

Breeding Value for Dry Matter Intake for Dutch Bull based on Combination of DGV for DMI and EBV for Predictors

Roel F. Veerkamp, Mario P.L. Calus, Gerben de Jong, René van der Linde, Yvette de Haas



Feed efficiency



- Feed efficiency
 - Feed important variable cost
 - Environmental/greenhouse gasses
 - “More for less”

- Objective: Develop (procedure to predict) feed intake breeding values for Dutch bull
 - Feed intake (DMI) data
 - Predictors yield and body size

The steps taken to get DMI BV

1. Combine data with weekly DMI records on cows
2. Estimate variance components (with yield and type) using fixed regression testday model
3. Obtain bull & cow genotypes (50k)
4. Estimate DGV for bulls using H-matrix (one-step)
5. Back solve DGV with genotypes to get SNP prediction equation for young bulls
6. Combine DGV of bulls with national EBV for type and production to get final DMI BV



1) Cow data

DMI:

#2538 cows

#3229 lactations,

#60,580 weekly DMI

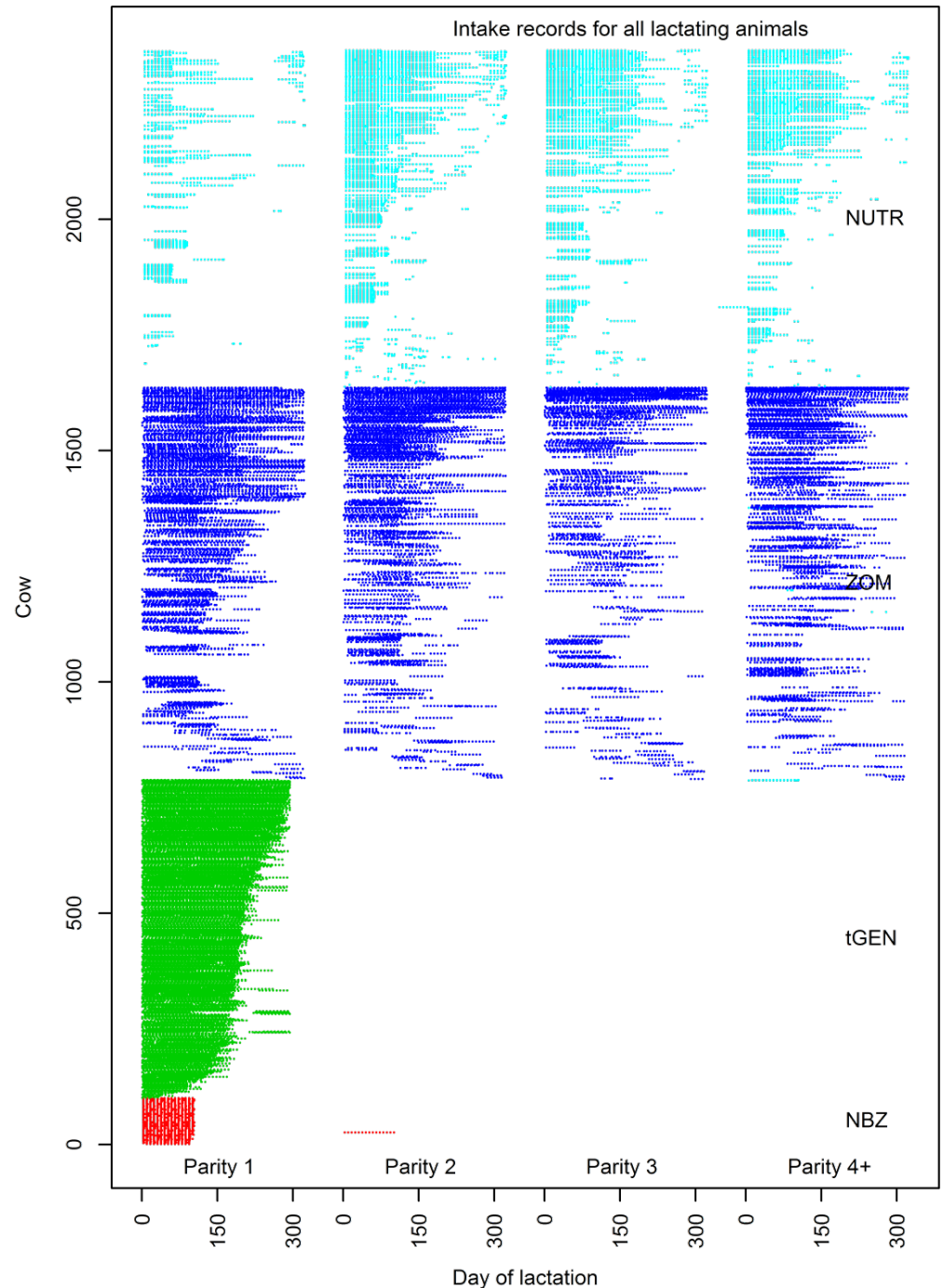
Milk, fat protein yield:

#8,417 lactations

#147,771 weekly

Stature and body
depth #2,272

Chest width #1,390



2) Variance component

- A fixed regression test-day model:
 - Genetic animal effect in parity 1, 2, 3+ for DMI, milk, fat and protein, plus stature, body depth and chest width
 - Fixed effects ...

- Residual, additive genetic and permanent environmental covariance matrices were 15x15.

- Type traits scored once during first parity, environmental covariance between type and DMI recorded at other days during the same lactation ← overestimated genetic correlations.

2) Variance components

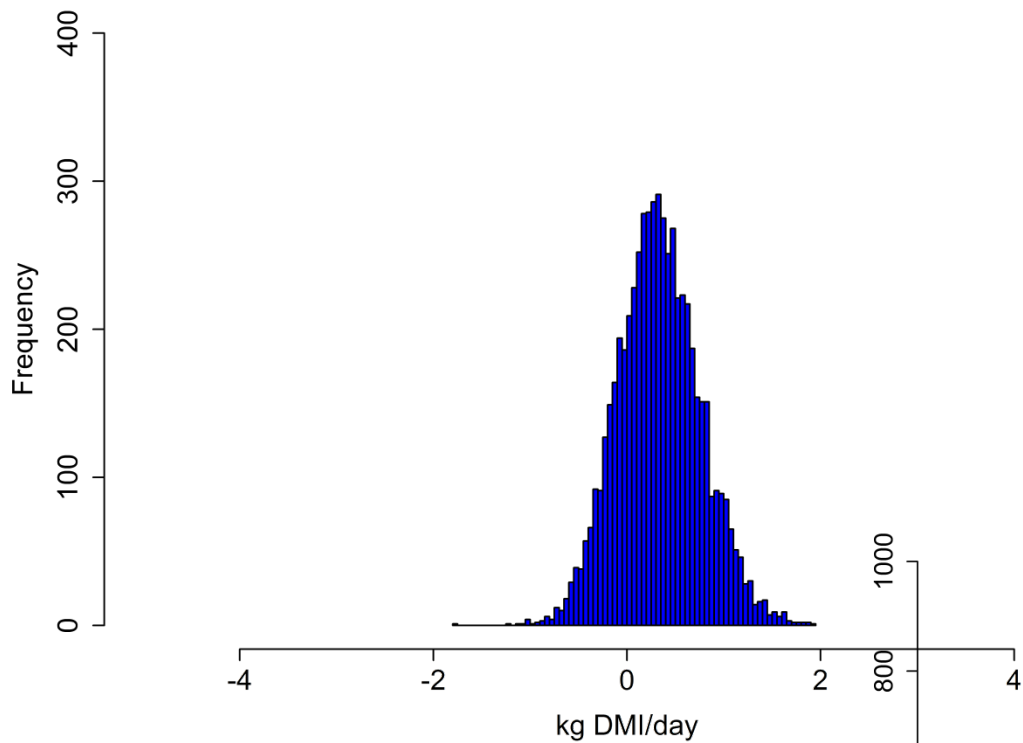
	h^2	DMI 2	DMI 3	Stature	Chest	Body	Yield
DMI 1	0.24	0.83	0.73	0.34	0.23	0.26	0.63
DMI 2	0.24		0.82	0.34	0.22	0.21	0.59
DMI 3	0.18			0.34	0.27	0.21	0.57



