



Genetic relationships between different measures of feed efficiency and the implications for dairy cattle selection indexes

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Introduction

- Feed intake represents >50 % of total costs of dairy production.
 - Dry matter intake (DMI in kg) is expensive to measure (*never mind actual energy intake in Mcal!*)
 - Tied to both economic and environmental sustainability.
- USDA grant (Vandehaar PI) generated ~5,000 DMI records on ~4,000 cows from 8 US research stations for >42 d of intakes between 50 and 200 DIM.
 - Genomic reliabilities for elite young bulls averaged 12% for RFI (Van Raden et al., 2018) based on use of reference population from USDA grant.
 - Other countries (Netherlands, Australia) have published genetic evaluations based on feed efficiency

Outline of talk

- Help provide a clear GENETIC distinction between various definitions of feed efficiency (FE) traits
 - Dry matter intake
 - Residual feed intake (RFI)
 - *Phenotypic vs genetic* RFI (pRFI vs. gRFI)
 - Feed Saved (FS) including *genetic* Feed Saved (**g**FS).
- Implications of FE trait choice for reliabilities of genetic evaluations and selection programs







phenotypic Residual Feed Intake (pRFI)

TWO STAGE MODEL

pRFI is not an observable trait: -> estimated residual from a first-stage statistical model:

$$\text{DMI} = \text{various environmental effects (e.g. CG)} + b_1 \text{MilkE} + b_2 \text{MBW} + b_3 \Delta \text{BW} + \varepsilon$$

$$- \text{RFI} = \hat{\varepsilon}$$

MilkE: Milk energy
MBW: metabolic body weight ($\text{BW}^{0.75}$)
 Δ BW: change in BW

RFI is a measure of metabolic efficiency

Second stage model is the quantitative genetic analysis model

$$pRFI = \mu + \mathbf{u}_{(\text{polygenic/genomic})} + \text{other cow-specific effects} + \mathbf{e}$$

potential random regression extensions for DIM-specific pRFI

Problem with pRFI: It is *phenotypically* independent of MilkE and MBW...but it *may not be genetically independent!*

→ Fails to recognize that genetic relationships between traits may differ from non-genetic relationships between traits!



An alternative approach to deriving genetic RFI (gRFI)

Originally introduced by Kennedy et al. (1993)

Multiple trait model approach due to Lu et al. (2015)



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An alternative approach to modeling genetic merit of feed efficiency in dairy cattle

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Genetic relationships

$$u_{DMI,j} = b_1^{(u)} u_{Milke,j} + b_2^{(u)} u_{MBW,j} + u_{gRFI,j}$$

$$\text{var}(u_{gRFI,j}) = \sigma_{u_{gRFI}}^2$$

Multiple trait (MT) model also adjusted for ΔBW (i.e. hybrid gRFI/pRFI approach)

Residual relationships

$$e_{DMI,j} = b_1^{(e)} e_{Milke,j} + b_2^{(e)} e_{MBW,j} + e_{gRFI,j}$$

$$\text{var}(e_{gRFI,j}) = \sigma_{e_{gRFI}}^2$$

(Kennedy et al. 1993 did not consider separate coefficients for residuals)

$$h_{gRFI}^2 = \frac{\sigma_{u_{gRFI}}^2}{\sigma_{u_{gRFI}}^2 + \sigma_{e_{gRFI}}^2}$$

MT model approach assures that Milke and MBW are **BOTH** *genetically* and *residually* independent of gRFI!

$$\text{cor}(u_{Milke,j}, u_{gRFI,j}) = \text{cor}(u_{MBW,j}, u_{gRFI,j}) = 0$$

$$\text{cor}(e_{Milke,j}, e_{gRFI,j}) = \text{cor}(e_{MBW,j}, e_{gRFI,j}) = 0$$

(Not true in Kennedy et al. 1993)

An application



Genome-wide association analyses based on a multiple-trait approach for modeling feed efficiency

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- Feed intakes on 6,937 Holstein cows from 16 research stations within 4 countries

$$\text{DMI (kg)} = \text{env. effects} + 0.33 \text{ MilkE (Mcal)} + 0.09 \text{ MBW (kg}^{0.75}\text{)} + pRFI \text{ (kg)}$$

Rearrange this expression:

$$\begin{aligned} i. e. \hat{b}_1 &= 0.33 \text{ kg/Mcal} \\ \hat{b}_2 &= 0.09 \text{ kg/kg}^{0.75} \end{aligned}$$

→ $pRFI = \text{corrected DMI} - 0.33 \text{ MilkE} - 0.09 \text{ MBW}$

- So..... $pRFI$ is a linear combination (“derivative trait”) of DMI, MilkE and MBW
 - Once you’ve conducted a MT analysis on DMI, MilkE and MBW, there is **NO NEED TO DO A SEPARATE ANALYSES** to compute heritability of $pRFI$ and genetic correlations of $pRFI$ with these or other traits (Kennedy et al., 1993).

