

# Nordic genetic evaluation for purebred beef cattle

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# Why go Nordic?

- Increase the accuracy of estimated breeding values
- Enable within breed comparison of cows and bulls across Nordic countries
- Is resource efficient



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# Nordic purebred beef evaluation

## Breeds

- Aberdeen Angus (AAN)
- Beef Simmental (SIM)
- Charolais (CHA)
- Hereford (HER)
- Limousine (LIM)

## Breeding values

- Calving
- Growth and carcass

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# Registrations

- Calving ease and calf survival scores (> 1998)
- Birth, weaning and post-weaning weights and carcass records since the 80's for DNK and SWE and 90's for FIN
- From: Farmers, technicians, test stations (SWE) and slaughterhouses

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# Calving traits

3 traits (12 breeding values)

- Calf survival (up to 24h)
- Calving ease
- Birth weight

2 groups

- First calving
- Later calving



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# Calving traits

## 3 traits (12 breeding values)

- Calf survival (up to 24h)\*
- Calving ease\*
- Birth weight\*

## 2 groups

- First calving
- Later calving

*\*maternal and direct breeding values*



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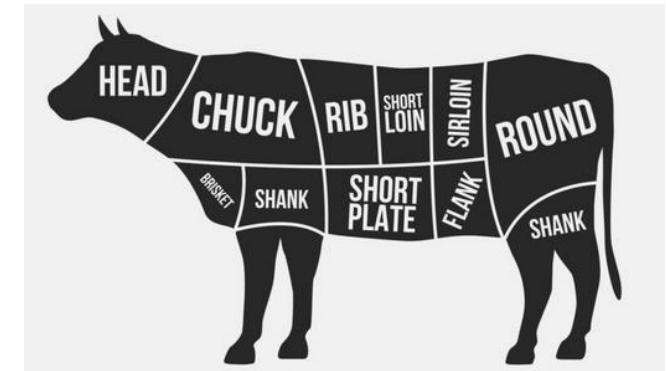


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# Weight/growth and carcass traits

## 7 traits (10 breeding values)

- Birth weight
- Weaning weight gain
- Post-weaning weight gain (FIN&SWE)
- Yearling weight (DNK)
- Slaughter daily gain
- EUROP conformation class
- EUROP fat class



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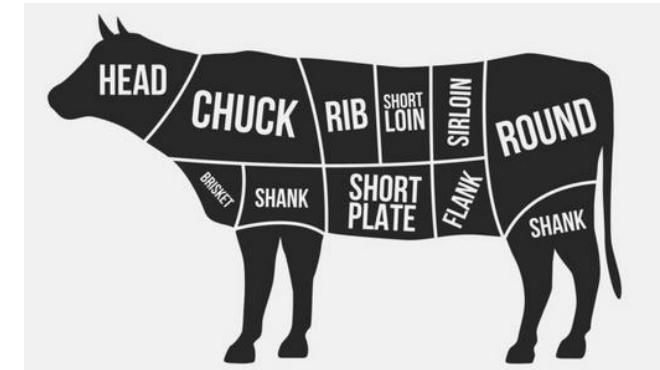
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# Methods for HV adjustment

- **Growth and carcass**
  - Simple adjustment
  - Country – year – breed – sex
- **Calving ease/Calf survival**
  - Snell scores
  - Country – year – breed – sex – primi- vs multiparous calvings \*

\* Small groups are merged

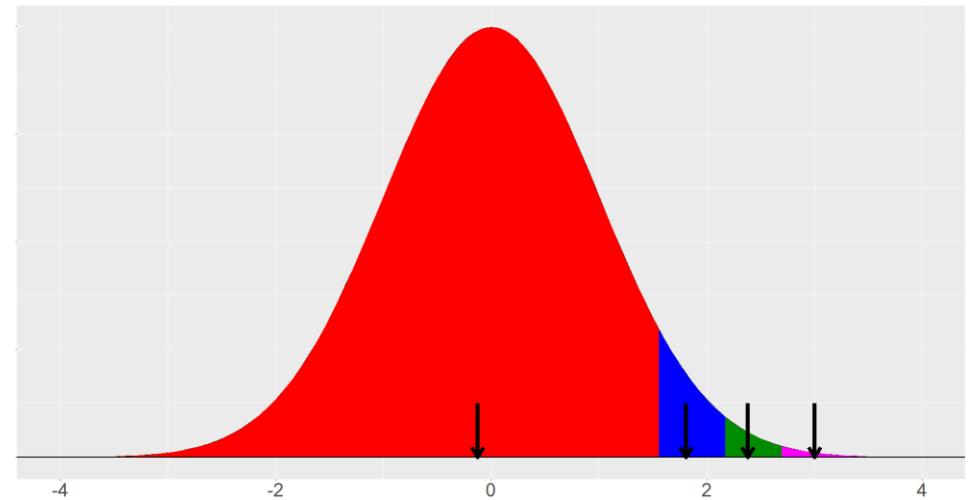
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# Calving, Snell scores

