

DEVELOPING A BOVINE KETOSIS RISK INDICATOR USING SPECTRAL ANALYSIS AND ANIMAL PHENOTYPE DATA

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Outline



- Introduction
- Materials and methods
- Results
 - Split sample cross validation
 - Four way cross validation
- Reporting
 - On national spectra
 - Alongside energy traits
- Conclusions





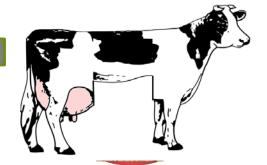


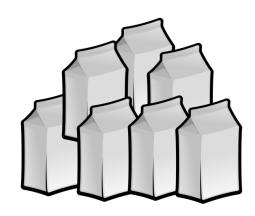












Healthy

Healthy



Ketosis is a metabolic disorder in which the body has to derive energy from ketone bodies

BHB = '-hydroxybutyrate and is a very stable 'ketone body'

NEFA = Non-esterified fatty acids and a measure of fat mobilisation

BHB mmol/l

Sub clinical ketosis



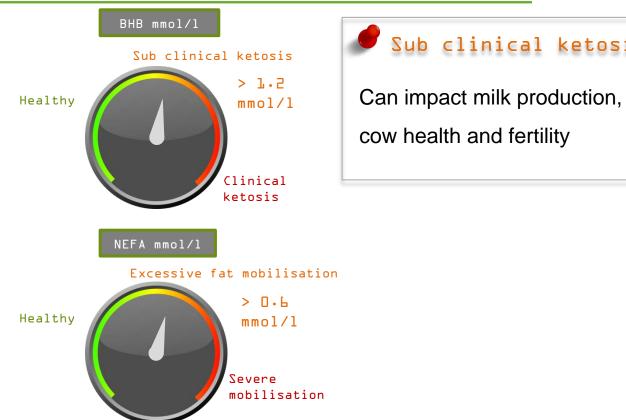
NEFA mmol/1

Excessive fat mobilisation





Sub clinical ketosis



lthy

lthy

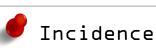




Heritability

Both BHB and NEFA are heritable

Estimates of 0.06 - 0.40 for BHB and 0.08 - 0.35 for NEFA (Koeck et al. 2014, Oikonomou et al., 2008, Jamrozik et al., 2016).



Nationally SCK of c. 30% (Macrae et al. 2012)



Sub clinical ketosis



NEFA mmol/l

Excessive fat mobilisation





Sub clinical ketosis

Can impact milk production, cow health and fertility

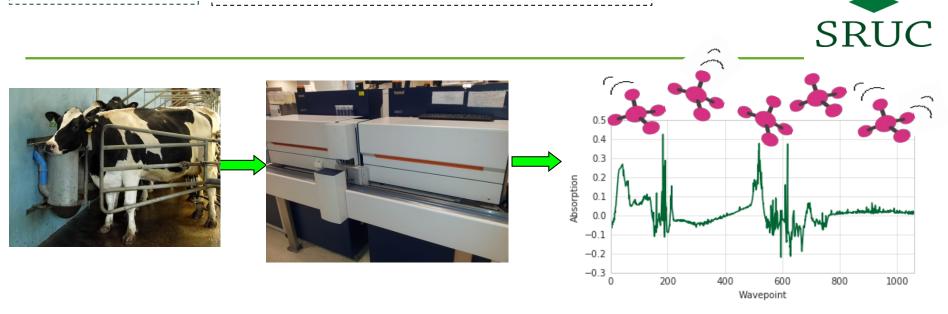


Clinical ketosis

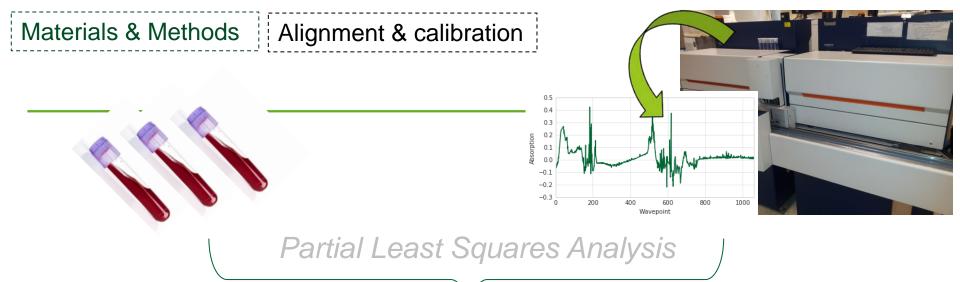
Loss of appetite, reduced milk yield, can induce hypoglycaemia, hyperketonaemia, immunosuppression

Introduction

Mid-infrared (MIR) technology



Objective : Can we detect levels of BHB and NEFA from milk MIR spectra?