Multiple trait analyses of FE component traits (Lu et al., 2018; JDS)

- Variances-covariances (VCOV)

– Genetic VCOV

Residual VCOV

$$\hat{\mathbf{G}} = \begin{bmatrix} \text{MilKE} & & \\ 2.69 & 0.14 & 1.10 \\ 0.14 & 26.42 & 2.61 \\ 1.10 & 2.61 & 1.08 \\ & \text{MBW} & \\ & & \text{DMI} \end{bmatrix}$$

$$\hat{\mathbf{R}} = \begin{bmatrix} \text{MilKE} & & \\ 9.50 & 4.27 & 3.36 \\ 4.27 & 31.98 & 4.18 \\ 3.36 & 4.18 & 3.52 \\ & \text{MBW} & \\ & & \text{DMI} \end{bmatrix}$$

$$\hat{h}_1^2 = \frac{\text{MilKE}}{2.69 + 9.50} = 0.22 \quad \hat{h}_2^2 = 0.45 \quad \hat{h}_3^2 = 0.23$$

Genetic correlations

Residual correlations

$$\hat{\boldsymbol{\rho}}_g = \begin{bmatrix} 1 & 0.02 & 0.64 \\ 0.02 & 1 & 0.48 \\ 0.64 & 0.48 & 1 \end{bmatrix}$$

$$\hat{\boldsymbol{\rho}}_e = \begin{bmatrix} 1 & 0.25 & 0.58 \\ 0.25 & 1 & 0.39 \\ 0.58 & 0.39 & 1 \end{bmatrix}$$

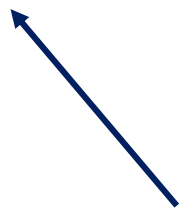
MilKE and MBW are potentially good predictors of DMI...
...genetically and phenotypically!

Example of Ecological Fallacy/Simpson's Paradox (Bello et al., 2012; JDS)

Within herd versus across herd relationships between milk yield and calving interval



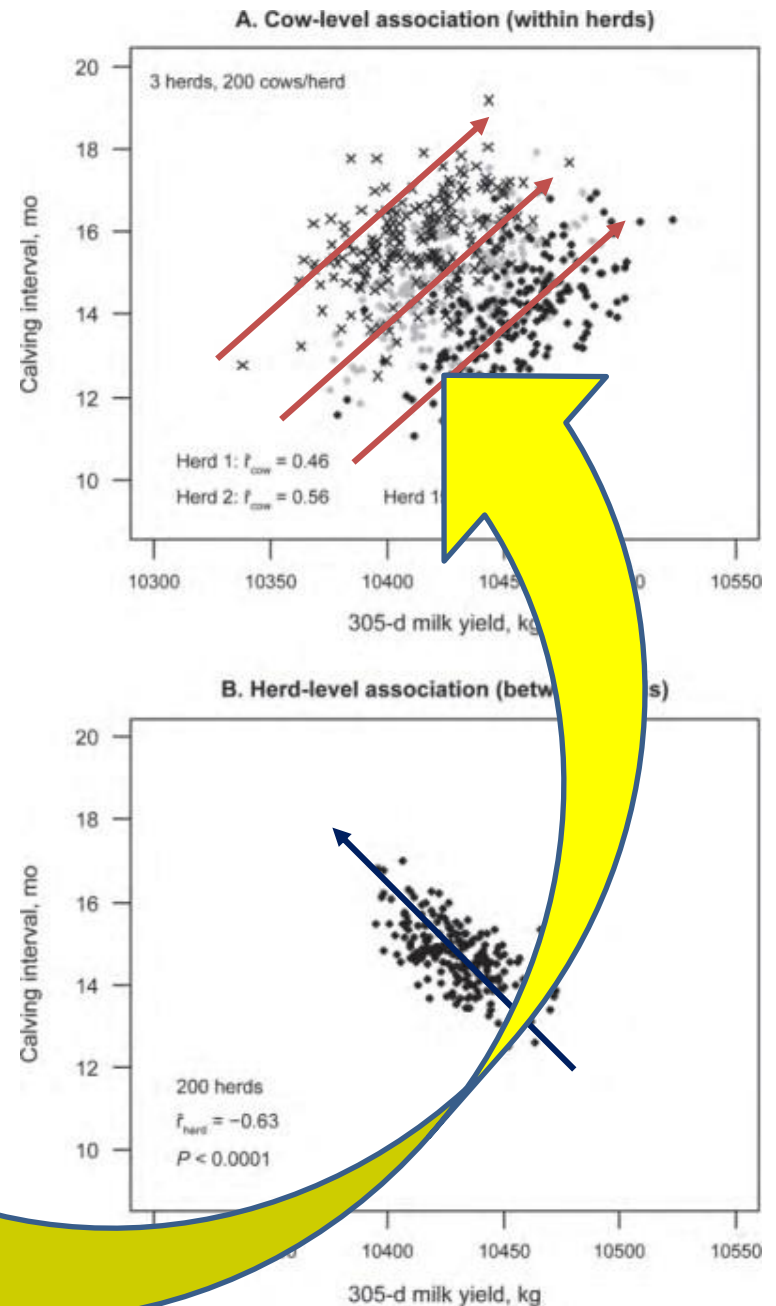
Positive (antagonistic) relationships between traits WITHIN herds



