

Technical challenges and opportunities of genomics in beef cattle

Some experiences from dairy cattle

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First came MACE

*Well, actually: first came regression
equations for each country
combination,
but never mind*

First came MACE

- Based on national (bull) EBVs
- Back-solving to “observations” y

- Using these in a multi-trait (multi-country) analysis

$$(D + A^{-1}k)\hat{a}_{\text{Nat}} = Dy$$

$$(D + A^{-1} \ddot{A} T^{-1})\hat{a}_{\text{Int}} = Dy$$

- No residual correlations, daughters have observations only in one country

Then came GMACE

- Based on national (bull) GEBVs
- Back-solving to “observations” y
- Using these in a multi-trait (multi-country) analysis

$$(D + D_g + A^{-1}k)\hat{g}_{\text{Nat}} = (D + D_g)y_g$$

$$(D + D_g + A^{-1} \ddot{A} T^{-1})\hat{g}_{\text{Int}} = (D + D_g)y_g$$

Consequences

- Residuals might not be uncorrelated
 - Several countries may use the same phenotypic (MACE) and genotypic information
 - Genomic predictions are repeated information of the same genetic merit, not independent measures, esp for major genes (e.g., DGAT1)
- Happens when more than one country submits GEBV for the same bull
 - Adjusted for by using fraction of common genotyped bulls and r_g

Consequences

- Residuals might not be uncorrelated
 - Leads to double-counting when calculating reliability, adjustment is needed.
- Also problems with variance estimates
- Several solutions suggested leading to current application, RobustGMACE
- Still not perfect
- MACE EBVs are used as input
- Not very time consuming analysis

Then came Intergenomics...

- Sharing of genotypes across several countries for Brown Swiss,
- Establish an international database of genotypes for the BSW populations at Interbull Centre, > 5000 bulls in ref pop
- Develop methodology to estimate GEBVs for traits on each country scale using a common ref pop
- Uses MACE EBVs

...and Interbeef

- Using real phenotypes to get EBVs
- Multiple-trait(country) animal model
- Phenotypes uploaded to IDEEA database

Interbeef milestones

2001 EUBEEVAL
FRA - IRL - GBR

2005 Variance components /
pilot ebvs
FRA - IRL - GBR
2breed
1 module

2008 Interbeef / IDEA

2014 Official EBVs
10 countries
2 breeds
4 modules

IDEA database

- Common Interbull & Interbeef
- International tag (AID)
 - breed||country||sex||tag
- Provide software for user
 - CheckPedig & CheckLinks
- User upload/query
- Statistics on uploaded files
 - Validated/duplicates/conflicts/corrected information



Main files

- File 601 = pedigree
 - File 602 = performance file
 - File 603 = parameter file
 - File 604 = ET file
-
- All files have a defined format
 - Using unique international tag
-
- Strict validation process on Pedigree (common to dairy) and performance

Genetic evaluations

- Multitrait across country model using raw phenotypes
- Run at Interbull center
 - Using MiX99
 - 2 x year (May – Sept) => 3 x year (Jan – June – Sept)
- EBVs and reliabilities in country's own scale
 - With few summary stats
 - According to Interbeef publication rules

Interbeef in numbers

	CHAROLAIS	LIMOUSINE
Pedigree size	4,960,799	2,972,065
...of which verified	4,947,304	2,963,985
...of which unverified	7,859	4,600
...of which marked as invalid	5,636	3,480
Number of ET animals	2,607	7,989
Number of International EBV	3,965,5328	2,966,9910
...of which publishable	407,158	128,1760
Solutions for fixed effects	254,569	174,936
Solutions for random effects	2,592	5,615

Interbeef in summary

- Scientific community
 - Technical group
 - Scientific advisory group
- Steering committee
 - Working group
- Interbeef = new service for breeders
 - Based on collaboration between countries

Current situation dairy

- Genomic evaluations have been based on genotyping progeny-tested bulls with very high reliability
 - “phenotype” with very high h^2

