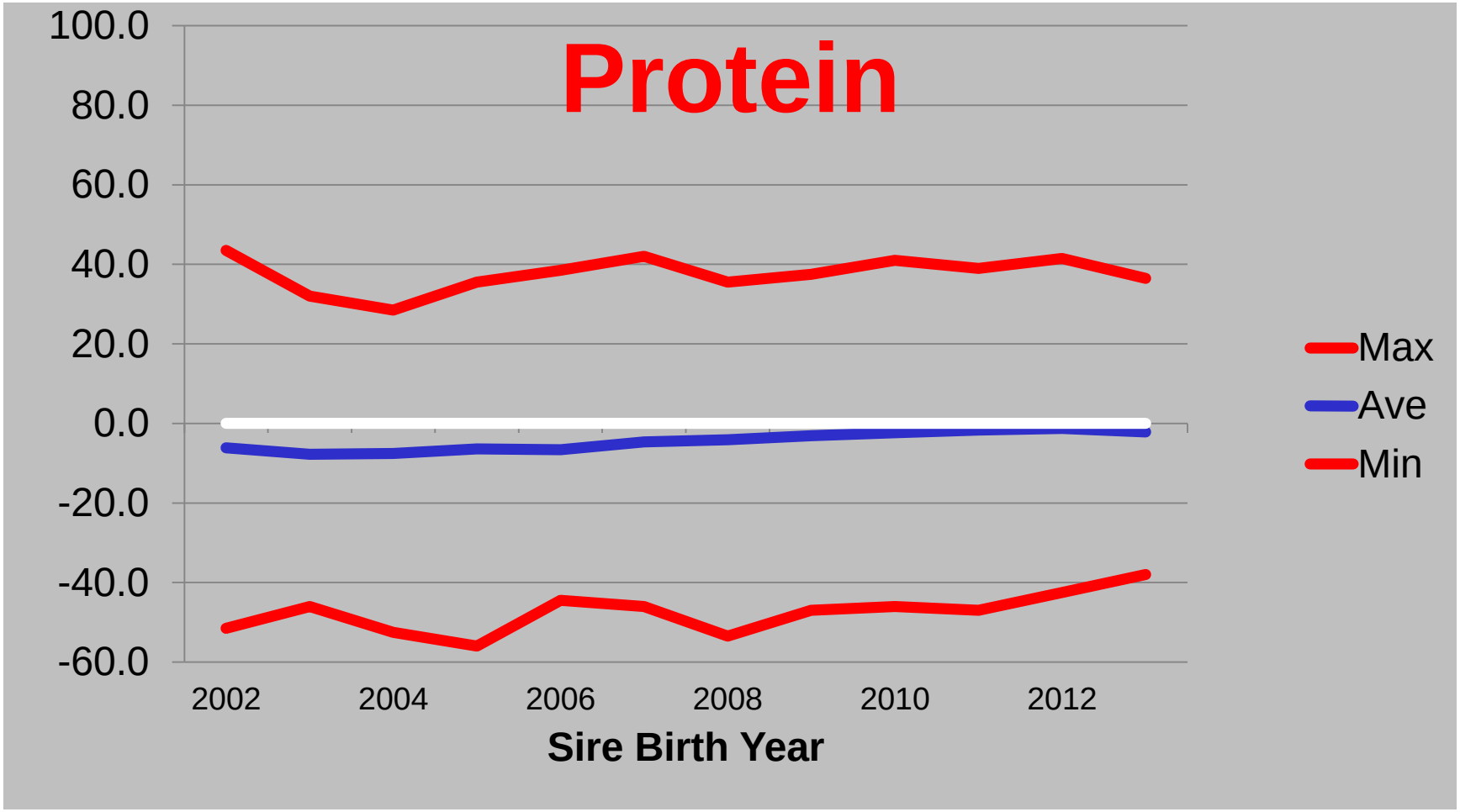
Range of MS_{EBV} with EBV ignoring genotypes (GPS bias)