Negative (beneficial) relationship between traits ACROSS herds

In turn, could anticipate differences in genetic and residual correlations between traits.

Use of *pRFI* fails to recognize this



Simply deriving *gRFI* coefficients from a MT analyses

$$\hat{\mathbf{G}} = \begin{array}{c} \begin{array}{|cc|c|} \hline \text{Milke} & \text{MBW} & \text{DMI} \\ \hline 2.69 & 0.14 & 1.10 \\ 0.14 & 26.42 & 2.61 \\ \hline 1.10 & 2.61 & 1.08 \\ \hline \end{array} \\ \begin{array}{l} \text{Milke} \\ \text{MBW} \\ \text{DMI} \end{array} \end{array} = \begin{array}{c} \begin{array}{|c|c|} \hline \hat{\mathbf{G}}_{\text{sink,sink}} & \hat{\mathbf{G}}_{\text{sink,source}} \\ \hline \hat{\mathbf{G}}_{\text{source,sink}} & \hat{\mathbf{G}}_{\text{source,source}} \\ \hline \end{array} \end{array}$$

$$\begin{bmatrix} \hat{b}_1^{(u)} \\ \hat{b}_2^{(u)} \end{bmatrix} = \hat{\mathbf{G}}_{\text{source,sink}} \left(\hat{\mathbf{G}}_{\text{sink,sink}} \right)^{-1} = \begin{bmatrix} 1.10 & 2.61 \end{bmatrix} \begin{bmatrix} 2.69 & 0.14 \\ 0.14 & 26.42 \end{bmatrix}^{-1} = \begin{bmatrix} 0.40 \text{kg / Mcal} \\ 0.097 \text{kg / kg}^{0.75} \end{bmatrix}$$

Similarly,

$$\hat{\mathbf{R}} = \begin{array}{c} \begin{array}{|cc|c|} \hline 9.50 & 4.27 & 3.36 \\ 4.27 & 31.98 & 4.18 \\ \hline 3.36 & 4.18 & 3.52 \\ \hline \end{array} \\ \begin{array}{l} \text{Milke} \\ \text{MBW} \\ \text{DMI} \end{array} \end{array} = \begin{array}{c} \begin{array}{|c|c|} \hline \hat{\mathbf{R}}_{\text{sink,sink}} & \hat{\mathbf{R}}_{\text{sink,source}} \\ \hline \hat{\mathbf{R}}_{\text{source,sink}} & \hat{\mathbf{R}}_{\text{source,source}} \\ \hline \end{array} \end{array}$$

$$\begin{bmatrix} \hat{b}_1^{(e)} \\ \hat{b}_2^{(e)} \end{bmatrix} = \hat{\mathbf{R}}_{\text{source,sink}} \left(\hat{\mathbf{R}}_{\text{sink,sink}} \right)^{-1} = \begin{bmatrix} 3.36 & 4.18 \end{bmatrix} \begin{bmatrix} 9.50 & 4.27 \\ 4.27 & 31.98 \end{bmatrix}^{-1} = \begin{bmatrix} 0.31 \text{kg / Mcal} \\ 0.089 \text{kg / kg}^{0.75} \end{bmatrix}$$

- You could do the same thing with *pRFI*! $\hat{\mathbf{P}} = \hat{\mathbf{G}} + \hat{\mathbf{E}}$

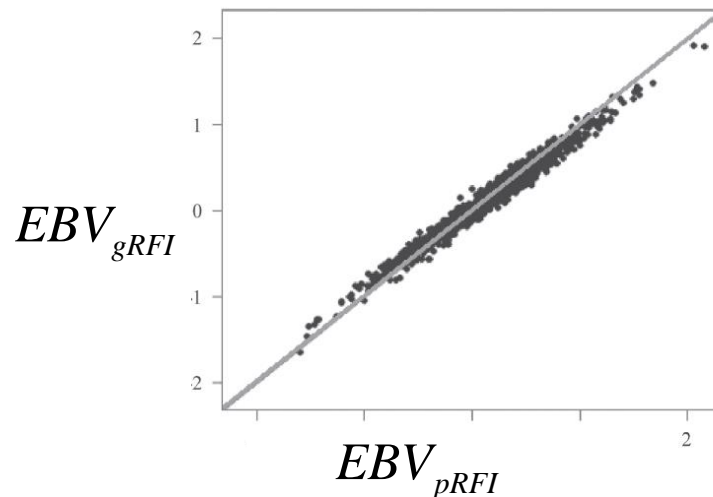
$$\begin{bmatrix} \hat{b}_1 \\ \hat{b}_2 \end{bmatrix} = \hat{\mathbf{P}}_{\text{source,sink}} \left(\hat{\mathbf{P}}_{\text{sink,sink}} \right)^{-1} = \begin{bmatrix} 0.33 \text{kg / Mcal} \\ 0.09 \text{kg / kg}^{0.75} \end{bmatrix}$$

