

Prediction of blood parameters of buffaloes from milk mid-infrared spectra

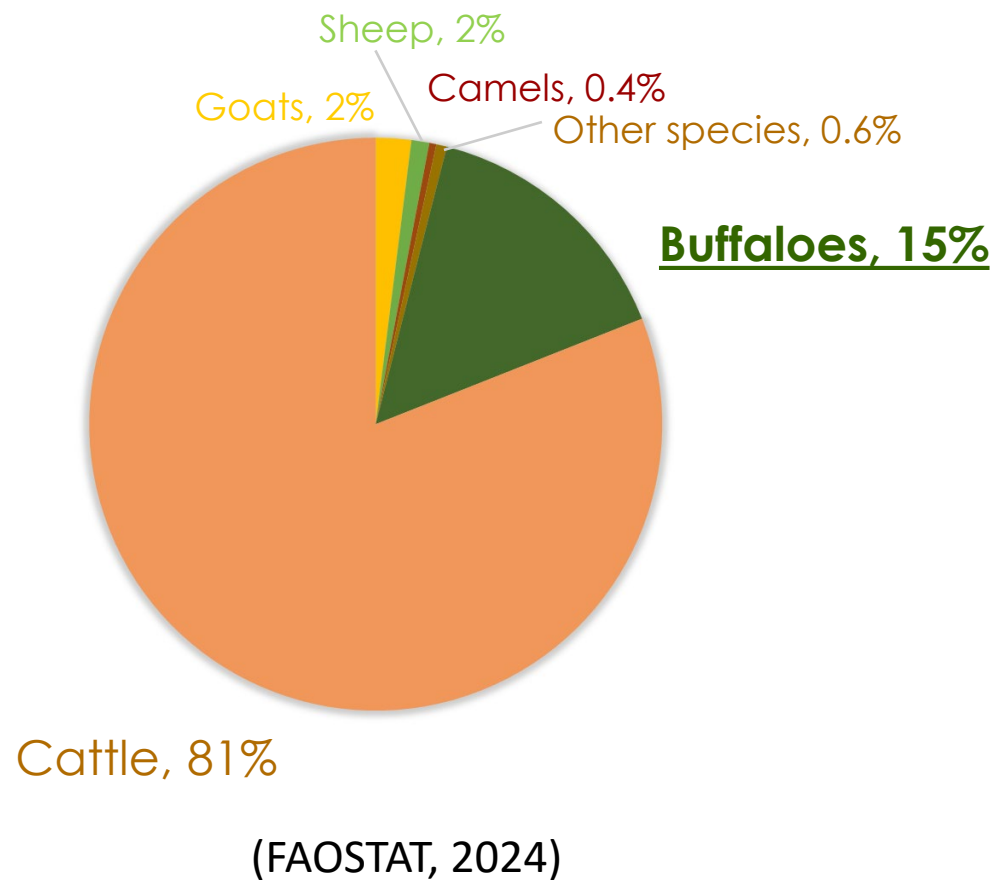
*Silvia Magro*¹, *Sergio Esposito*², *Gianluca Neglia*², *Giovanni Niero*¹, *Massimo De Marchi*¹

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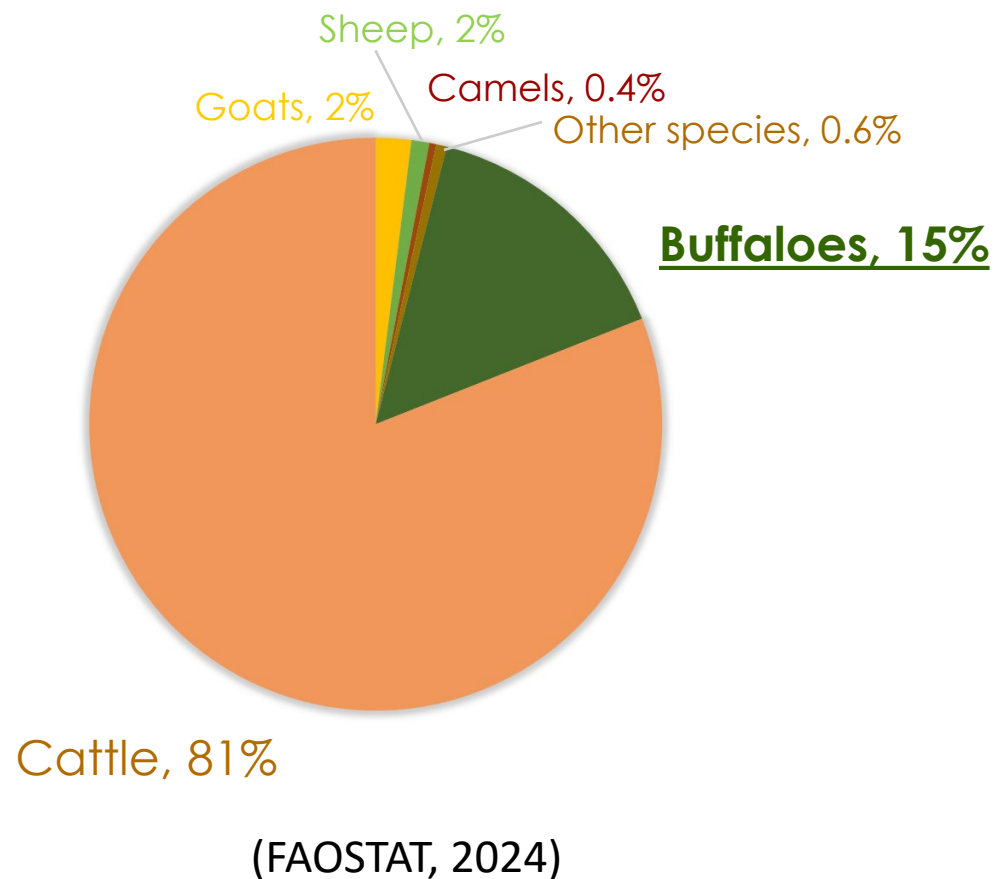
INTRODUCTION

World milk production:



INTRODUCTION

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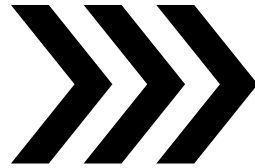
In Italy:

'Mozzarella di Bufala Campana' cheese

Protected Designation of Origin (PDO) by the European Community
(Regulation 1107/96 of 12 June 1996)



INTRODUCTION



Progressive intensification of the system:

- an increase in the size of the herd
- the adoption of intensive/semi-intensive farming techniques (originally intended for cattle)

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- ✓ maximize the efficiency of the dairy sector
- ✓ improve the yield and quality of milk and cheese

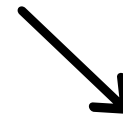


INTRODUCTION



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Management issues that also impact animal welfare and health



INTRODUCTION

Blood metabolic profile testing allows for monitoring **metabolic health** and **nutritional status**.

