

Genomic information in routine evaluation – Genomic prediction, blending and publication criteria NAV

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Bulls with known EBV and markers (SNPs) create "DNA-dictionary"



Quality of the dictionary depends on the size of the reference population

SNPs



Deregressed proofs (DRP)

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Abbreviations

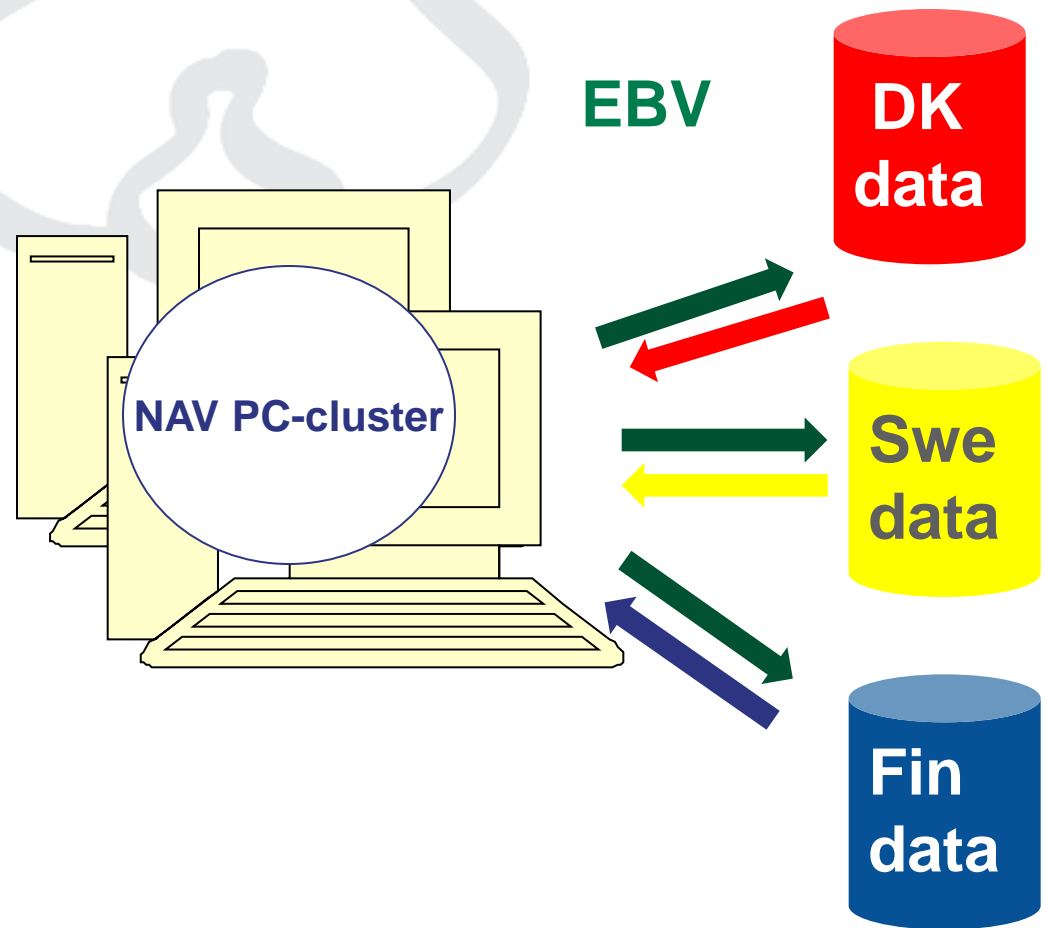
- **DGV (SNP effects)**
 - Direct Genomic Value
- **EBV (phenotypic data from farms) – DRP**
 - Estimated breeding value
- **GEBV (SNP effects + phenotypic data)**
 - Genomic Enhanced Breeding value

