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Simulating genetic progress for traits with expensive phenotyping

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Content

- Some examples traits with expensive phenotyping
- NrfTwin - Digital twin of Geno breeding program
- What genetic progress can we expect with respect to:
 - Different number of phenotypes collected
 - Different economic weights
 - Different genetic correlations
- Conclusions



Acknowledgement

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- Train@Ed



TRAIN@Ed

- SkatteFUNN



Photo: Håvard Melbø Tajet

Two examples of expensive phenotyping

- At Geno we are phenotyping around 1000 cows per year for roughage intake and enteric methane
- What genetic progress can we expect for these traits in 10 years?



Session III - New traits; today at 16:45; Karoline A. Bakke: Genetic correlations between daily dry matter intake, body weight and enteric methane in Norwegian Red dairy cows

Roughage intake



Photo: Janez Jenko

Enteric methane

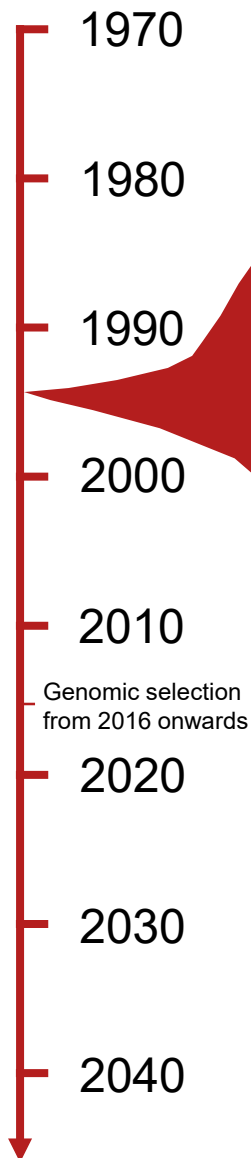


Photo: Nathalie Bjørneby

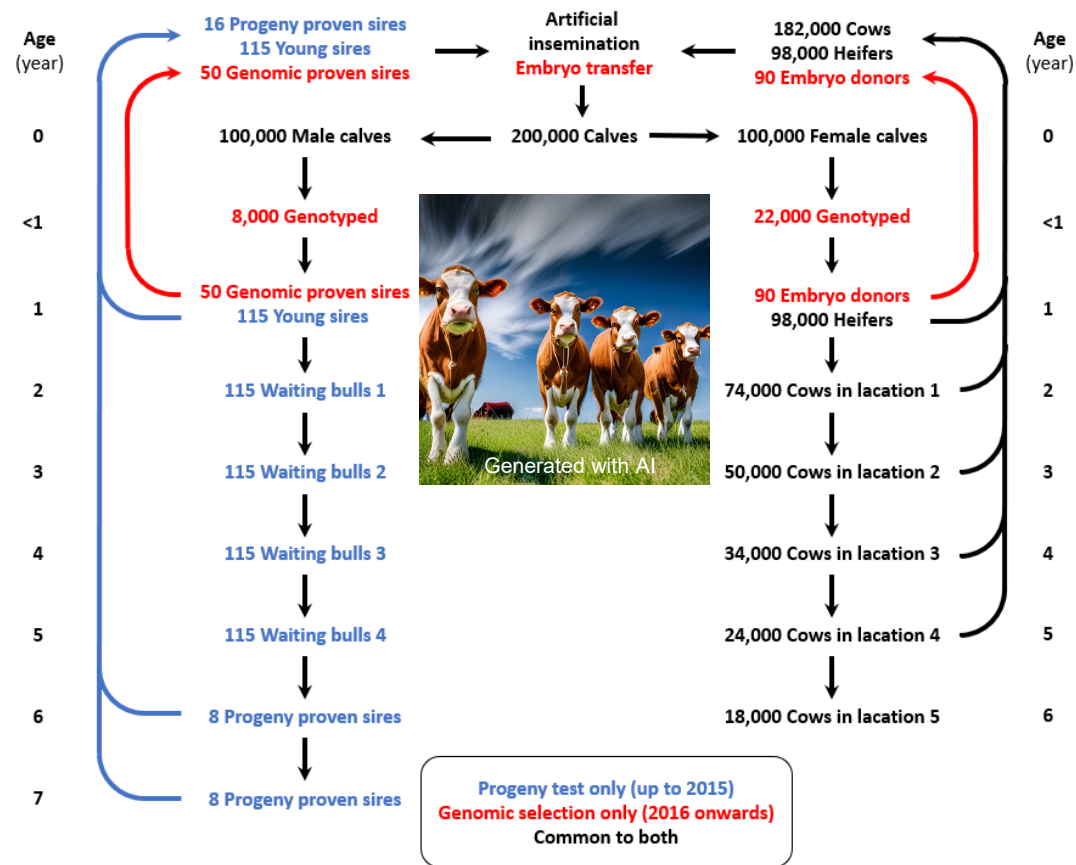
NrfTwin – Digital twin of Geno breeding program