- high costs
- labour
- animals' stress



conducting extensive blood
analyses on a large scale



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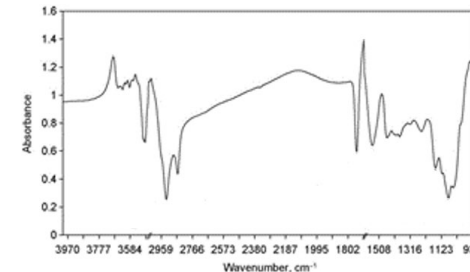
- high costs
- labour
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conducting extensive blood analyses on a large scale



Utilizing mid-infrared (MIR) spectra of milk to predict blood traits may present an effective opportunity.



AIM

The present study aims to test the ability of MIR to predict blood traits using milk spectra collected from the same buffalo.



MATERIAL & METHODS



310 buffaloes



9 farms

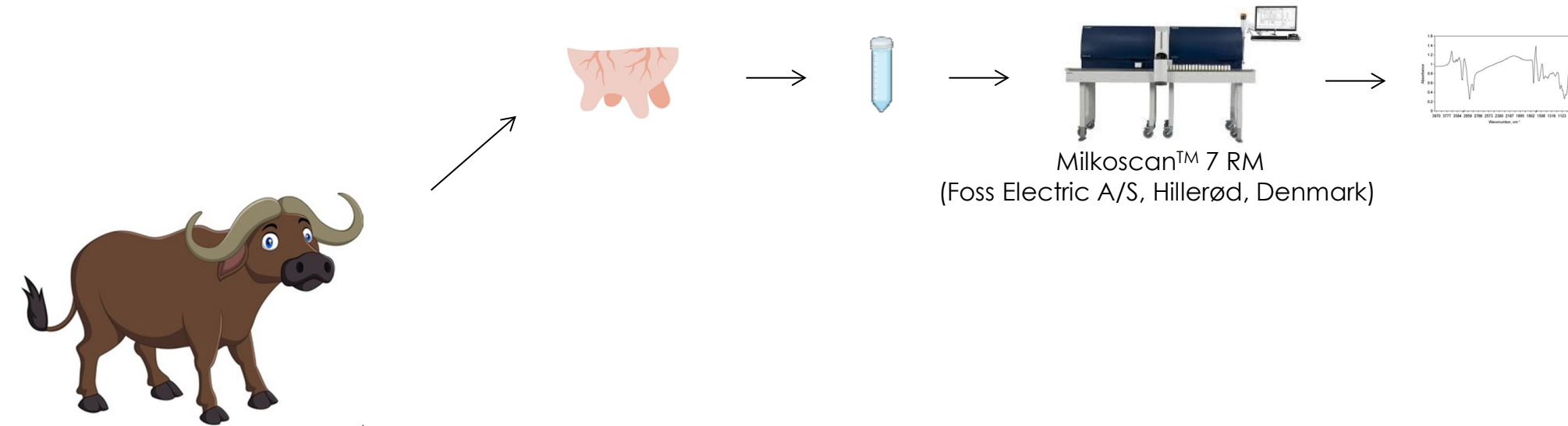


From February to September 2022

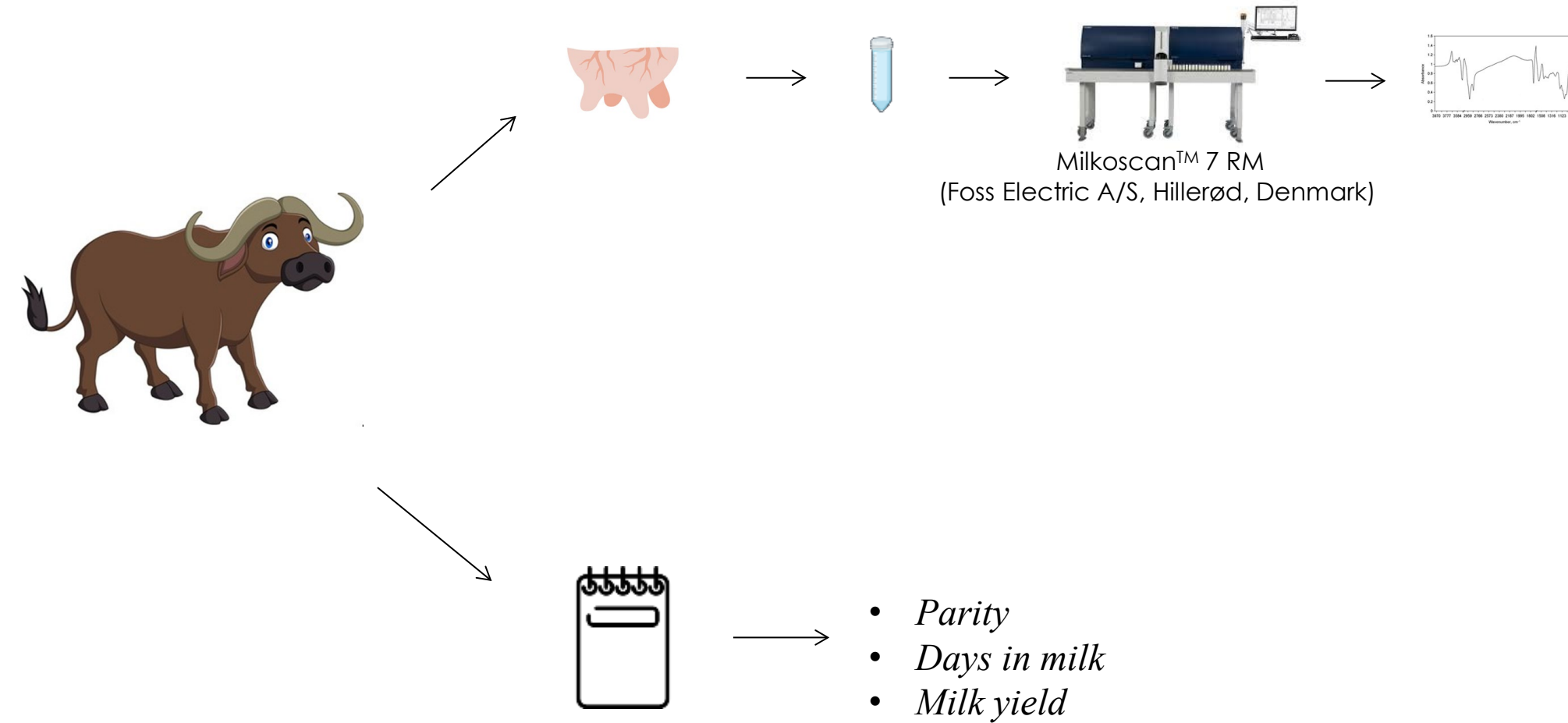
Individual blood and milk samples
were collected during the morning milking.



