Genotype plus Environment
Integration for a more sustainable dairy production system

Wallonie recherche CRA-W

Prediction of energy status of dairy cows using milk MIR spectra

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Global objective of the project

Optimise production efficiency, fertility, health and environmental footprint of dairy cows:

First step:

Develop models predicting **phenotypes of interest** based on easily-measured and large scale **biomarkers in milk**:

- -Milk glycan
- -Milk metabolites
- **-Milk MIR spectra**

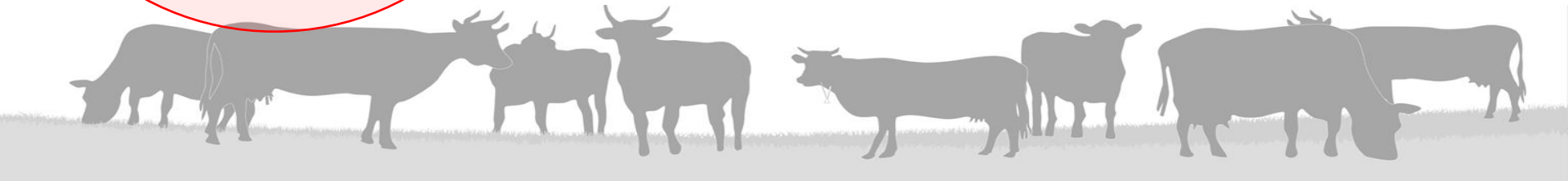
Final steps:

Genomic study : Genome-Wide Association Study (GWAS) to relate genotype to phenotypes of interest
~15 000 cows

→ **Breeding**

Management study: new management strategies at herd and cow level to improve phenotypes of interest
~600 cows

→ **Advisory tools**



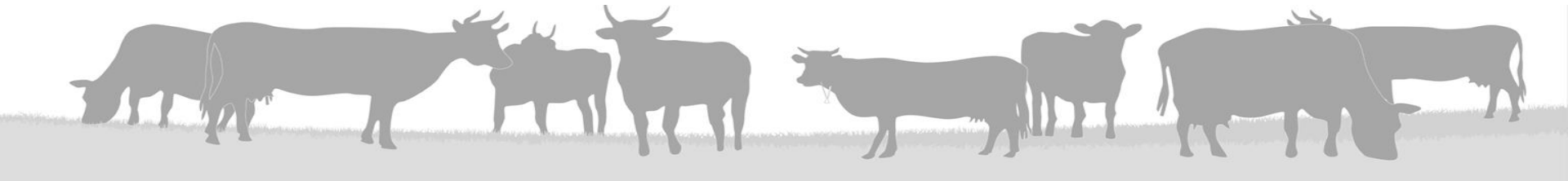
Objective

Develop models predicting **phenotypes of interest**:

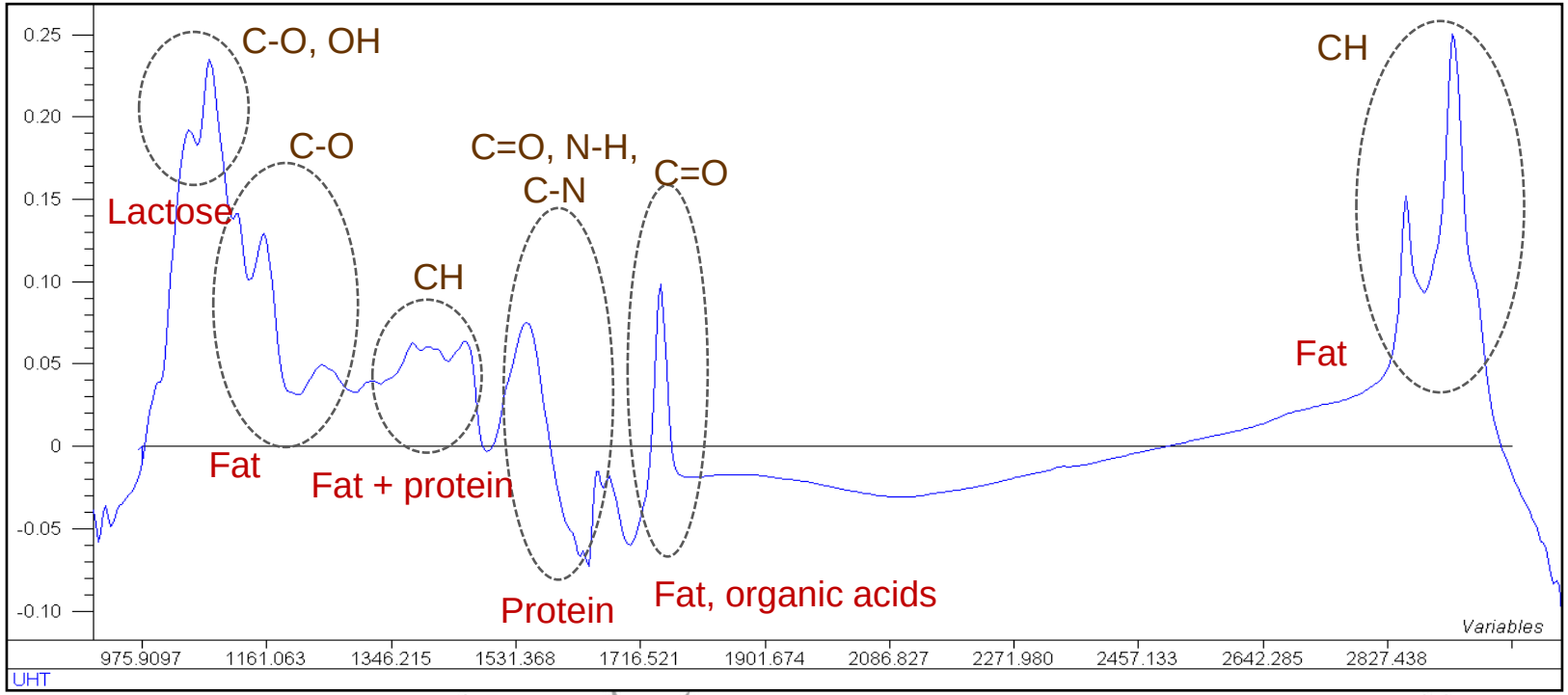
MIR ⟶ Energy status:

