

EAAP 2019 Ghent

Potential use of MIR spectra in the prediction of hoof disorders in Holstein Friesians

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² CRV BV

³ Walloon Agricultural Research Center (CRA-W)



Context



Context



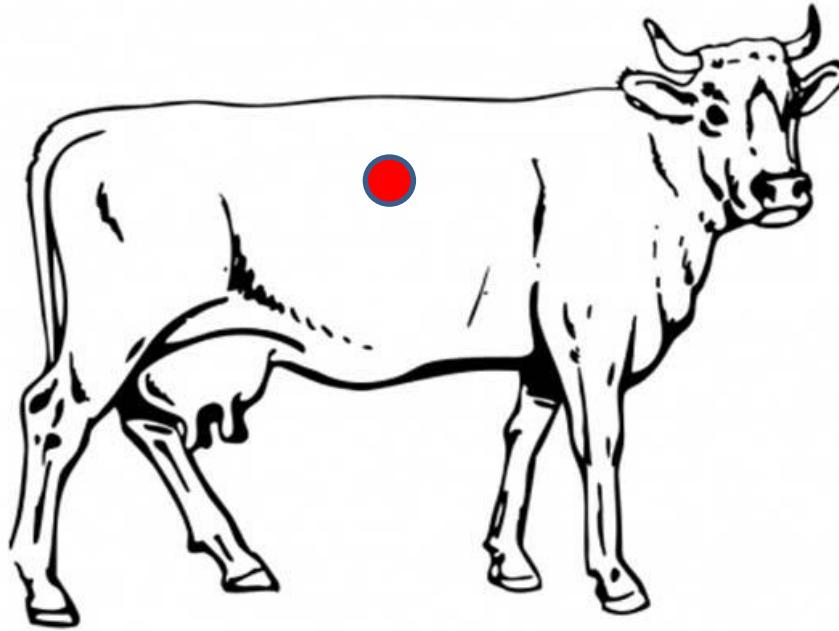
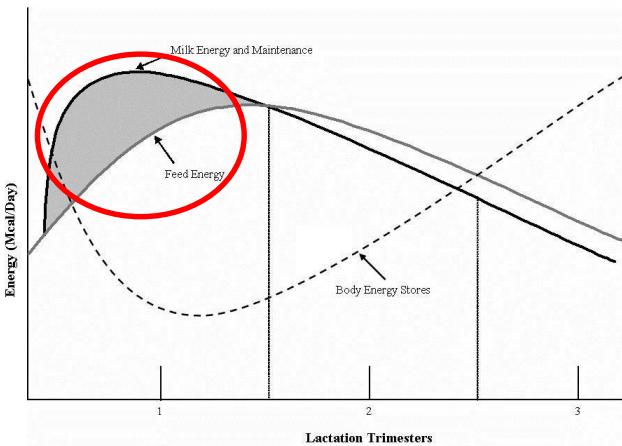
Context



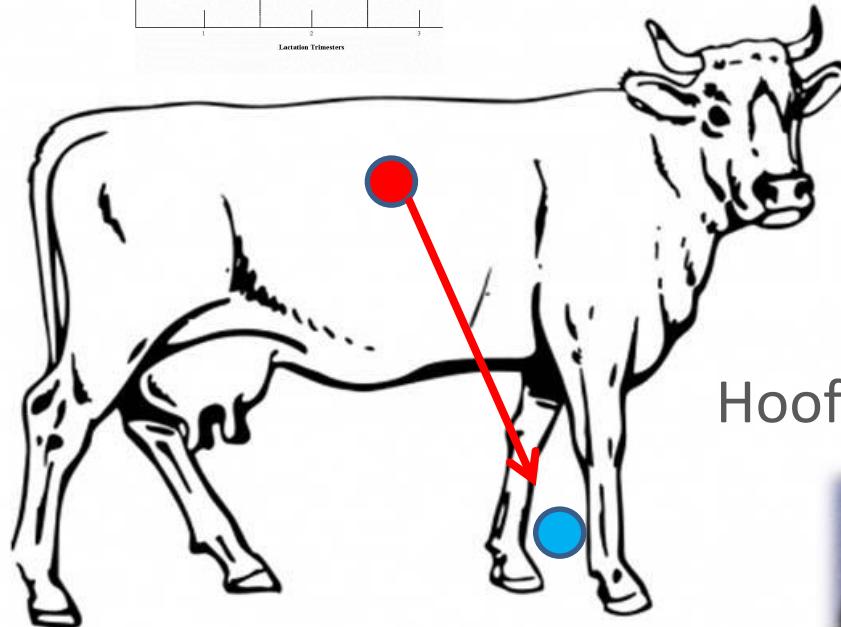
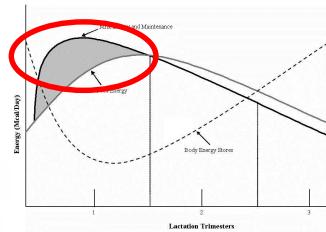
Context