Identical to conventional regression approach yet allows for missing data

gRFI vs *pRFI* comparisons (Lu et al., 2018)

Genetic parameters

Trait	Genetic variance	Residual variance	Heritability
<i>pRFI</i>	0.40 ± 0.05	2.09 ± 0.05	0.16 ± 0.02
<i>gRFI</i>	0.38 ± 0.05	2.09 ± 0.05	0.15 ± 0.02



Partial regressions of DMI on energy sink traits (Milke & MBW)

Trait	Component	Partial regression on Milke ($kg/Mcal$)	Partial Regression on MBW ($kg/kg^{0.75}$)
<i>pRFI</i>	Phenotypic	$\hat{b}_1 = 0.33 \pm 0.06$	$\hat{b}_2 = 0.09 \pm 0.02$
<i>gRFI</i>	Genetic	$\hat{b}_1^{(u)} = 0.40 \pm 0.02$	$\hat{b}_2^{(u)} = 0.097 \pm 0.008$
	Residual	$\hat{b}_1^{(e)} = 0.31 \pm 0.01$	$\hat{b}_2^{(e)} = 0.089 \pm 0.005$

Genetic relationships are stronger than residual relationships between DMI with Milke and MBW!

Actually, you never ever need to explicitly compute a RFI once you've done a multiple trait analyses on component traits!!!

e.g., Recall $u_{DMI} = b_1 u_{Milke} + b_2 u_{MBW} + u_{pRFI} = 0.33u_{Milke} + 0.09u_{MBW} + u_{pRFI}$

$$\begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -b_1 & -b_2 & 1 \end{bmatrix} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \end{bmatrix} \quad \text{or more specifically} \quad \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.33 & -0.09 & 1 \end{bmatrix} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \end{bmatrix}$$

Therefore

$$\text{var} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.33 & -0.09 & 1 \end{bmatrix} \mathbf{G} \begin{bmatrix} 1 & 0 & 0 & -0.33 \\ 0 & 1 & 0 & -0.09 \\ 0 & 0 & 1 & 1 \end{bmatrix} \quad \text{Let's use } \hat{\mathbf{G}} = \begin{bmatrix} 2.69 & 0.14 & 1.10 \\ 0.14 & 26.42 & 2.61 \\ 1.10 & 2.61 & 1.08 \end{bmatrix}$$

such that

$$\text{var} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{pRFI} \end{bmatrix} = \begin{bmatrix} 2.69 & 0.14 & 1.10 & 0.19 \\ 0.14 & 26.42 & 2.61 & 0.15 \\ 1.10 & 2.61 & 1.08 & 0.48 \\ 0.19 & 0.15 & 0.48 & 0.40 \end{bmatrix} \quad \Rightarrow \quad \rho \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0.02 & 0.64 & 0.18 \\ 0.02 & 1 & 0.48 & 0.05 \\ 0.64 & 0.48 & 1 & 0.73 \\ 0.18 & 0.05 & 0.73 & 1 \end{bmatrix}$$

Could similarly derive:

$$\text{var} \begin{bmatrix} e_{Milke} \\ e_{MBW} \\ e_{DMI} \\ e_{pRFI} \end{bmatrix} = \begin{bmatrix} 9.50 & 4.27 & 3.36 & -0.19 \\ 4.27 & 31.98 & 4.18 & -0.15 \\ 3.36 & 4.18 & 3.52 & 2.02 \\ -0.19 & -0.15 & 2.02 & 2.10 \end{bmatrix} \quad \Rightarrow \quad \rho \begin{bmatrix} e_{Milke} \\ e_{MBW} \\ e_{DMI} \\ e_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0.25 & 0.58 & -0.04 \\ 0.25 & 1 & 0.39 & -0.02 \\ 0.58 & 0.39 & 1 & 0.74 \\ -0.04 & -0.02 & 0.74 & 1 \end{bmatrix}$$

Note that $\hat{h}_{pRFI}^2 = \frac{0.40}{0.40 + 2.10} = 0.16$

Just like in Lu et al. (2018)...but without doing the additional analysis on pRFI!