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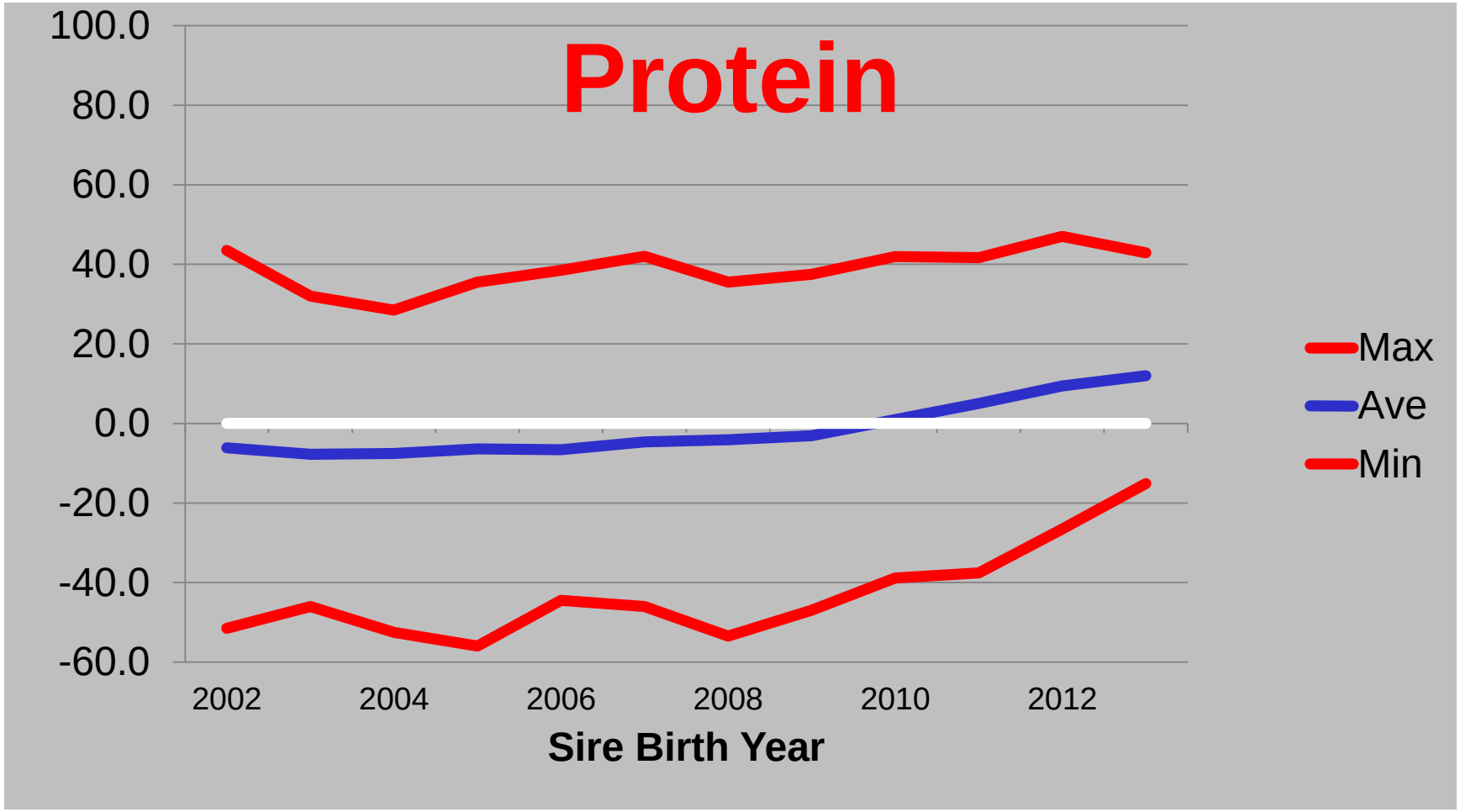
Range of MS_{EBV} with EBV adjusted for GPS: b_{EBV}*1.50



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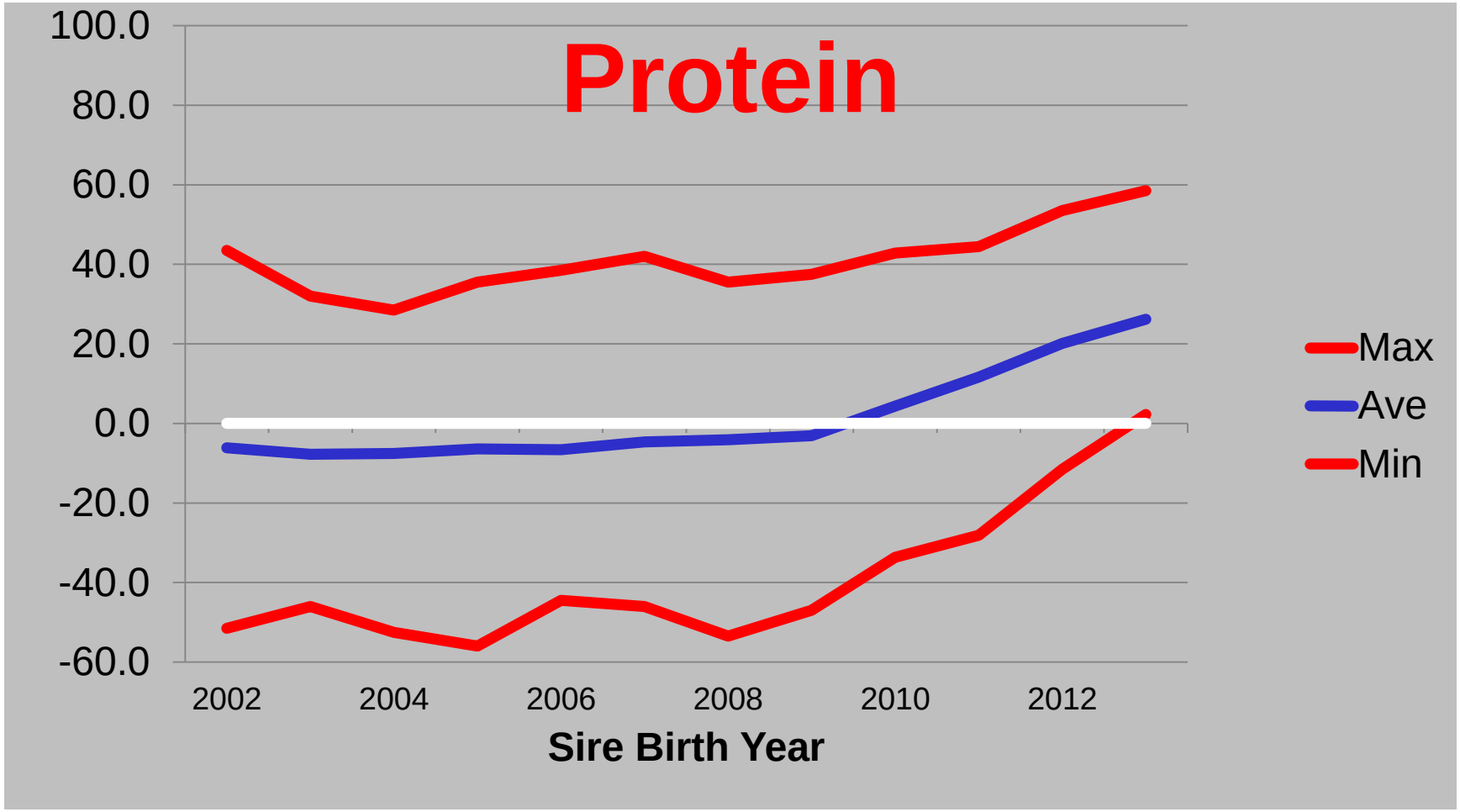
Range of MS_{EBV} with EBV adjusted for GPS: b_{EBV}*2.00