Hypothesis



Hypothesis



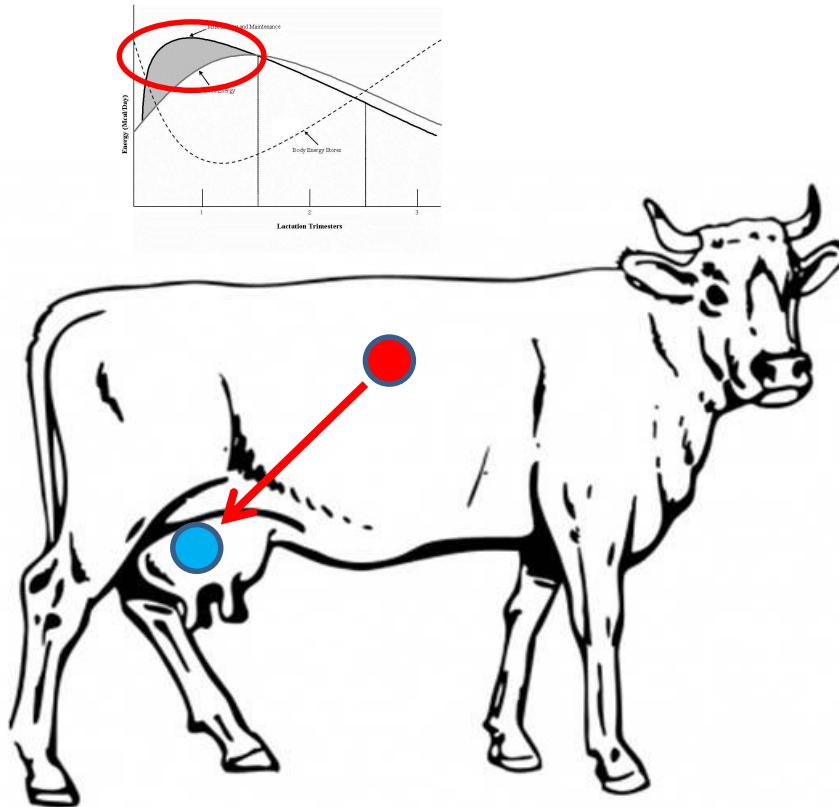
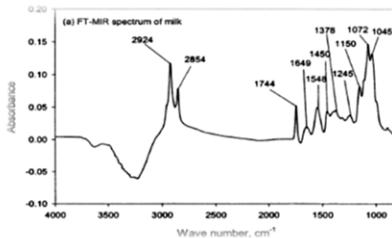
Hoof disease score



Hypothesis



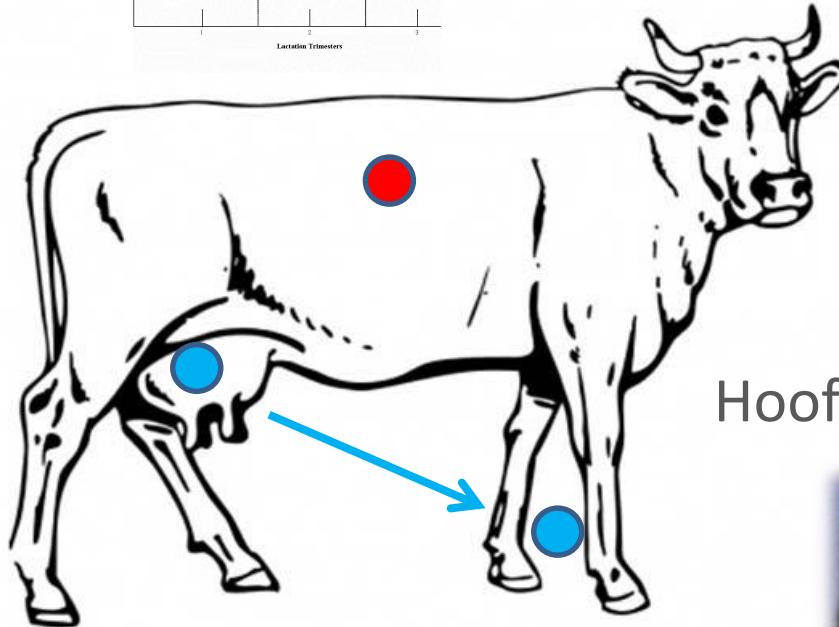
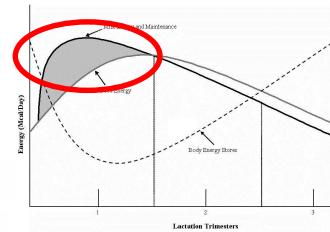
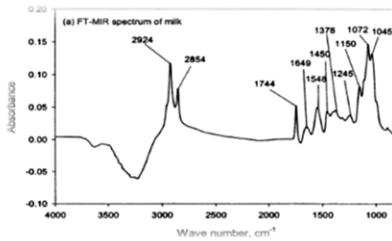
Milk composition
=
MIR spectra



