The use of novel phenotyping technologies in animal breeding

Henk Bovenhuis, ABG, Wageningen University & Research

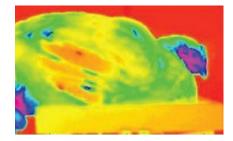




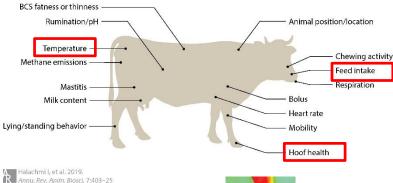


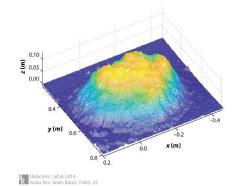


Novel phenotyping technologies - sensors



Temperature



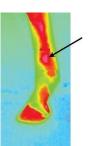


Sensors:

- Machine vision (cameras)
- Sound
- Accelerometers
- Electronic nose
- GPS
 -





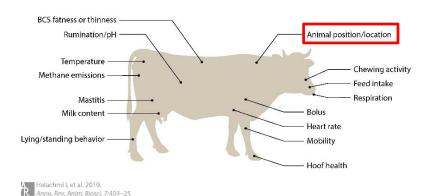


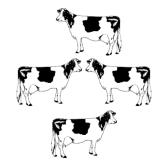
Halachmi I, et al. 7019. Annu. Rev. Anim. Biosci. 7:403–25

inflammation in the leg

individual feed intake

Novel phenotyping technologies - sensors





Behaviour: social interactions Disease: Transmission Infection

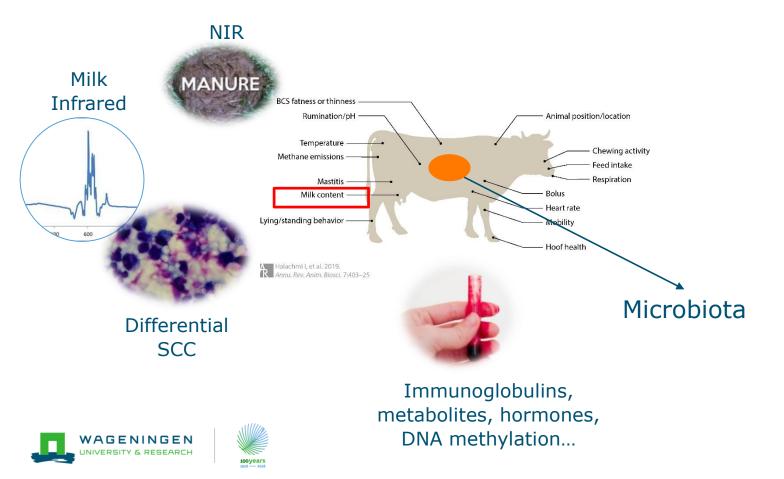
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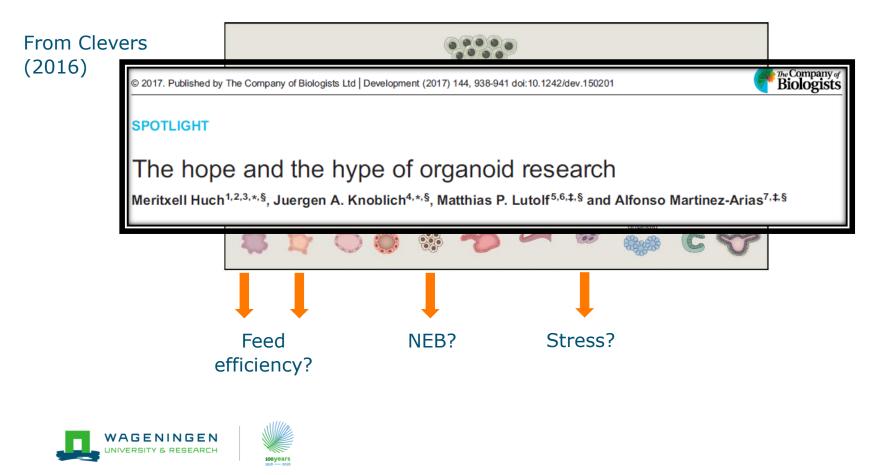