Fertility:
-IGF-I level and LH inhibition (Butler, 2000)
-Uterine health (Hammon, 2006)

Health:
-Inflammation (Esposito 2013)
-Immune response (Hammon, 2006)
-Digestive issues: ketosis, DA… (Collard, 2000)
-Locomotive issues (Collard, 2000)



Why MIR?



- **Position** of the peaks → **Qualitative** analysis
- **Intensity** of the peaks → **Quantitative** analysis

Why MIR?

- Already available
- Fast
- Cheap

Milk control

MIR

© Bentley

Milk composition

Fat

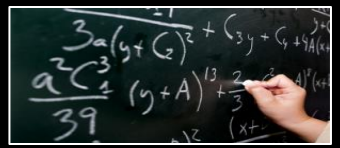
Proteins

Urea

Lactose

…

Models



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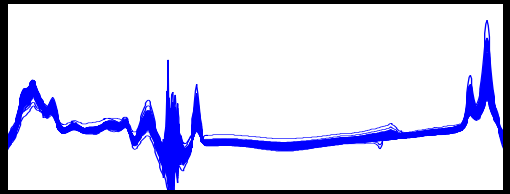
MIR spectra of each cow



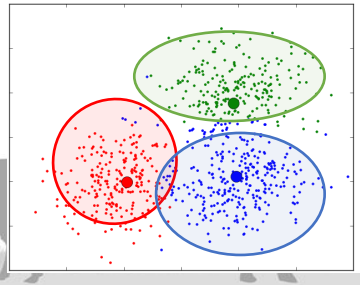
Objective

Develop models predicting **phenotypes of interest**:

MIR ⟶ Energy status:

- Feed related phenotypes

- Blood components
- Global metabolic status using the clusters metodology



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Develop models predicting **phenotypes of interest**:

MIR → Energy status:

- Feed related phenotypes

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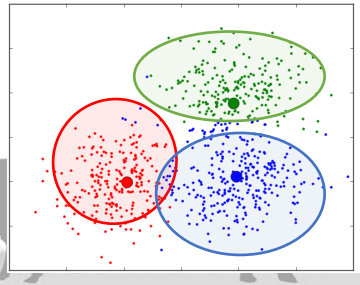


Materials & Methods

Experiments

- 6 experimental farms
- Common sampling protocol
- 235 cows

- Holsteins
- Calving to DIM 50

	# Cows	PP	MP	MY	Feed diet roughage
AFBI (UK)	61	18	43	31.6	Grass
AU (Denmark)	35	11	14	35.5	Corn/grass
CRAI (Italy)	45	8	37	29.3	Triticale
CRA-W (Belgium)	31	13	18	30.5	Corn/grass/sugarbeet
FBN (Germany)	27	3	24	37.5	Corn/grass
UCD (Ireland)	36	2	34	30.5	Corn/grass
TOTAL	**235**	**55**	**180**	**32.1**	

Phenotypes of interest

Feed related phenotypes

- Energy balance = $NE_{Intake} - NE_{Milk} - NE_{Maintenance}$ (NRC, 2001)
- RFI = DMI – PDMI (with $PDMI = (0.372 * FCM + 0.0968 * BW^{0.75}) * (1 - e^{(-0.192 * (WeekOfLactation + 3.67))})$ (NRC, 2001)
- DMI Observed

Measured daily

Daily DMI measurment in 3 farms (132 cows)

Phenotypes of interest

Blood plasma metabolites and hormones

- Glucose ~ energy
- IGF-I ~ liver status
- NEFA ~ mobilization
- BHB ~ (sub)clinical ketosis

DIM14 & 35

Sampling in the 6 farms (235 cows)

