



Genomic selection for feed efficiency in dairy cattle: a complex objective

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Outline

Gross efficiency versus metabolic efficiency

Genomic prediction of measures related to intake

- Australia and New Zealand
- Australia, Netherlands and UK
- Australia, Canada, Denmark, Ireland, Germany, Netherlands, New Zealand, UK, USA

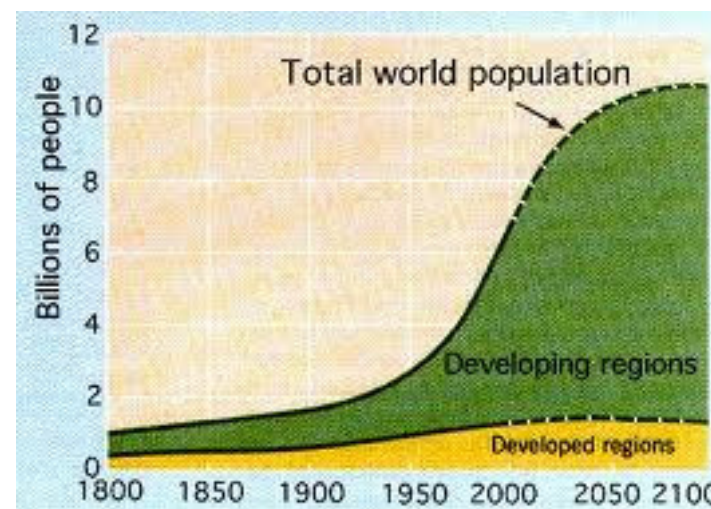
Feed efficiency traits in the breeding objective

Importance of feed efficiency

Feed a growing population

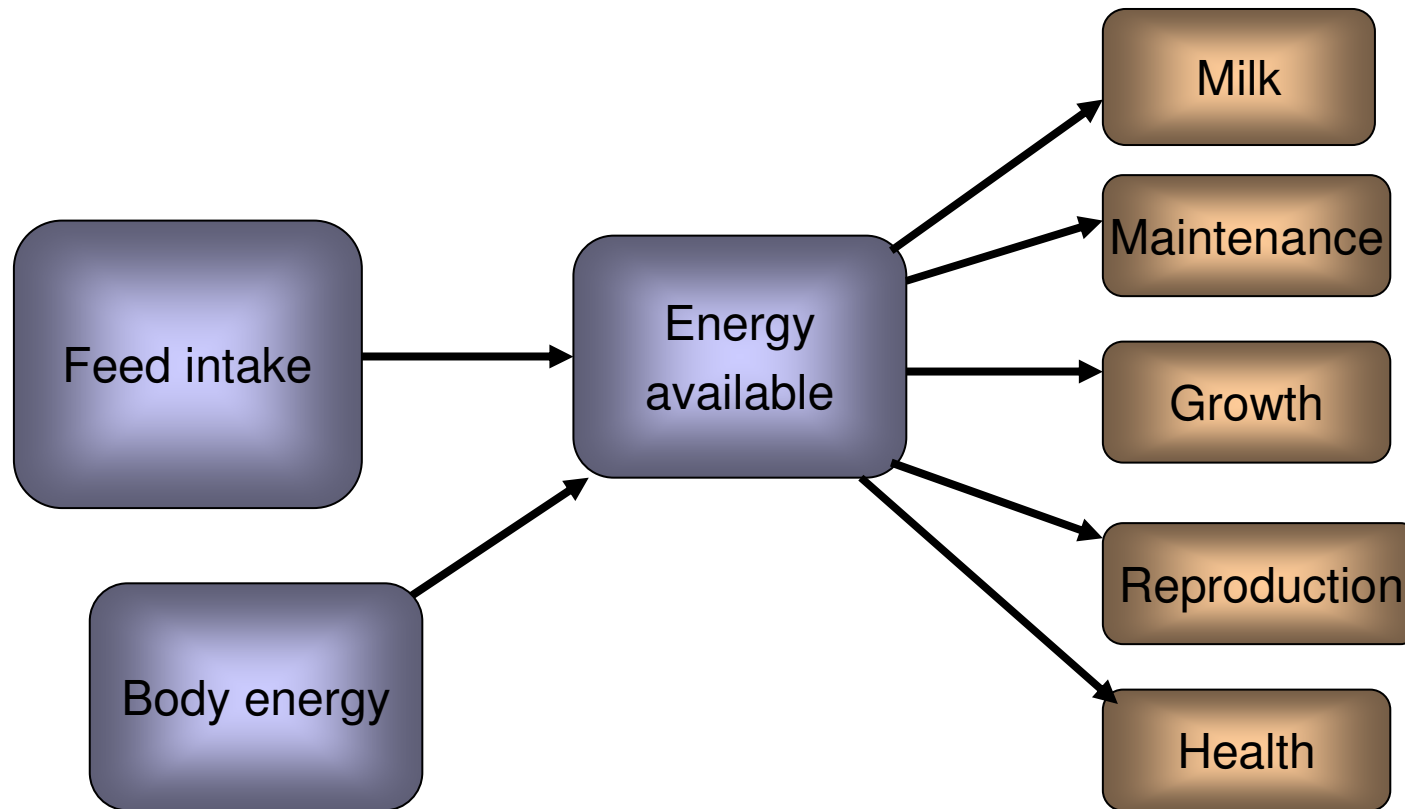
Feed is a major variable cost in animal production