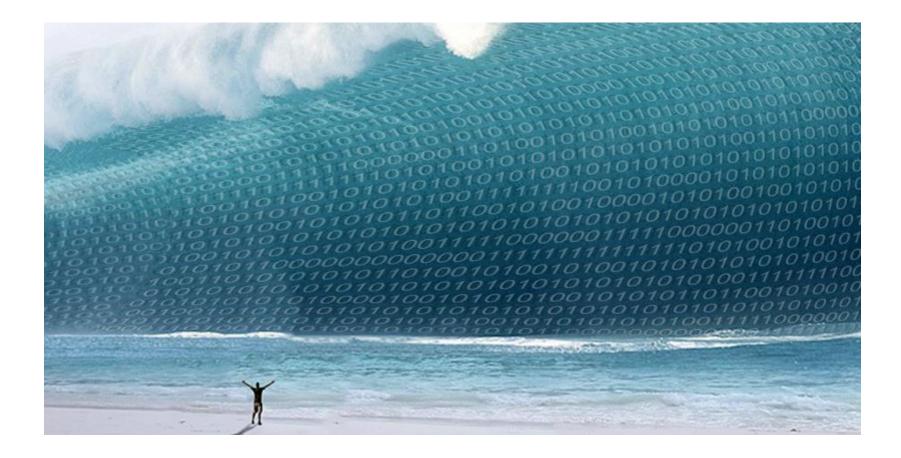


Novel phenotyping technologies – "omics"



Novel phenotyping technologies – organoids

















Management indicators

Larger farms / More cows per farmer

Less (quality) time individual cow

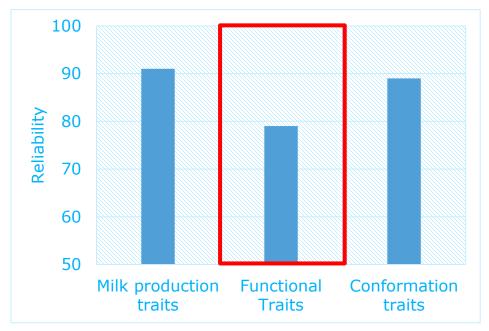
How does the farmer know what the cow needs/wants?



AMS



Do breeders need additional phenotypes??



$$\mathsf{H} = \mathsf{v}_1 \mathsf{A}_1 + \mathsf{v}_2 \mathsf{A}_2 + \dots$$

Additional breeding goal traits??

Average reliability published EBV Dutch HF bulls (n=950, 12-2018)



Do breeders need additional phenotypes??

- Environmental impact Feed efficiency, Methane emission, Phosphorus efficiency, Nitrogen efficiency....
- Cow Health Disease resistance, longevity....
- Product quality Manufacturing, Nutritious value



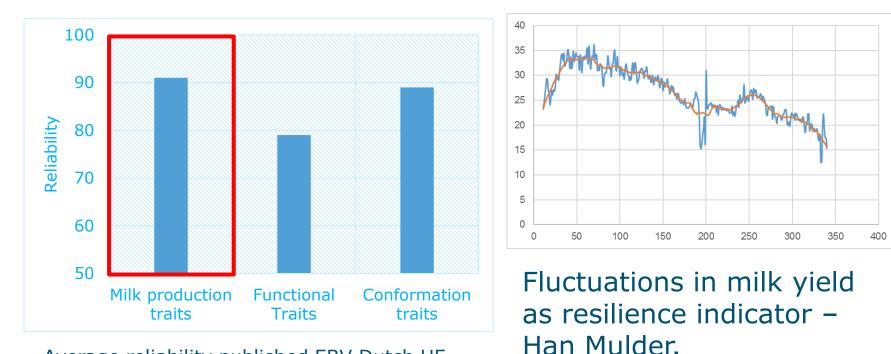








Do breeders need additional phenotypes??



Average reliability published EBV Dutch HF bulls (n=950, 12-2018)





Requirements ??

Accuracy and bias

Price

- High-throughput
- Non-destructive







Use??

- Research
- Management
- > Breeding value estimation
- Payment









Research

Management

- Breeding value estimation
- Payment





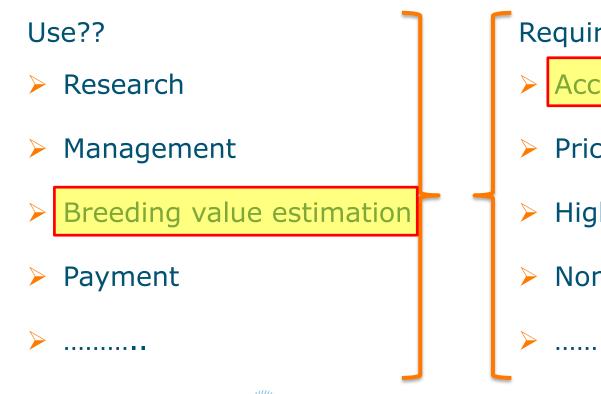


Requirements ??

