

ERFARINGER MED
SINGLE- STEP
GENOMISK SELEKSJON

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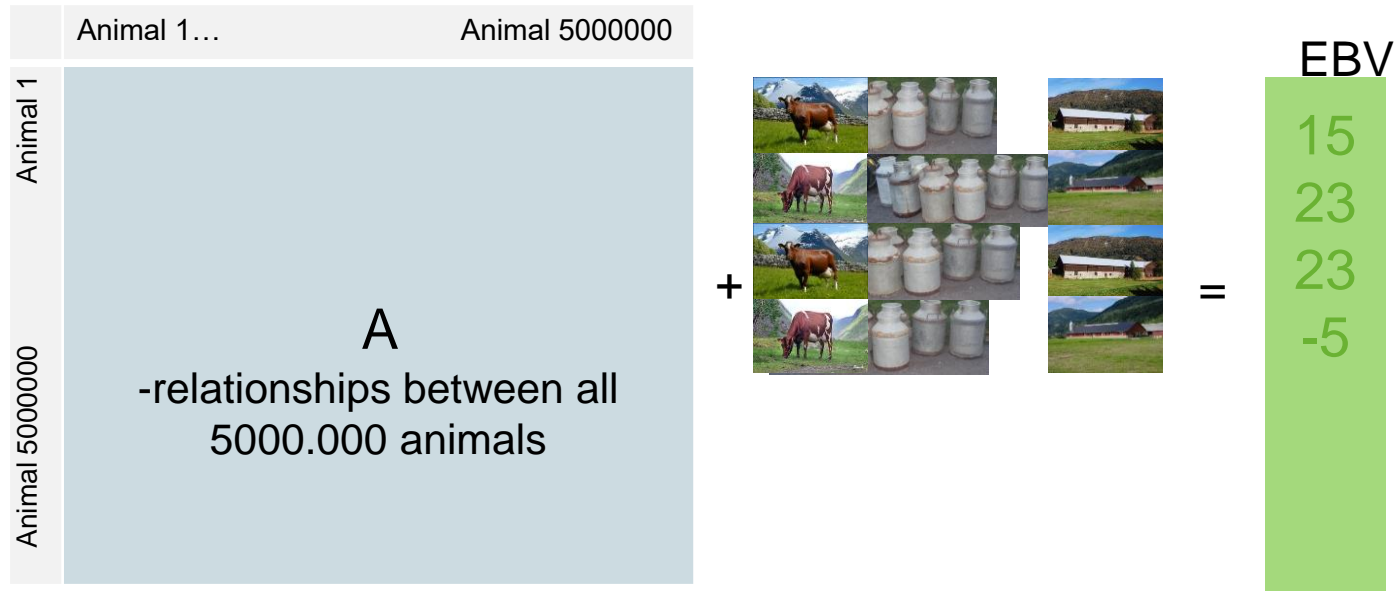
NÖK-konferansen, Rättvik, 23-25. juli, 2018

Milestones in implementation of GS in Norwegian Red

- ▶ 2012/2013
 - Implementation of two step GS for preselection of young bulls for progeny testing
- ▶ February 2016
 - Implementation of single step GBLUP
 - GS-bulls => Elite bulls
- ▶ January 2017
 - Implementation of BULLIT - breeding values estimated every time we receive genotypes (2-3 weeks)
 - Heifers incl. young new born calves and cows - updated EBVs every run
- ▶ June 2017
 - Farmer initiated genotyping
 - 18.000 females first year
- ▶ June 2018
 - Genetic groups ssGBLUP
 - New genomic relationship matrix in ssGBLUP, (imputed to 109.000 SNPs)

Traditional estimation of breeding values (BLUP)

- Utilises pedigree based relationship- phenotypes and other relevant information



Two-Step genomic selection

Step 1. Utilises pedigree-info and phenotypes as previous slide (BLUP)