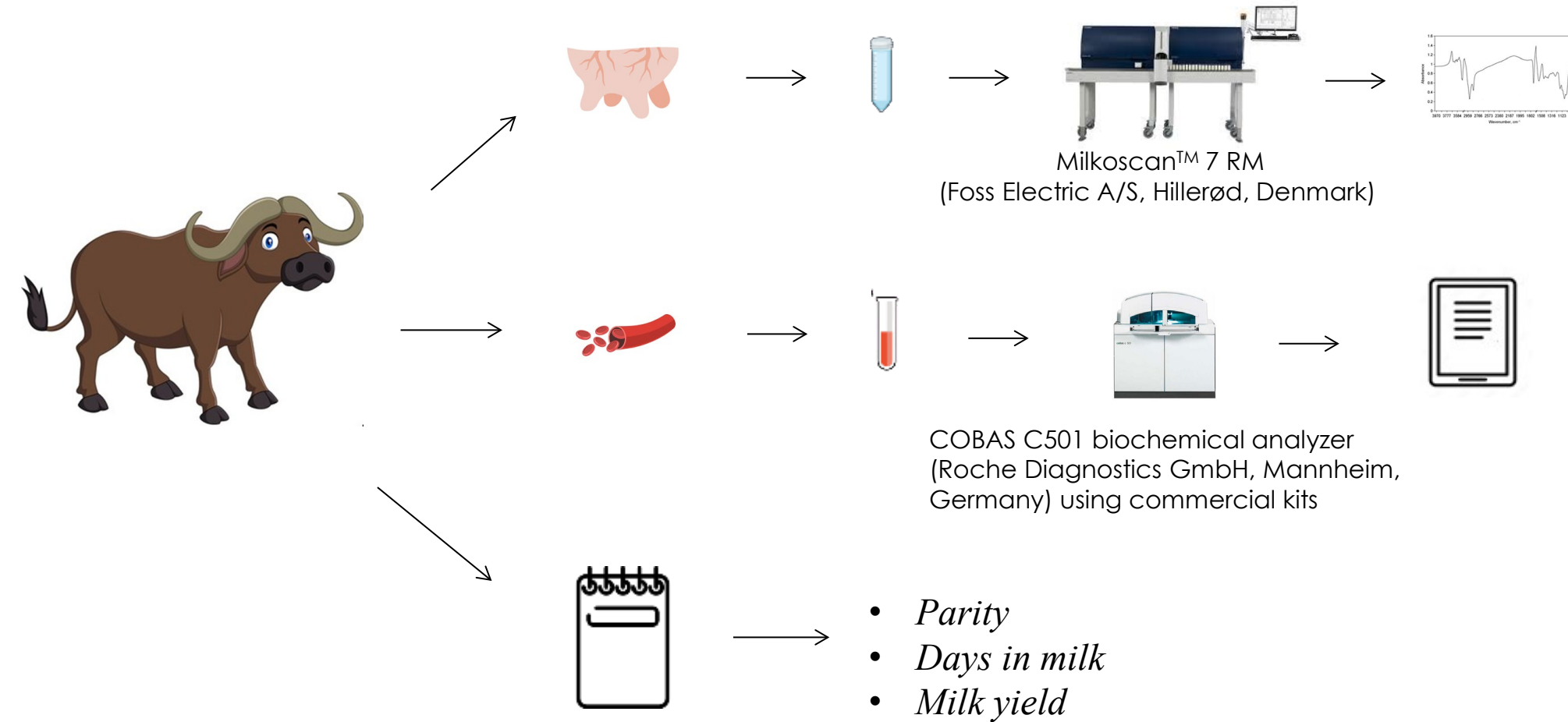
MATERIAL & METHODS



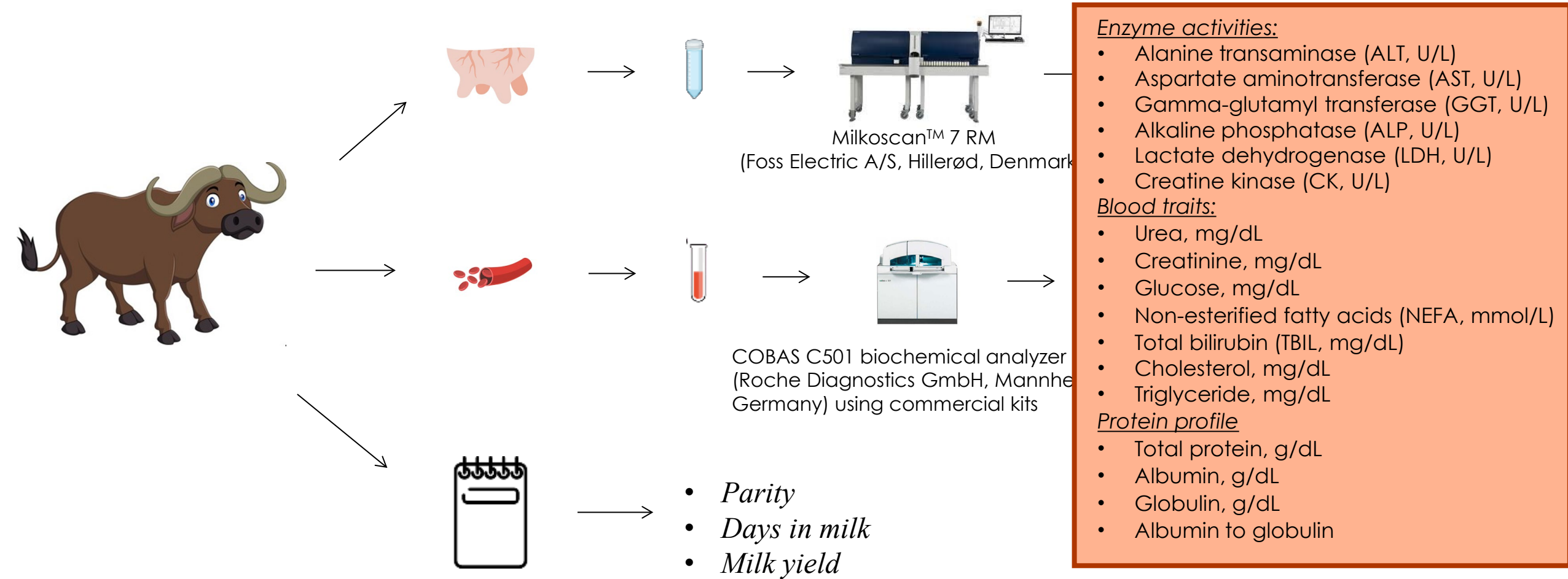
MATERIAL & METHODS



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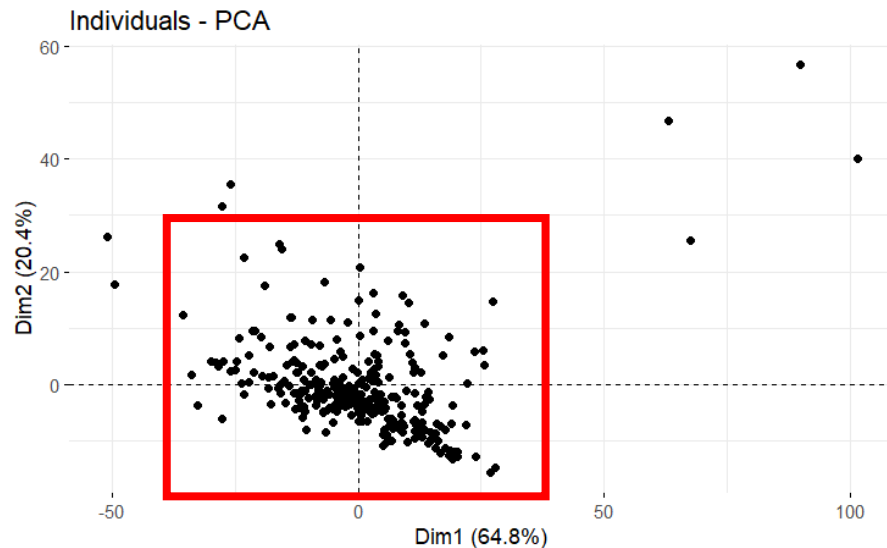
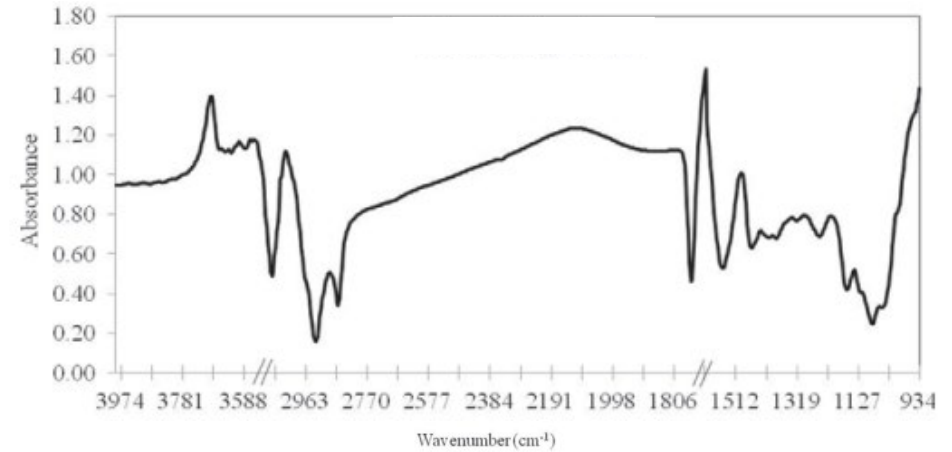
MATERIAL & METHODS



MATERIAL & METHODS

Mid-infrared prediction models

Spectral regions known to be associated with noisy water absorption wavelengths were discarded
-> **leading to 338 wavelengths**



Preliminary analysis of the spectral data was conducted using principal component analysis (PCA) to identify anomalous samples in terms of the MIR spectrum -> **8 spectra were discarded**

For non-distributed blood traits, a logarithmic transformation was applied (CK, NEFA; TBILT).



MATERIAL & METHODS

Mid-infrared prediction models

The **partial least squares (PLS)** analysis was carried out using the 'trainControl' function available in the R package 'caret' :

- ✓ The models were fine-tuned using leave-one-out cross-validation, and the number of latent variables was set automatically but capped at a maximum of 15 to avoid overfitting.
- ✓ Spectral data points were centered and scaled.