Accuracy and bias

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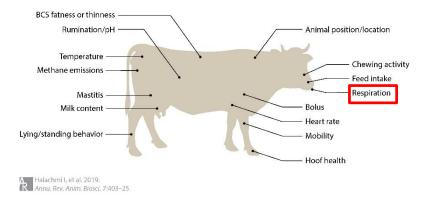


Requirements ??

Accuracy and bias

Price

- High-throughput
- Non-destructive



Sensors:

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Sniffer CH4 $ightarrow h^2 \approx 0.10$ $ightarrow r \approx 0.25$ $ightarrow herd \approx 0.60$



J. Dairy Sci. 101:9619–9620 https://doi.org/10.3168/jds.2018-14704 © American Dairy Science Association[®], 2018.

Letter to the Editor: Challenging one sensor method for screening dairy cows for reduced methane emissions

P. Huhtanen*¹ and A. N. Hristov†

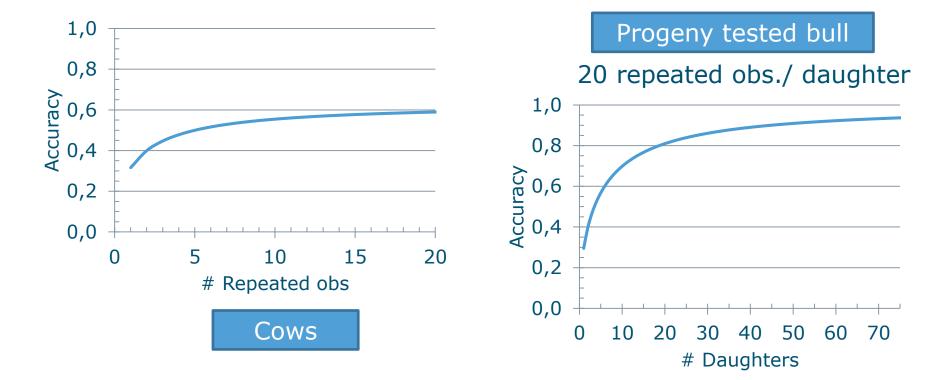
*Department of Agricultural Science, Swedish University of Agricultural Sciences, S-90183 Umeå, Sweden †Department of Animal Science, The Pennsylvania State University, University Park 16802

"... the need for high throughput methodology, e.g. for screening large numbers of animals for genomic studies, **does not in itself justify the use of methods that are inaccurate, imprecise, or biased**" (Hammond et al., 2016).



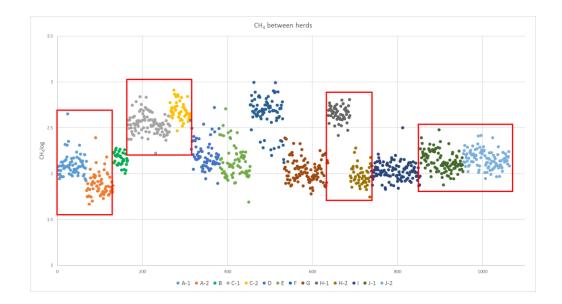


Accuracy of EBV- h²=0.10, **r=0.25**





Bias due to Herd effects



 $Y = HTD + \dots$ Anim + PE + e







Systematic "errors"



$$H = v_1A_1 + v_2A_2 + \dots + v_nCH_4$$

Genetic
correlation
$$I = b_1X_1 + b_2X_2 + \dots + b_nCH_4 - sniffer$$

Sniffer CH4 as **indicator** for "true" CH4.







Use??