Analyzed at UCD & Aarhus university

Phenotypes of interest

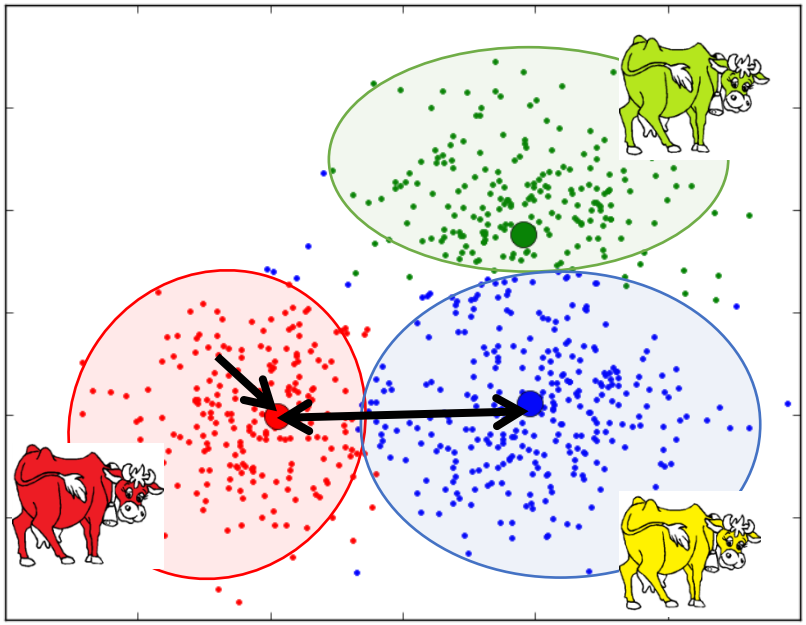
Blood metabolites and hormones are usefull when used togheter

→ Clusters:

- Combination of the blood metabolites and hormones into 3 groups of cow status

K-means nearest neighbour clustering

K=3



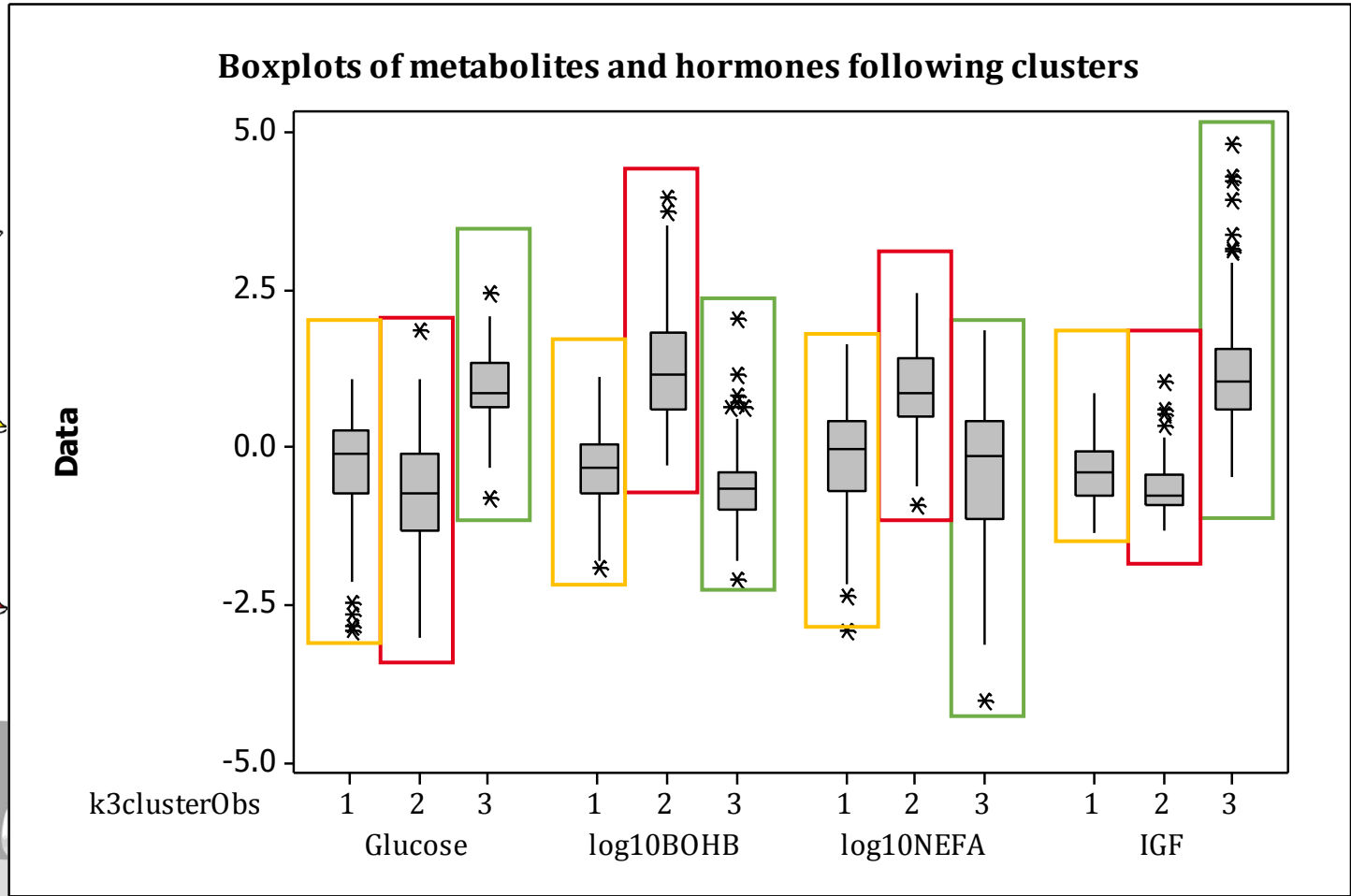
Phenotypes of interest

- Metabolic clusters

3 : healthy cows

1 : intermediate cows

2: imbalanced cows



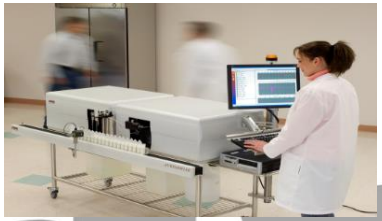
MIR analysis of milk

- Analyzed locally or at CRA-W
- Twice per week
- AM & PM (weighted average)

- Foss and Delta

MIR standardisation

- Different instruments
- Standardisation step needed



MIR standardisation

- Different instruments
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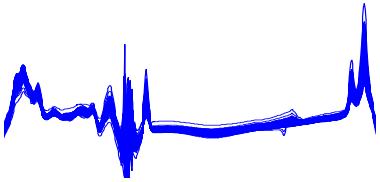
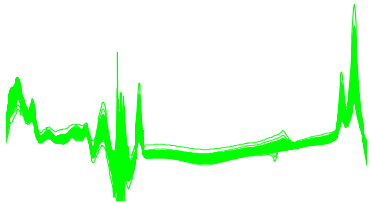
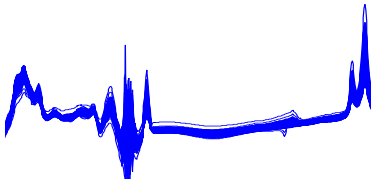
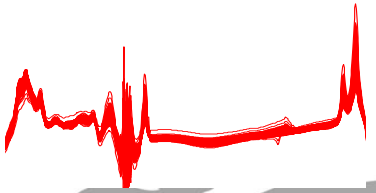
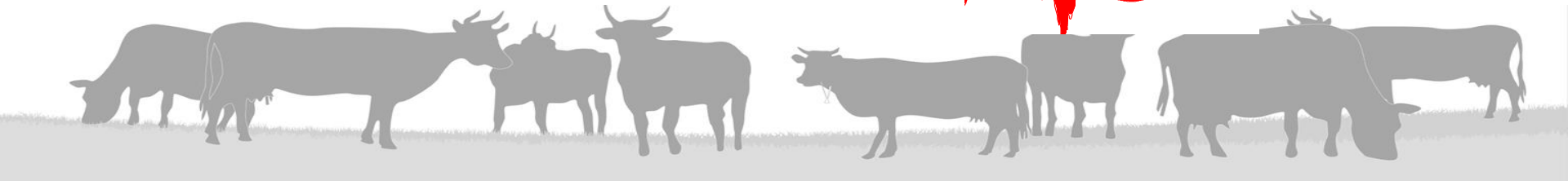