Predicted NEFA

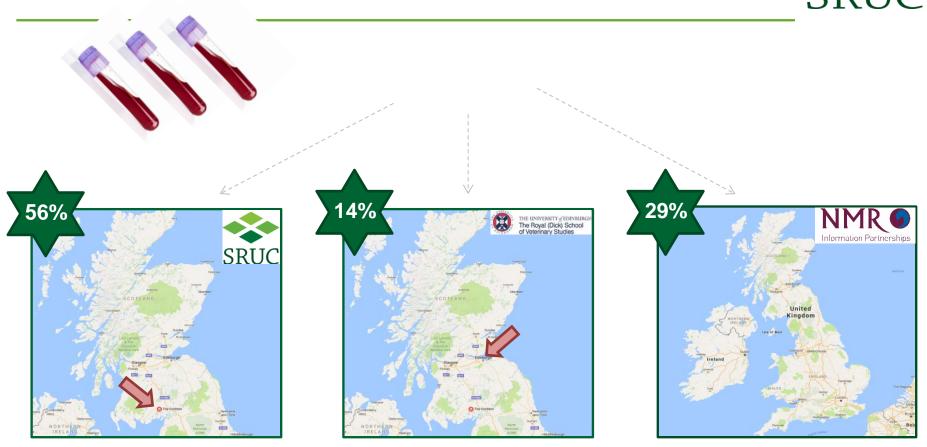


Fatty acids (Soyeurt et al., 2011)

Energy traits (McParland et al., 2011

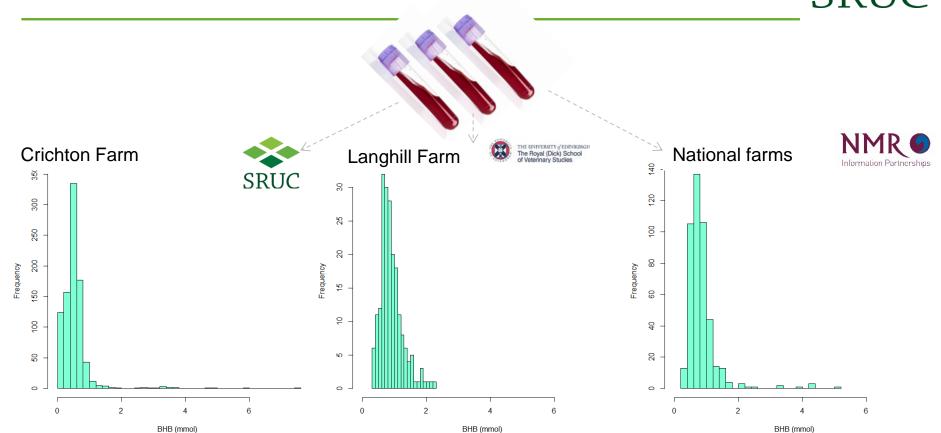
Materials & Methods | Sourcing reference data: Location





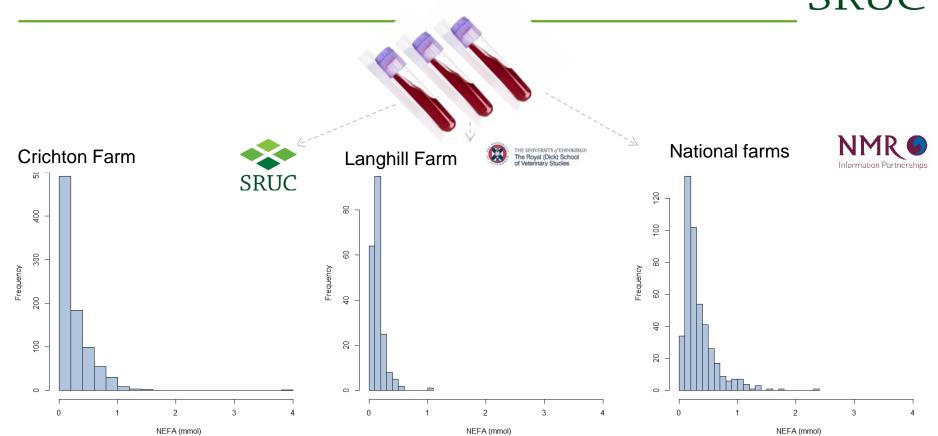
Materials & Methods | Sourcing reference data: distributions





