

#### INCLUDING GENETIC GROUPS AS FIXED OR RANDOM EFFECTS IN LARGE SCALE SINGLE-STEP GENOMIC PREDICTIONS

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Avler for bedre liv



#### Agenda

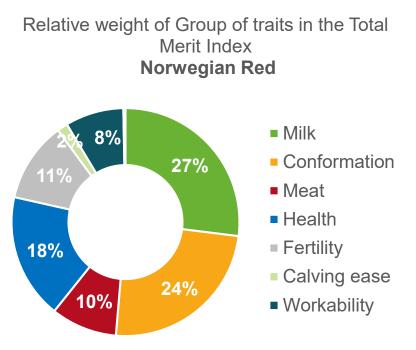
Overview of breeding scheme of Norwegian Red

- Breeding goal
- Implementation of genomic selection
- ssGBLUP based breeding programme
  - Challenges and biases
  - Solutions
- Genetic groups as random effect reduces some biases



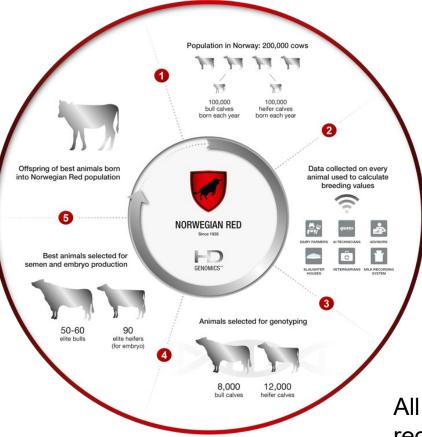
## Norwegian Red

- Breed Established in 1935 by Geno (farmer owned cooperative)
- Dual purpose breed (milk and meat)
- From 70's health and fertility in breeding goal
  - > 40 traits included
- 2012 genomic selection (SNP-BLUP) of test bulls
- 2015 ssGBLUP, switched from progeny testing to GS bulls





## Norwegian Red – breeding programme



130000 genotypes=>ssGBLUP

<u>30.000 + new genotypes/year</u> 8.000 bull calves 6.000 heifer calves 16.000 + females (producer init.)



All elite bulls and embryo heifers are regenotyped on 777K (1823 bulls)



#### Challenges with biases

- Inflation (young genotyped animals overpredicted)
  - Selection of SNPs for the H<sup>-1</sup> matrix is crucial
  - Method for building H<sup>-1</sup> (setting allele frequencies equal to 0.5)
- Level-bias (Nordbø et al 2019. EBV Increase, after genotyping)
  - Strict filtering of SNPs within and across SNPchips
  - Not adding anything to diag(G) before inverting
- Genetic groups
  - Genotyped animals with unknown ancestors are over-predicted
  - Animals with genotyped offspring and unknown ancestors are overpredicted



## 3-trait repeatability animal model for milk

- 3 traits (milk, %protein, %fat) ssGBLUP with genetic groups using QP transformation on A<sup>-1</sup> (approximation)
- 124493 genotyped animals
- 8.1 mill. 305d records (1st-5th lactation) on 3.8 mill. animals
- 4.8 mill animals in pedigree, 118 genetic groups
- Mix99

#### Gen.corr. and heritabilities

Milk 0	.42		
Protein% -0	.44	0.61	
Fat% -0	.36	0.62	0.36

#### H<sup>-1</sup> :

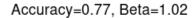
- Imputation: to 777k: 122k SNPs
- Allele frequency: 0.5
- Scaling: G=ZZ'/k -> mean(diag(G))=1
- Weight A-matrix: 10%
- hginv\_lapack\_para

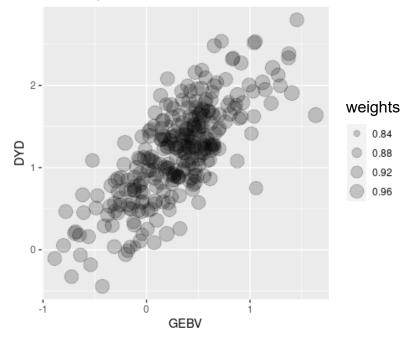


## Validation: Interbulls GEBV-test

- Masking 5 year of data.
- Prediction of GEBVs on reduced data set
- Compare with DYDs
- Weighted linear regression

	Milk		Fat	%	Protein%	
	R <sup>2</sup>	β	R <sup>2</sup>	β	R <sup>2</sup>	β
org	0.573	1.02	0.63	0.96	0.699	1.11