- Research
- > Management
- Breeding value estimation

X

X

 $\mathbf{\Lambda}$

X

Payment







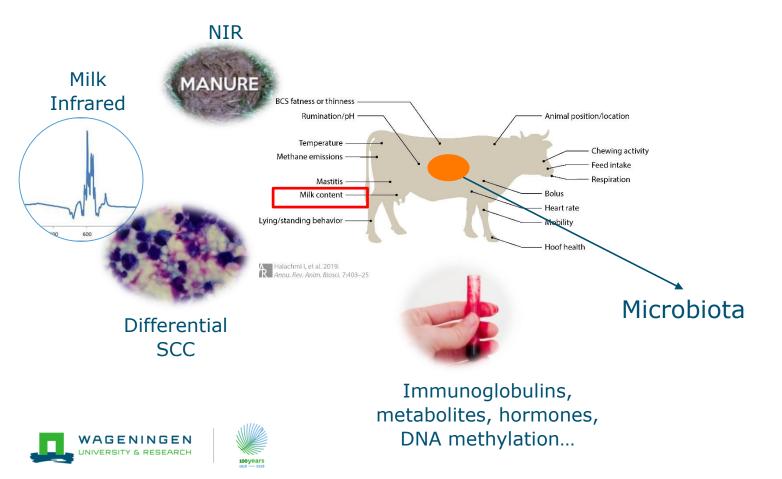
Inaccurate and biased sensor data can provide valuable information for selective breeding.

"Nice to have" vs "Need to have"





Novel phenotyping technologies – "omics"





J. Dairy Sci. 102:6288–6295 https://doi.org/10.3168/jds.2018-15684 © American Dairy Science Association®, 2019.

Validation strategy can result in an overoptimistic view of the ability of milk infrared spectra to predict methane emission of dairy cattle

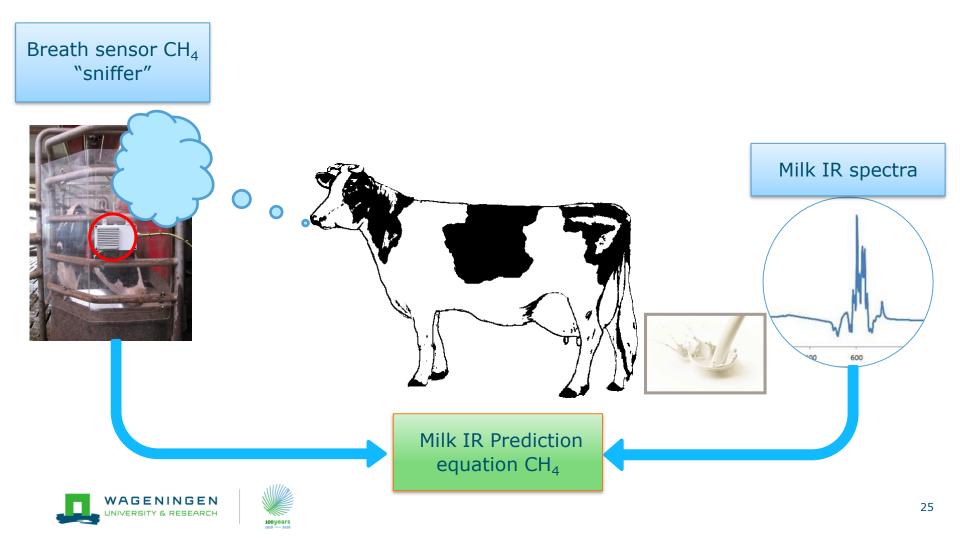
Qiuyu Wang and Henk Bovenhuis*

Animal Breeding and Genomics Group, Wageningen University, PO Box 338, 6700AH, Wageningen, the Netherlands









Data

CH₄ Sniffer in AMS Average over 5-day period: 2 days before, during and 2 days after milk recording

- IR spectra Qlip Selected set of 275 IR wavenumbers
- Animals 801 cows on 10 commercial herds





Methods

- Partial Least Squares Regression
- Validation Strategy Random Cross-Validation







Calibration

n=640 (80%)

Validation n=161 (20%)





Results – validation R²

Prediction	Random CV R ²
Infrared	0.49

$R_{cv}^2 = 0.49$ is within the range of published values (0.13-0.72)







Calibration

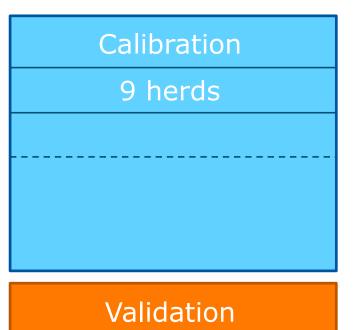
n=640 (80%)

Validation n=161 (20%)





Block cross validation



Herd 10

Results – validation R²

Prediction	Random CV R ²	Block CV R ²
Infrared	0.49	0.01

Cross validation strategy has a big impact on the results (and conclusions)!!