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Flow from phenotypes to EBV

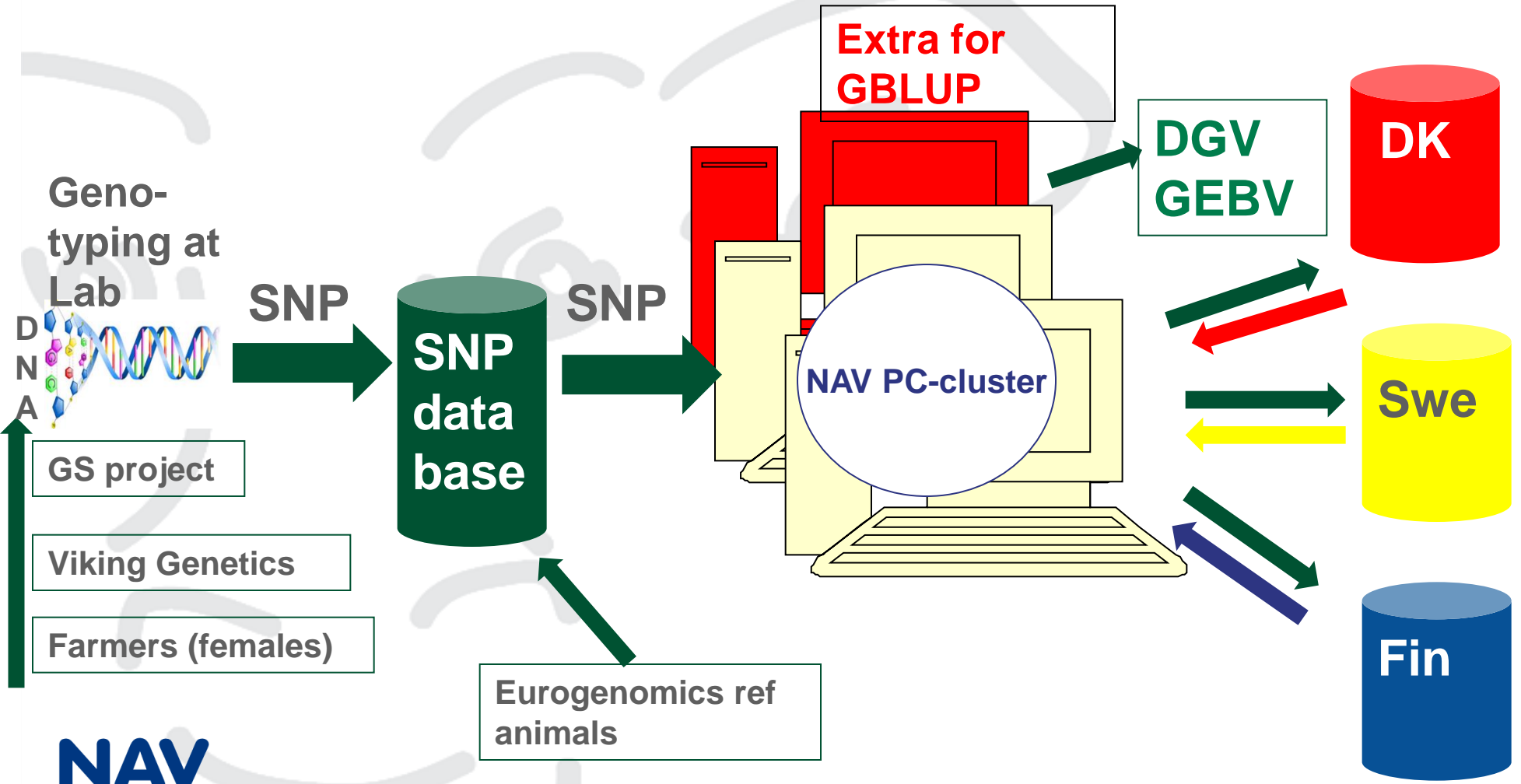


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Flow from DNA+phenotypes to GEBV



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Flow from DNA+phenotypes to GEBV

Requires 3 runs for all traits

1. Traditional EBV estimation
2. Genomic prediction to get DGV
3. Bi-variate blending estimation (EBV&DGV) to get GEBV

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Flow from DNA+phenotypes to GEBV

Requires 2 runs for all traits

1. Traditional EBV estimation
- 2.
- 3.
4. One step combine genomic prediction and blending

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Flow from DNA+phenotypes to GEBV

- DGVs/GEBVs have to be estimated often (wish from VG each month) – (>40 traits for all 3 breeds)
- EBV (traditional evaluations) – 4 times a year

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Flow from DNA+phenotypes to GEBV

- A lot of evaluations require things are streamlined
- We need to develop it stepwise:
It means we will not be able to estimate DGVs 12 times a year from primo 2011 (VG wish)