Step 2. Includes EBV* (deregressed BV) from step 1 and all genomic information

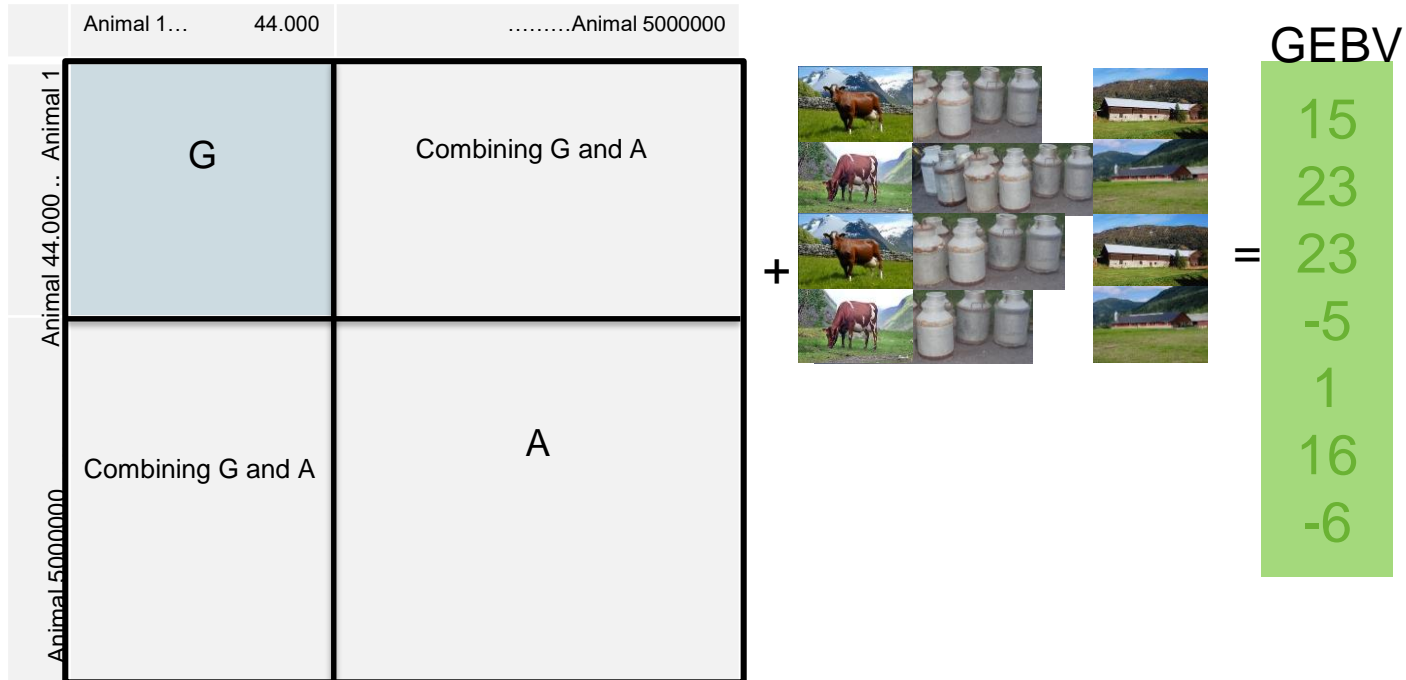
	Animal 1...	Animal N
Animal1	G -Genomic relationships between genotyped animals	
Animal N ...		
Animal N ...		
Animal N ...		

+ EBV* = GEBV

15	15
23	23
23	23
-5	-5
	1
	16
	-6

Singel Step Genomic Selection

- All pedigree-info, all genotypes and all phenotypes are utilised in one simultaneous analysis



Why did Geno choose the single step method?

- ▶ Two step:
 - Larger populations => CPU may be challenging with single step
 - Advantage: Can handle very large number of genotyped animals
 - Disadvantage: Selection bias may be a problem

- ▶ Single step:
 - Smaller populations => CPU is not a problem
 - Advantage: Avoids selection bias, utilise all genotyped animals, higher accuracy
 - Disadvantage: Struggling with number of genotyped animals beyond 100.000 + other bias issues (imputation+harmonizing A and G)

- ▶ Pragmatic approach
 - Choose the method that performs best – cross validation

 - **For the Norwegian Red population Single Step performed best** (International studies support this)

Cross Validation - Which method for EBV-calculations predicts the future performance of the cows best?