(Kuhn, 2008)



RESULTS




Descriptive statistics

Blood trait	Mean (SD)	Range	CV, %
<i>Enzyme activities</i>			
ALT, U/L	45.17 (10.97)	17.30 - 94.00	24.3
AST, U/L	130.50 (28.95)	63.60 - 327.00	22.2
ALP, U/L	287.94 (189.90)	19.74 - 1,528.00	66.0
GGT, U/L	30.52 (8.06)	13.00 - 66.02	26.4
LDH, U/L	1,256.22 (205.12)	652.00 - 1,845.00	16.3
CK, U/L	178.00 (76.65)	53.00 - 793.00	43.1
<i>Blood traits</i>			
Urea, mg/dL	60.01 (16.83)	21.00 - 129.90	28.0
Creatinine, mg/dL	1.62 (0.32)	0.90 - 2.70	19.8
Glucose, mg/dL	67.34 (11.92)	25.30 - 115.00	17.7
NEFA, mmol/L	0.95 (0.94)	0.07 - 3.16	98.9
TBIL, mg/dL	0.27 (0.30)	0.00 - 4.34	111.1
Cholesterol, mg/dL	122.22 (32.50)	38.90 - 283.00	26.6
Triglyceride, mg/dL	18.57 (12.45)	0.00 - 45.10	67.0
<i>Protein profile</i>			
Total protein, g/dL	6.93 (0.72)	4.73 - 8.73	10.4
Albumin, g/dL	3.40 (0.26)	2.55 - 4.07	7.6
Globulin, g/dL	3.53 (0.57)	2.18 - 5.05	16.1
Albumin-to-globulin	0.99 (0.15)	0.59 - 1.57	15.2

CV, coefficient of variation

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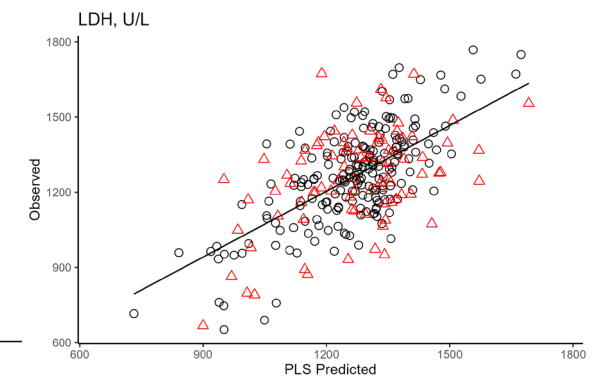
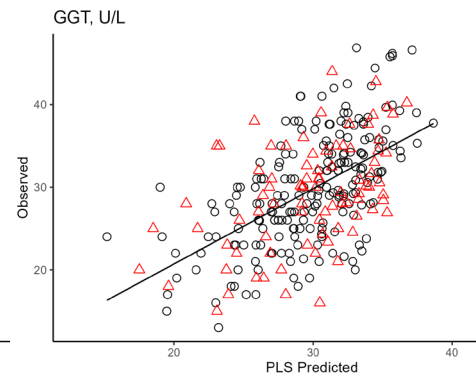
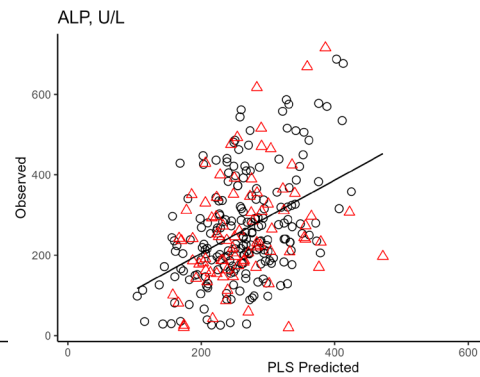
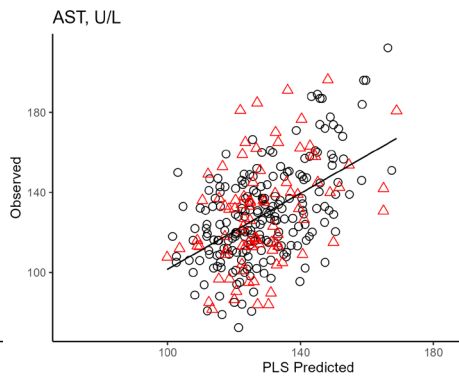
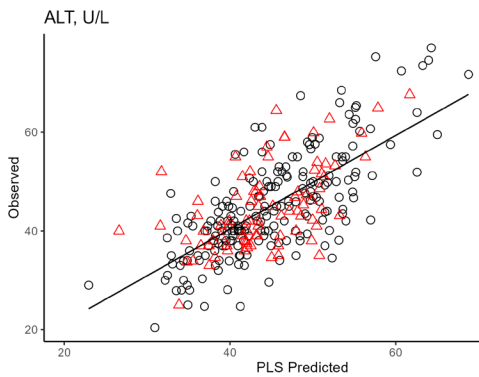
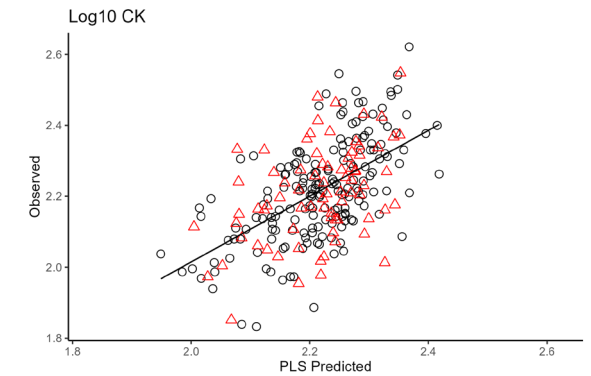
CV, coefficient of variation

RESULTS

Enzyme activities

Trait	LV	Calibration (70%)		Validation (30%)	
		R^2_c	SE_c	R^2_v	SE_v
ALT, U/L	10	0.51	6.87	0.35	7.90
AST, U/L	9	0.33	19.83	0.15	23.92
ALP, U/L	6	0.20	118.21	0.14	127.53
GGT, U/L	6	0.36	5.28	0.21	6.08
LDH, U/L	11	0.47	138.73	0.26	176.44
Log ₁₀ CK	8	0.37	0.11	0.14	0.13