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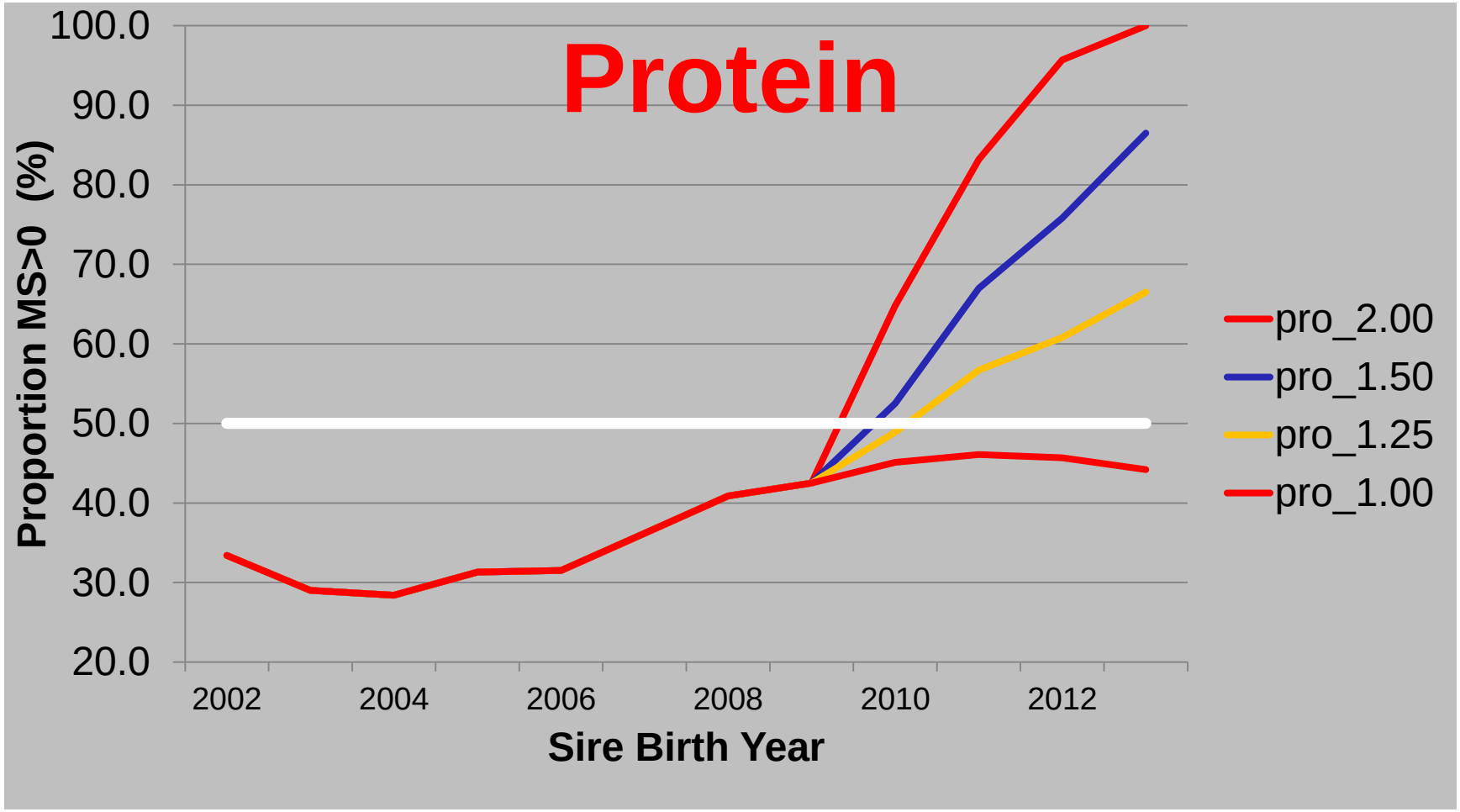
GPS bulls are the best full-sibs: move %MS>0 from 50% ~> 100%