Same thing is true for gRFI!

$$\begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -b_1^{(u)} & -b_2^{(u)} & 1 \end{bmatrix} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \end{bmatrix} \quad \Rightarrow \quad \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.40 & -0.10 & 1 \end{bmatrix} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \end{bmatrix}$$

Using estimates from Lu et al. (2018)

Therefore

$$\Rightarrow \text{var} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.40 & -0.10 & 1 \end{bmatrix} \mathbf{G} \begin{bmatrix} 1 & 0 & 0 & -0.40 \\ 0 & 1 & 0 & -0.10 \\ 0 & 0 & 1 & 1 \end{bmatrix} \quad \text{Let's use } \hat{\mathbf{G}} = \begin{bmatrix} 2.69 & 0.14 & 1.10 \\ 0.14 & 26.42 & 2.61 \\ 1.10 & 2.61 & 1.08 \end{bmatrix} \text{ from Lu et al. (2018)}$$

such that

$$\Rightarrow \text{var} \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \end{bmatrix} = \begin{bmatrix} 2.69 & 0.14 & 1.10 & 0 \\ 0.14 & 26.42 & 2.61 & 0 \\ 1.10 & 2.61 & 1.08 & 0.38 \\ 0 & 0 & 0.38 & 0.38 \end{bmatrix} \quad \Rightarrow \quad \rho \begin{bmatrix} u_{Milke} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0.02 & 0.64 & 0 \\ 0.02 & 1 & 0.48 & 0 \\ 0.64 & 0.48 & 1 & 0.60 \\ 0 & 0 & 0.60 & 1 \end{bmatrix}$$

Genetic correlations

Key points/reminders

“Restricted selection index”
(Kennedy et al., 1993)

u_{gRFI} uncorrelated with u_{Milke} and u_{MBW}

$$\text{COV}(u_{DMI}, u_{gRFI}) = \sigma_{u,RFI}^2$$

$$\text{CORR}(u_{DMI}, u_{gRFI}) = \sqrt{\sigma_{u,gRFI}^2 / \sigma_{u,DMI}^2}$$

Deriving residual covariance parameters for gRFI

$$\begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \\ e_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -b_1^{(e)} & -b_2^{(e)} & 1 \end{bmatrix} \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \end{bmatrix} \quad \longrightarrow \quad \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \\ e_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.31 & -0.09 & 1 \end{bmatrix} \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \end{bmatrix}$$

Different from Kennedy et al. (1993)..they re-use $b_1^{(u)}$ and $b_2^{(u)}$

Using estimates from Lu et al. (2018)

Therefore

$$\text{var} \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \\ e_{gRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.31 & -0.09 & 1 \end{bmatrix} \mathbf{R} \begin{bmatrix} 1 & 0 & 0 & -0.31 \\ 0 & 1 & 0 & -0.09 \\ 0 & 0 & 1 & 1 \end{bmatrix}$$

Let's use $\hat{\mathbf{R}} = \begin{bmatrix} 9.50 & 4.27 & 3.36 \\ 4.27 & 31.98 & 4.18 \\ 3.36 & 4.18 & 3.52 \end{bmatrix}$
from Lu et al. (2018)

such that

$$\text{var} \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \\ e_{gRFI} \end{bmatrix} = \begin{bmatrix} 9.50 & 4.27 & 3.36 & 0 \\ 4.27 & 31.98 & 4.18 & 0 \\ 3.36 & 4.18 & 3.52 & 2.09 \\ 0 & 0 & 2.09 & 2.09 \end{bmatrix}$$

Residual correlations

$$\rho = \begin{bmatrix} e_{MilKE} \\ e_{MBW} \\ e_{DMI} \\ e_{pRFI} \end{bmatrix} = \begin{bmatrix} 1 & 0.25 & 0.58 & 0 \\ 0.25 & 1 & 0.39 & 0 \\ 0.58 & 0.39 & 1 & 0.77 \\ 0 & 0 & 0.77 & 1 \end{bmatrix}$$

- Key points/reminders

– e_{gRFI} uncorrelated with e_{MilKE} and e_{MBW}

$$\text{COV}(e_{DMI}, e_{gRFI}) = \sigma_{e,RFI}^2$$

$$\text{corr}(e_{DMI}, e_{gRFI}) = \sqrt{\sigma_{e,gRFI}^2 / \sigma_{e,DMI}^2}$$

$$\hat{h}_{gRFI}^2 = \frac{0.38}{0.38 + 2.09} = 0.15$$

Feed Saved

- Currently popular feed efficiency trait (AUS, CRV)
- Pryce et al., 2015

– Recall $DMI_{adj} = b_1 (Milke - \overline{Milke}) + b_2 (MBW - \overline{MBW}) + pRFI$

Combine together

• $pRFI$



• Energy required for maintenance = $b_2 (MBW - \overline{MBW})$



- *Feed saved (FS)*

$$FS = - \left(b_2 (MBW - \overline{MBW}) + pRFI \right) = - \left(DMI_{adj} - b_1 (Milke - \overline{Milke}) \right)$$

Easier for industry to understand

- Why not consider **genetic Feed Saved** (u_{gFS})?

$$u_{gFS} = - \left(b_{MBW}^{(u)} u_{MBW} + u_{gRFI} \right) = - \left(u_{DMI} - b_{Milke}^{(u)} u_{Milke} \right)$$

- i.e. genetic rather than phenotypic regressions...just as with *gRFI*!!