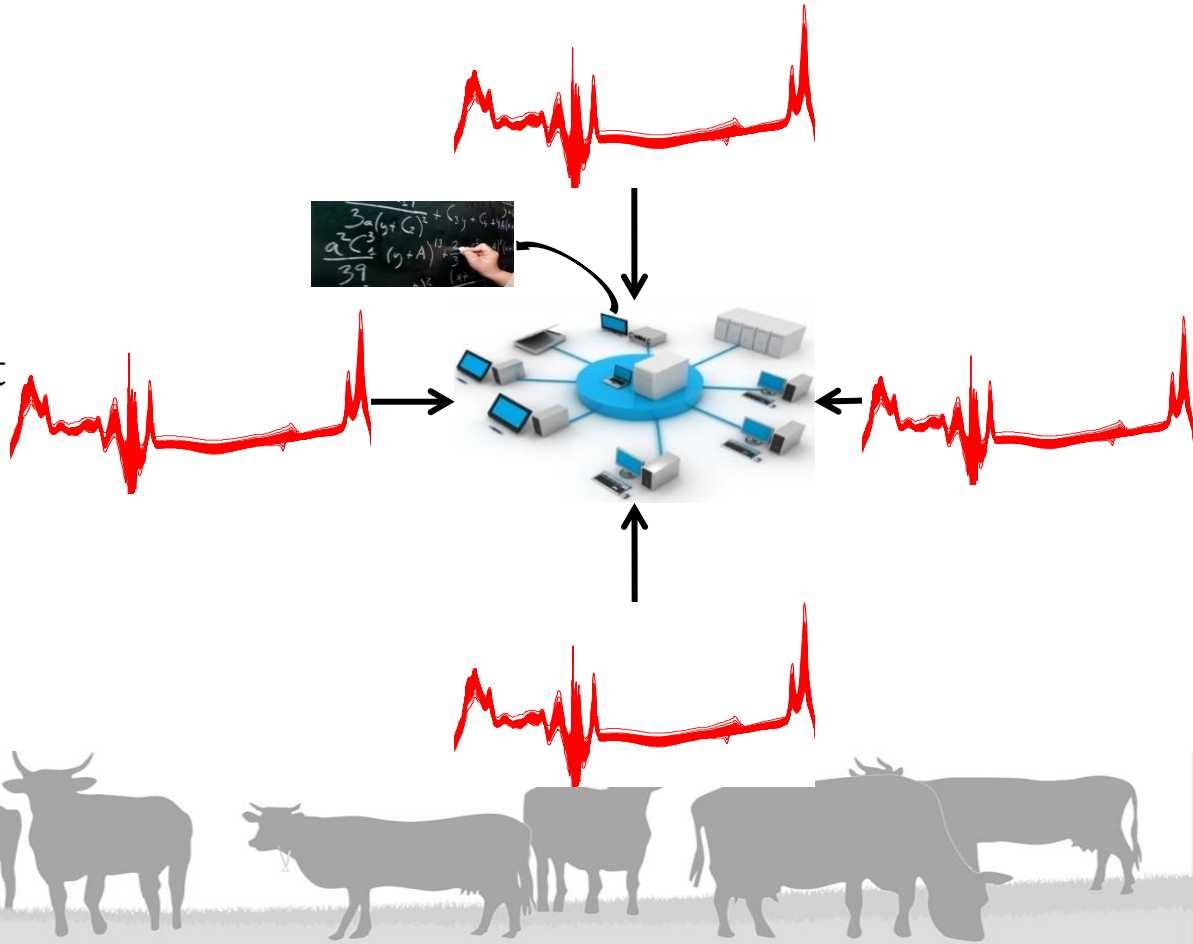






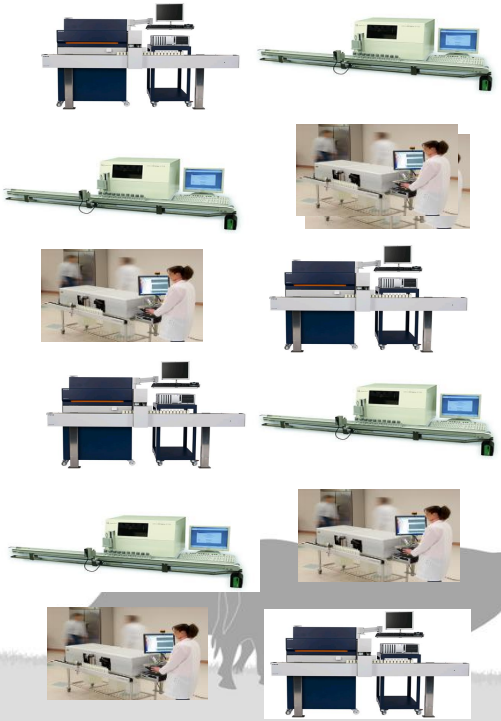
MIR standardisation

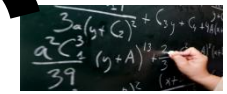
-
- Harmonize the spectral format
- Creation of common models