Environmental impact – greenhouse gases

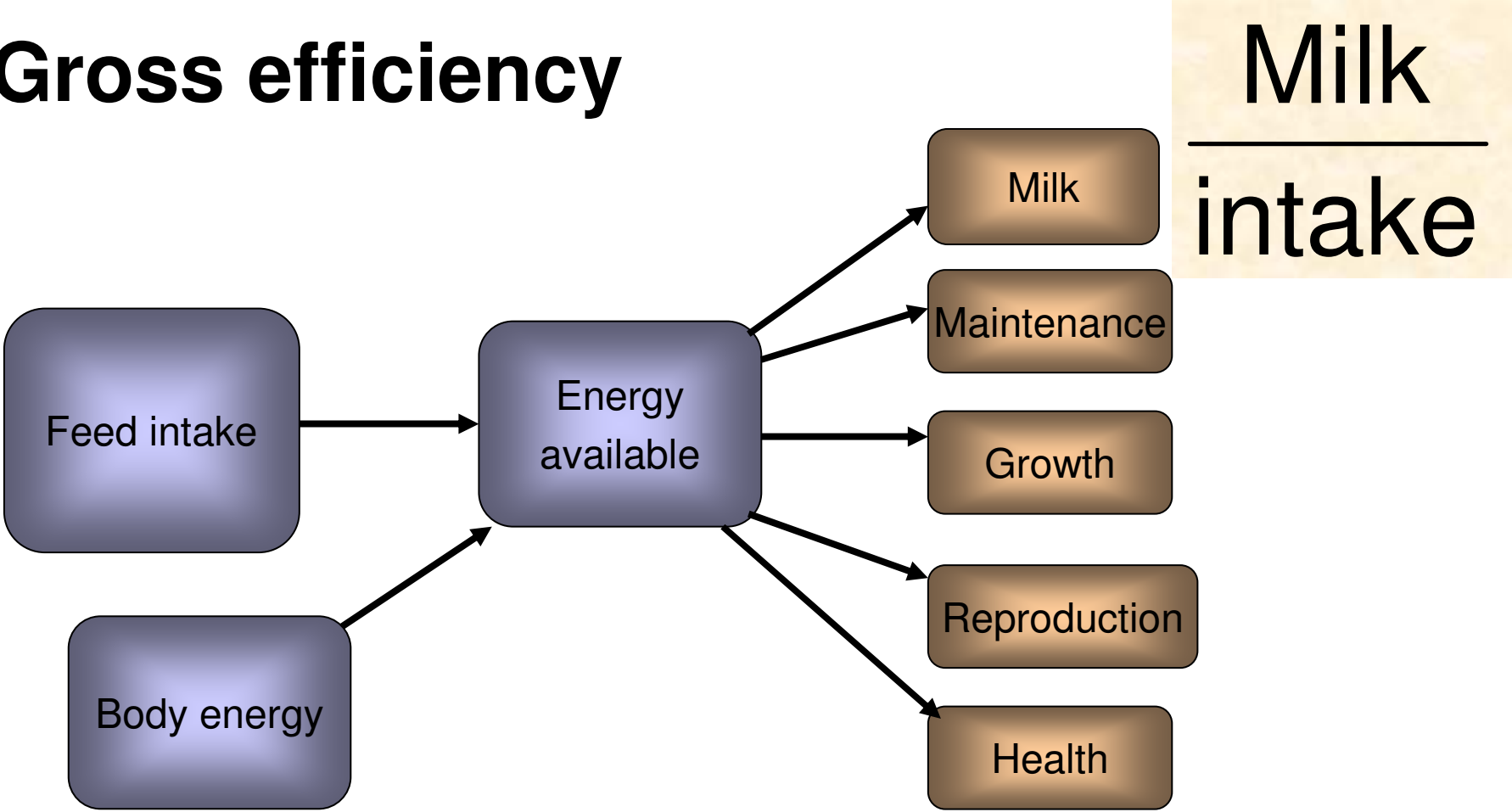


stconsultant.blogspot.com

Feed utilisation complex (simplified)

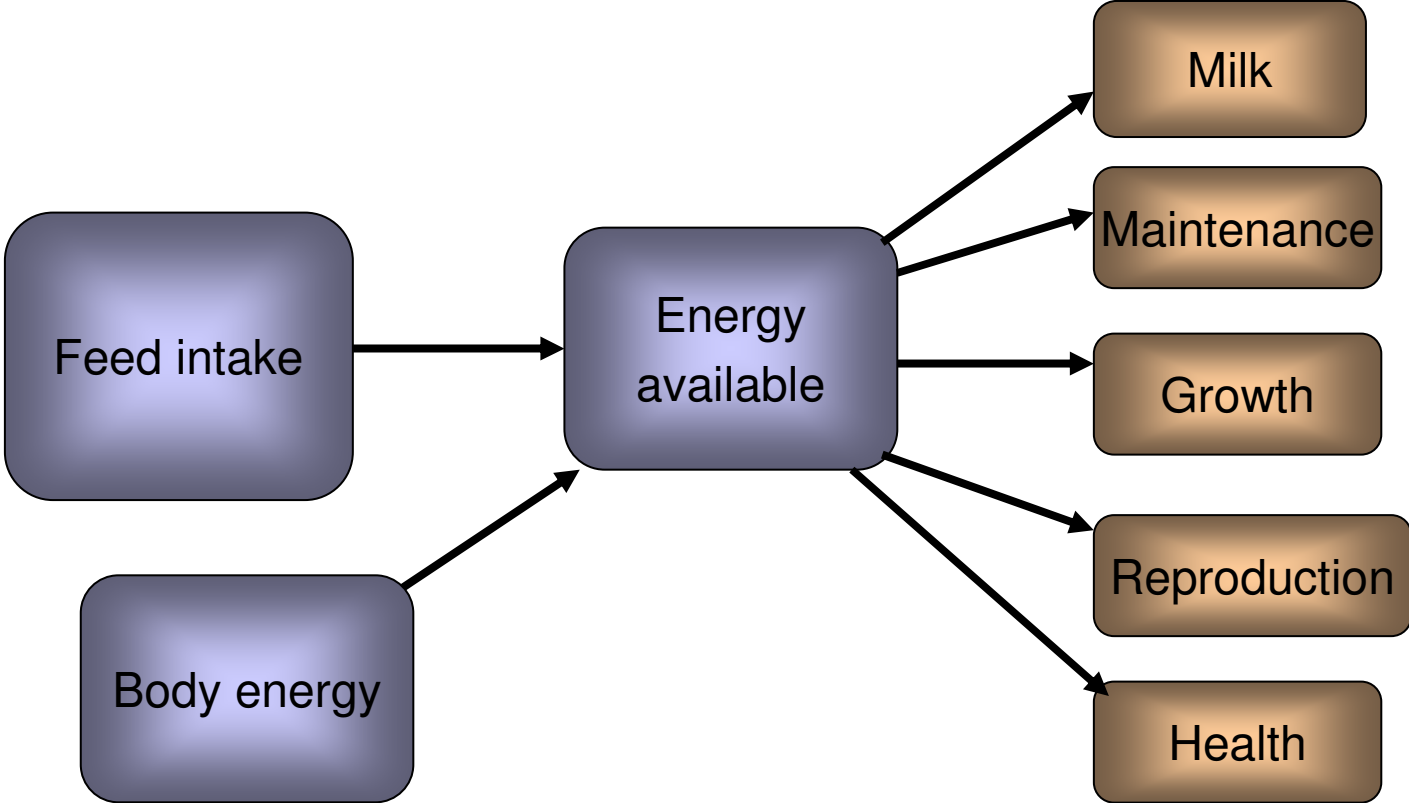


Gross efficiency



Gross efficiency

$$\frac{\text{Output}}{\text{intake}}$$



Countries that select for gross efficiency

Australian Profit Ranking (APR)

New Zealand (Breeding Worth; BW)

Others?....