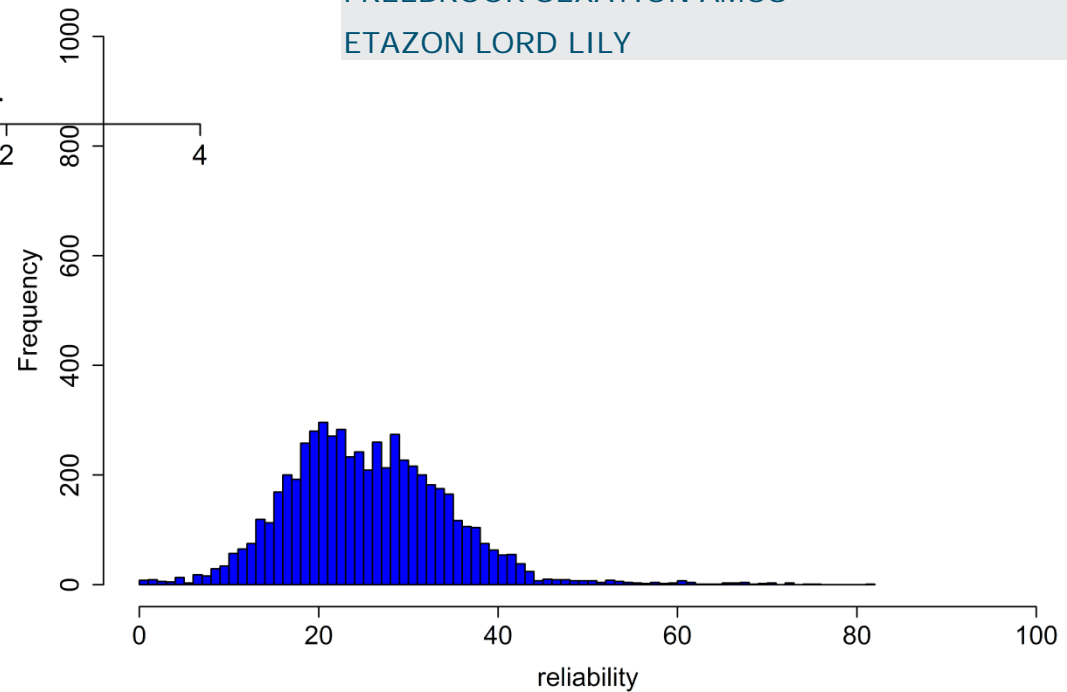
3 + 4) Estimate DGV using H-matrix

- Genotypes were available for 1,013 cows (with DMI records) and 5,967 sires with 41,235 SNP
- Combined pedigree and genomic relationship matrix, weight on the G versus A matrix of 0.95
- Dense: genomic breeding values for DMI (DGV) were estimated using MIXBLUP, (<http://www.mixblup.eu/>).
- (ASREML to get reliability)

Genomic DGV DMI



SKALSUMER SUNNY BOY
DELTA CLEITUS JABOT
EASTLAND CASH
ETAZON CELSIUS
DOWNALANE CELLO
F16 ROCKET C
ETAZON LABELLE
CARLIN M IVANHOE BELL
BIS-MAY TRADITION CLEITUS
FREEBROOK SEXATION AMOS
ETAZON LORD LILY



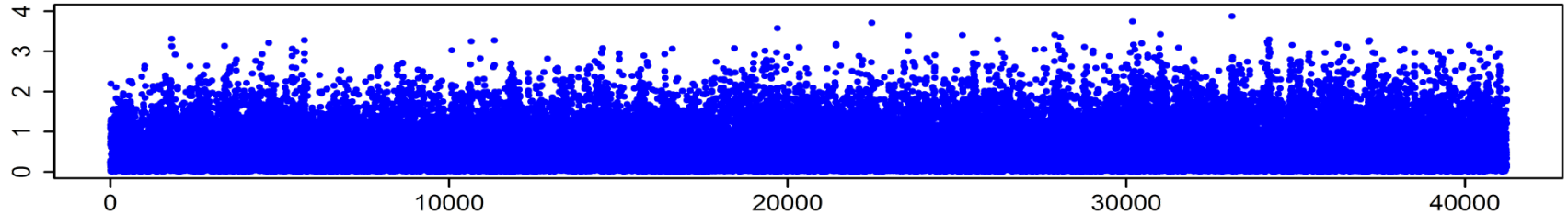
5) Back solve DGV with genotypes to get SNP prediction equation for young bulls