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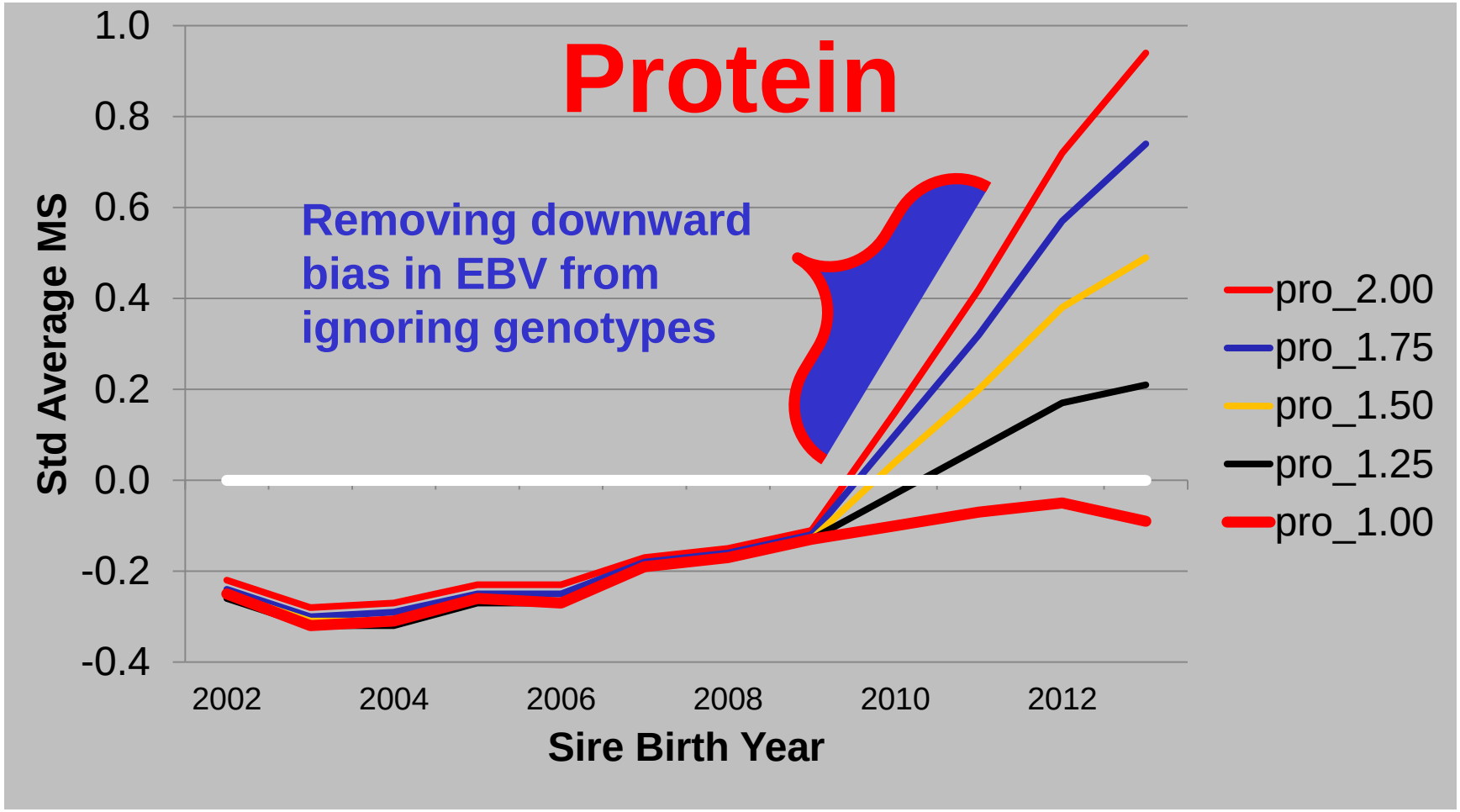
GPS affects on ITB validation Test4 (Trends in average MS)