$$\frac{\text{income} - \text{costs}}{\text{kg DM}}$$

Approximated using maintenance and production requirements

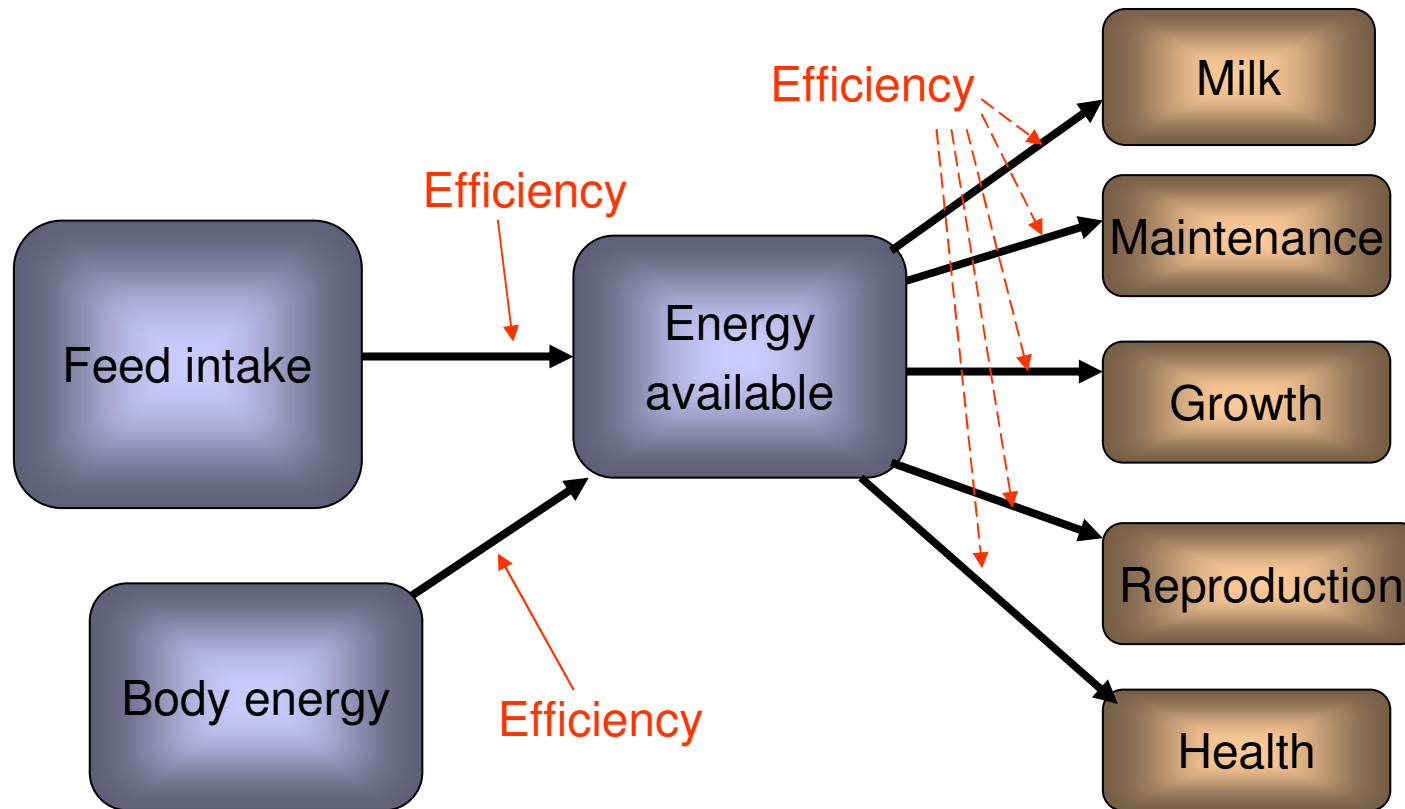
Genetic gain in milksolids and liveweight in the 10 years prior to and after introduction of BW in NZ

	Milksolids	Liveweight
1986-1996	+19.7 kg	+15.5 kg
1996-2006	+25.1 kg	+3.1 kg

(Harris et al., 2007; AAABG)



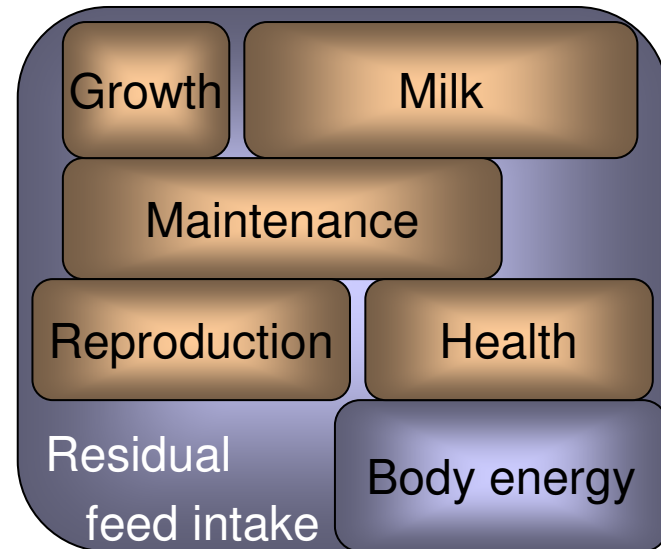
Metabolic efficiency



Metabolic efficiency

Metabolic efficiency is the efficiency of converting feed into growth, milk, maintenance etc.

Residual feed intake (RFI) is the difference between actual feed intake and predicted feed intake



Data required to calculate residual feed intake in **lactation**

Requirement – accurate measurements of:

Dry matter intake (*expensive*)

Liveweight (*not often measured* – predicted using type)

Liveweight change/growth (*difficult*)

Milk, fat and protein (*easy!*)

Body condition score (*difficult*)

Energy for reproduction, health (*usually not included*)

Data required to calculate residual feed intake in **growing heifers**

Requirement – accurate measurements of:

Dry matter intake (**expensive**)

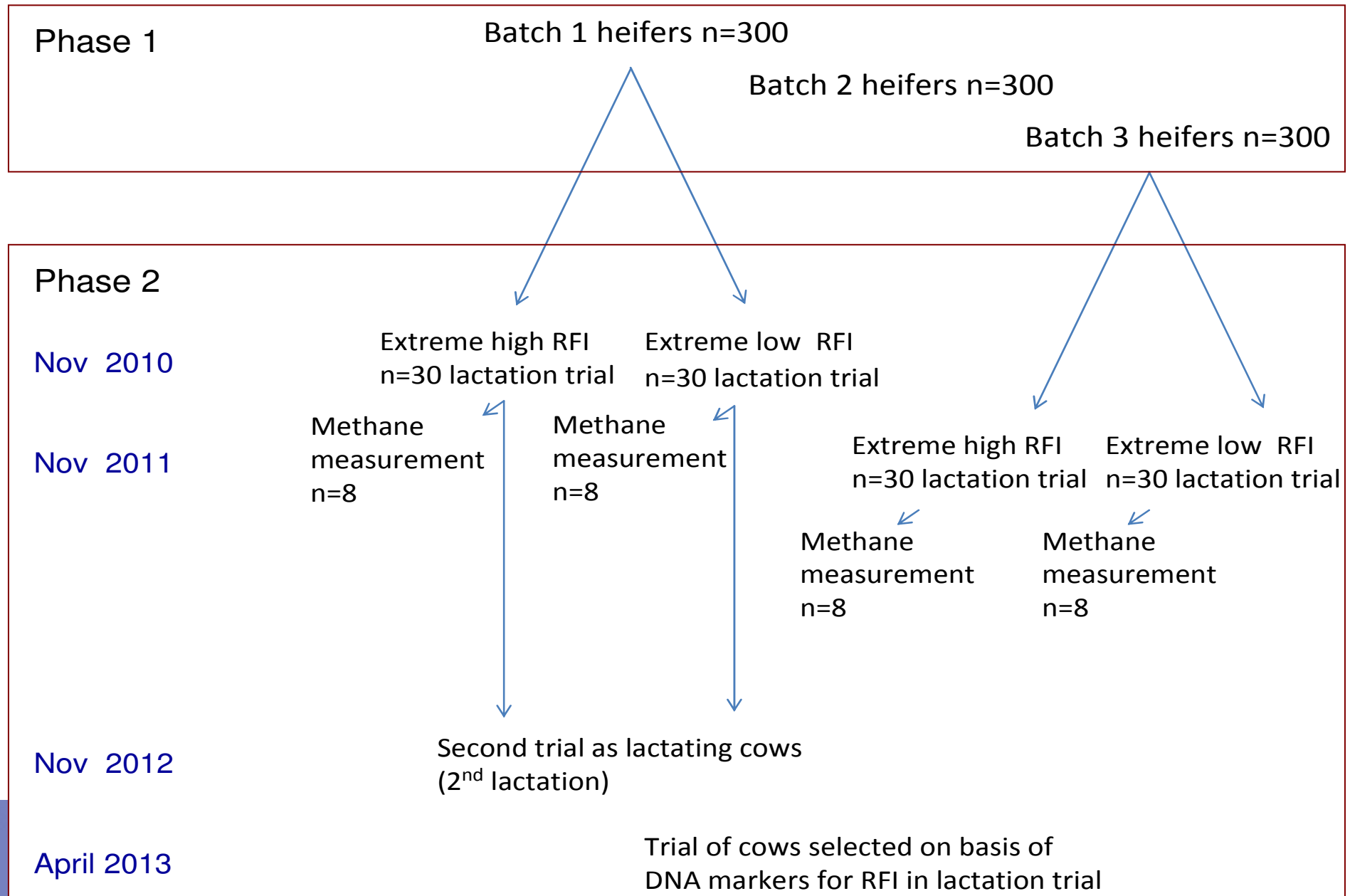
Liveweight (**OK**)