Accuracies for GEBVs

- Accuracies of GEBVs based on sires with many daughters
 - High “heritability” of both production and functional traits, 0.95 and 0.75 respectively
 - “Phenotypes” are daughter averages
 - Accuracy depends mainly on number of bulls, N_p

$$r_{g\hat{g}}^2 = \frac{N_p h^2}{N_p h^2 + M_e} q^2$$

Daetwyler, 2009 thesis

where $M_e = 2N_e L / \ln(4N_e L)$

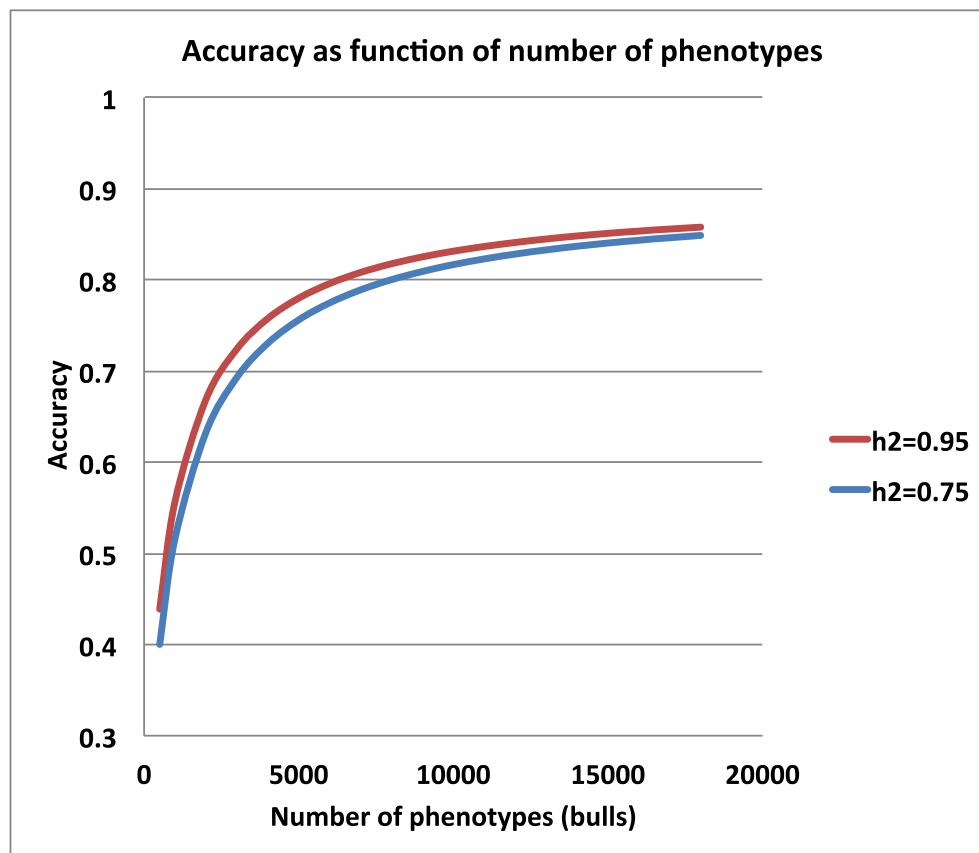
Goddard, 2008

Effective number of chromosome segments

Dublin 24-26 Nov 2014

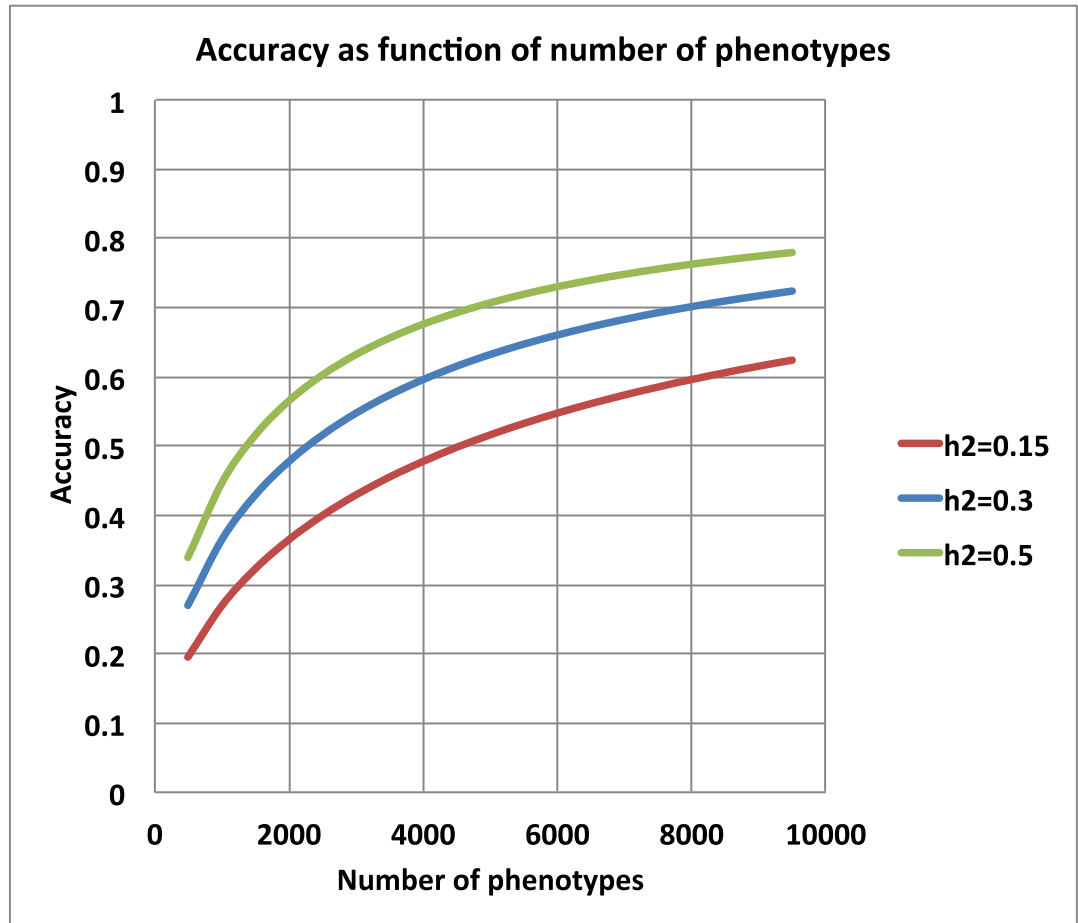
Accuracies for GEBVs

- We are running out of bulls and new progeny-tested bulls are not introduced



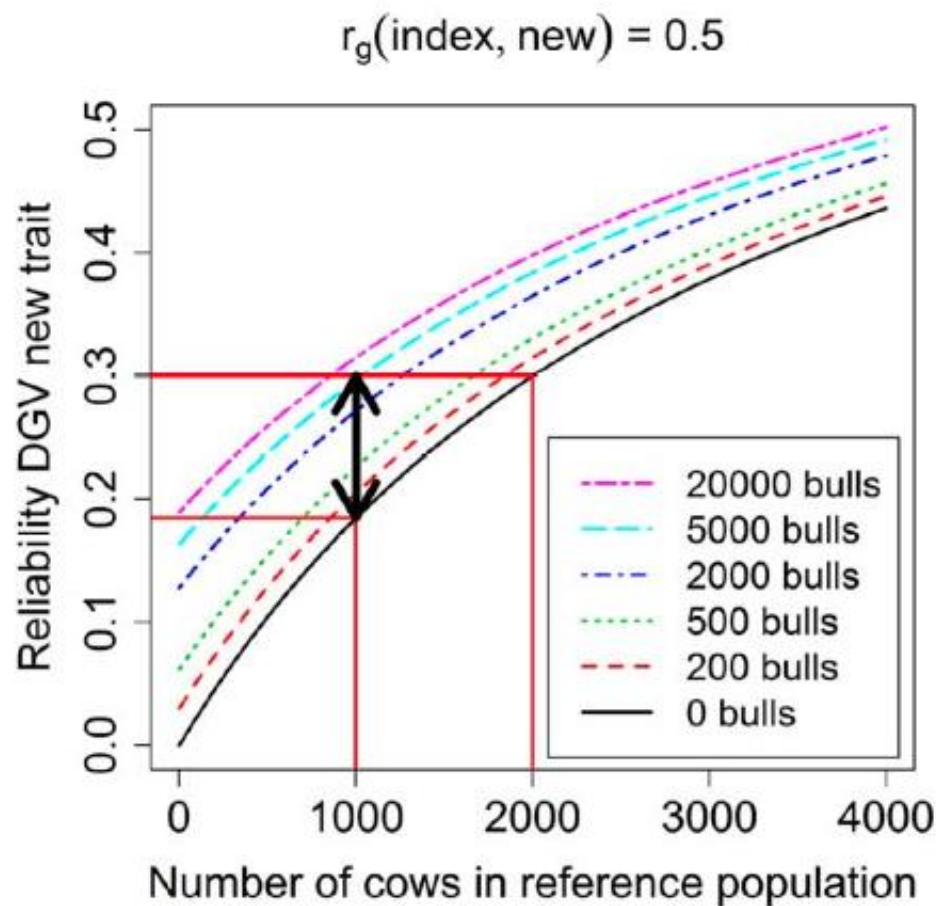