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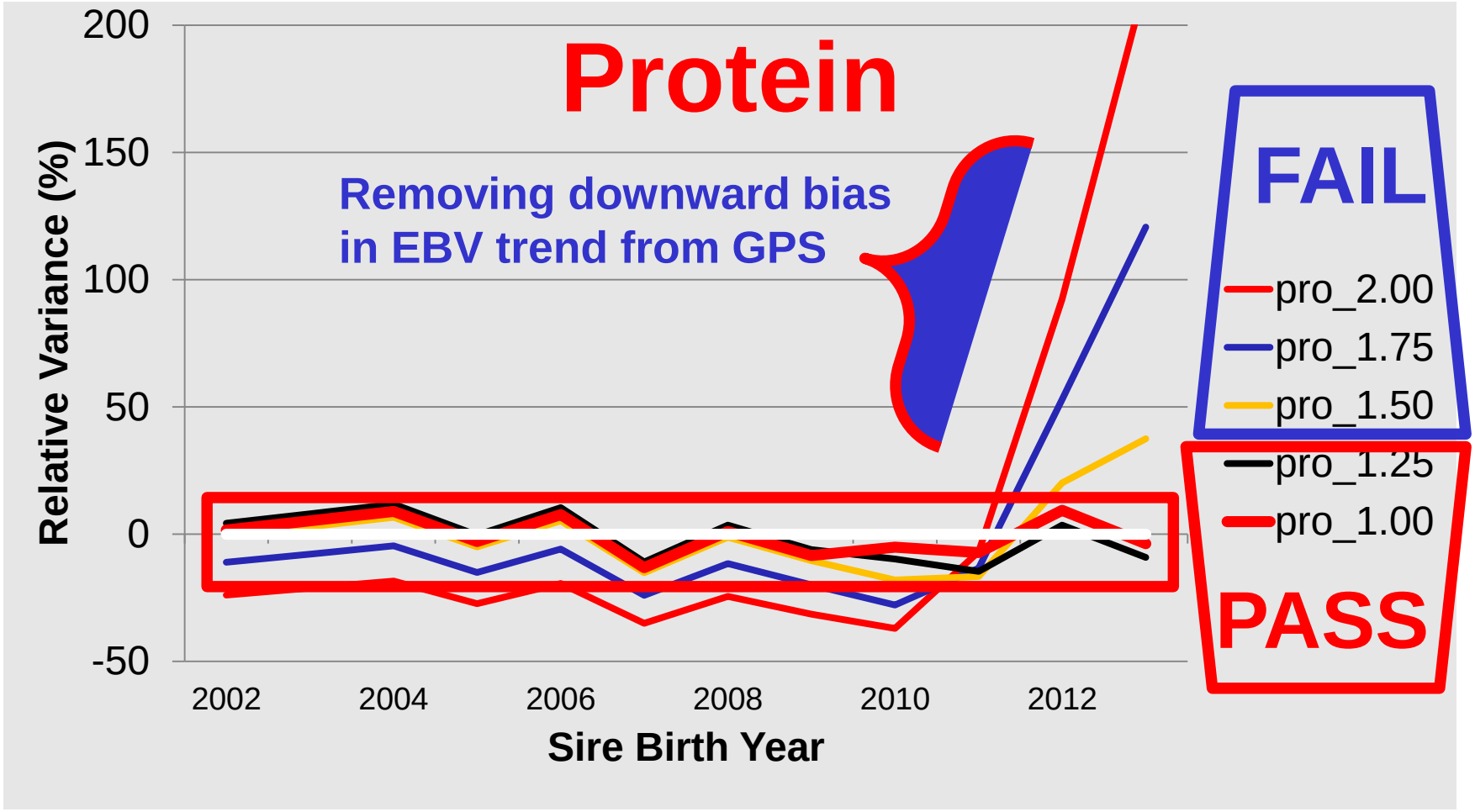
GPS affects on ITB validation Test4 (Trends in variance)



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MS Variance Test
Protein

- **If EBV without genotypes include GPS bias, then the biased EBV will PASS the variance trend test (ITB test 4)**
- **If EBV are corrected to account for GPS, then the unbiased EBV will FAIL the variance trend test (ITB test 4)**
  - Intensity of GPS is **HIGH** for **Protein**