Historical breeding program
from 1970
to 2020

Alternative future breeding
programs from
2021 to 2030



One year in Geno's historical breeding program



Questions we would like to answer

- What genetic progress can we expect if we increase the number of phenotypes?
- What genetic progress can we expect with different economic weights?
- What genetic progress can we expect with different genetic correlations with index trait?

Phenotyped animals
are also genotyped

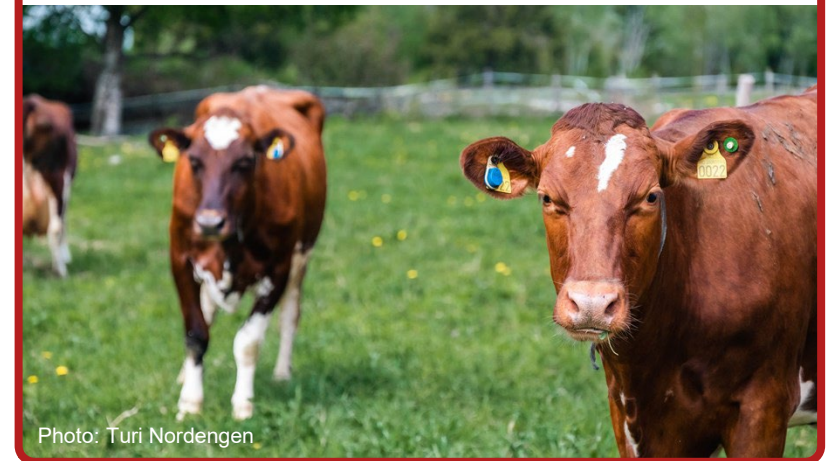


Photo: Turi Nordengen

Material and methods

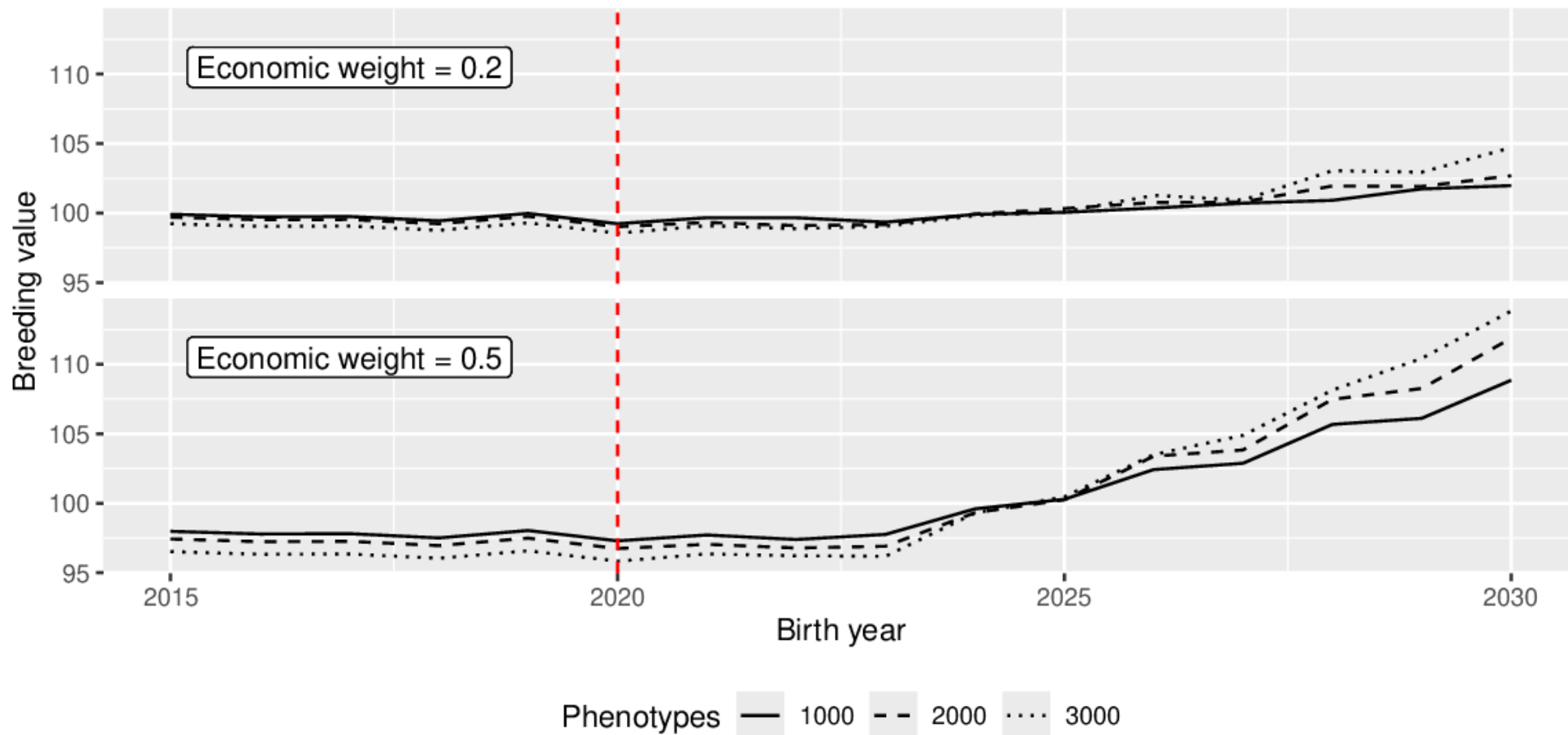
- 50 years of historical breeding
 - Selection on index trait ($h^2 = 0.192$)
 - Expensive trait ($h^2 = 0.3$)
- 10 years of Future breeding
 - With either 1000, 2000, or 3000 phenotypes per year
 - Economic weight of either 0.2 or 0.5
 - Genetic correlation of either 0, 0.3, or 0.6
- Running each scenario in 10 replicates