Materials & Methods | Sourcing reference data: distributions







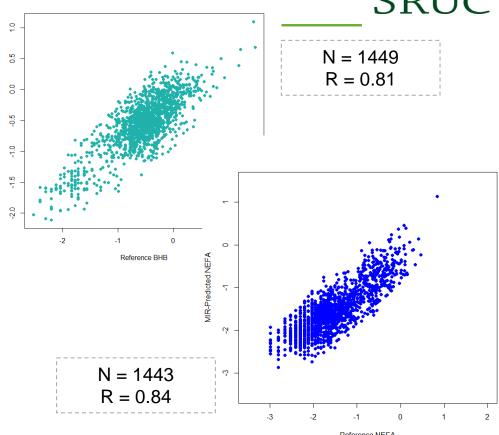
- Spectral data standardised in accordance with Grelet et al., 2016. as part of the Optimir project.
- Transformation of reference data
- Data thinning (similar to Grelet et al. 2016)
- Restrictions on residuals in defining outliers
- Feedback from receiver operating characteristic curves (sensitivity and specificity, area under the curve)
- Inclusion of various phenotypic traits alongside spectral data in the PLS
- Optimal number of factors to use in the model according to SAS

Results

Split sample validation



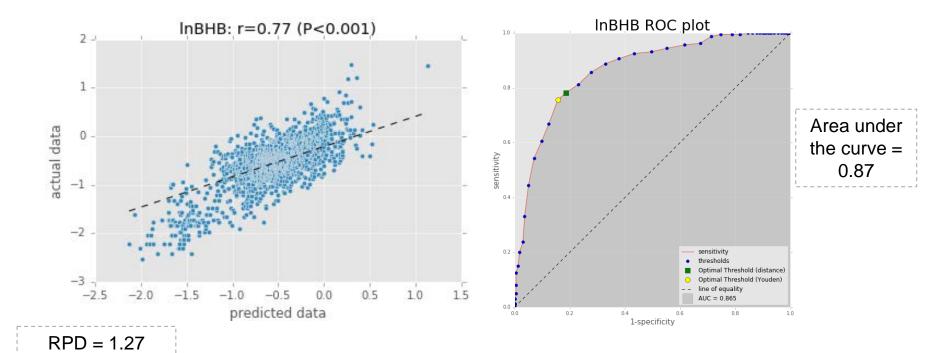
- Converged upon a tool
 - Using data from all sources
 - Residuals > 2 stdev of the global press considered outliers and removed
 - Both traits (natural) log transformed
- Split sample validation
- R = square root of the coefficient of determination