► Cow validation

- Mask phenotypes of a set of cows
- Calculate EBVs
- Correlate the EBVs with the masked phenotypes

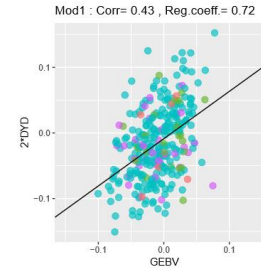
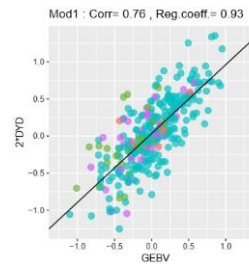
► Bull validation

- Mask phenotypes of daughters and sisters of a set of proven bulls (simulate the state of a young bull calf)
- Calculate EBVs of the bulls
- Correlate the EBVs with the phenotypic performance of the daughters (Daughter Yield Deviations)

► Parameters of interest

- Correlation - Accuracy
- Slope - Bias (inflation)
- Bias on mendelian sampling:

$$Mean(EBV) = \frac{SireEBV + DamEBV}{2}$$



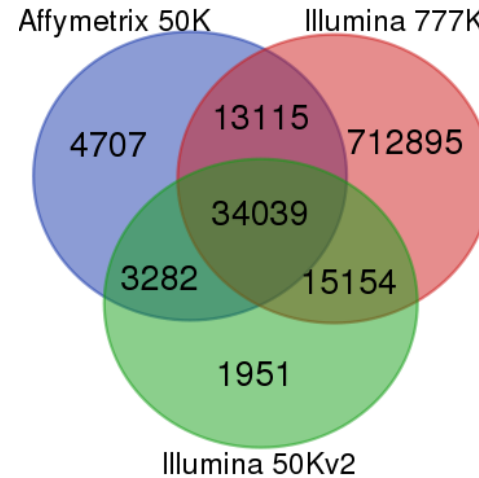
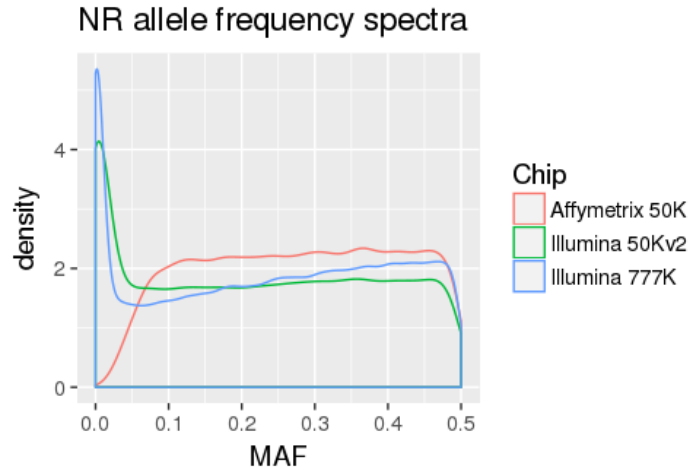
Genotypes – individuals

SNP chip	Genotyped males	Genotyped females	Time
Affymetrix 25K	2.316		->2009
Illumina 50K v1	1.242		2009-2010
Illumina 50K v2	4.337	451	2010-2015
Custom Affy 50K	9.171	26.469	2014->
Illumina 777K	2.018		sporadic
Total	17.686	26.920	SUM=44.606

Some bulls are genotyped on more than one chip, $\Sigma > 17.686$

- Genotyped most AI-sires from 1970 onwards

Genotypes – chips



NRF-customized Affymetrix chip (2014)

- Removed low-MAF and low-quality SNPs from Illumina chips
- Good overlap with Illumina 50K & 777K for imputation
- Selected SNPs for important traits (polled, caseins, QTLs from GWAS)

Effect of including cow genotypes in the ssGBLUP

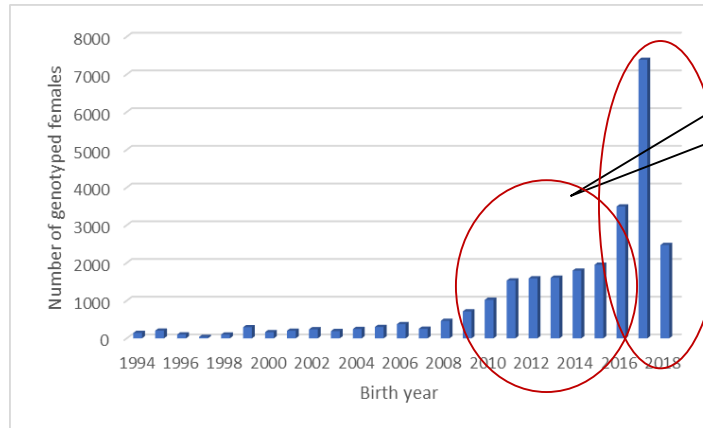
Calculations from winter 2017

- 8000 genotyped cows included

	Accuracy, no genotyped cows	Accuracy, 8000 genotyped cows	Increased accuracy, percentage
No of ins 1st to 4th lact	0.71	0.73	3.2 %
CFI, 1st to 4 th lact	0.48	0.50	3.7 %
Milk yield, kg prot 1st to 4th lact	0.72	0.75	4.1 %