Hypothesis



Milk composition
=
MIR spectra



Hoof disease score

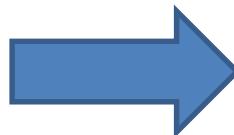


(CRV 2019)

Mid-infrared technology

MIR analysis

Milk samples



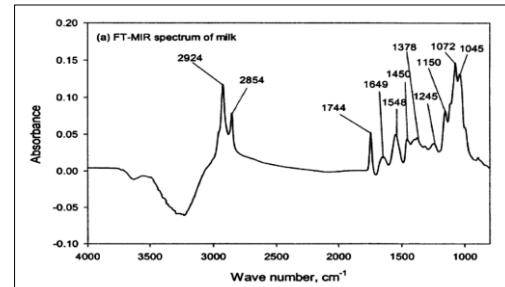
MIR spectra

Prediction

Novel components

- BHB, acetone ...

Cow health status



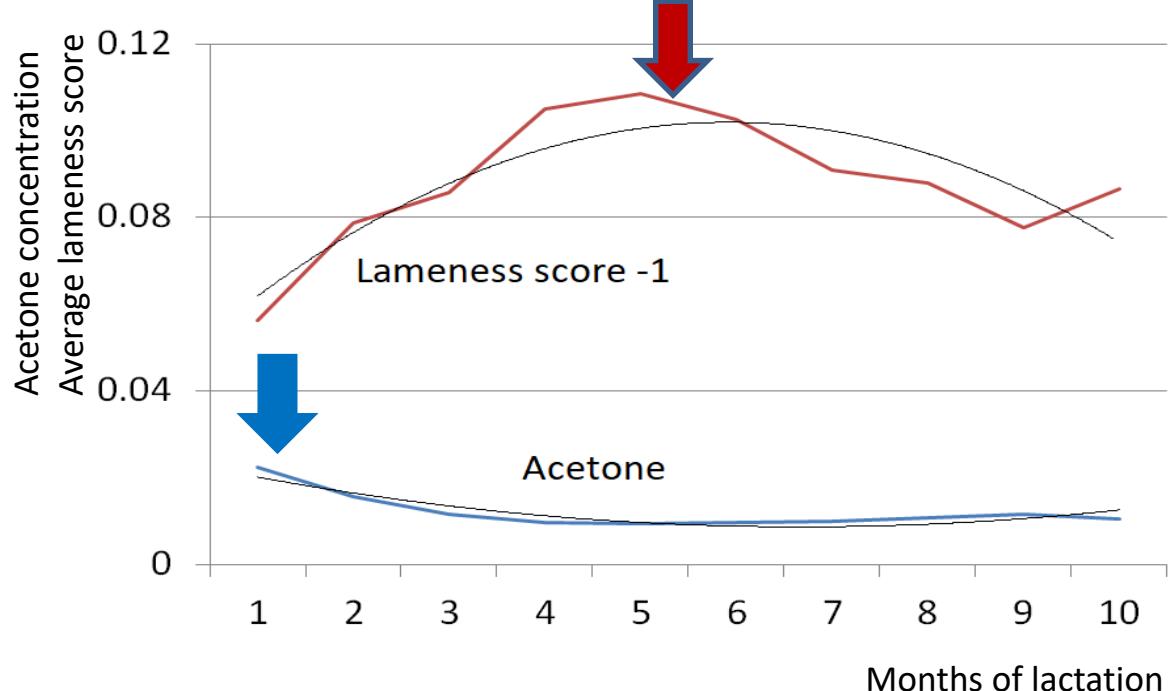
Reference values





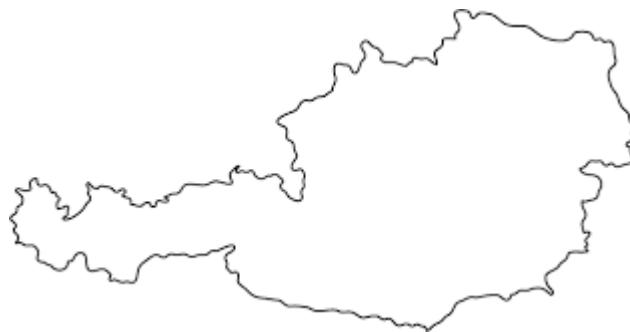
Previous research

- ▶ Milk Metabolites
- ▶ Locomotion scores



Previous research

▶ Austrian data



Zucht
Data
EDV-DIENSTLEISTUNGEN GMBH

A. Mineur *et al.*, EAAP 2018

Present research

▶ Dutch data



CRV

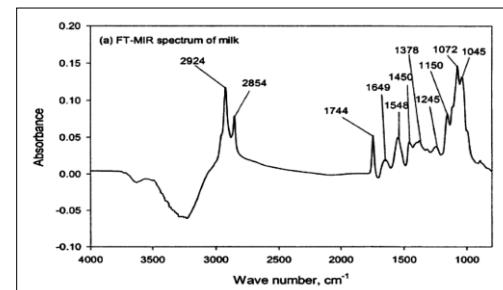
Previous research

- ▶ Austrian data
- ▶ MIR based metabolites

[BHB]
[acetone]
[citrate]

Present research