Liveweight change/growth (**OK**)

Residual feed intake (RFI) heifer trial

- Beef industry has demonstrated selection for RFI is possible
- Collect RFI data and DNA from 2000 calves (Aus & NZ)
- Develop genetic and physiological tests that can be used to predict RFI of animals
- Create a herd of high and low efficiency animals for further research

Experimental design





- Modified existing research feedlot
- 56 to 70 day trial period plus additional adaptation period
- DMI every meal, liveweight 2x per week
- Electronics designed specifically for the project



- Modified existing
- 56 to 70 day
- DMI every mo
- Electronics d



EID reader

Feed bin

Load cells

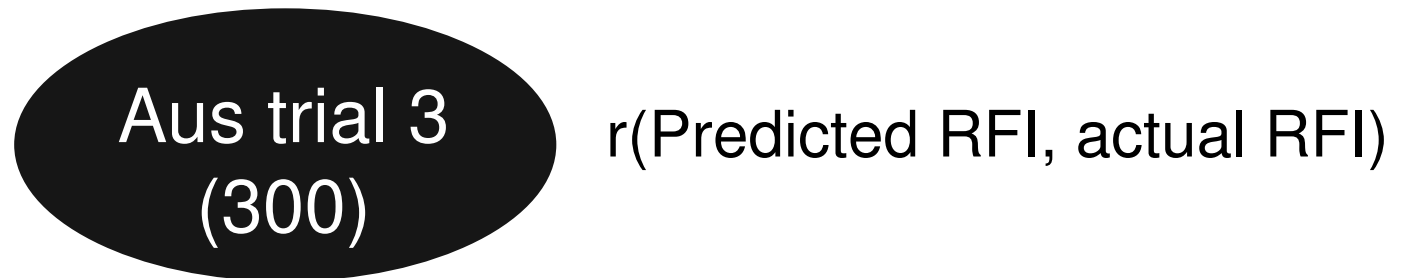
Genetic improvement is feasible

Trait	Heritability (average \pm SE)	Phenotypic SD
RFI (kg/d)	0.27 (\pm 0.12)	0.44
Liveweight (kg)	0.32 (\pm 0.12)	21.9
DM intake (kg)	0.17 (\pm 0.10)	0.85
Growth rate (kg/d)	0.22 (\pm 0.10)	0.13

Genomic predictions



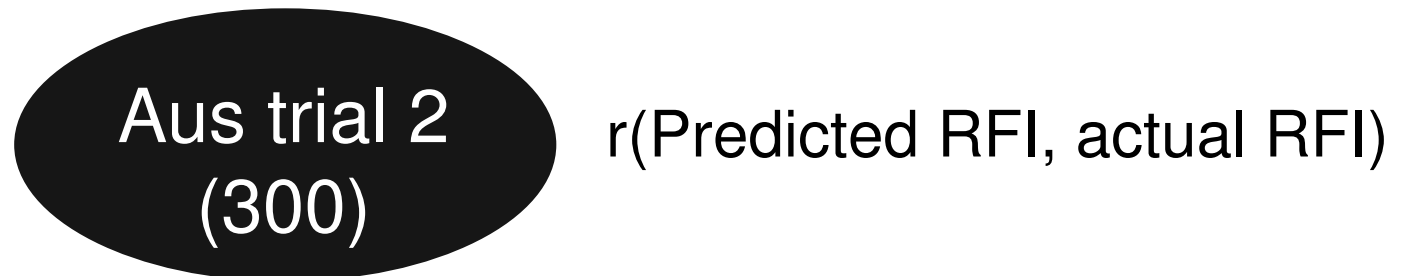
Prediction Equation $RFI = x_1 + x_2 + x_3 + x_4 + \dots + x_{625,000}$



Genomic predictions



Prediction Equation $RFI = x_1 + x_2 + x_3 + x_4 + \dots + x_{625,000}$



Results: Accuracy of genomic predictions

Validation	GBLUP	BayesMulti
AU trial 1	0.28	0.41
AU trial 2	0.31	0.39
AU trial 3	0.29	0.42
Average	0.29	0.41



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Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers

Genomic predictions

NZ heifers
(1000)