Accuracies for GEBVs

- We need to genotype cows, but lower h^2
- Need many cows
- Incentive for genotyping cows: w/in herd selection



Measuring and genotyping cows

- *Need to combine traits measured in cow populations with traits measured in bull reference population*
- *(Calus et al., 2011)*



Future?

- Using real phenotypes and sharing genotypes to get GEBVs
- Using single-step genomic BLUP
- Using information from both genotyped and non-genotyped animals

$$\begin{bmatrix} \hat{e} \\ \hat{u} \\ \hat{e} \end{bmatrix}' \begin{bmatrix} X'X & X'Z \\ Z'Z + aH^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} \hat{e} \\ \hat{u} \\ \hat{e} \end{bmatrix}' \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ \hat{e} & G^{-1} - A_{22}^{-1} \\ \hat{e} & 0 \end{bmatrix}$$



VALUE PROPOSITION

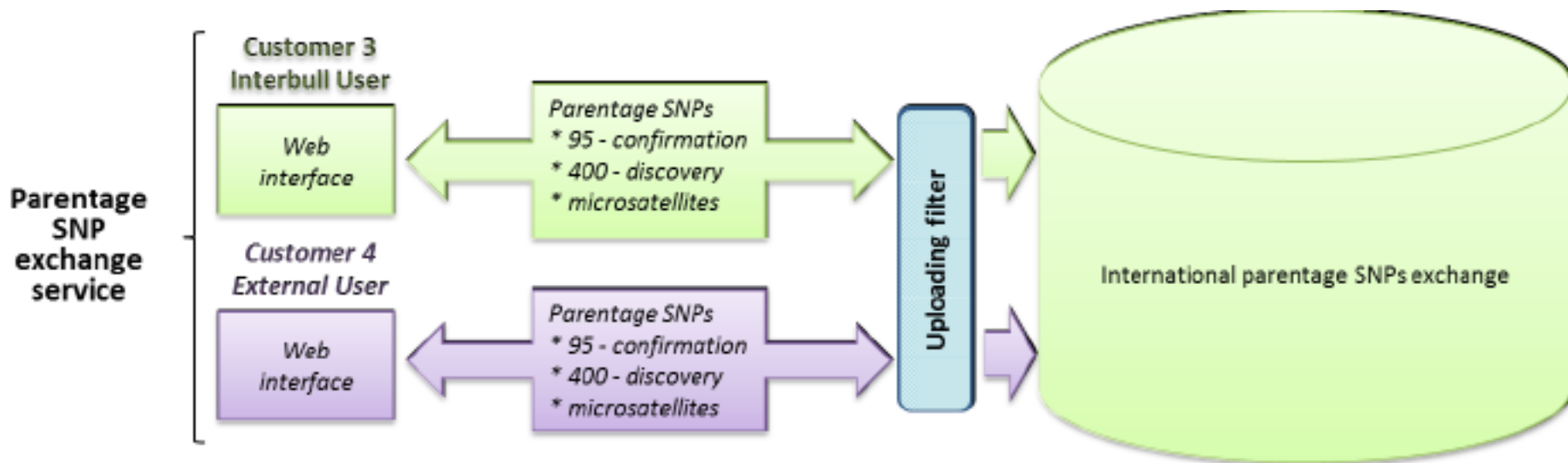


- Establish the **INFRASTRUCTURE** necessary for international cooperation based on **SNP** data
- Optimize customer investments in genotyping by **AVOIDING DUPLICATION**
- Establish **STANDARD PROTOCOLS FOR GENOMIC DATA EXCHANGE**
- Become the international source of **BOVINE PARENTAGE SNPS**
- Facilitate **MULTILATERAL SNP DATA EXCHANGE** by establishing a common repository and customer driven access rules
- (Provide affordable **GENOMIC DATA STORAGE** for small populations)