- Given the proportions in each category, replace category labels (e.g., 1-4) by the expected value on the underlying scale
- Distance between categories adjusted for frequency distribution



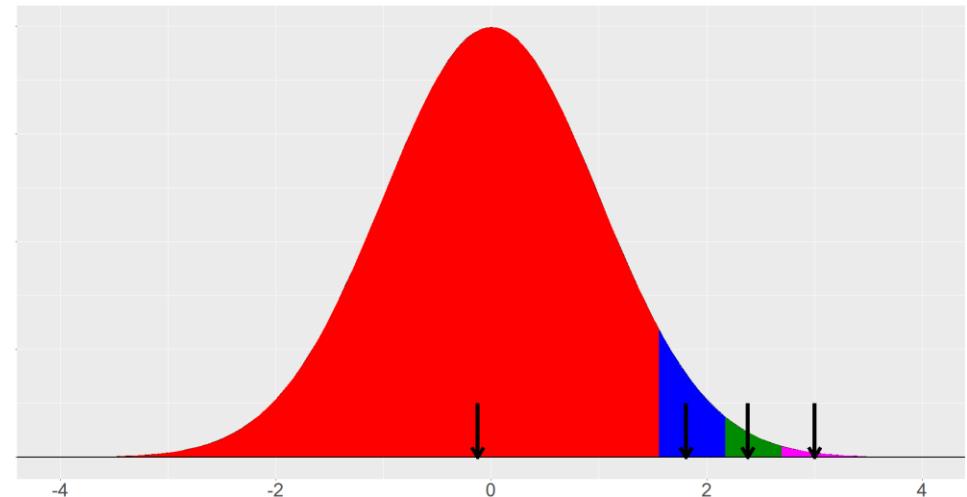
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# Calving, Snell scores

- Given the proportions in each category, replace category labels (e.g., 1-4) by the expected value on the underlying scale
- Distance between categories adjusted for frequency distribution
- More realistic breeding values for cows with difficult calving



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# Genetic parameters

- Estimated for Charolais and Hereford and applied them within breed group (Continental and British)
- Pattern of **genetic correlations** among traits was remarkably similar for Charolais and Hereford.
- Same principle applied in both, the calving and the growth/carcass evaluation

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# Breed-wise multi-trait animal model

## Fixed

- Country-sex
- Country-twin (*only carcass*)
- Country-year-month
- Country-dam age-time
- CG: Herd-birth year
- Adjustment for age at weighing (*only carcass*)

## Random

- Animal genetic
- Maternal genetic
- Dam permanent environmental (maternal)