Other possibilities

Residual milk energy (Coleman et al., 2010):

- Switch the trait order : adjust MilkE for MBW & DMI

$$u_{MilkE,j} = b_{DMI}^{(u)*} u_{DMI,j} + b_{MBW}^{(u)*} u_{MBW,j} + u_{gRMilkE,j}$$



$$u_{gRMilkE,j} > 0$$

- i.e. use genetic regressions.



$$u_{gRMilkE,j} < 0$$

- *Feed Conversion or Gross efficiency **ratio***

$$\frac{DMI}{MilkE} \text{ or } \frac{MilkE}{DMI}$$

...difficult to work with... not normally distributed and need to express EBVs relative to a baseline-> option: use a Bayesian approach (Shirali et al., 2018)

NOT DISCUSSED FURTHER: linear measures are more highly related to profit (selection indexes, IOFC) than ratio measures!

Relationship between alternative FE traits

Derivative traits

$$\begin{bmatrix} u_{MilKE} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \\ u_{gFS} \\ u_{gRMilKE} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -b_{MilKE}^{(u)} & -b_{MBW}^{(u)} & 1 \\ b_{MilKE}^{(u)} & 0 & -1 \\ 1 & -b_{MBW}^{(u)*} & -b_{DMI}^{(u)*} \end{bmatrix} \begin{bmatrix} u_{MilKE} \\ u_{MBW} \\ u_{DMI} \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ -0.40 & -0.10 & 1 \\ 0.40 & 0 & -1 \\ 1 & 0.13 & -1.32 \end{bmatrix} \begin{bmatrix} u_{MilKE} \\ u_{MBW} \\ u_{DMI} \end{bmatrix}$$

Although you don't need to record MBW for FS!...*it's a potential predictor trait for FS!*

Using the same \hat{G} as provided earlier:

Genetic correlations

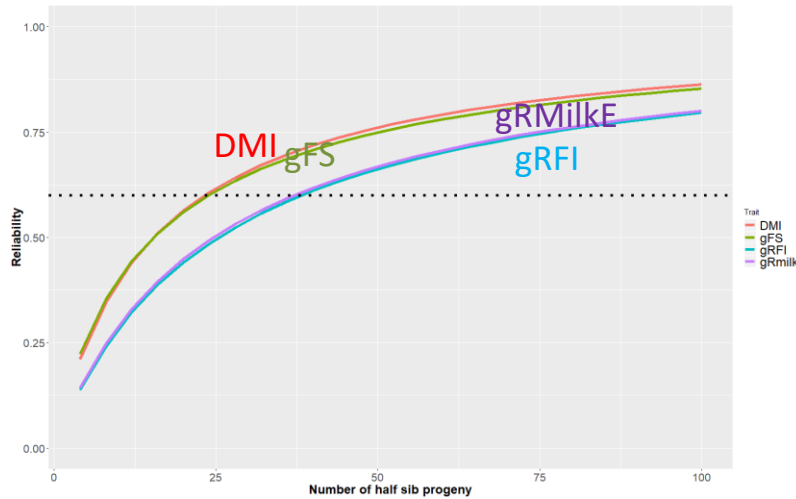
$$\hat{\rho} = \begin{bmatrix} u_{MilKE} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \\ u_{gFS} \\ u_{gRMilKE} \end{bmatrix} = \begin{bmatrix} 1 & 0.02 & 0.64 & 0 & -0.01 & 0.68 \\ 0.02 & 1 & 0.48 & 0 & -0.63 & 0 \\ 0.64 & 0.48 & 1 & 0.60 & -0.77 & 0 \\ 0 & 0 & 0.60 & 1 & -0.78 & -0.73 \\ -0.01 & -0.63 & -0.77 & -0.78 & 1 & 0.57 \\ 0.68 & 0 & 0 & -0.73 & 0.57 & 1 \end{bmatrix}$$