MIR standardisation

- Models can be used on all instruments in further steps of the project





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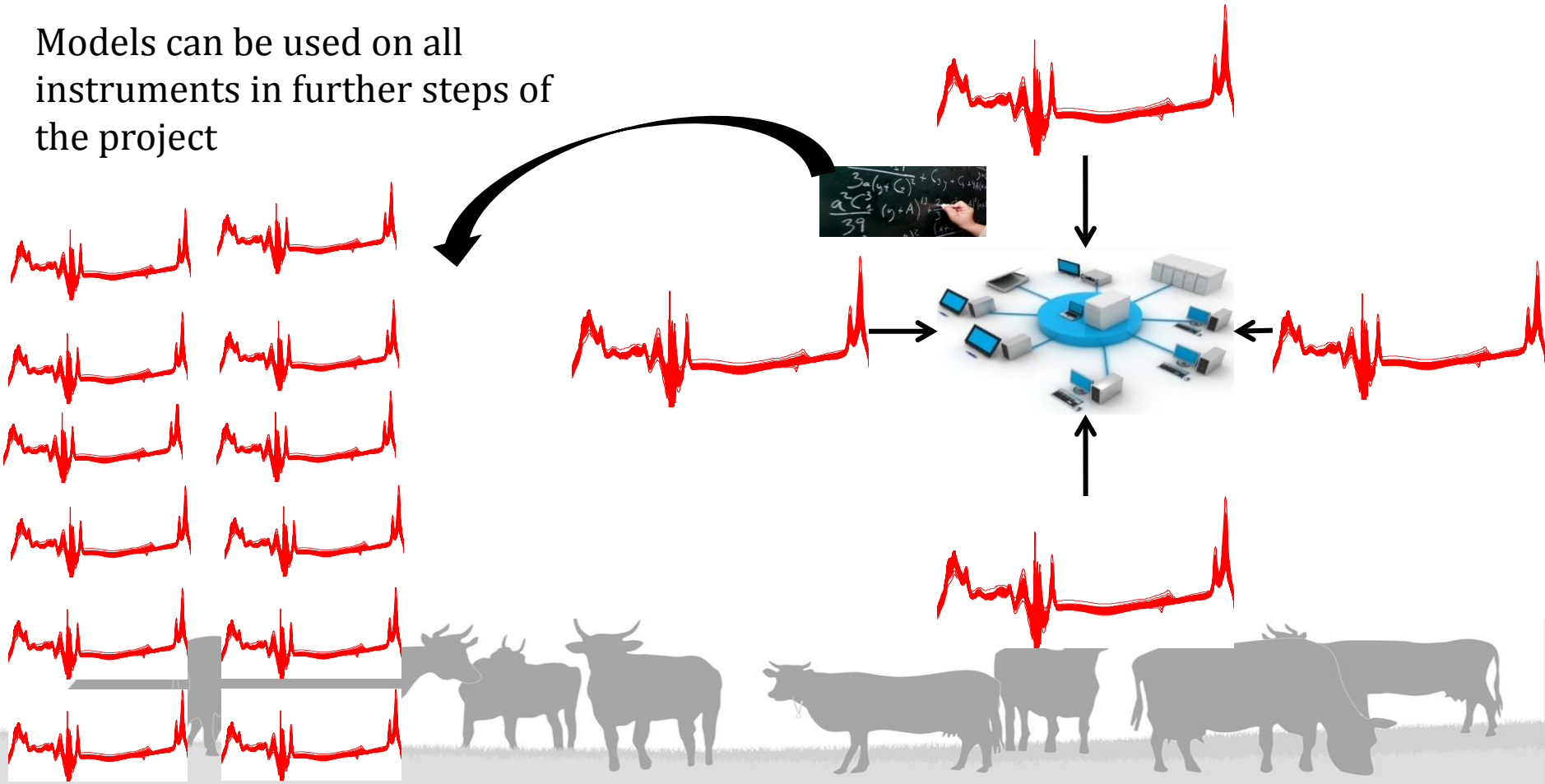
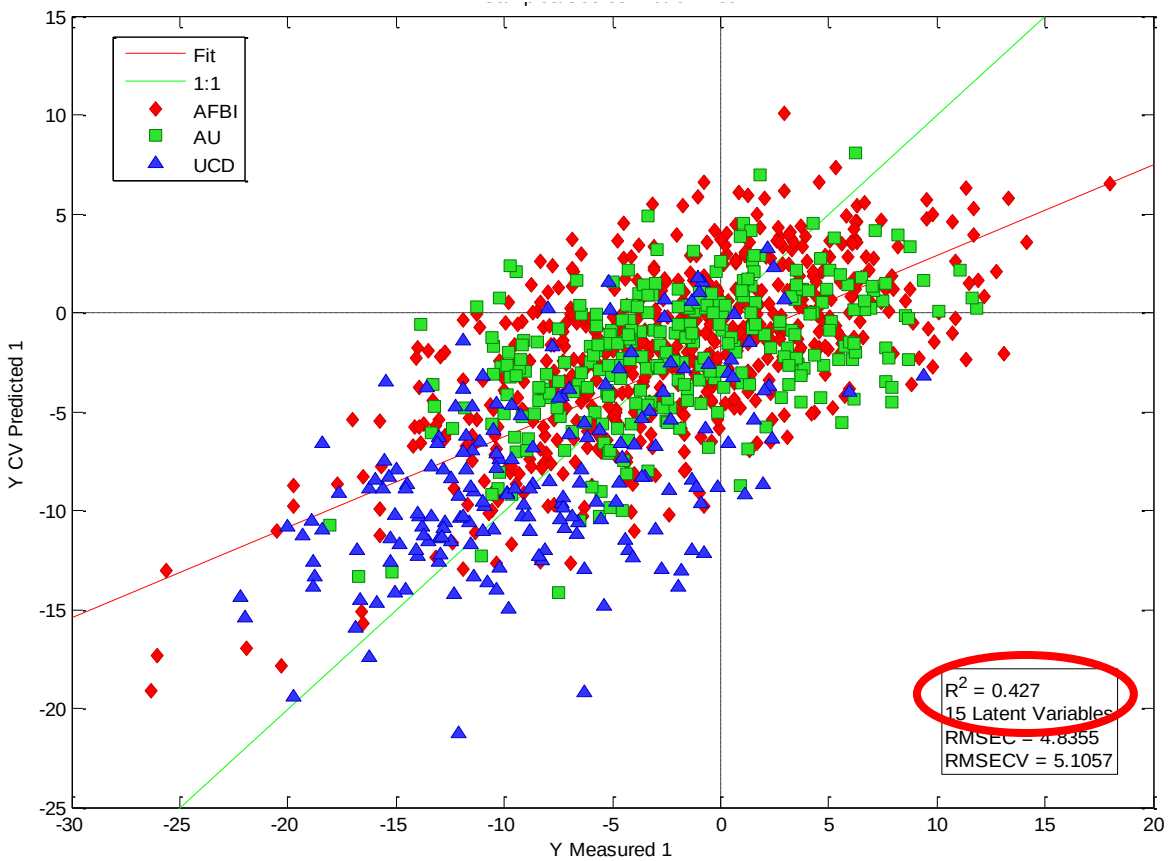