Genotypes +
Phenotypes

Prediction Equation $RFI = x_1 + x_2 + x_3 + x_4 + \dots + x_{625,000}$



Aus heifers

$r(\text{Predicted RFI, actual RFI})$

Results: Accuracy of genomic predictions

Validation	GBLUP	BayesMulti
Australia	0.14	0.21
New Zealand	0.01	0.03



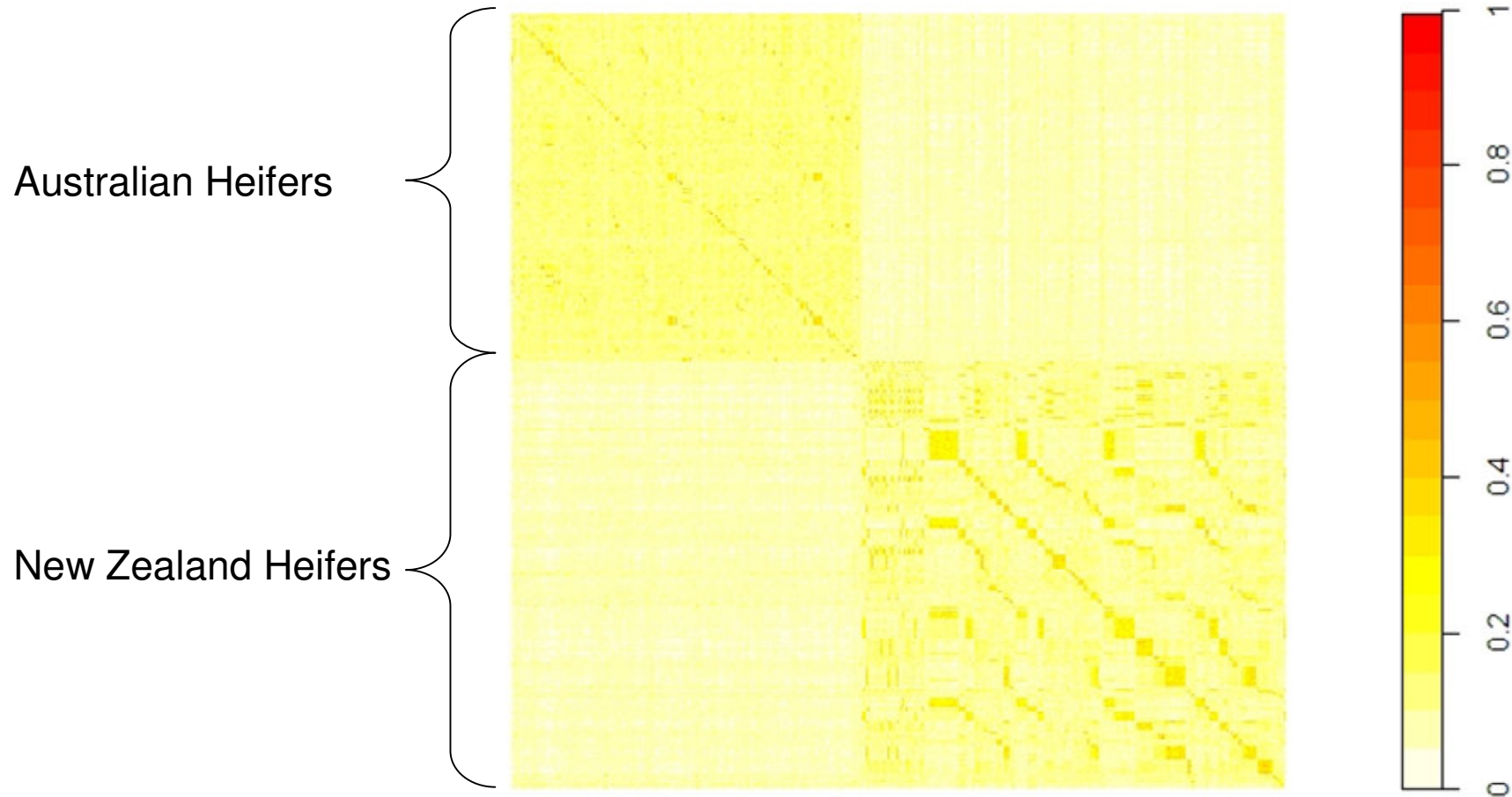
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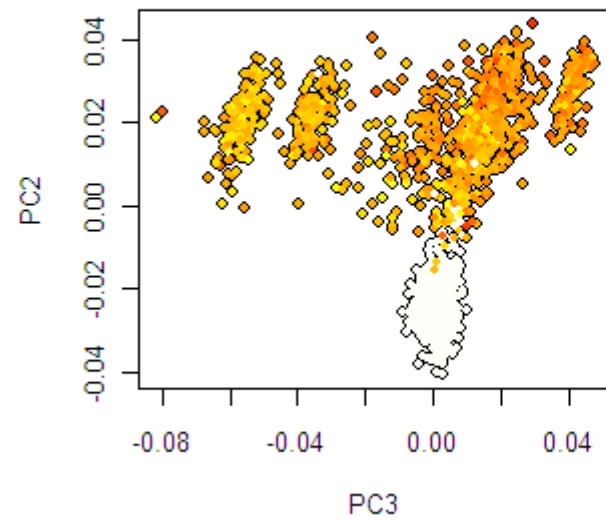
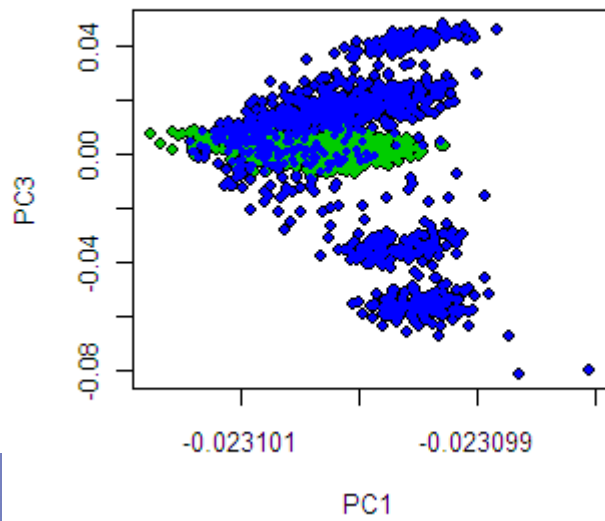
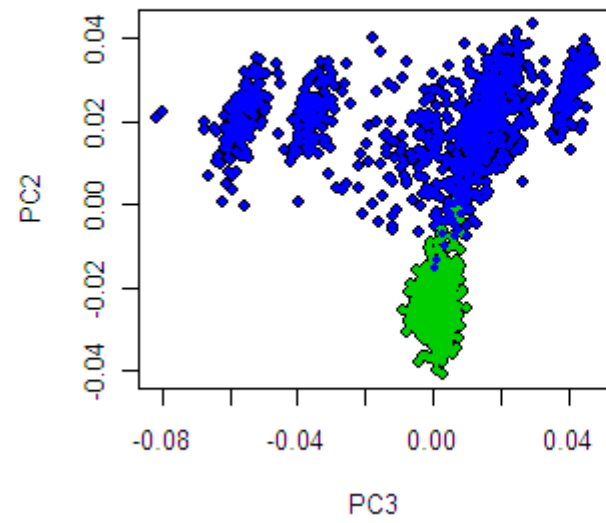
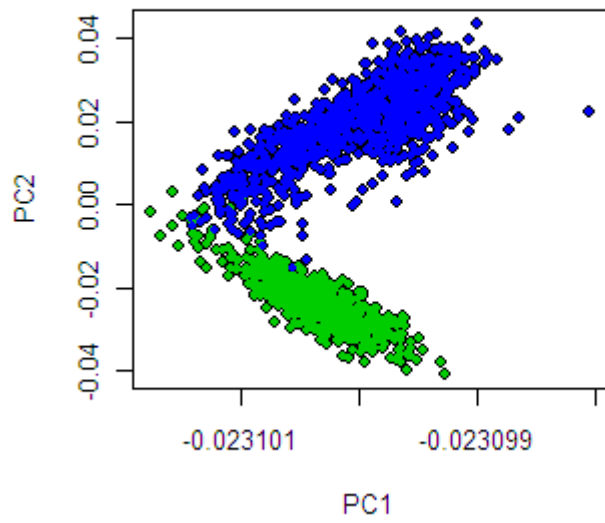
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Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers

Results

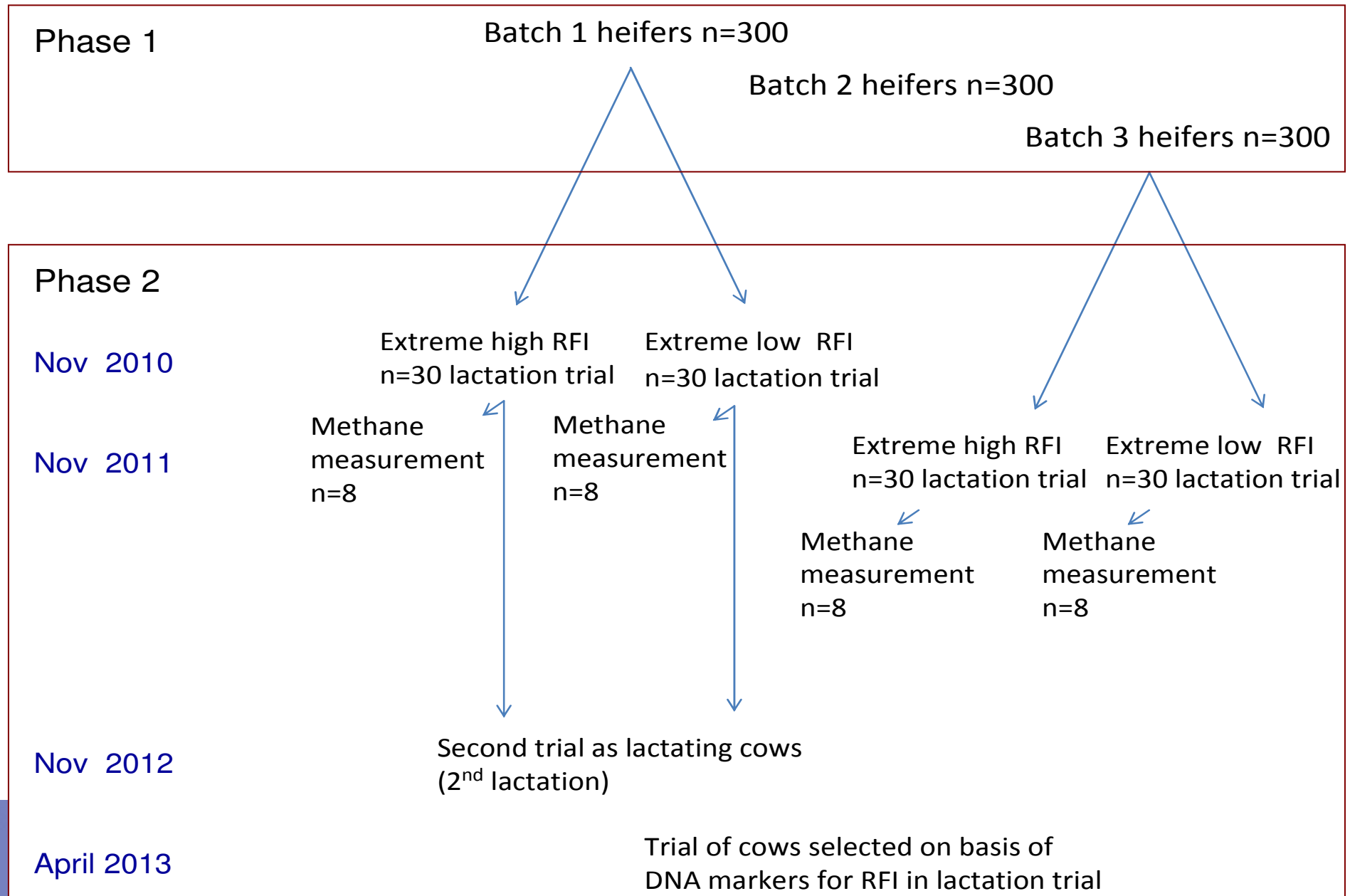




Does RFI_calf predict RFI_lact?



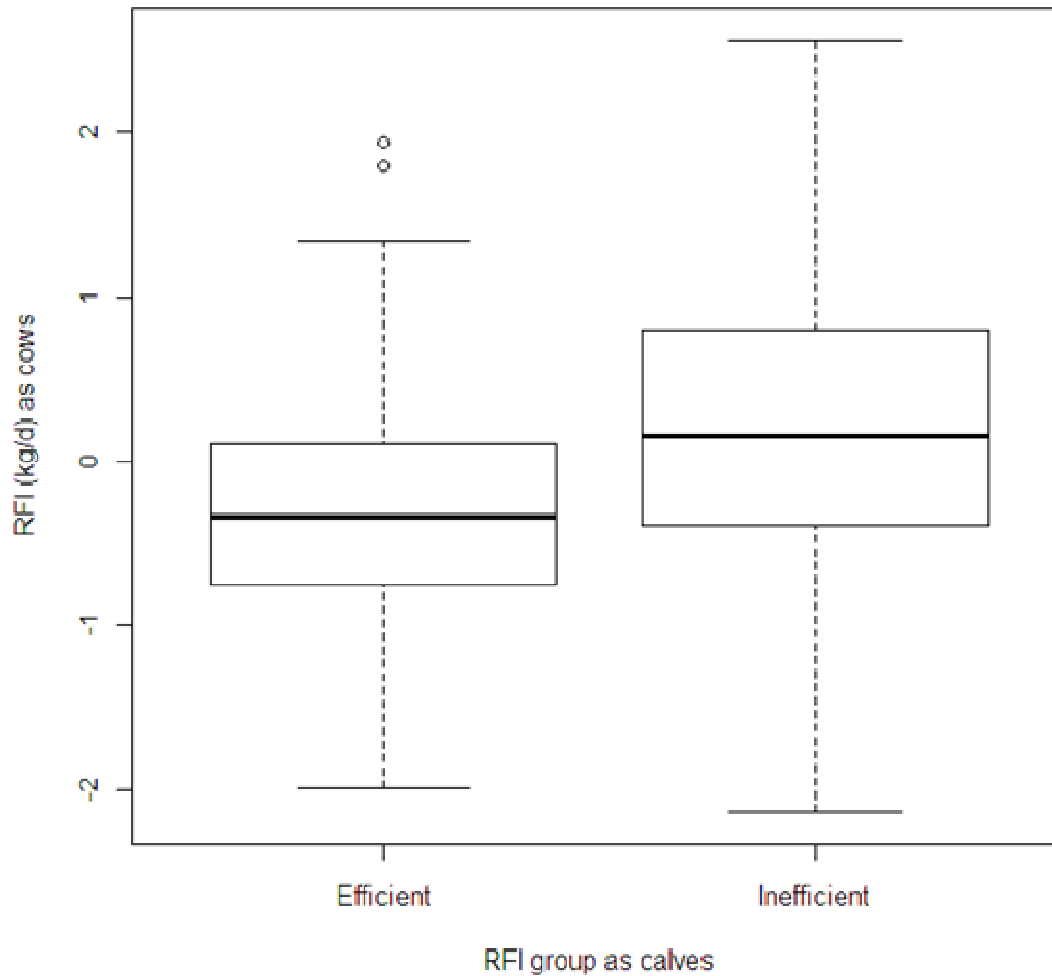
Experimental design



Does RFI_calf predict RFI_lact?

