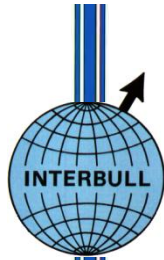


ITC – Tallinn, Estonia

25th August 8.00-12.30

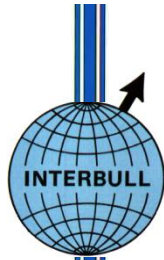
27th August 15.15-17.00



Robust MACE - validation

- Preliminary conclusion
 - No significant differences between MACE and GMACE – no model offers better predictability on all scales
 - Technical challenging
- Next step
 - Investigate if preliminary conclusion is too general – look at local issues.
 - How does each models deal with genomic pre-selection bias?





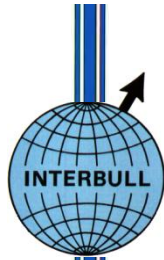
Genomic preselection

- Report from investigation by Luke, Finland of an idea deriving YD from Single Step and use those for calculating EBVs – seem not to work as expected
- Still need for better understanding of discrepancy between genetic trend from Single Step and traditional EBV evaluation



SNP MACE

- We have to be very clear in what we are aiming for and can expect from SNP-MACE
 - MACE will not continue to work
 - SNP-Mace a future way to get foreign phenotypic information included in national "GEBVs"
 - A feasibility project – and there are many unsolved issues



Genomic reliabilities

- Aim - develop standard procedure for Genomic reliabilities
- Done
 - Standard procedure ready
- Next step
 - Validate procedure (countries invited)
 - Finetuning
 - Implementation