- ▶ Dutch data
- ▶ MIR spectra



Previous research

- ▶ Austrian data
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A. Mineur *et al.*, EAAP 2018

Present research

- ▶ Dutch data
- ▶ MIR spectra
- ▶ Hoof disease scores

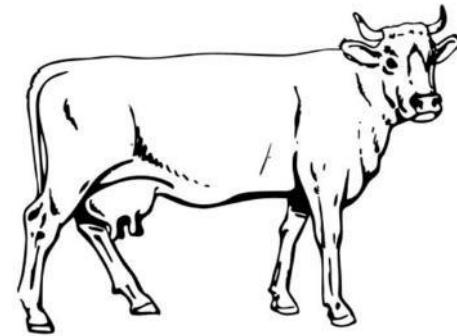


(CRV 2019)

Data

▣ Holstein Friesian, 2013 - 2018

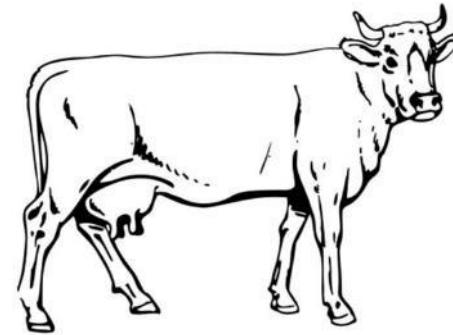
- 267 009 cows
- 2299 herds



Material and methods

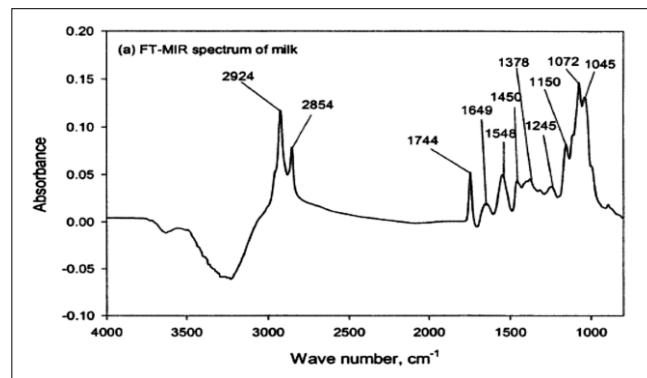
▣ Holstein Friesian, 2013 - 2018

- 267 009 cows
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▣ MIR spectra: 3 154 241

- 1060 total wavenumbers
- First derivative
- 212 selected wavenumbers



Data

► Hoof scores: 386 676

- 0 = healthy
- 1 = light, 2 = moderate, 3 = severe disorder
- 6 diseases



(CRV 2019)