LV = Latent Variables



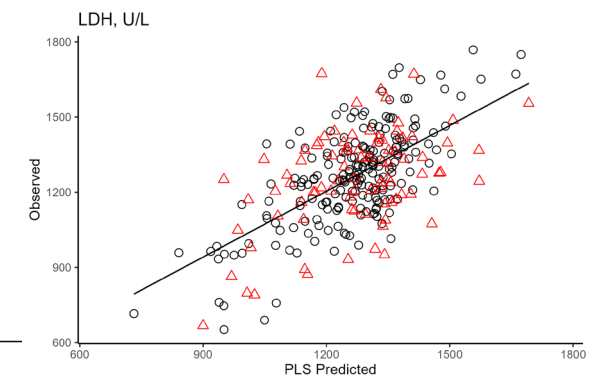
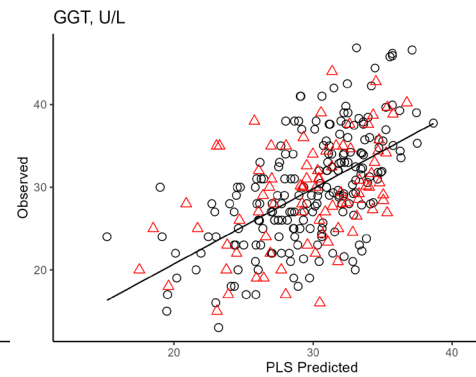
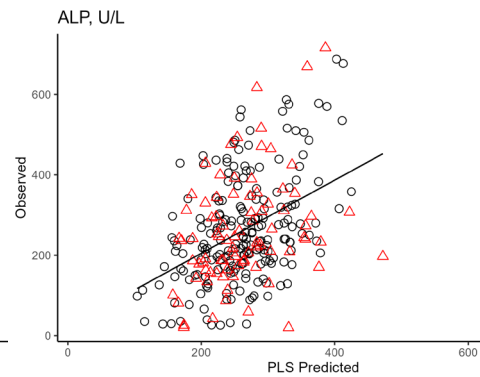
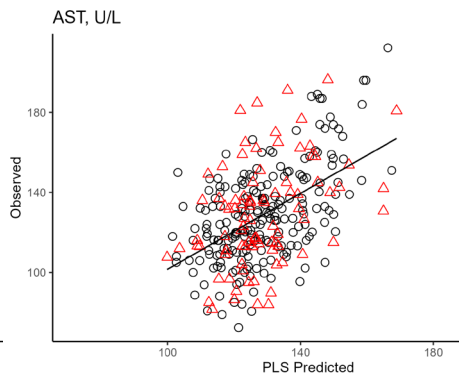
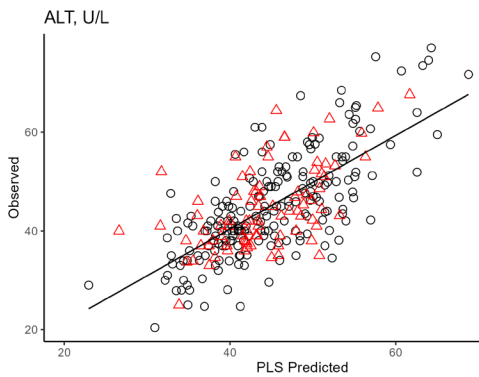
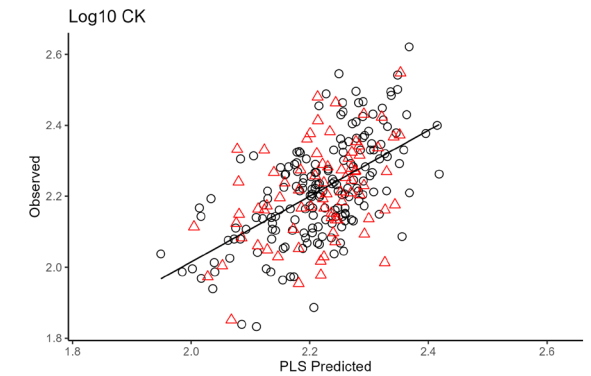
● calibration set, ▲ validation set