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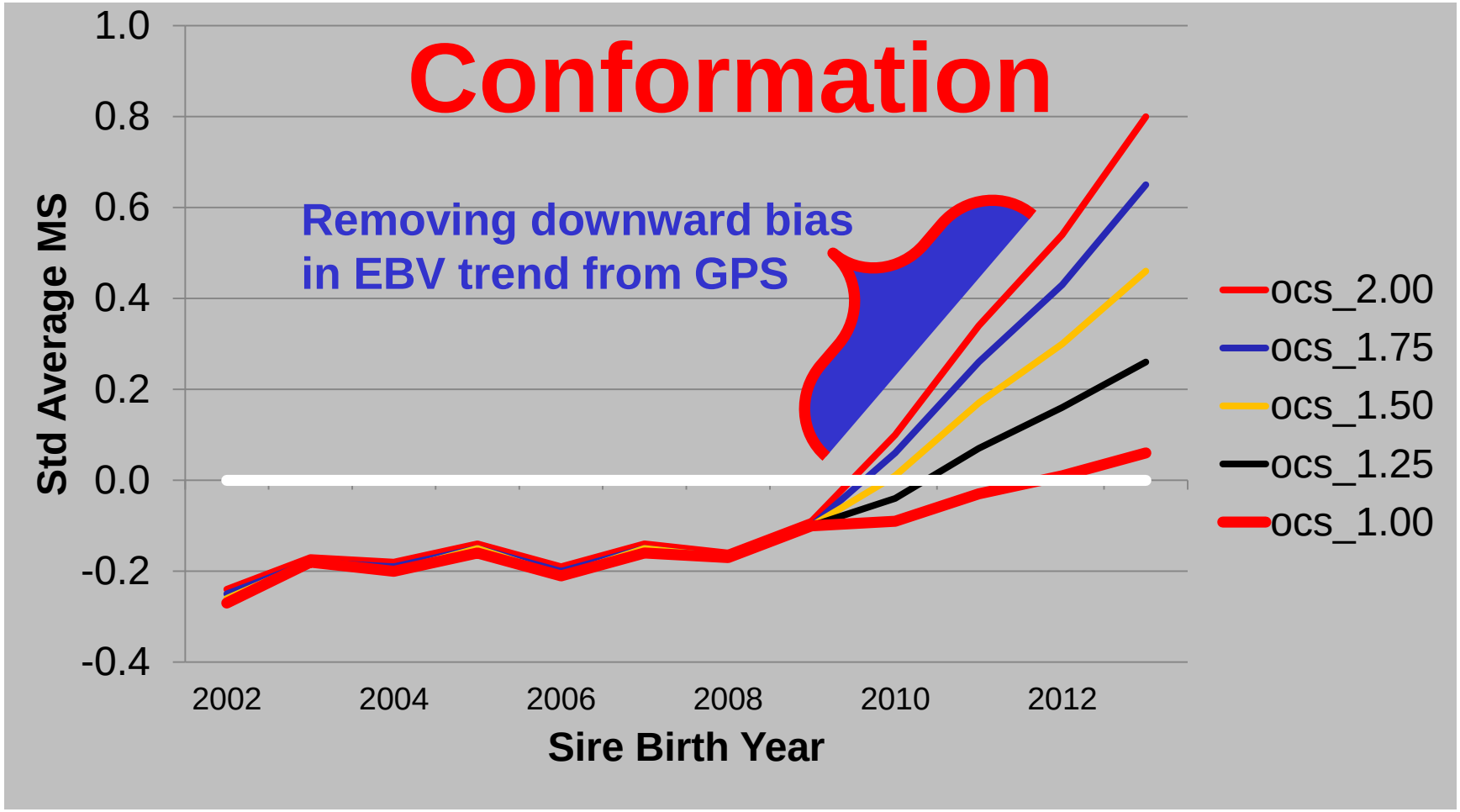
GPS affects on ITB validation Test4 (Trends in average MS)



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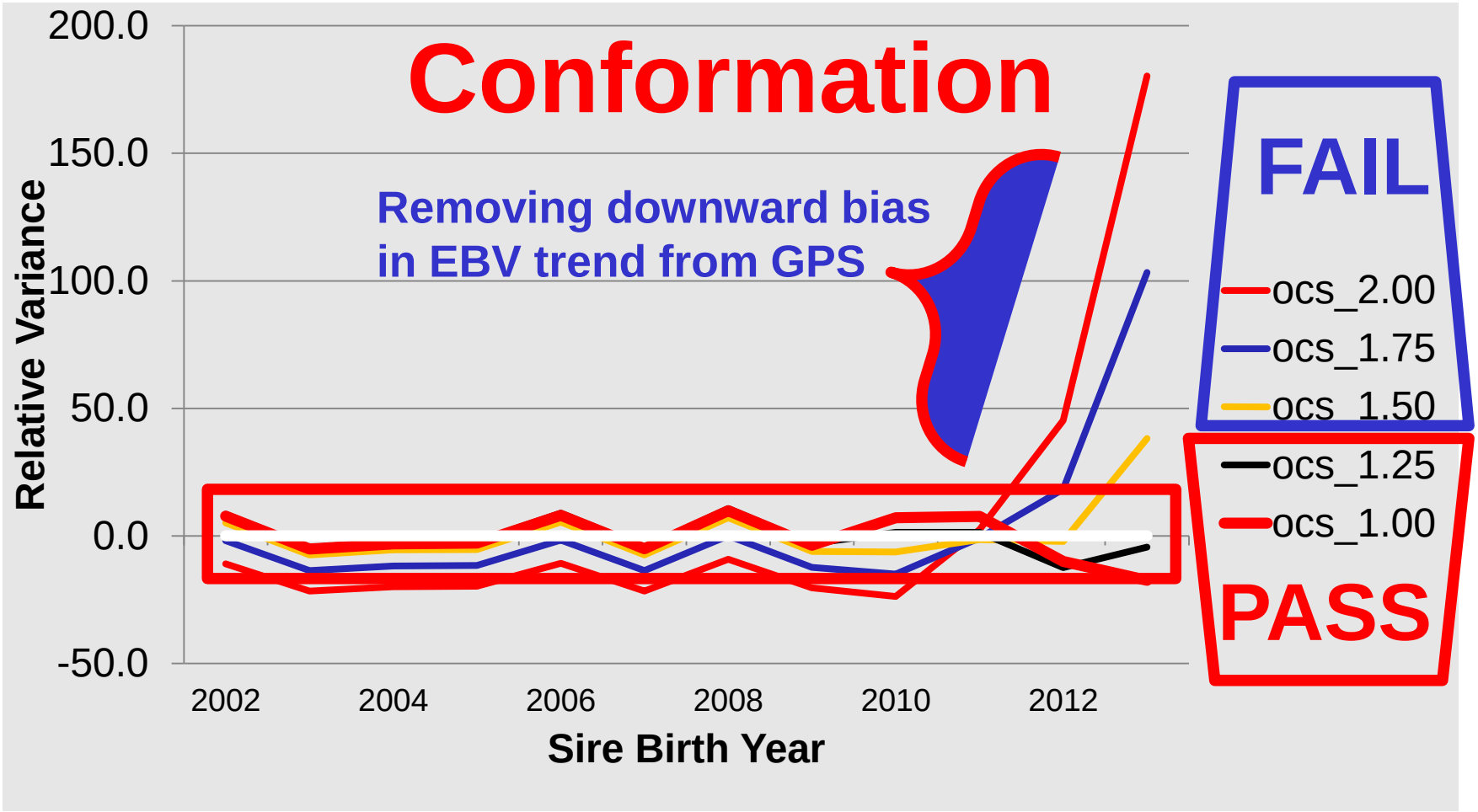
GPS affects on ITB validation Test4 (Trends in variance)