MilKE and MBW are **NOT** predictors of gRFI...genetic independence

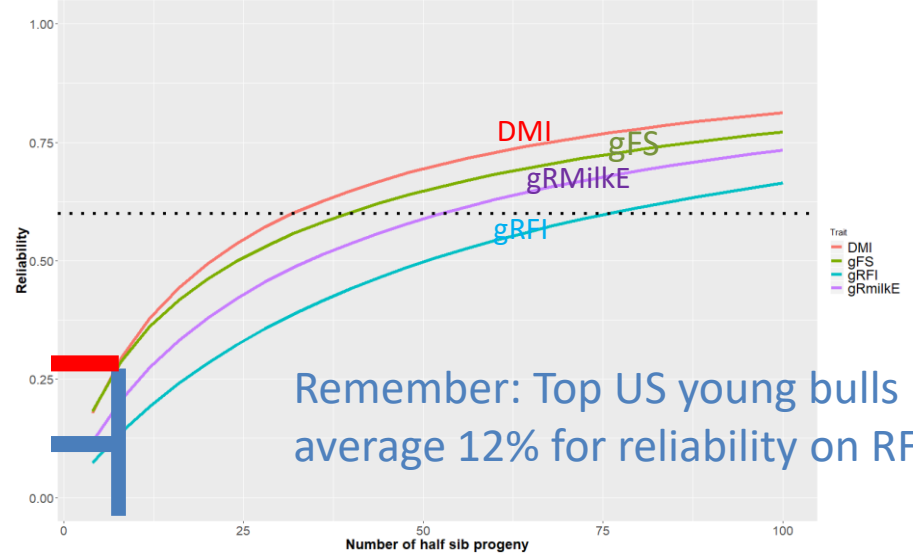
$$\hat{h}_{DMI}^2 = 0.23 > \hat{h}_{gFS}^2 = 0.21 > \hat{h}_{gRMilKE}^2 = 0.17 > \hat{h}_{gRFI}^2 = 0.15$$

PTA reliabilities on sires for different proportions of daughters having DMI records (all daughters have MilkE, MBW records)

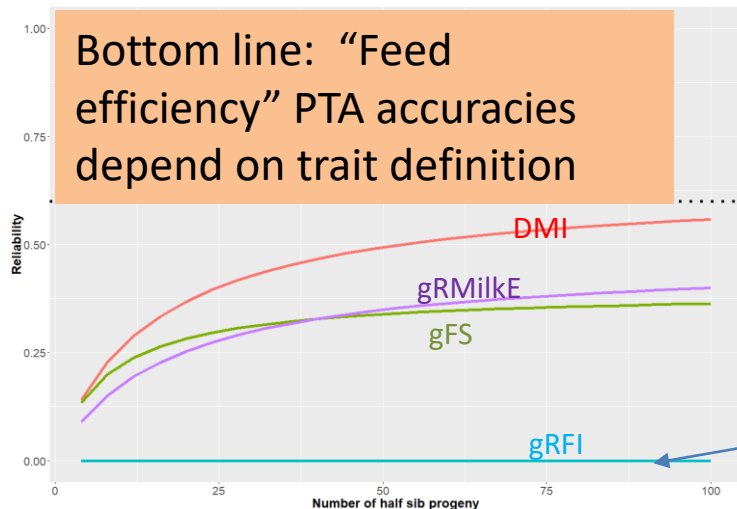
100% of daughters having DMI records



50% of daughters having DMI records



No daughters having DMI records



$$\rho \begin{bmatrix} u_{MilkE} \\ u_{MBW} \\ u_{DMI} \\ u_{gRFI} \\ u_{gFS} \\ u_{gRMilkE} \end{bmatrix} = \begin{bmatrix} 1 & 0.02 & 0.64 & 0 & -0.01 & 0.68 \\ 0.02 & 1 & 0.48 & 0 & -0.63 & 0 \\ 0.64 & 0.48 & 1 & 0.60 & -0.77 & 0 \\ 0 & 0 & 0.60 & 1 & -0.78 & -0.73 \\ -0.01 & -0.63 & -0.77 & -0.78 & 1 & 0.57 \\ 0.68 & 0 & 0 & -0.73 & 0.57 & 1 \end{bmatrix}$$

Want meaningful genetic evaluations on metabolic efficiency (RFI)??...then you need DMI records!

Selection index as a function of DMI

- Suppose efficiency index ($EI.. \$/d$) only involves MilkE, MBW, & DMI.

$$EI = v_1 EBV_{MilkE} + v_2 EBV_{MBW} + v_3 EBV_{DMI} \quad \text{economic weights} \quad \begin{cases} v_1 > 0 \\ v_2 : ? \\ v_3 < 0 \end{cases}$$

- Assume:

- $v_1 = \$0.60/\text{Mcal}$ (based on milk fat prices)

- $v_2 = 0$ (don't factor in feed costs here!...that's already in v_3 !!!)