***The genetic model also includes:  
Genetic groups***

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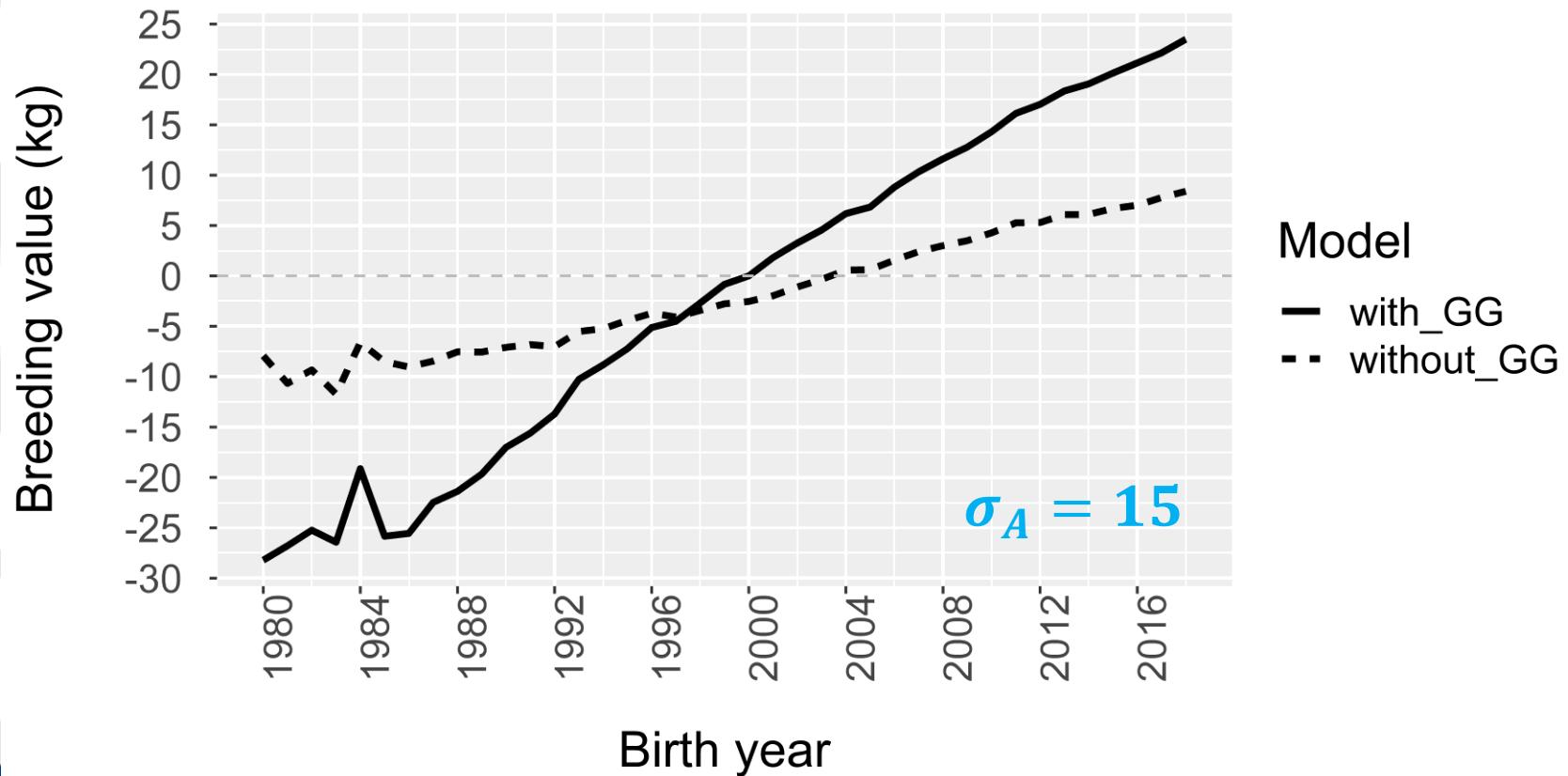


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# Genetic Groups definition

- Selection path: Differences in **genetic level between genders** are assumed to be **negligible**
- Based on **country of origin** and **year of birth**
  - Danish, Finish, Swedish, European, American, Canadian and “rest” (*Non-Nordic countries and breeds other than the breed of evaluation are pooled together*).
  - 10-year groups (capture the trend)
  - GG > = 100 animals

# Genetic trends Angus, weaning weight gain, direct



# Properties of the breeding values

- **Stability:** EBVs from successive evaluations (more data)
  - Correlations
  - Standardized EBV change (*as a function of reliability and genetic standard deviation*)
- **Validation:**
  - Legarra and Reverter method
  - AI sires used in more than one country

# Summary

- First joint **Nordic EBVs** for calving, weight gain and carcass traits for pure beef cattle published **in November 2021**



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- First joint Nordic EBVs for calving, weight gain and carcass traits for pure beef cattle published in November 2021
- In the process of establishing joint composite EBVs



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# Summary

- First joint Nordic EBVs for calving, weight gain and carcass traits for pure beef cattle published in November 2021
- In the process of establishing joint composite EBVs
- Coming next:
  - Include more breeds
  - Include fertility
  - Genomic prediction



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