DD = digital dermatitis

ID = interdigital dermatitis

IH = interdigital hyperplasia

SH = sole haemorrhage

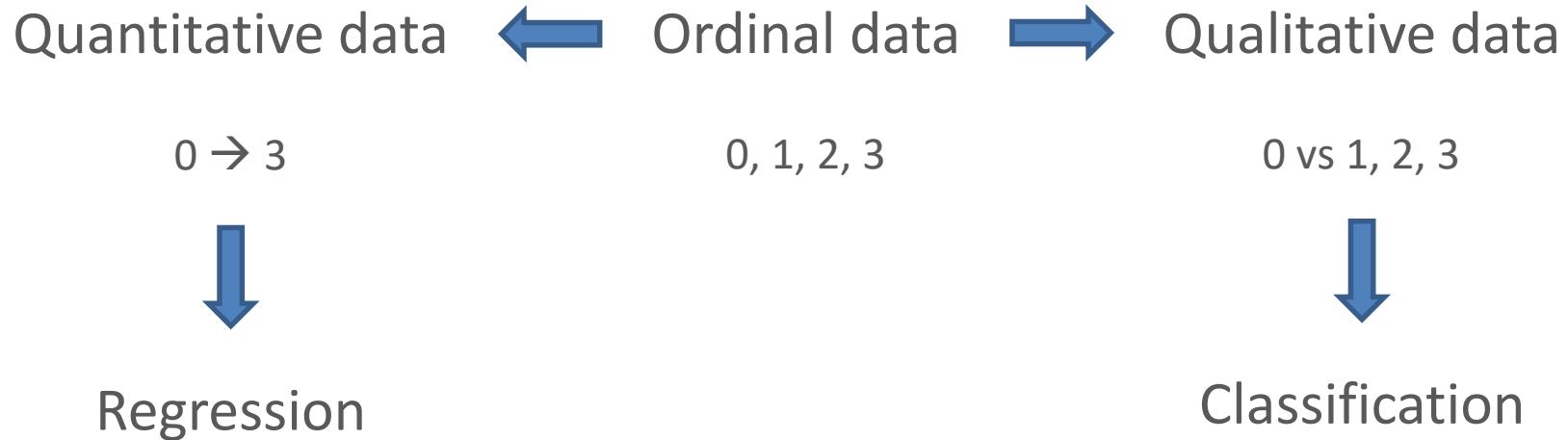
SU = sole ulcer

WL = white line disease

HD = hoof disorder

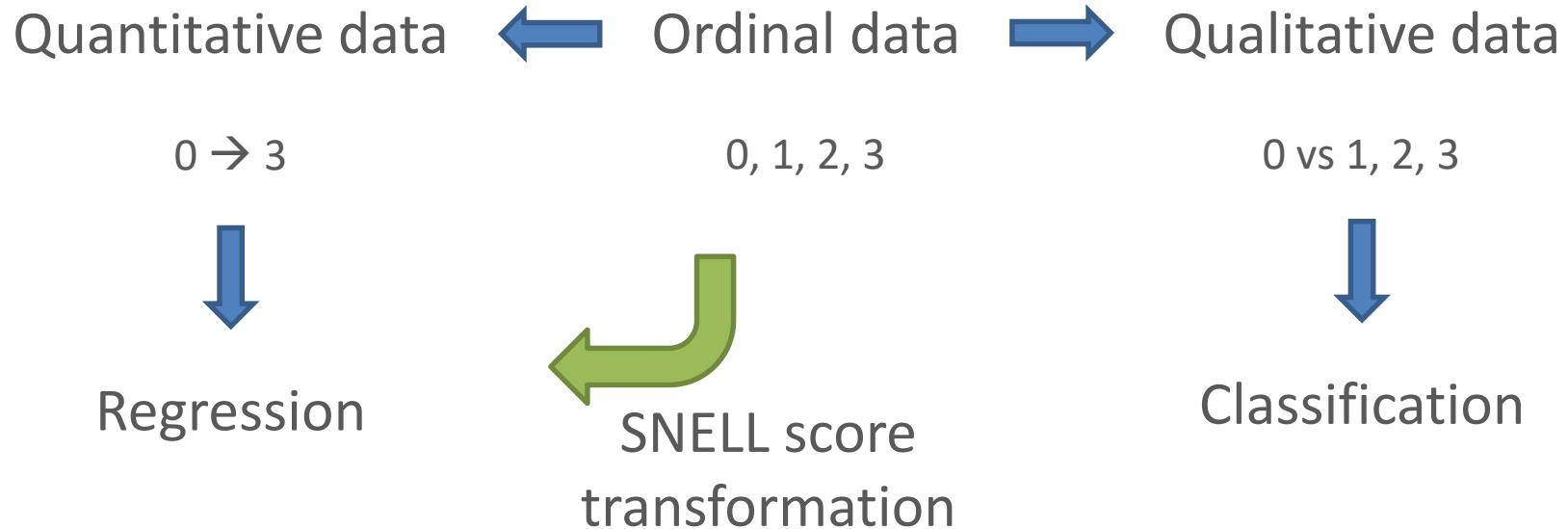


Material and methods





Material and methods



Material and methods

► SNELL scores

- Scaling procedure, ordinal data to numerical scores
- Better assumption of normality (distribution)