- Our experiment
 - 108 heifers measured (in two batches) for
 - Dry matter intake (DMI)
 - Liveweight, liveweight change (BW)
 - Body condition score, change (BCS)
 - Milk volume, lactose, protein, milk
 - Over 32 days, with 14 day adjustment
- $DMI = BW + BW\Delta + BCS + BCS\Delta + \text{milk} + \text{protein} + \text{fat} + \text{lactose} + RFI_{\text{lact}}$

Does RFI calf predict RFI_lact?



Both cohort#1 and cohort#3 data

Significant at $P < 0.01$

Difference between efficient/inefficient cows ~ 0.6kg day

Can we get higher accuracies by sharing data?



Shared data

Australia (DPI)

- 843 calves with genotypes (624,930 SNPs)

RobustMilk (SAC & WLR)

- 599 Dutch cows with genotypes (37,069 SNPs)
- 359 Scottish cows with genotypes (37,069 SNPs)

Common

- 40 bulls genotyped in both datasets

Accuracy of genomic selection for dry matter intake (shared data)

Multi-trait model

	Within	Shared
Australia	0.38 (0.03)	0.39 (0.04)
UK	0.30 (0.04)	0.33 (0.03)
Netherlands	0.33 (0.10)	0.34 (0.09)

de Haas et al, in press (JDS)

DEPARTMENT OF
PRIMARY INDUSTRIES

biosciences
research

Global dry matter initiative (gDMI)

Led by Roel Veerkamp

Combine DMI phenotypes

Common pedigree

Combine genotypes



Key research questions:

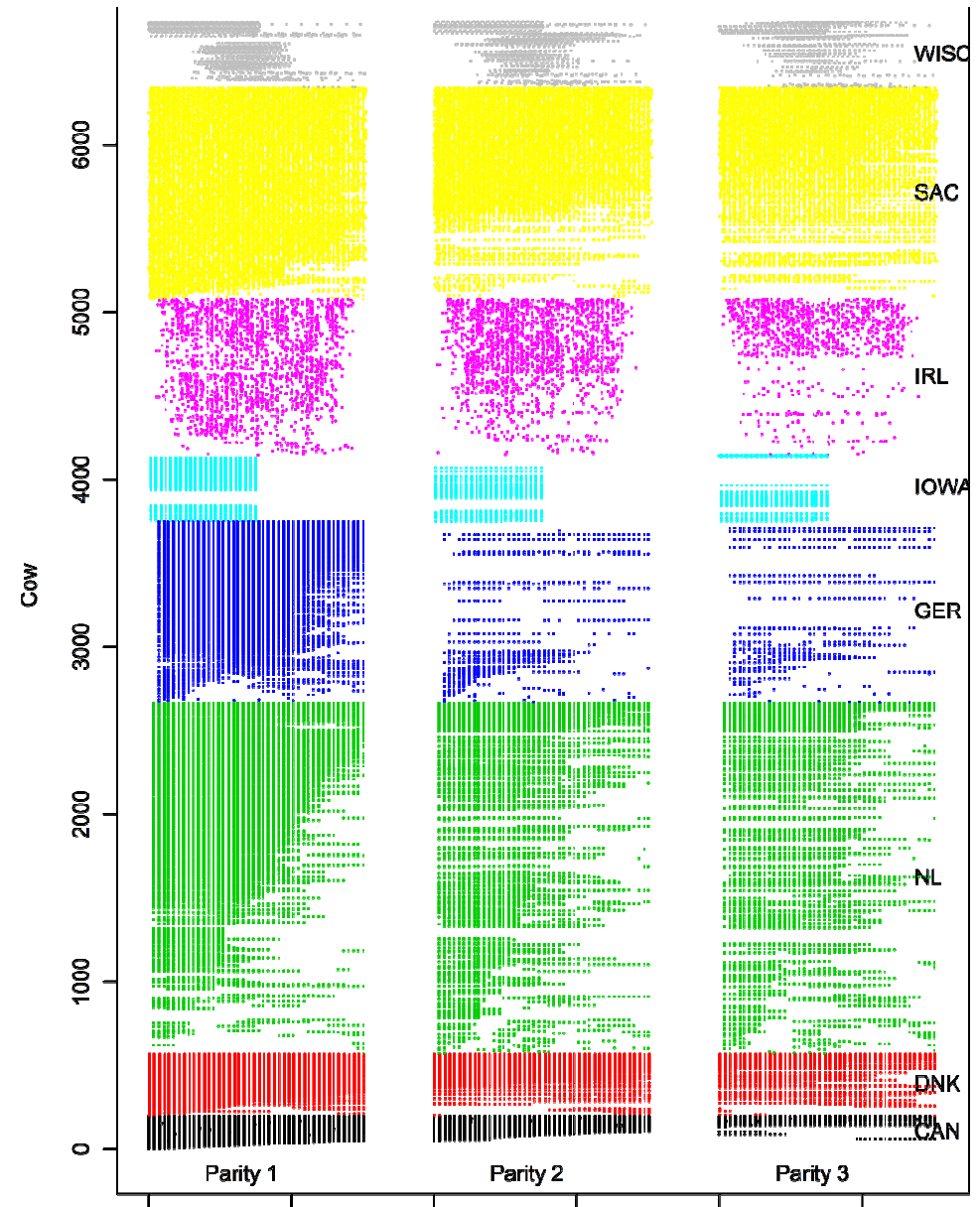
- Genomic similarity between population?
- How to combine, homogenise and standardise phenotypes?
- Can we predict DGV for DMI for different partners?