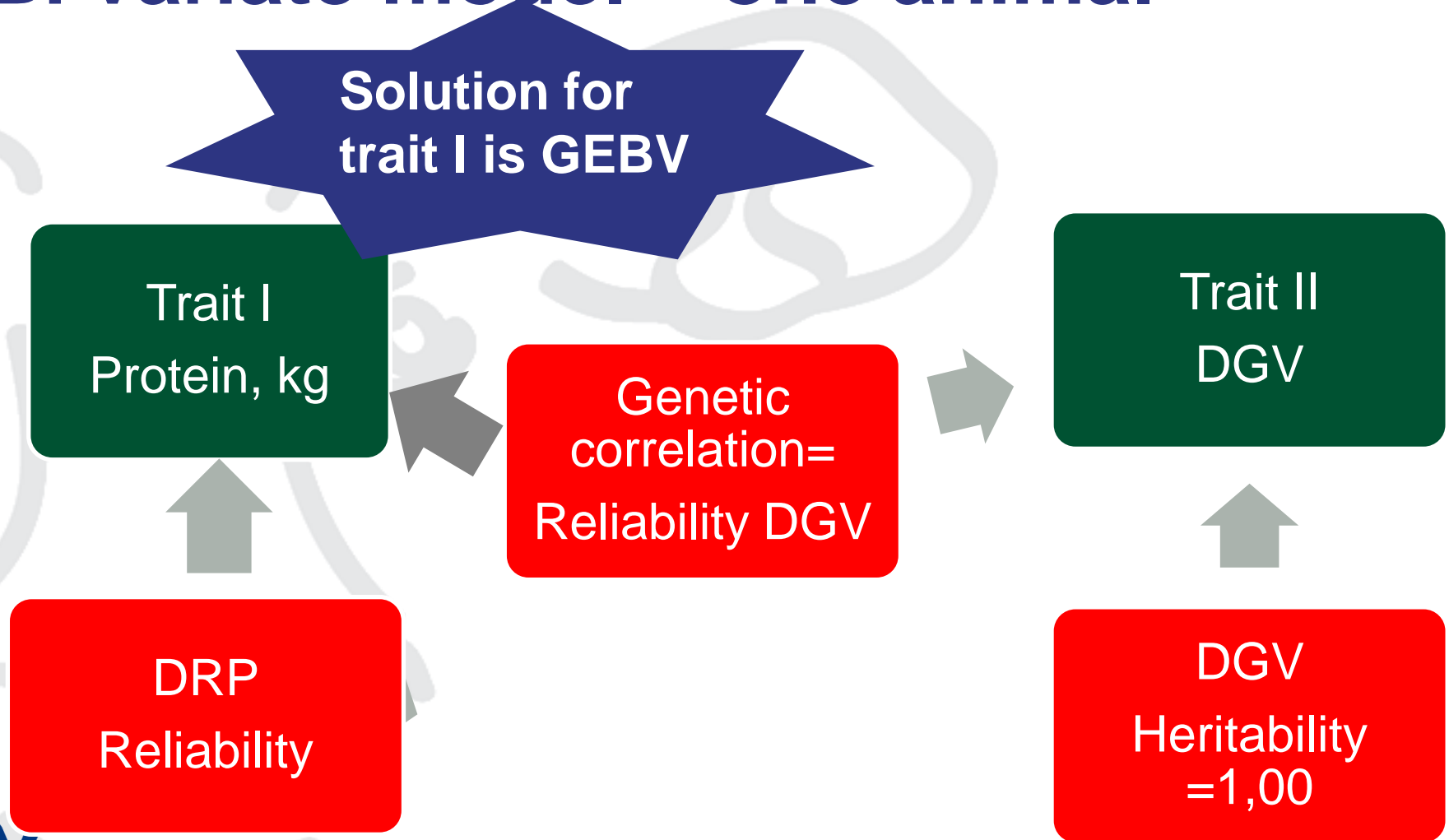
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Eksample protein – BLUP

Bi variate model – one animal



Blending in two steps

1. Early 2011 (May 2011)

- DRP for bulls and DGVs
- All candidates and bulls get GEBVs

2. Later 2011

- DRP for cows and DGVs
- All animals get GEBVs - also female relatives to genotyped animals

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DRP

1. We have a method for calculation of **DRP** for bulls from **EBV** (Strandén & Mäntysaari, 2010)
2. We investigate if the method works for estimation of **DRP** from cows from **EBVs**. (MTT is working on it)

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1. What will happen in practice – **DRP bulls**

- Pedigree information adds very little extra information
- EBVs for bulls with milking daughters will change significantly for functional traits, but also for yield, if reliability is moderate
reliability DGV = reliability EBV

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2. What will happen in practice–

DRP cows

- EBVs for genotyped cows will change significantly – DGV gives a lots of new information – **reliability DGV >> reliability EBV**
- EBVs for cows related to genotyped animals can also be changed a bit.

How to estimate GEBV for combined traits e.g mammary system?

- Blending DGV and EBV for linear udder traits
or
- Blending DGV for udder and EBV for udder

Analyses ongoing!

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Ongoing work – genomic selection

- **NAV do unofficial routine run for all three breeds**
- **Test based on Holstein about blending, combining traits, reference bulls, DRP cows etc.**
- **Two step versus one step (all breeds)**

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Key points - publication rules

- **GEBVs will be published on national data bases after each genomic prediction run (we might need only to update animals genotyped since last prediction to avoid a lot changes in GEBVs due to rounding off)**

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Key points - publication rules

- **Until we get DRP for females the problematic animals to handle is cows with own performance since we are not able combine own records and genomic information for these categories of animals an update on databases are not possible – problematic traits are yield, type and mastitis. National organisation will be responsible for sending the farmers GEBVs for tested cows.**

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Key points - publication rules

Males:

- **Publication of GEBVs for VG AI bulls at 20 month age (after "test" inseminations)**
- **Discarded bull calves not published due to agreements about reference bulls and ongoing GS project. (VG has to make agreement with farmers telling that GEBVs will only be official if the bull is selected)**

Practical implementation

- NAV hope to publish the first official GEBVs early 2011 (**May 2011**), BUT several things need **still** to be tested and clarified before it is possible
- GEBV for Holstein might be published before GEBV for RDC and Jersey

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