- SNP prediction equations (a_j) ([Stranden and Garrick \(2009\)](#)):
were obtained from the vector \mathbf{u} with DGV for bulls
$$\mathbf{a} = \mathbf{DZ}'(\mathbf{ZDZ}')^{-1}\mathbf{u}.$$

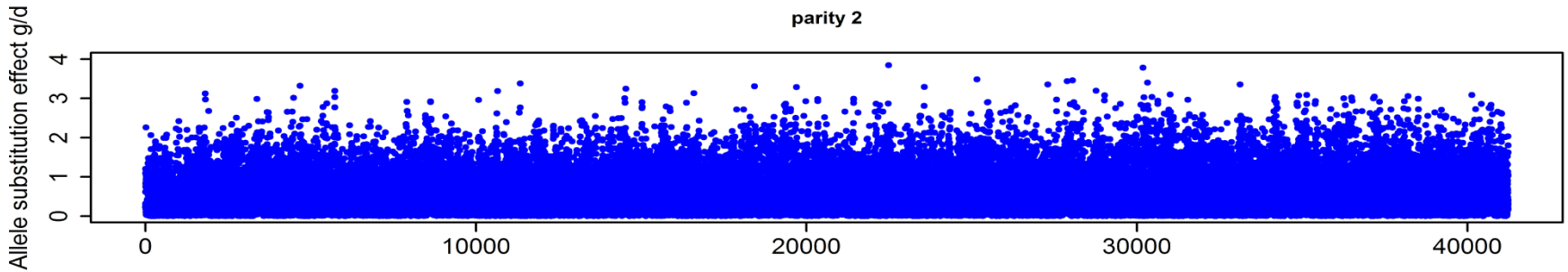
Where \mathbf{Z} is the centered design matrix, \mathbf{D} is an identity matrix, and \mathbf{a} is the derived vector with effects for each SNP.

