

Imputation and pedigree verification

Kevin Byskov, Line Hjortø and Anders Fogh



Se "European Agricultural Fund for Rural Development" (EAFRD)

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mælkeafgiftsfonden

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Females tested in the LD-project (spring 2013)

- 7571 animals genotyped
 - 22 deleted due to low callrate

Country	JER	RDC	Total
Denmark	3835	532	4367
Sweden	78	1233	1311
Finland	-	1871	1871
Total	3913	3636	7549

How many genotypes are accepted?

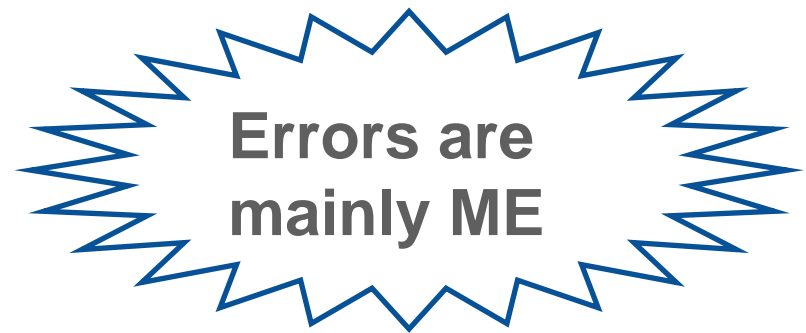
- **% approved, routine: 96-97 %**

Percent approved per breed, LD-project

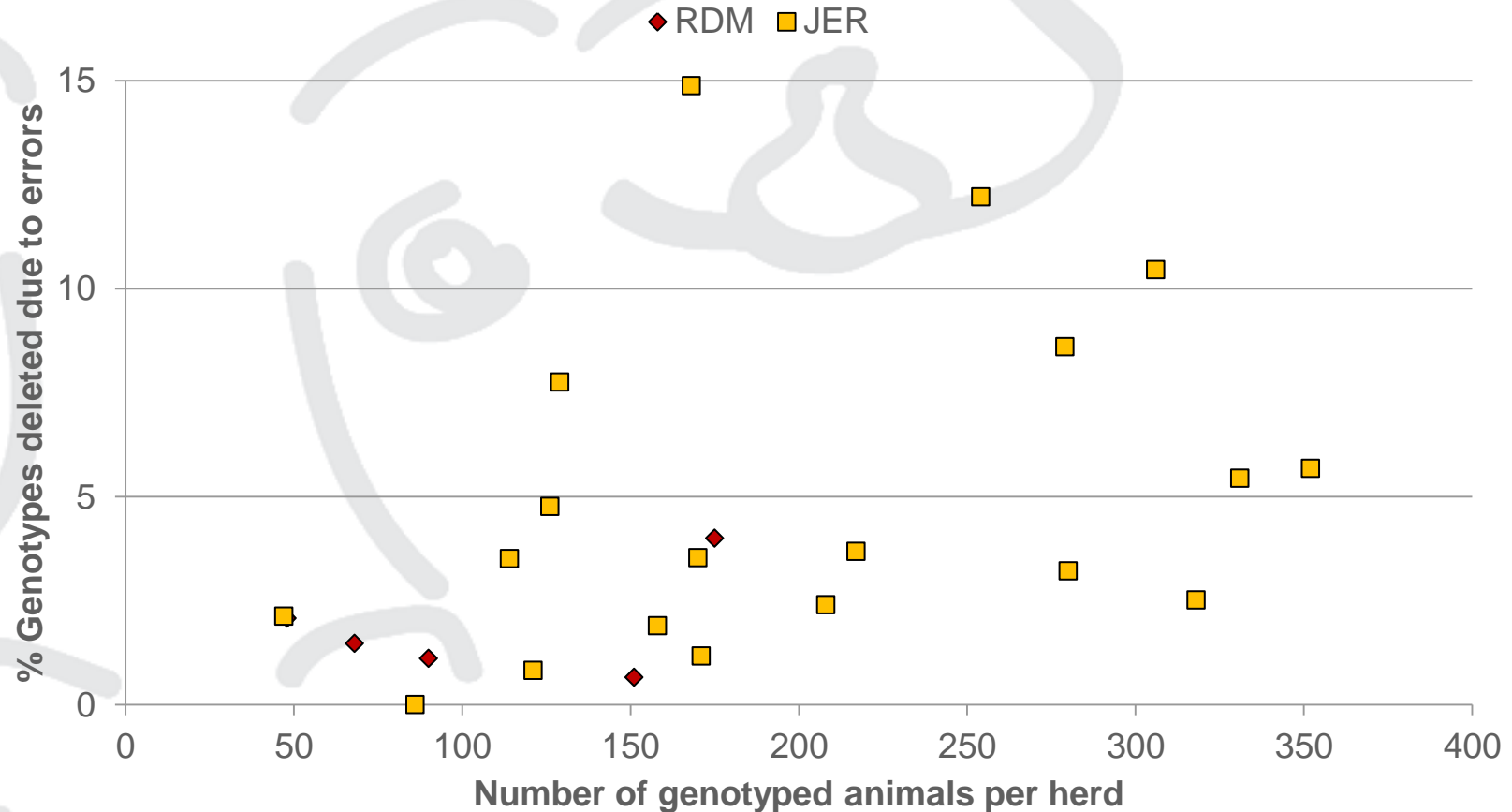
- JER: 94.5 %
- RDC: 97.9 %

Percent approved per country, LD-project

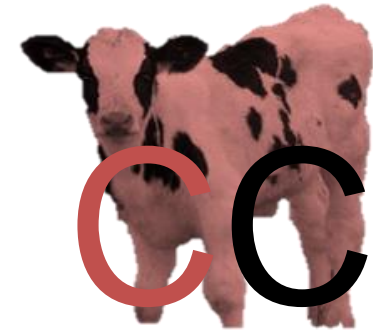
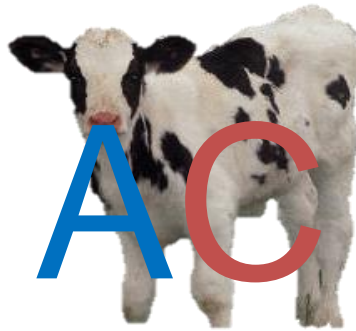
- DNK: 94.9 %
- SWE: 97.6 %
- FIN: 98.0 %



% deleted genotypes – Danish herds



Principle behind Mendel Error Check



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Mendel Error Check - Failed



- Rejected pedigree or sire is unknown / not genotyped
 - search for potential parents
- Technique similar as for ME-Check
 - Counting opposite homozygous loci
- Result is returned to VG or Växa
 - When errors are corrected genotype can be included again – farmers responsibility

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Imputation

- When pedigree, sex, and ID is verified the genotype can be imputed
- HOL - **FImpute**
 - **Quick & accurate in homogeneous populations**
- RDC & JER - **Beagle**
 - **Slow** but **accurate and robust**