Results

MIR prediction of feed related phenotypes

- Energy balance (Mcal/d)
- PLS
- 132 cows
- 1069 data in the model

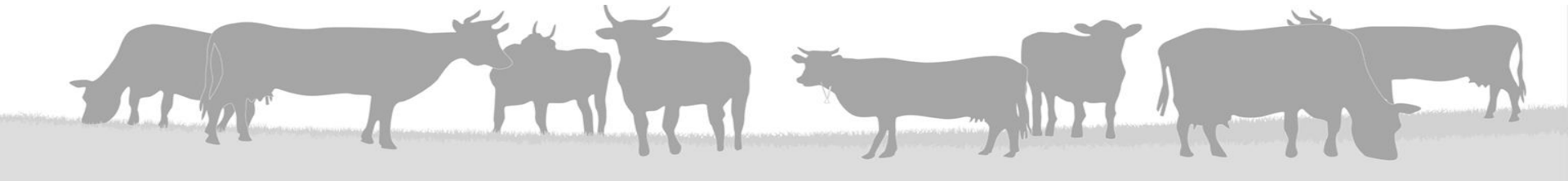
- 15 latent variables
- CV 10 subgroups



MIR prediction of feed related phenotypes

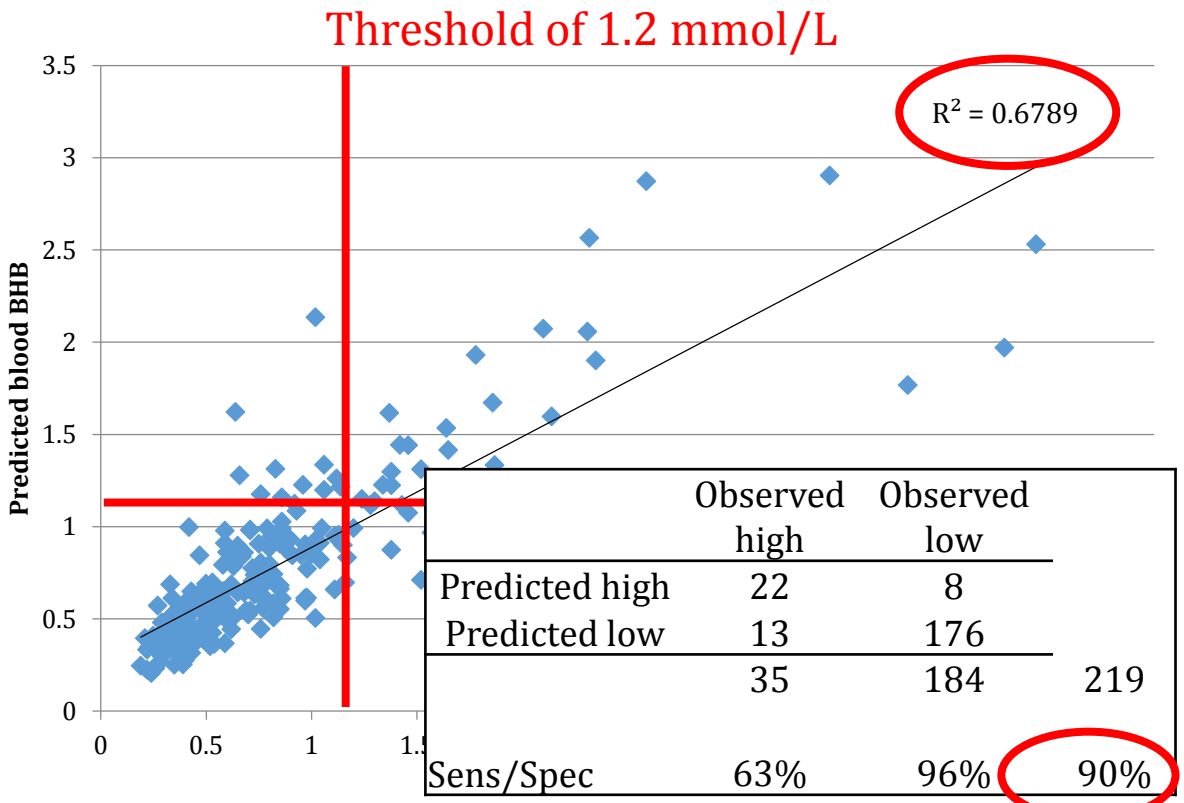
- PLS, LOOCV

	Predictor traits	n	#LV	R^2cv	RMSECV
Energy balance (Mcal/d)	MIR	1069	15	0.43	5.1
Energy balance (Mcal/d)	**MIR, DIM, FPCM**	1098	12	**0.51**	4.8
RFI (kg/d)	MIR	1115	14	0.46	2.9
RFI (kg/d)	MIR, DIM, FPCM	1097	14	**0.53**	2.7
DMI (kg/d)	MIR	1052	14	0.47	3.2
DMI (kg/d)	MIR, DIM, FPCM	1098	8	**0.59**	2.9