Phenotypes

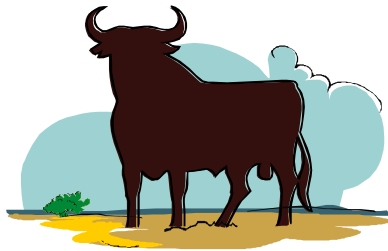
#cows: 5000

#lactations: 11700

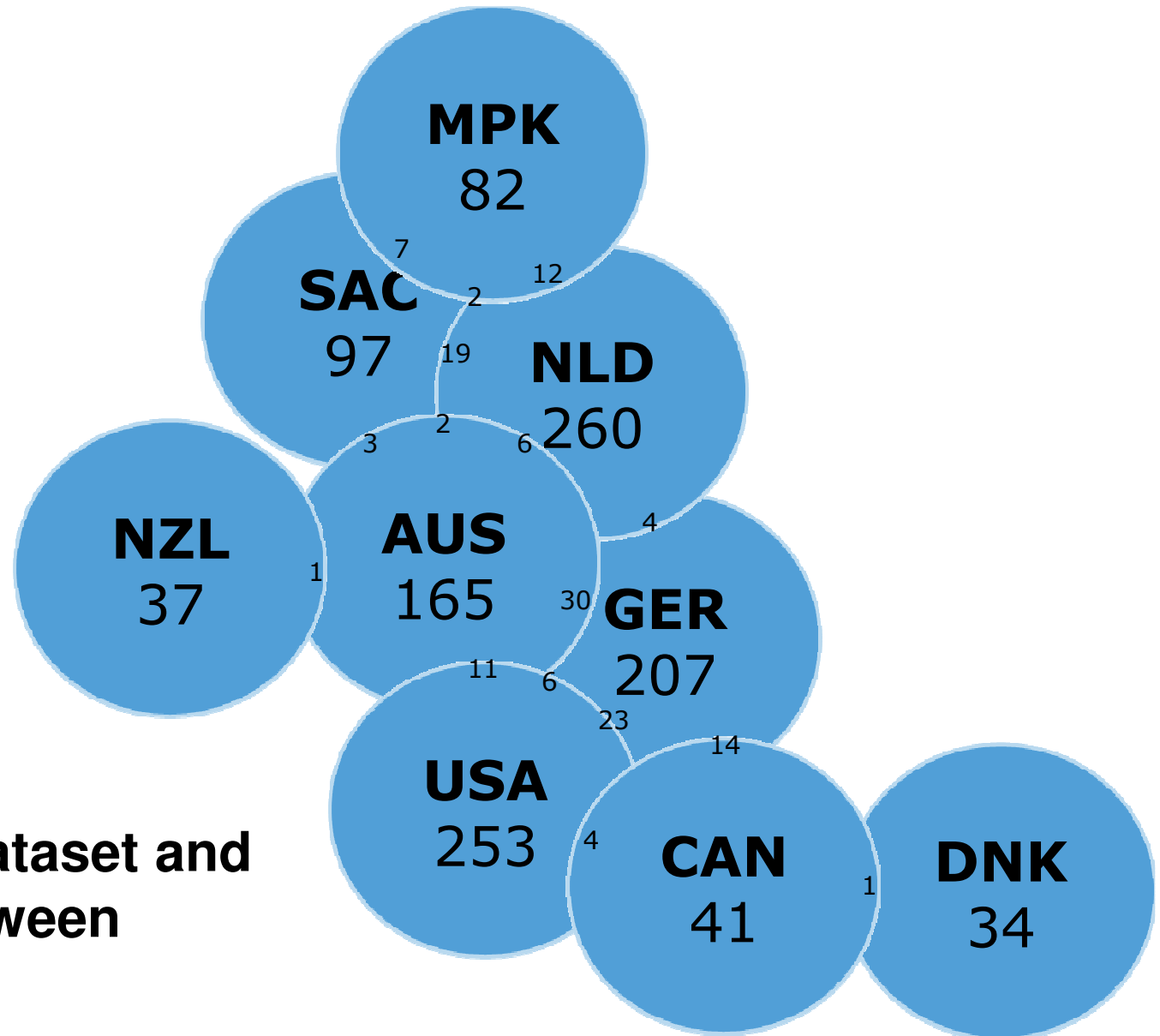
#calves: 1800



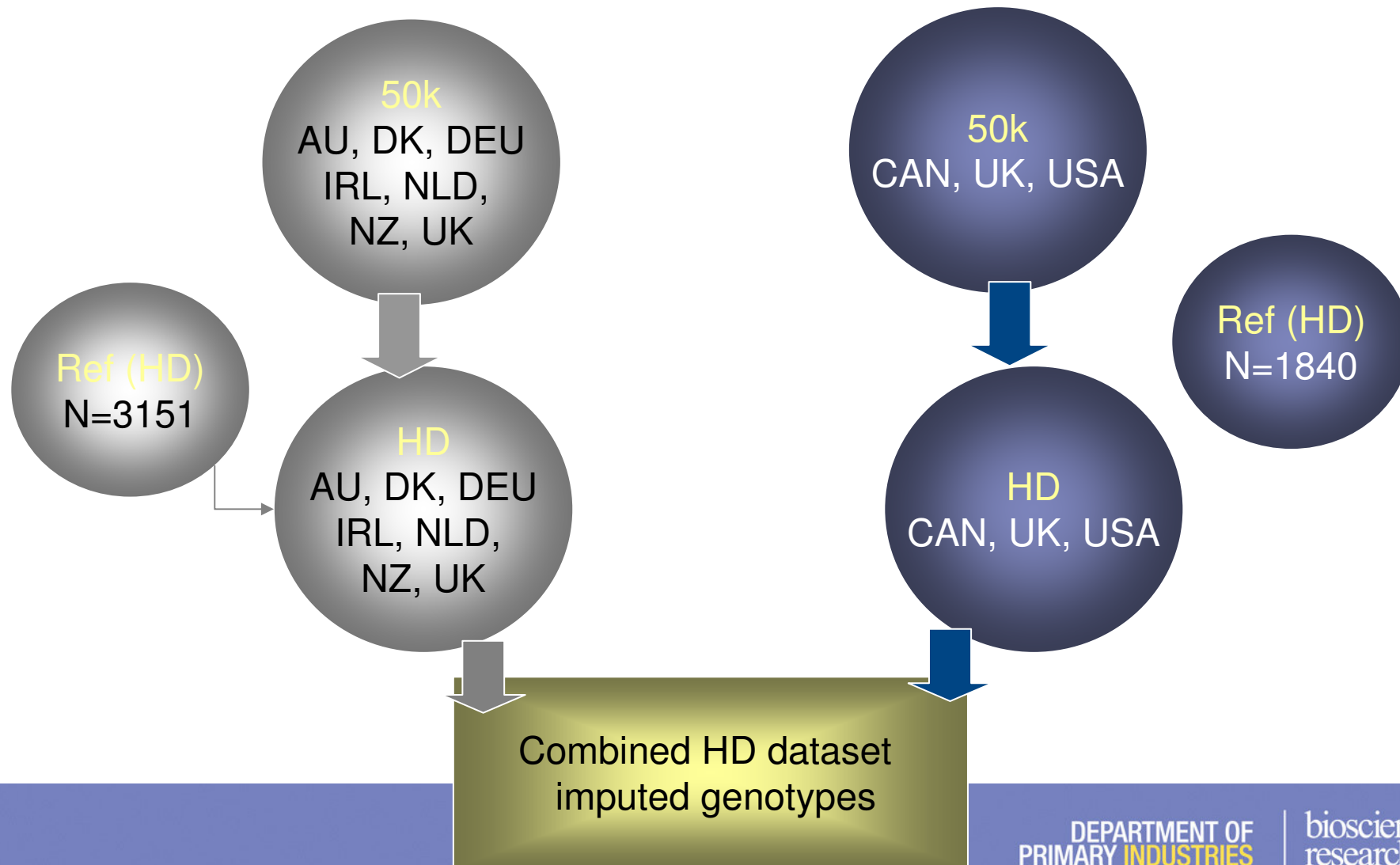
Pedigree



**Sires in each dataset and
in common between
datasets**



Genotypes



Breeding goal

Residual feed intake or dry matter intake?

Selection for RFI could lead to an improvement in metabolic efficiency

Risky if not confident that mobilisation of body tissue is correctly adjusted

RFI could just be indicator of body reserve mobilisation!

Do genetic correlations between RFI and other traits exist?

RFI independent of milk, liveweight, growth phenotypically

Not necessarily the case genetically

Selecting for reduced DMI (as part of a multi-trait index) probably more sensible

Still require a measure of body reserves (e.g. BCS) in breeding objective, so that you do not reduce DMI at the expense of BCS

Conclusions

- Feed efficiency is important in dairy production
- Selection is possible using genomic selection
- A challenge is to increase the accuracies of prediction
 - combine data internationally and use multi-trait genomic prediction models



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- American Society of Animal Science
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- Gardiner Foundation
- ADHIS
- gDMI colleagues

Global Dry Matter Initiative (gDMI)