5) Back solve DGV with genotypes to get SNP prediction equation for young bulls

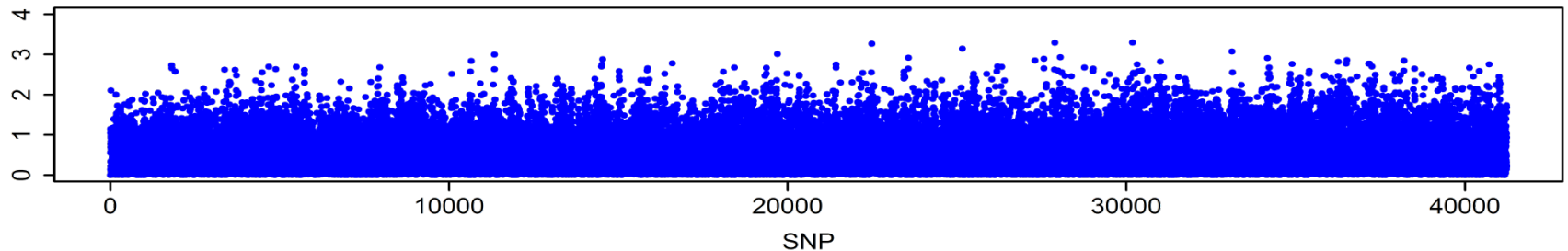
parity 1



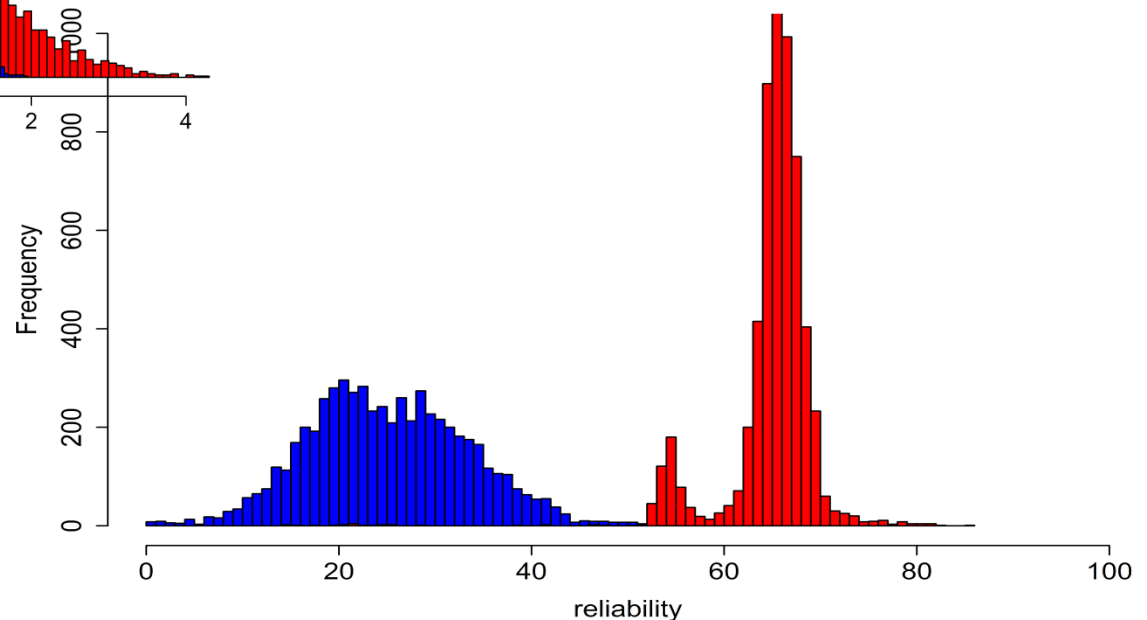
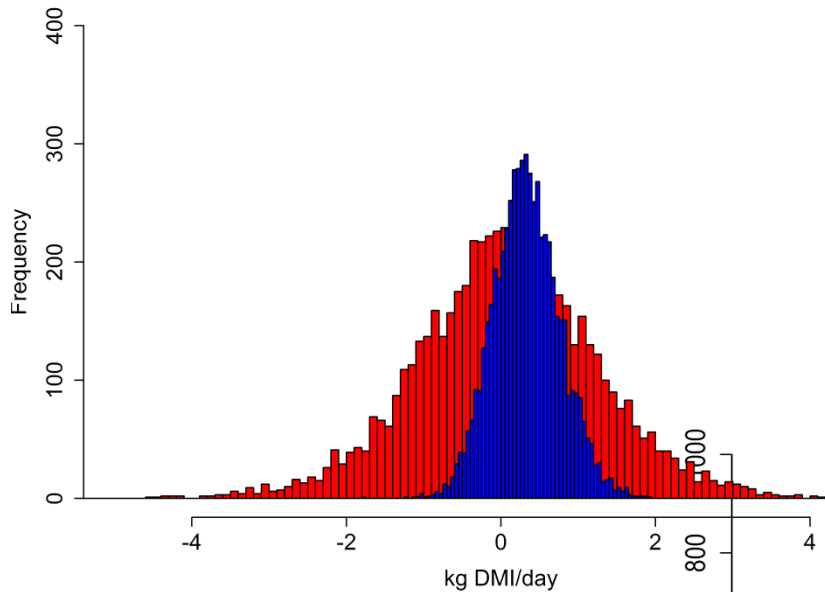
parity 2