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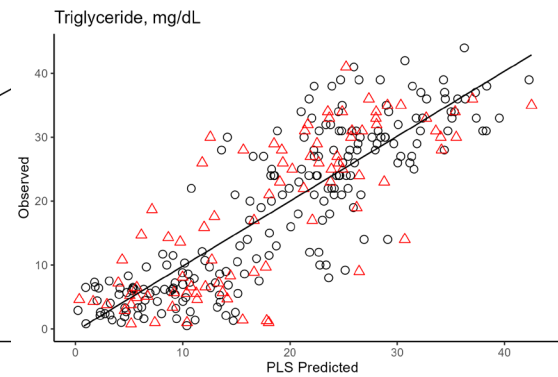
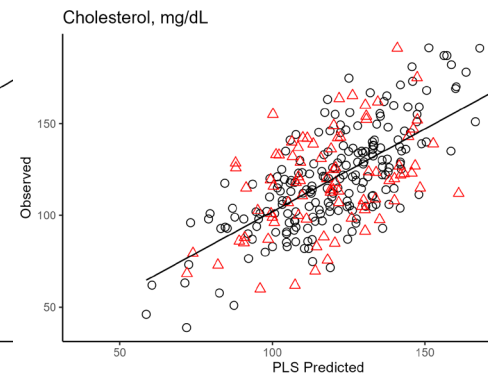
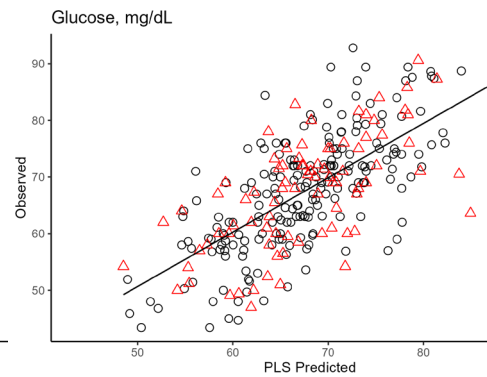
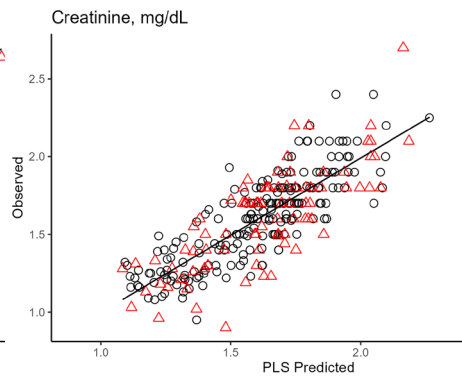
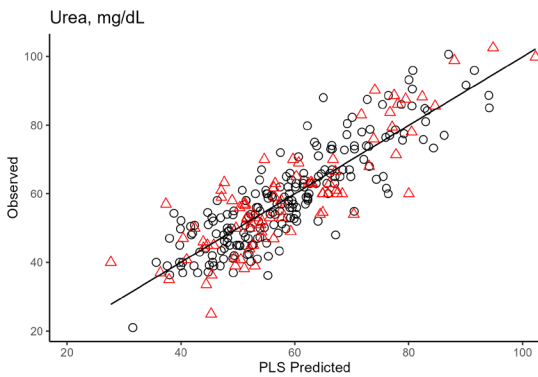
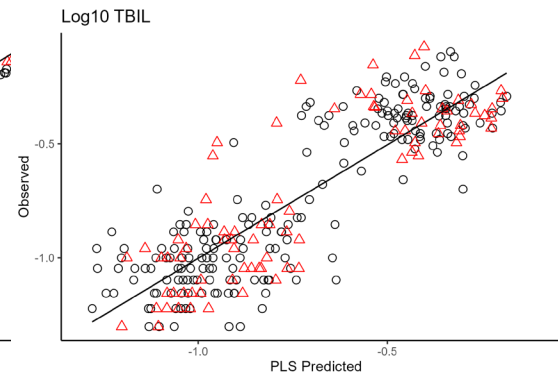
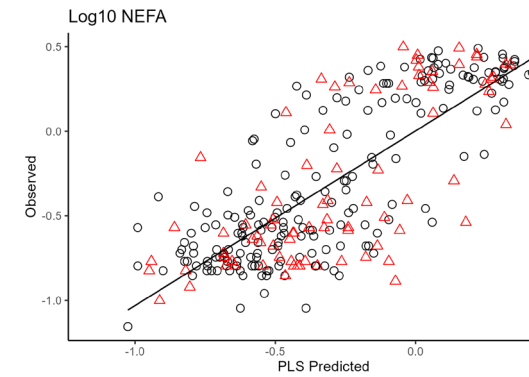
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RESULTS