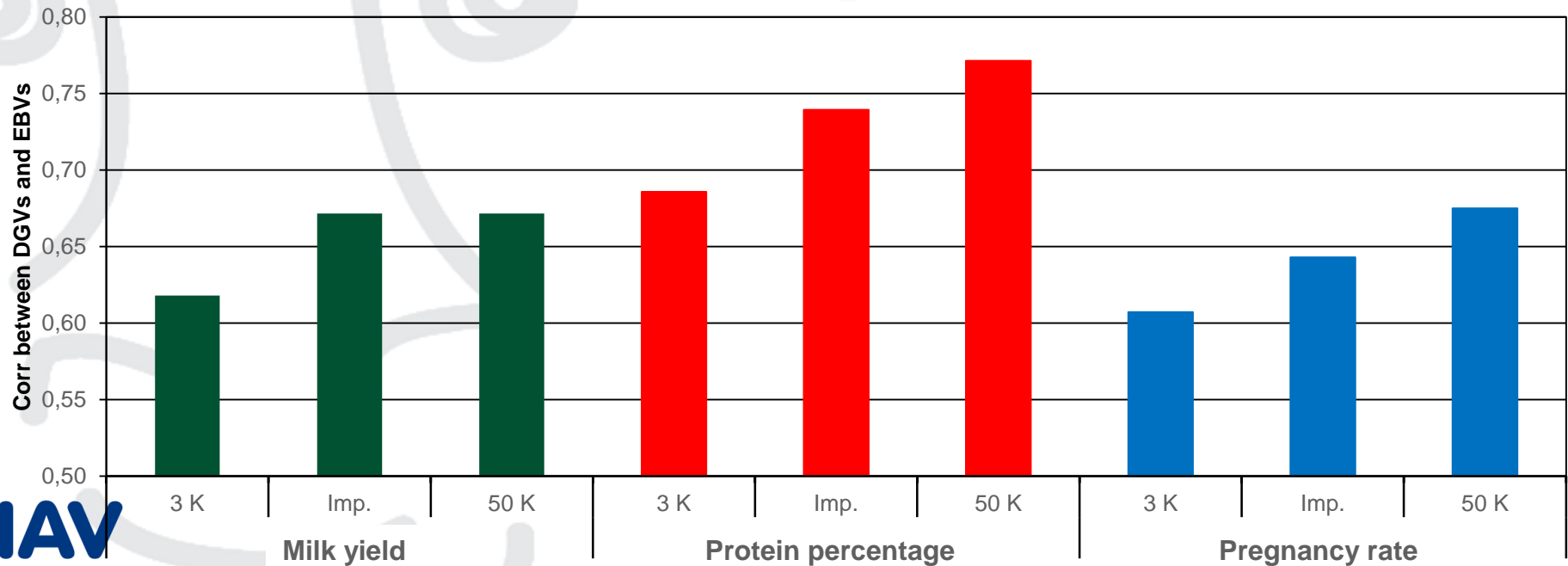
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Why do we impute?

- Accuracy of GEBV
 - 54K > imputed LD > LD



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American Jersey; modified after Weigel et al., 2010

Why do we impute?

- Cows (in referencegroup - RDC and Jersey) and heifers
 - **Low density chip**
- Illumina Bovine 54K chip
 - Version 1 and 2
- Eurogenomics (Holstein) og GENO (RDC)
 - NLD (HOL) and Geno (RDC) has previously used another chip

NAV Missing calls



Basics

- **SNP = Single Nucleotide Polymorphism**
- **At animal level**

2	2	2	2	2	1	2	0	0	2	1	1	2	2	1	1
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- **Homozygote for one allele = 0**
- **Heterozygote = 1**
- **Homozygote for the other allele = 2**

- **At chromosome level**

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	0	1

- **Variant A = 0**
- **Variant B = 1**

SNP Reference animals genotyped with 54K

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	0	1
1	1	1	1	1	0	1	0	0	1	0	0	0	1	0	1
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0
0	0	0	0	1	1	1	0	0	1	1	1	1	1	1	0
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0

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Modified after Marchini & Howie, 2010

SNP candidate animals genotyped with LD

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	0	1
1	1	1	1	1	0	1	0	0	1	0	0	0	1	0	1
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0
0	0	0	0	1	1	1	0	0	1	1	1	1	1	1	0
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0

1	?	?	?	1	?	1	?	0	1	0	?	?	1	?	0
1	?	?	?	1	?	1	?	0	1	1	?	?	1	?	0

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Utilize information from reference

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	0	1
1	1	1	1	1	0	1	0	0	1	0	0	0	1	0	1
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0
0	0	0	0	1	1	1	0	0	1	1	1	1	1	1	0
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0

1	?	?	?	1	?	1	?	0	1	0	?	?	1	?	0
1	?	?	?	1	?	1	?	0	1	1	?	?	1	?	0

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Impute missing values

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	0	1
1	1	1	1	1	0	1	0	0	1	0	0	0	1	0	1
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0
0	0	0	0	1	1	1	0	0	1	1	1	1	1	1	0
1	1	1	0	0	1	0	0	1	1	1	0	1	1	1	0

1	1	1	1	1	1	1	0	0	1	0	0	1	1	1	0
1	1	1	1	1	0	1	0	0	1	1	1	1	1	1	0

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Imputation finished

- **Genotypes checked for errors and imputed are then used as input for genomic predictions**

Questions?

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