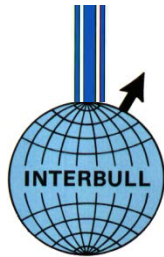


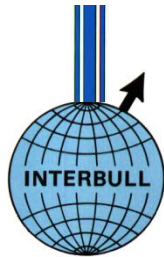
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- ITC activities since Nantes meeting
 - 2 working groups
 - GMACE (Pete Sullivan, Jette Jakobsen, Poul Van Raden, Gerben de Jong and Zengting Liu)
 - Genomic reliabilities (WG for standardization of genomic reliability computations: Bevin Harris (chair), Mario Calus, Martin Lidauer, Vincent Ducroq, Zengting Liu, and Poul Van Raden)
 - ITC recommendation in relation to changed GMACE method



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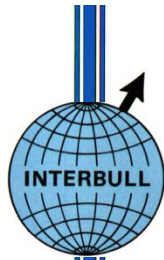
- Post processing of correlations
 - Decided and implemented since august 2013
 - All traits to be post processed – was not the case for conformation traits
 - Non Holstein breeds shall use Holstein correlations as priors for all traits
 - 0.3 as a lower limit for conformation



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Genetic correlations

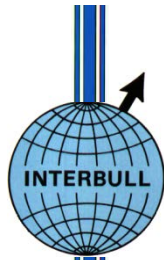
- Overview and general discussion across traits about post processing windows
- Actions – focus on protein:
 - Poor linked countries - apply priors also for Holstein?
 - Strong linked countries low estimated correlations (outside trait window)
- Working group Raphael Mrode, Esa Mantysaari, Tom Lawlor and Hossein Jorjani will come up with proposals



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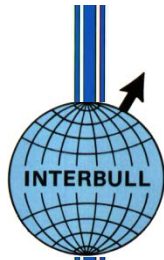
MS trend validation (project MTT-Interbull-NAV)

- IB4 pilot run April 2014
 - 3 high heritability traits use both male and female EBVs
 - 2 low heritability traits stick to sire EBVs
- Results/feed-back/next step
 - Easy program to use more breeds and results
 - 26% country x trait combinations outside current limits – what should be the limit?
 - Working group behind the project will look closer at:
 - The results in relation to HV correction, population size, and distribution of deviations/bias
 - Needs to get results from more breeds and traits to give a full picture - countries might be contacted by IBC



Working group genomic reliability - time line august 2013

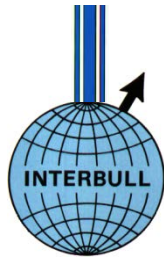
- Create simulated data set
 - Key features: vary reference set size, low and high h^2 , vary clusters of relatedness
- Compare model and validation reliabilities
- Develop "computationally simple" method applicable to a number of genomic models (
- Test method(s) on simulated and real data
- Recommended method(s) reported in Berlin 2014



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Status genomic reliabilities from working group

- Approximations of model based reliabilities very promising (tested by Martin Lidauer and Bevin Harris)
- Model reliabilities versus validation reliabilities - not solved - simulation work has to be done
- The working group has not a final recommendation ready yet in relation to genomic reliabilities

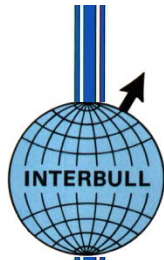


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Genomic reliabilities

- Still a strong need to get international recommendations

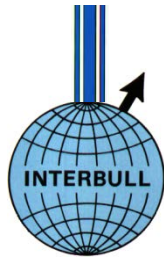
- An extension paper describing state of art will be produced by (Joao Durr, Pete Sullivan+ITC+WG reliabilities)
 - to be used on webpage + magazine etc
 - to give industry a better understanding of genomic reliabilities



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GEBV test review

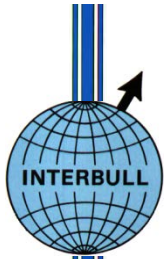
- b_1 (slope expectation $b_1=1$)
 - Current acceptable if $b_1 > 1$
 - ITC recommend to establish a upper threshold for b_1
 - Working group to come up with a final recommendation Paul Van Raden, Esa Mantysaari, and Zengting Liu



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GEBV test review

- b0 or mean
 - Need to focus on top bulls $GEBV=EBV$
 - IBC create basic for further discussions of a possible test in ITC
- Handling GEBV test when number of validation bulls is limited – current criteria has to be more clear - use of domestic bulls only or/and foreign bulls?



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■ GMACE

- Nothing new
- Details about the method used in the test run February 2014

■ Robust MACE

- French presentation at the open meeting
- Further actions to be discussed during and after the open meeting