- $v_3 = - \$0.25/\text{Kg}$ (feed costs...AS IS)

- Elsie's EBVs $EBV_{MilkE} = +1.6\text{Mcal}$; $EBV_{MBW} = +5.0\text{kg}^{.75}$; $EBV_{DMI} = +1.0\text{kg}$



$$EI = 0.60(+1.6) + 0(+5.0) - 0.25(+1.0) = +\$0.71/d$$

Write same efficiency index...but now as a function of gRFI!

- From Lu et al. (2018):

$$EBV_{DMI} = b_{MilkE}^{(u)} EBV_{MilkE} + b_{MBW}^{(u)} EBV_{MBW} + EBV_{gRFI}$$

- Plug this into

$$EI = v_1 EBV_{MilkE} + v_2 EBV_{MBW} + v_3 EBV_{DMI}$$

Genetic-Economic Discounts for DMI when RFI is specified in index

$$\begin{aligned}
 EI &= v_1 EBV_{MilkE} + v_2 EBV_{MBW} + v_3 \left(b_{MilkE}^{(u)} EBV_{MilkE} + b_{MBW}^{(u)} EBV_{MBW} + EBV_{gRFI} \right) \\
 &= \left(v_1 + v_3 b_{MilkE}^{(u)} \right) EBV_{MilkE} + \left(v_2 + v_3 b_{MBW}^{(u)} \right) EBV_{MBW} + v_3 EBV_{gRFI} \\
 &= \left(0.60 - 0.25(0.40) \right) EBV_{MilkE} + \left(0 - 0.25(0.10) \right) EBV_{MBW} + (-0.25) EBV_{gRFI} \\
 &= 0.50 EBV_{MilkE} - 0.025 EBV_{MBW} - 0.25 EBV_{gRFI}
 \end{aligned}$$

gRFI for Elsie



$$\begin{aligned}
 EBV_{gRFI} &= EBV_{DMI} - b_{MilkE}^{(u)} EBV_{MilkE} - b_{MBW}^{(u)} EBV_{MBW} \\
 &= +1.0 - 0.40(+1.6) - 0.10(+5.0) = -0.14
 \end{aligned}$$

Lu et al. (2015)

EI as function of gRFI:

$$EI = 0.5(1.6) - 0.025(5.0) - 0.25(-0.14) = \$0.71/d$$

Same as before!!!!

Selection Index Weights

EI being function of which FE trait?	Actual (relative) economic weight on MilkE	Actual (relative) economic weight on MBW	Actual (relative) economic weight on FE trait	Elsie's Efficiency Index (EI)
DMI	0.60 (79%)	0 (0%)	-0.25 (21%)	\$+0.71
gRFI	0.50 (74%)	-0.025 (12%)	-0.25 (14%)	\$+0.71
gFS	0.50 (81%)	0 (0%)	-0.25 (19%)	\$+0.71

Actual weights on FE trait don't change!

Reliability of EI does not change whether EI is written as function of DMI, gRFI, gFS (or pRFI or pFS or residual milk energy for that matter)!!!

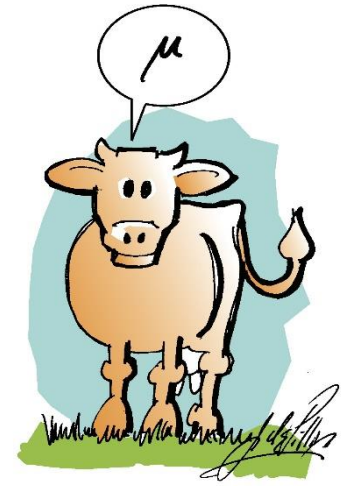
Conclusions for genetic evaluation of Feed Efficiency (FE)

- DMI vs RFI vs FS...vs whatever. **DOES IT MATTER??**
 - Actual selection index (SI) does (**SHOULD**) **NOT** change if it's a function of DMI, FS or RFI...**even though h^2 of FE traits vary from each other.**
 - It might only matter if breeders wish to deviate from SI and upweight *biological efficiency* (RFI) or *economic efficiency* (FS)
- Of the 3 (DMI,RFI,FS), FS might be the most economically meaningful FE EBV to report, but RFI still most relevant for metabolic efficiency studies(e.g. GWAS -> Lu et al., 2018)...FS is a genetically more complex trait
 - Strongly advocate the use of **genetic regressions** for both FS and RFI given potential differences in genetic versus residual relationships between component traits.
 - g_{RFI} g_{FS} g_{RMilKE} ✓

Other issues to contend with in selection indexes

- **Badly need genetic correlation** estimates between DMI/RFI/FS and other traits in NM\$
- RFI/FS sink coefficients may be changing systematically over time:
 - e.g. b_2 on (M)BW.... \uparrow
 - implies that genetic/residual correlations are changing between DMI and (M)BW ?
 - Substantial heterogeneity in $pRFI$ coefficients (Tempelman et al., 2015) and $gRFI$ coefficients (Lu et al., 2017) across herds and rations as well.

THANK YOU!



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