MIR prediction of blood metabolites and hormones

- BHB blood
- PLS
- 235 cows
- 219 samples
- Log transformation
- Random removing of low values
- LOOCV
- 8 LV

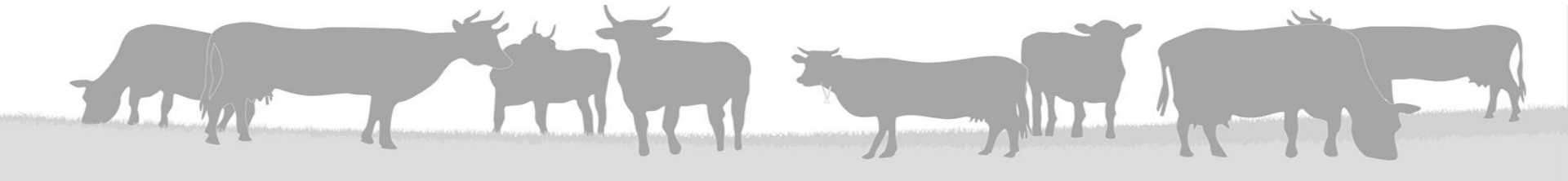


	Observed high	Observed low	
Predicted high	22	8	
Predicted low	13	176	
	35	184	219
Sens/Spec	63%	96%	90%

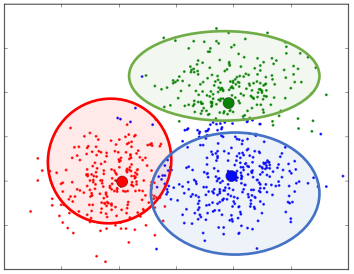
MIR prediction of blood metabolites and hormones

- PLS, LOOCV

Phenotype	n	#LV	R^2cv	RMSECV
Blood NEFA (micro-ekv/L)	392	12	0.37	302
Blood Glucose (mmol/L)	378	8	0.43	0.39
Blood BHB (mmol/L)	219	8	0.68	0.37
Blood IGF-I (mg/L)	378	12	0.59	47.18



MIR prediction of energy status clusters



- MIR, MY, Parity
- PLS-DA, 6LV

	Healthy	Intermediate	Imbalanced	
Predicted Healthy	90	31	8	
Predicted Intermediate	15	110	15	
Predicted Imbalanced	8	33	54	
	113	174	77	364

MIR prediction of energy status clusters

- MIR, MY, Parity
- PLS-DA, 6LV

	Healthy 	Intermediate 	Imbalanced 		Sens	Spec	Glob acc.
Predicted Healthy 	90	31	8		80%	84%	
Predicted Intermediate 	15	110	15		63%	84%	70%
Predicted Imbalanced 	8	33	54		70%	86%	
	113	174	77	364			

MIR prediction of energy status clusters

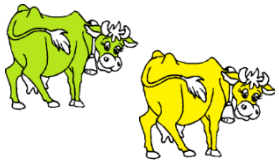
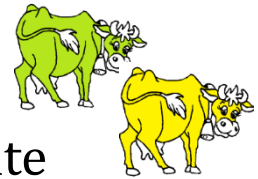
- MIR, MY, Parity
- PLS-DA, 6LV

	Healthy	Intermediate	Imbalanced		Sens	Spec	Glob acc.
Predicted Healthy	90	31	8		80%	84%	
Predicted Intermediate	15	110	15		63%	84%	70%
Predicted Imbalanced	8	33	54		70%	86%	
	113	174	77	364			

Only 4.4% of extreme misclassification

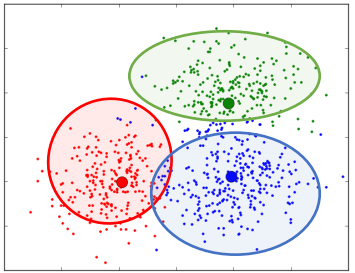
MIR prediction of energy status clusters

- MIR, MY, Parity
- PLS-DA, 6LV

	Healthy-or-Intermediate 	Imbalanced 		Sens	Spec	Glob acc.
Predicted Healthy or Intermediate 	246	23		70%	86%	82%
Predicted Imbalanced 	41	54				
	287	77	364			

Conclusions

- MIR models on energy status:
  - Direct EB, RFI or DMI
  - Blood BHB and IGF-I
  - Global metabolic status using the clusters metodology



- Variable accuracy following traits

- To be used in genomic studies
- Herd or individual cows management tools

Thank you for your attention!

Acknowledgments and Disclaimer

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