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MS Variance Test
Conformation

- **If EBV without genomics include GPS bias, then the biased EBV will PASS the variance trend test (ITB test 4)**
- **If EBV are corrected to account for GPS, then the unbiased EBV will FAIL the variance trend test (ITB test 4)**
  - Intensity of GPS is **HIGH** for **Conformation**

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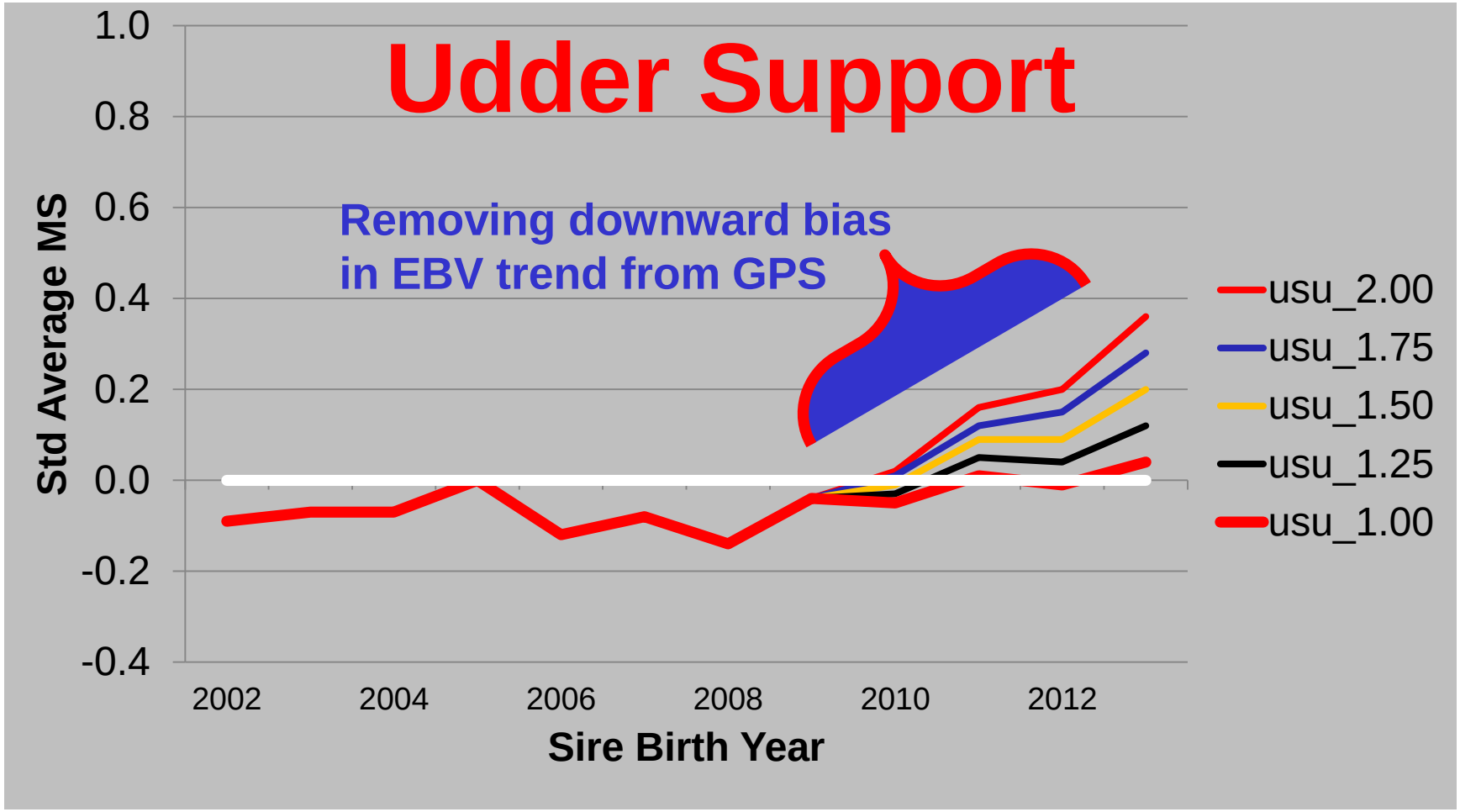
GPS affects on ITB validation Test4 (Trends in average MS)