"Negative control"

Selected 114 wavenumbers from the Water Absorption Regions:

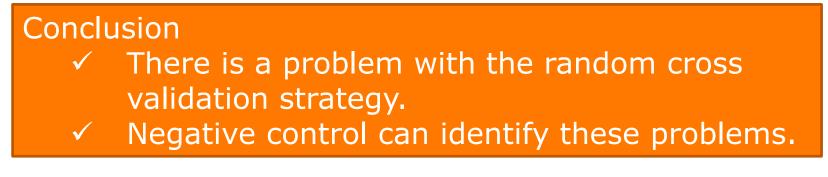
- ✓ contain mainly "noise"
- ✓ not informative for predicting milk composition Expected $R^2 \approx 0$





"Negative control"

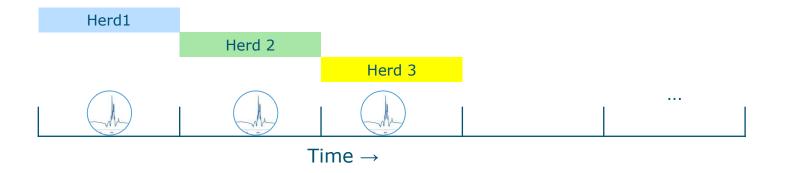
Prediction	Random CV R ²	Block CV R ²
Infrared	0.49	0.01
Negative control	0.25	0.03







Diagnosis



- Confounding of "herd" and "date of IR" analysis
- Random Cross Validation: errors associated with "date of IR" analysis explain between herd differences in CH₄



Is this a special case??

- Confounding "herd" and "date of IR" analysis
- Differences due to herds 60% variation
- CH₄ respiration chambers???
 Ring test calibration of respiration chambers in the UK suggest substantial "batch effects" (Gardiner et al. 2015)





OPINION

Tackling the widespread and critical impact of batch effects in high-throughput data

Jeffrey T. Leek, Robert B. Scharpf, Héctor Corrada Bravo, David Simcha, Benjamin Langmead, W. Evan Johnson, Donald Geman, Keith Baggerly and Rafael A. Irizarry

NATURE REVIEWS GENETICS

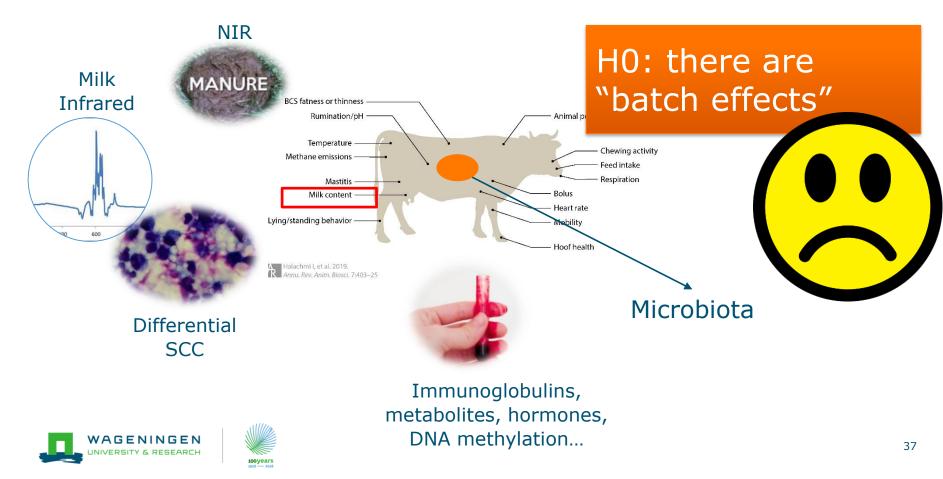
VOLUME 11 OCTOBER 2010 733

"One often overlooked complication with such studies is **batch effects**, which occur because measurements are affected by laboratory conditions, reagent lots and personnel differences.





Novel phenotyping technologies – "omics"



Conclusions

- Inaccurate and biased sensor data can provide valuable information for selective breeding.
- Choose your validation strategy carefully.
- H0: high throughput data are affected by "batch effects".