SEC = 0.4SDEP = 0.35

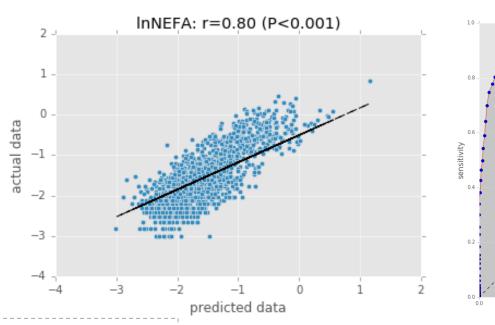
4 way cross validation

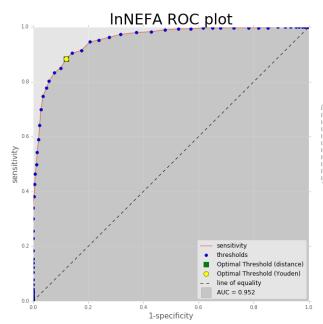




4 way cross validation







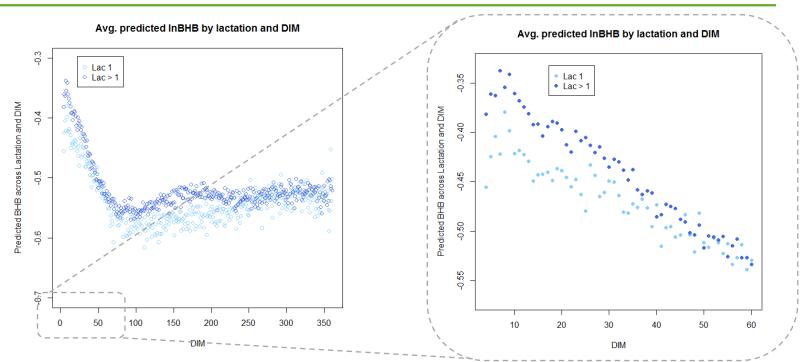
Area under the curve = 0.95

RPD = 0.81

SEC = 0.48

SDEP = 0.71



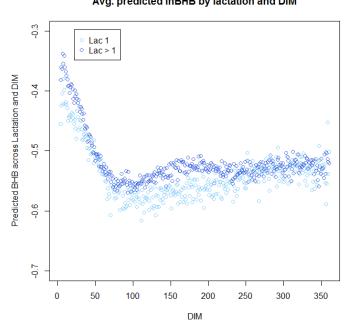


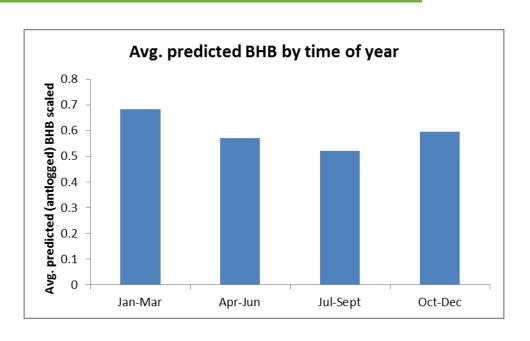
Reporting

National

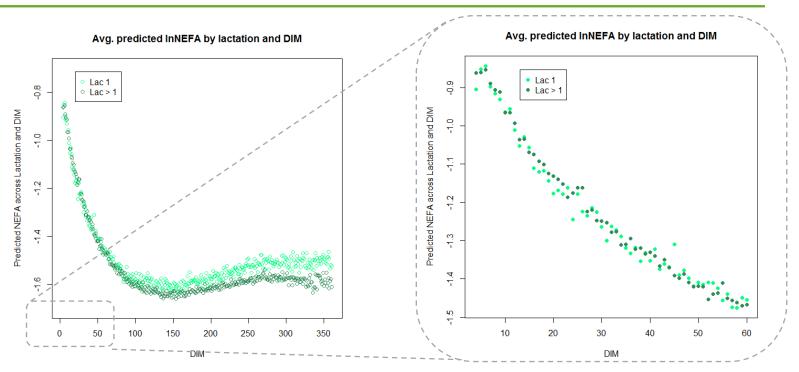






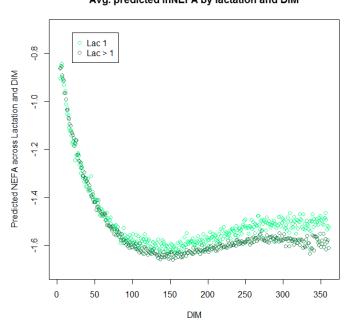


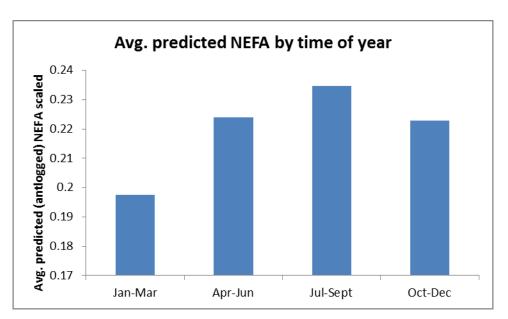




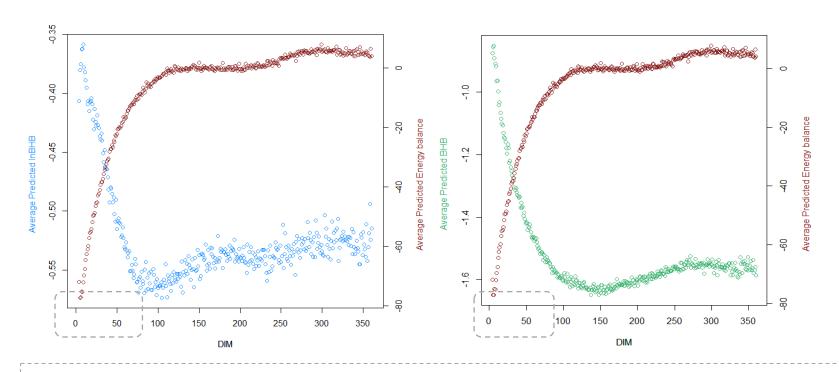




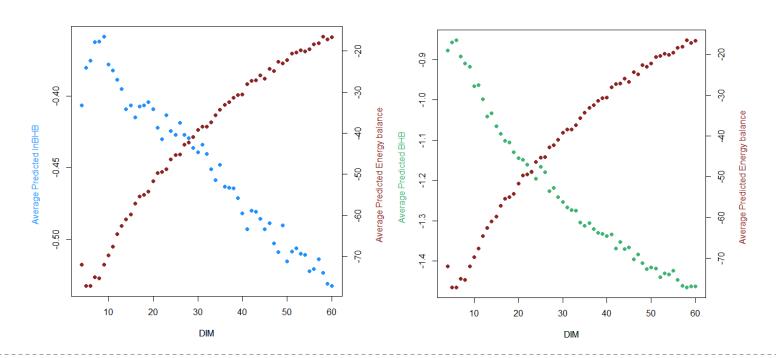












Conclusions



- Demonstrated the ability to predict BHB and NEFA using MIR
- Could be used routinely as an early-indicator of potential health issues
- Energy balance predicted routinely from MIR at NMR; BHB and NEFA predictions due to accompany these

Acknowledgements



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