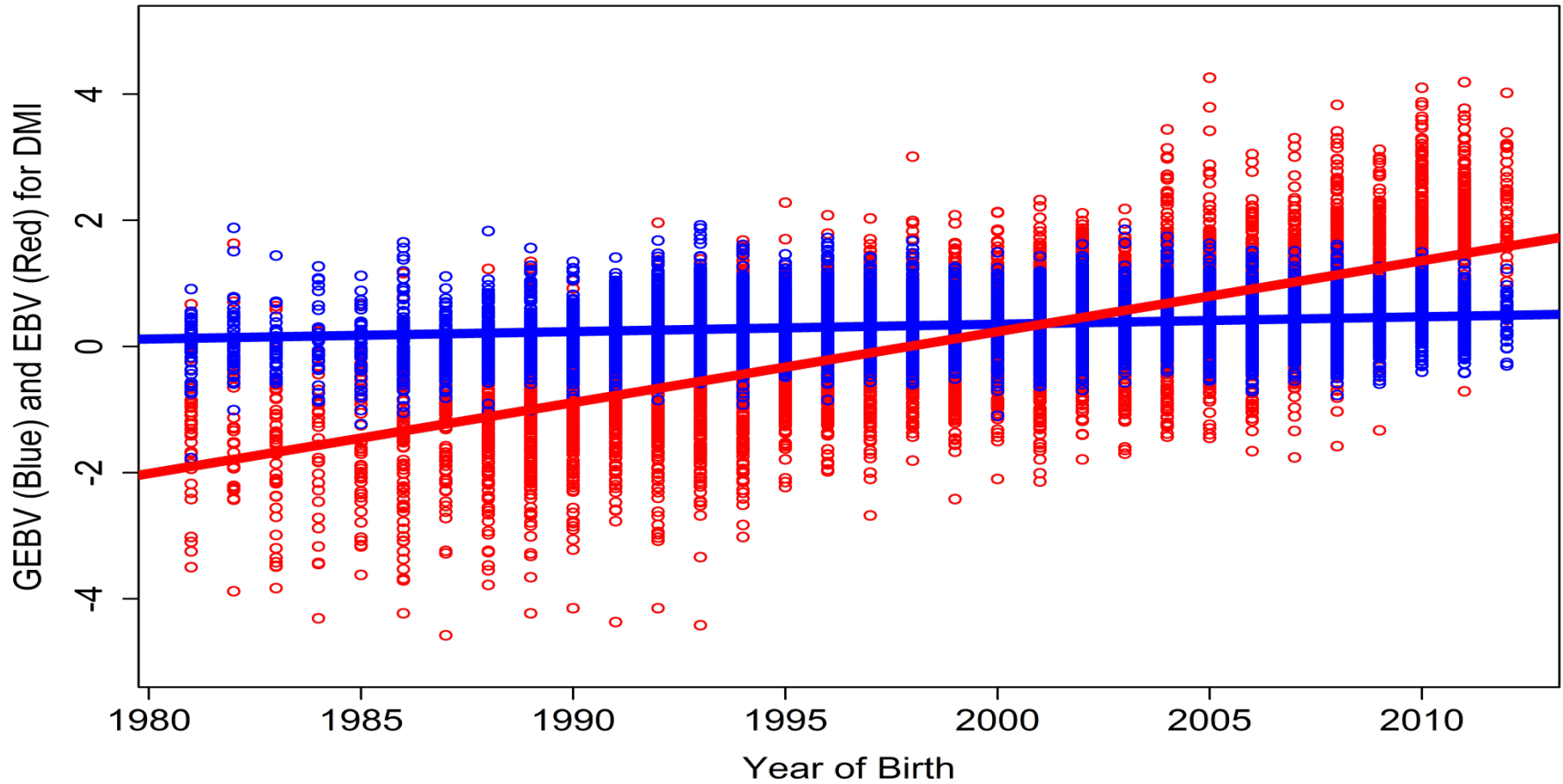
parity 3



6) Combine DGV of bulls with national EBV for type and production to get final DMI BV



Genetic trends

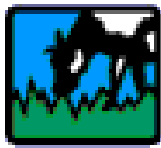


Conclusions

- Selection for feed efficiency a realistic prospect
 - Yield and type make a good first step
 - Genomics should identify 'net efficient cows'
- Combine data internationally (gDMI)
- Utilisation: include in selection indices

Acknowledgements

- Dutch:



Productschap
Zuivel



- USDA project:



United States
Department of
Agriculture

National Institute
of Food and
Agriculture