- Standardization of breeding values:

$$EBV = m + k * \frac{rEBV - mEBV}{sEBV}$$

Where EBV is standardised breeding value; $m = 100$; $k = 12$; $rEBV$ raw breeding value; $mEBV$ is the mean of the breeding values of females born between years 2023 and 2028; $sEBV$ is the standard deviation of the bulls breeding values born between April 2011 and March 2016.

Results



Increase the number of phenotypes

1000 phenotypes



Genetic progress after 10 years is

64.1 points

for index trait

2.7 points

for expensive trait

2000 phenotypes



Genetic progress after 10 years is

63.9 points

for index trait

3.7 points

for expensive trait

3000 phenotypes



Genetic progress after 10 years is

63.4 points

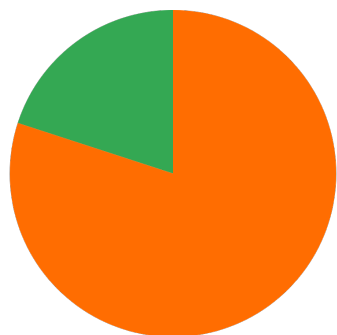
for index trait

6.2 points

for expensive trait

Different economic weights for expensive trait

Economic weight = 0.2



Genetic progress after 10 years is

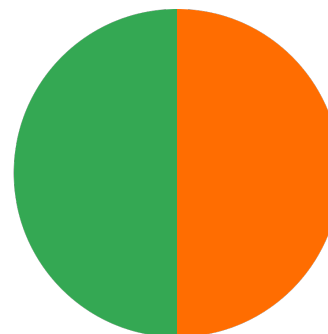
64.1 points

for index trait

2.7 points

for expensive trait

Economic weight = 0.5



Genetic progress after 10 years is

58.7 points

for index trait

11.6 points

for expensive trait

The effect of genetic correlation

No correlation between index trait and expensive trait

Genetic progress after 10 years is

64.1 points

for index trait

2.7 points

for expensive trait

Correlation between index trait and expensive trait = 0.3

Genetic progress after 10 years is

64.4 points

for index trait

20.9 points

for expensive trait

Correlation between index trait and expensive trait = 0.6

Genetic progress after 10 years is

64.2 points

for index trait

38.6 points

for expensive trait

Conclusions

- Collecting more phenotypes from genotyped animals improves genetic gain
- Higher economic weights for expensive trait improves genetic gain for expensive trait but slows down the genetic progress for the index trait
- Higher genetic correlation between expensive trait and index trait leads to a higher genetic improvement
- Phenotyping expensive traits for estimation of genetic parameters is very important

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Thank you 😊



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