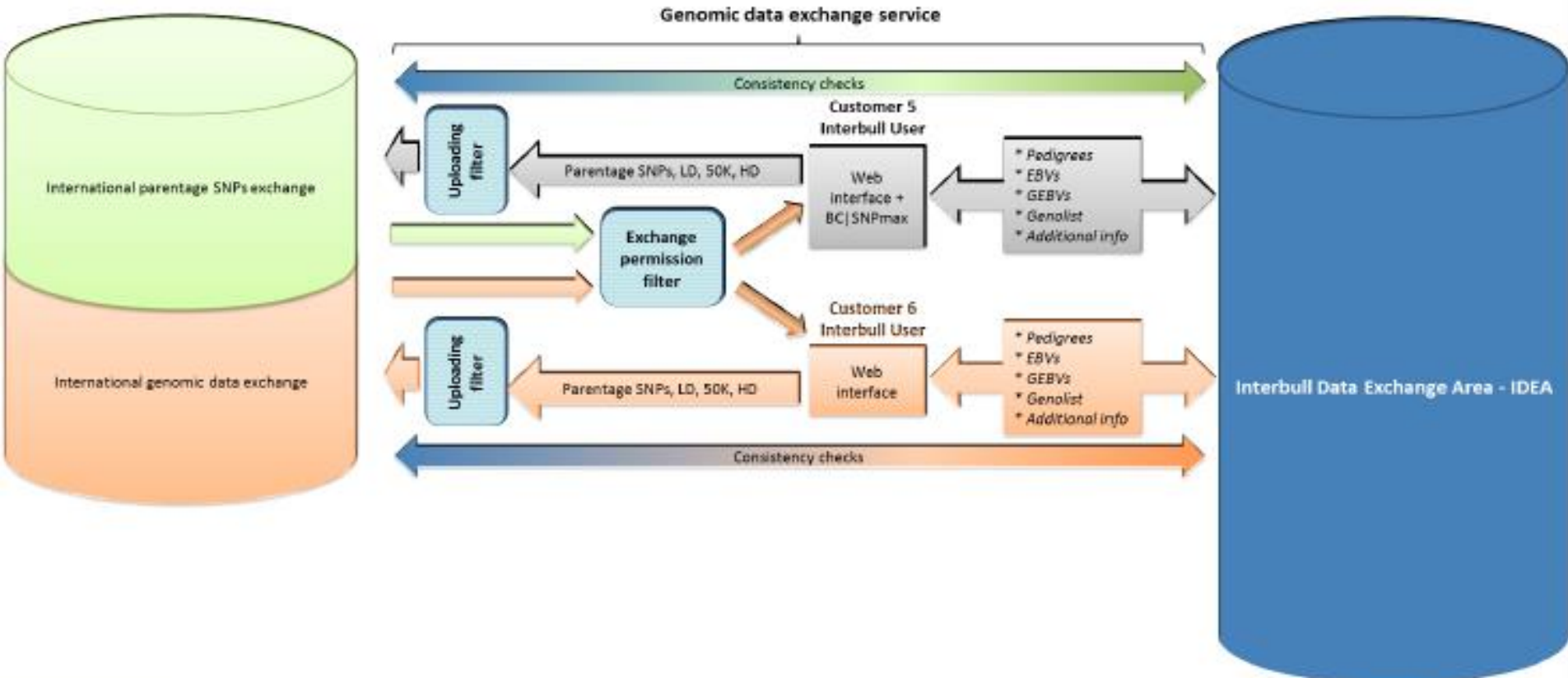
Future?

- First step of GenoEx is Parentage SNP exchange



Future?

- Could be extended to genomic data exchange



Future?

- Could be extended to genomic data exchange and allowing exclusive areas for certain customers (e.g., small countries)