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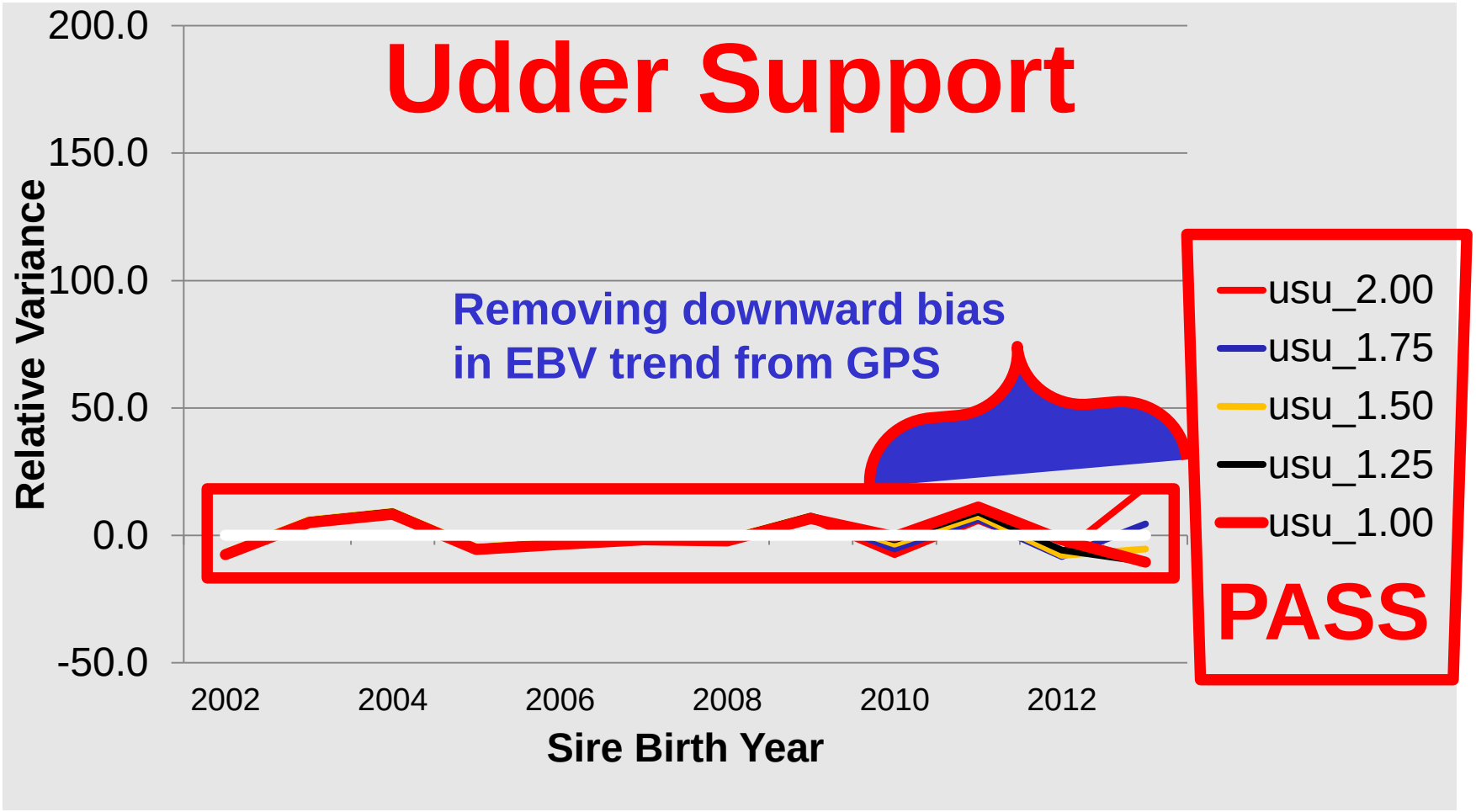
GPS affects on ITB validation Test4 (Trends in variance)



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MS Variance Test
Udder Support

- **If EBV without genomics include GPS bias, then the biased EBV will PASS the variance trend test (ITB test 4)**
- **If EBV are corrected to account for GPS, then the unbiased EBV will PASS the variance trend test (ITB test 4)**
  - Intensity of GPS is **LOW** for **Udder Support**

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Summary

- **Software is flexible, efficient, easy to use**
- **Results of the validation test are NOT RELEVANT to decide inclusion/exclusion of national EBV as input to MACE**
  - GPS-Biased EBV pass the test
  - Unbiased EBV fail the test
- **Software is a very useful tool for "GE systems mining"**
  - Good quality information/data is generated, to allow detailed tracing and post-analysis of within and between family estimates of genetic differences... To improve understanding of GE systems behaviours and for developing improved systems