SH 2013		0	1	2	3	
	Absolute frequency	79225	22771	7005	911	109912
	Relative frequency	0,72	0,21	0,06	0,01	
SNELL 2013		-0,36	0,93	1,75	2,64	



Model

- ▶ Fixed effect correction of MIR spectra
 - Herd-test day
 - Lactation group: 1, 2, 3+
 - Month of lactation
- ▶ Equal numbers of 0, 1, 2, 3 hoof scores

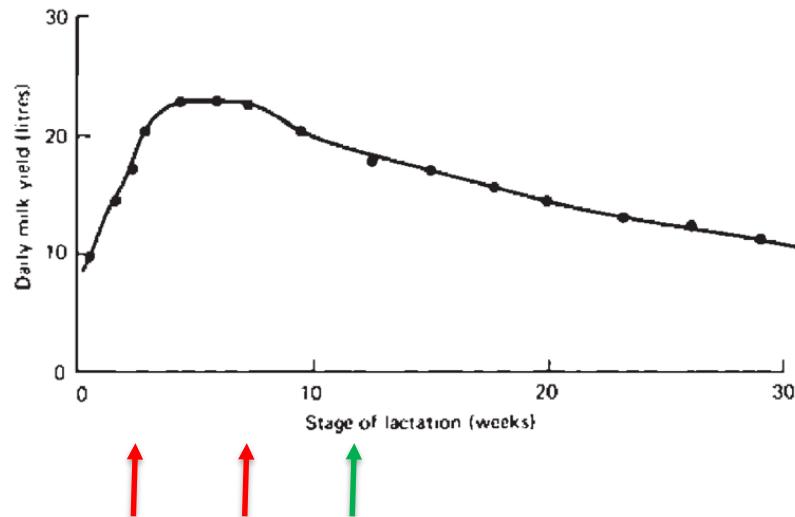
Model

► Predictive variables

- MIR 1 – 212 per months

► Predicted variable

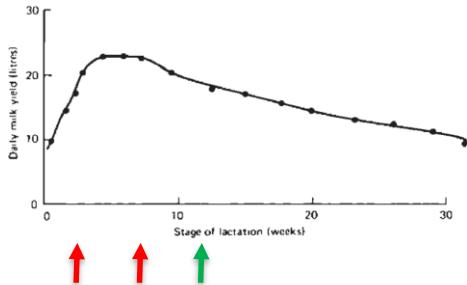
- Hoof score in following month



Model

► Predictive variables

- MIR 1 – 212 per months
- Outliers: GH > 5



► Predicted variable

- Hoof score in following month



► Regression

- SNELL scores

► Classification

- Hoof scores
- 0 = healthy
- 1, 2, 3 = diseased

Results

▶ Regression (PLS)

- N=5200
- HD = combined disease
- SH = sole haemorrhage
- SU = sole ulcer
- WL = white line disorder
- Month 5, predicted by MIR month 1, 2, 3, 4

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hoof lesion	R ²	R ^{2cv}
HD SNELL 5	0,094	0,042
SH SNELL 5	0,039	-0,22
SU SNELL 5	0,100	0,048
WL SNELL 5	0,062	0,004

Results

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 - Sole Ulcer month 5
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Results

▶ Classification (PLS-DA)

- Sole Ulcer month 5
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	healthy	diseased	total	sensitivity (%)	specificity (%)	global accuracy (%)
predicted healthy	1173	735	1908			
predicted diseased	760	1203	1963	61%	62%	61%
total	1933	1938	3871			

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Conclusion

► Routine management

- Low R^2
- Insufficient sensitivity & specificity

Conclusion & future research

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► Breeding applications

- Phenotypes as proxies

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- Genetic correlations?

Conclusion & future research

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- Phenotypes as proxies
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- EBV calculation

Acknowledgements

► CRV



► National Fund for Scientific Research



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Thank you

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