Level-bias ≈ 0 (average change in EBV when being genotyped)

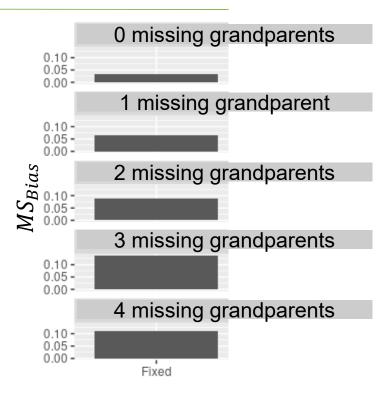


## Validation: Mendelian sampling?

• Compare EBVs with parentage average for groups of animals.

$$MS_{Bias} = Mean\left(\frac{EBV - 0.5(EBV_p + EBV_m)}{\sigma_g}\right)$$

- Genotyped animals or animals
  with genotyped offspring
- Method for fitting genetic groups
  - Fixed effects
  - Random effect

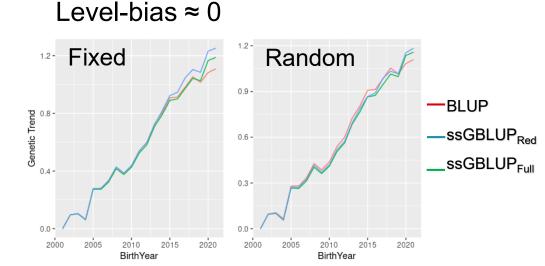


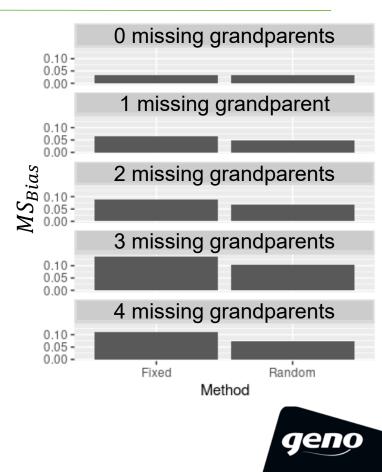


#### Genetic groups as random effect ( $\sigma_{G}^{2}$ ) vs. fixed

#### Interbulls GEBV-test:

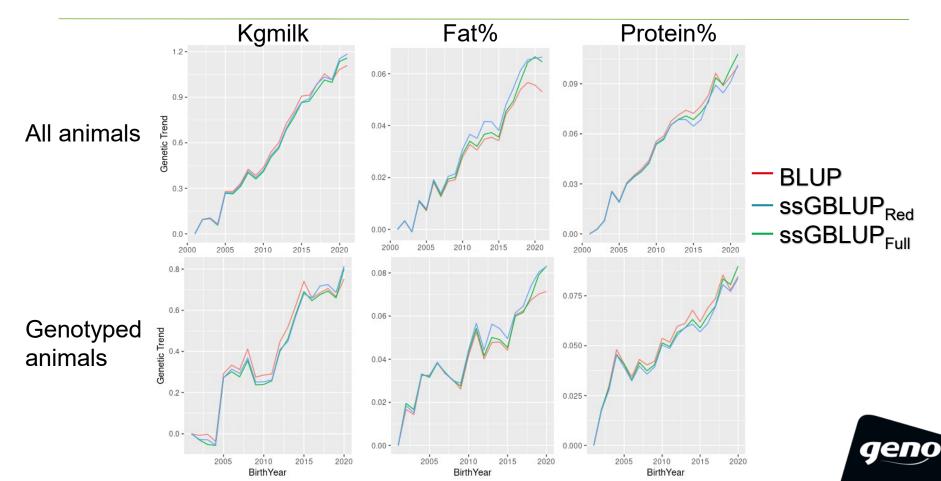
	Milk		Fat	%	Protein%	
	R <sup>2</sup>	β	R <sup>2</sup>	β	R <sup>2</sup>	β
Fixed	0.573	1.02	0.63	0.96	0.699	1.11
Random	0.574	1.02	0.63	0.96	0.700	1.11





### **Genetic Trends**

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#### Acknowledgements

- We want to thank for funding this research through the project 309611, «Large scale single step genomic selection in practice»
- The Research Council of Norway
- NMBU, LUKE, Norsvin SA and Geno SA



# QUESTIONS?