

Impact of Genomic Pre-selection on MACE

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To study the impact of the GPS bias on MACE, We need to simulate GPS in MACE input

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+ Modify MACE

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STEP 1: Get DRP with no GPS





STEP 2: Simulate GPS effects

Modify the MS terms from Step 1

- Only for one country Cou1
- Only for bulls with birth year >=2005

Their MS terms were raised with a constant (MS+) corresponding to 10% selection intensity and 60% reliability (as in Tyrisevä et al., 2013)

On Cou1 scale: MS+_cou1= SDgen_cou1 * i * rel

On country Cou2 scale: MS+_cou2= b_cou1:cou2 * MS+_cou1

Where $b_cou1:cou2 = r_g_{12} * SD_{(BVcou2)} / SD_{(BVcou1)}$



However: this not what we get If the country does not account for GPS effects



STEP 3: Simulate GPS bias at the national level





SIMULATION: DATA

Protein, 30 countries

Simulated DRP for all countries

- CONTROL: No GPS
- GPS: GPS effects for Cou1
- GPS_biased: GPS bias for Cou1

Simulated National EBV for Cou1

- EBV_0: Before GPS
- EBV_true: GPS effects
- EBV_biased: GPS bias

Current Scenario: GPS effects exist only in Cou1 Cou1 has GPS bias



SIMULATION: RESULTS

MS MEANS

MS+ on COU1 scale=0.69 MS+ on COU2 scale=0.66 r_{G} [COU1, COU2]= 0.89





SIMULATION: RESULTS

DRP

DRP COU1 bulls on COU1 scale





SIMULATION: RESULTS

National EBV cou1



∆G COU1 bulls

GPS bias = Prediction error = EBV_biased -EBV_true



IMPACT ON MACE

Three MACE Evaluations

The three different sets of de-regressed proofs:

Control, GPS, GPS_biased

Were used as input for the current MACE system



MACE RESULTS

ON COU1 SCALE



 ΔG COU1 bulls

Prediction error MACE vs NAT



On average 92% of the GPS bias gets into MACE proofs



CONCLUSION

MACE does not accommodate the GPS bias

MACE needs to be modified