Status July 2018

- Total of 26.606 genotyped females included



Ca 8000 new genotyped cows with phenotypes
=> Increased accuracy since 2017

New genotyped cows with phenotypes
=> Increase accuracy next years

Genotyping strategy

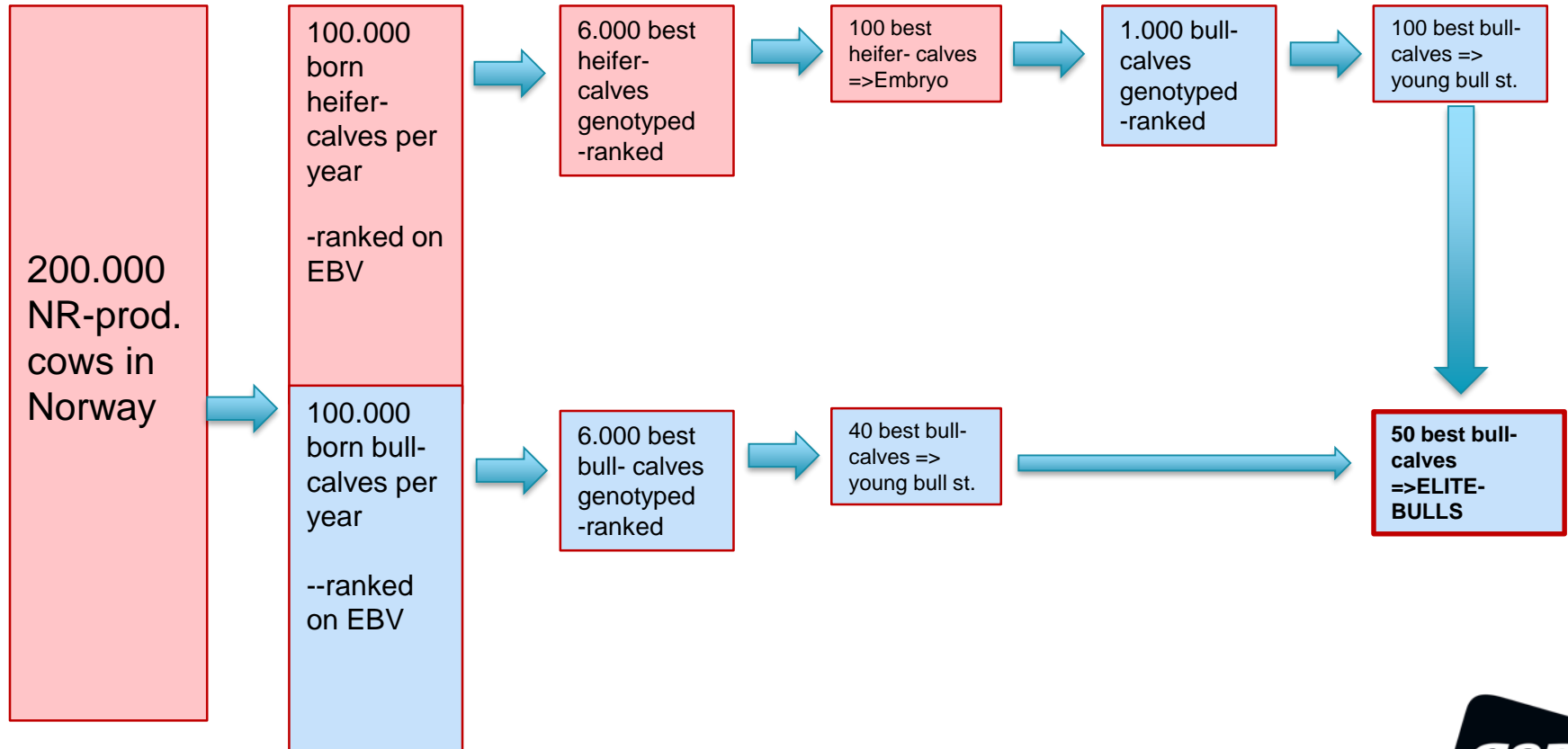
Norwegian Red Customised Affy 50K Chip:

Genotyping strategy for Norwegian Red	
Bull calves	6 000
Heifer calves	6 000
Farmer initiated females	18 000
New genotypes per year	30 000