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Urea, mg/dL	13	0.76	7.11	0.72	8.31
Creatinine, mg/dL	14	0.71	0.16	0.51	0.22
Log ₁₀ NEFA	9	0.68	0.27	0.55	0.33
Log ₁₀ TBIL	11	0.76	-0.27	0.69	0.20
Glucose, mg/dL	14	0.44	7.63	0.29	8.67
Cholesterol, mg/dL	15	0.58	18.08	0.24	25.06
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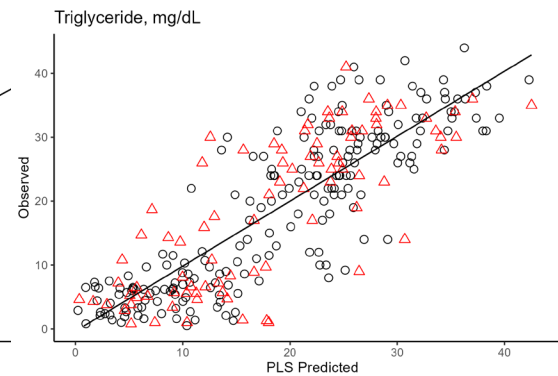
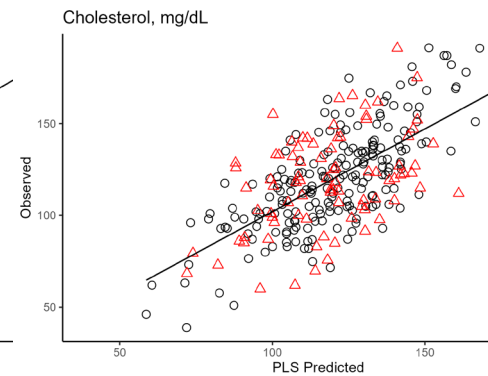
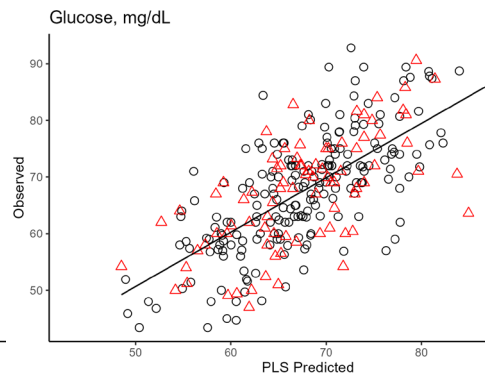
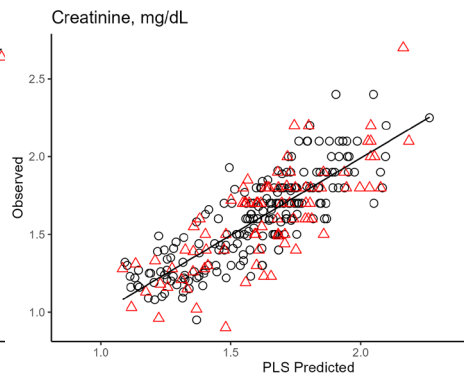
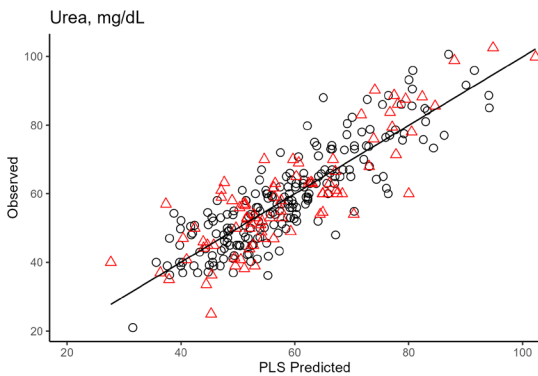
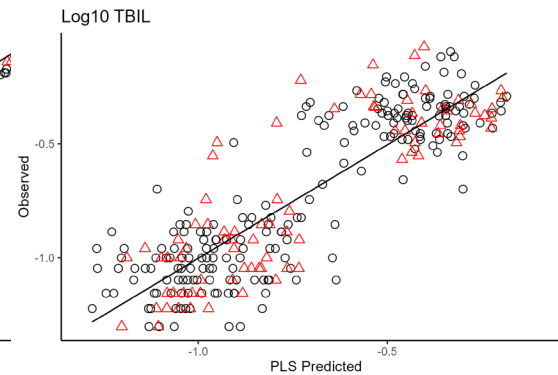
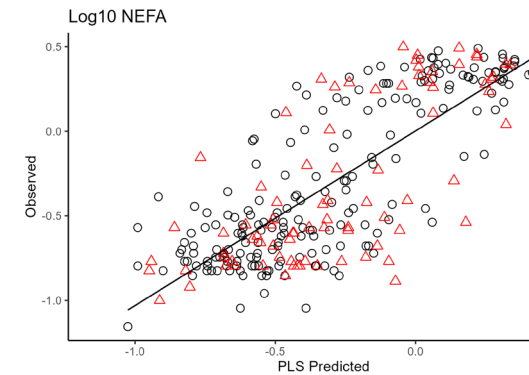
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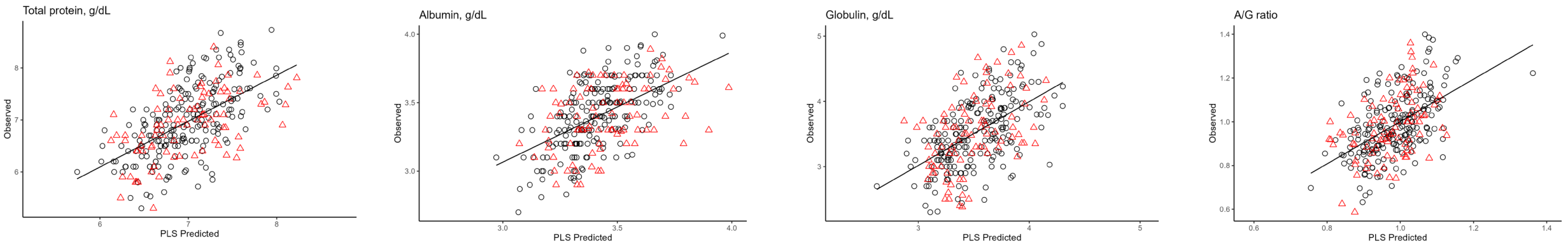
● calibration set, ▲ validation set

RESULTS

Protein profile

Trait	LV	Calibration (70%)		Validation (30%)	
		R^2_c	SE_c	R^2_v	SE_v
Total protein, g/dL	6	0.20	118.21	0.14	127.53
Albumin, g/dL	10	0.37	0.20	0.15	0.23
Globulin, g/dL	6	0.32	0.45	0.24	0.49
A/G ratio	7	0.32	0.45	0.24	0.49

LV = Latent Variables



● calibration set, ▲ validation set

CONCLUSIONS

Predict something present in the blood using the milk spectrum is challenging -> **INDIRECT PREDICTION**

- Low-moderate R^2 were as expected
- Phenotypes predicted from the milk spectra can be valuable for genetic investigations at the population level and for design of breeding programs



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Concentration of several blood traits (urea, TIBL, NEFA, creatinine, and triglyceride) can be considered as good enough for:

- ✓ POPULATION SCREENING: monitoring metabolic health of buffaloes in dairy herd
- ✓ CARRYING OUT SELECTIVE BREEDING



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Further efforts should be made to understand if MIR spectra coupled with **machine learning algorithms** can result in an improvement of the models' accuracy.





Thank you for attending

Ph.D. COURSE **ANIMAL & FOOD SCIENCE**
UNIVERSITY OF PADOVA

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DAFNAE
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Large-scale phenotyping in dairy sector using milk MIR spectra: Key factors affecting the quality of predictions

C. Grelet^a, P. Dardenne^a, H. Soyeurt^b, J.A. Fernandez^a, A. Vanlierde^a, F. Stevens^a, N. Gengler^b, F. Dehareng^{a,*}

Table 4

Characteristics of the 7 K-mean clusters resulting from the classification of 57 milk MIR models following their mean-centered cross-validation RPD, relative RMSE and R^2 .

Cluster	RPDcv	Relative RMSEcv	R^2 cv	Interpretation for application
1	> 6	<5%	> 0.97	Any application
2	4.2–6	<10%	0.94–0.97	Quality control
3	3–4.2	<10%	0.89–0.94	Quantitative screening
4	2–3	<25%	0.74–0.89	Rough screening
5	1.5–2	<25%	0.55–0.74	Allows to compare groups, discriminate high or low values
6	1.5–2	>25%	0.55–0.74	Highly imprecise, can be used to detect extreme values
7	< 1.5	–	< 0.55	Not recommended

Near-infrared technology: getting the best out of light: a short course in the practical implementation of near-infrared spectroscopy for the user

P. Williams - 2004 - PDK Projects, Incorporated

- R^2 between 0.50 and 0.65 -> detection of extreme values or comparison of groups.
- R^2 between 0.66–0.81 -> approximate screening
- R^2 between 0.82–0.90 -> good quantitative screening
- $R^2 \geq 0.91$ -> punctual prediction