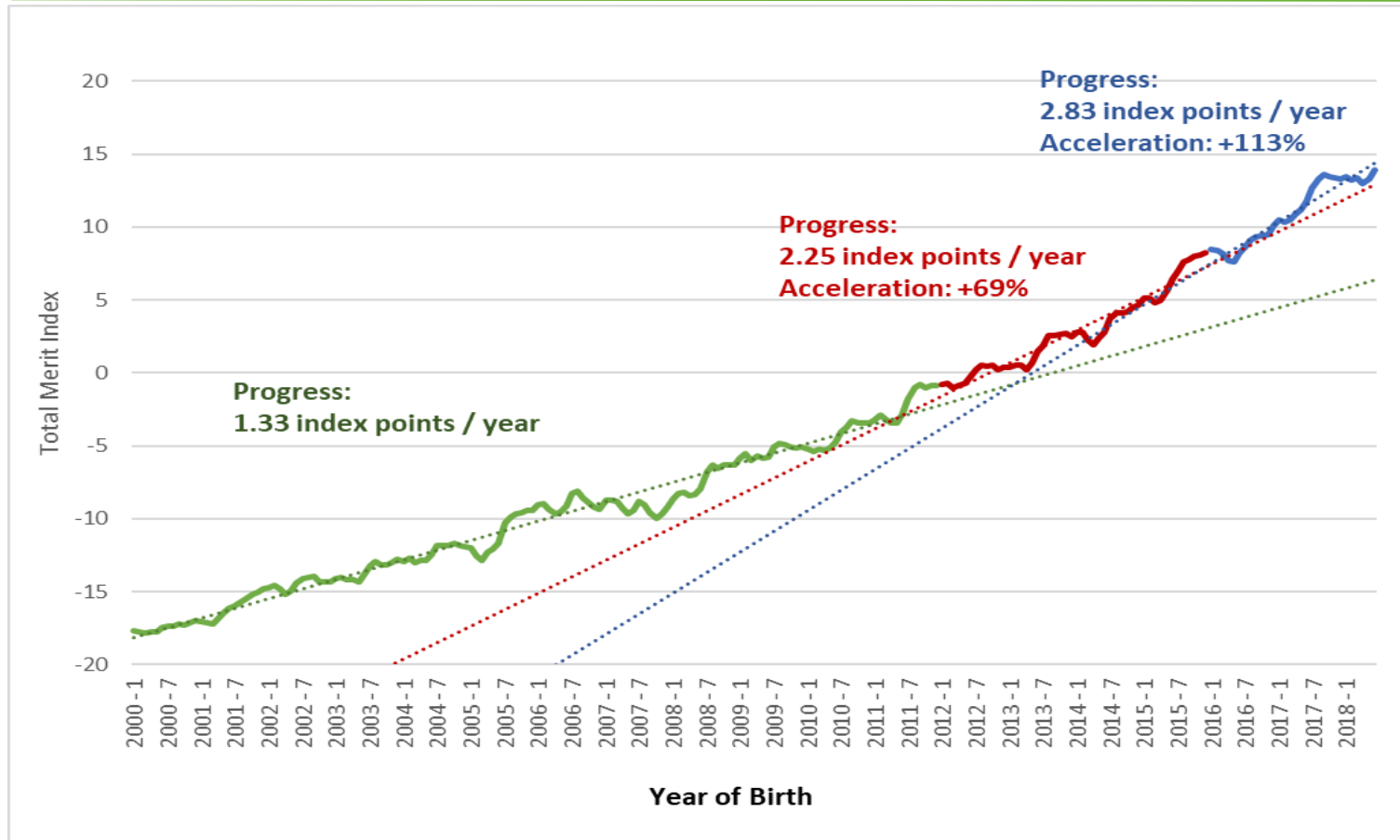
Illumina 777K Chip:

Regenotype all new elite bulls + embryo heifers continuously as they enter AI-station

Future selection strategy



Genetic trend



Conclusion

- ▶ SSGBLUP gives higher accuracy for **Norwegian Red**
- ▶ SNP clean-up and imputation has removed most bias issues
- ▶ Genotyping of cows increases accuracy on young bulls in addition to dams
- ▶ Geneic gain is accelerating and is expected to do so in the next generations
- ▶ Geno will continue improving
 - BLUP models
 - Utilisation of genomic information
 - Selection strategies
 - **Genetic gain**



Thank you!

