Smarter

SMAll RuminanTs breeding for Efficiency and Resilience

WP1 – Task 1
Phenotypes related to Feed Efficiency in Small Ruminants

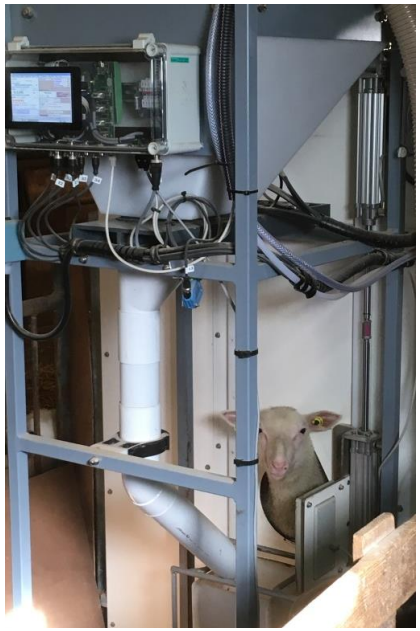
INRAE

SMARTER Final meeting

22nd May 2023

This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Grant Agreement n°772787

Estimates of **feed efficiency** for selection purposes require the acquisition of **individual intake** records



Expensive …
Time consuming …

Only possible on experimental farms

Objectives

- Defining possible proxies
- Testing them to quantify the quality of prediction
- Applying them on commercial farms

Investigation only in experimental farms,

with **total individual records of feed intake**

Dairy sheep

Spain

40 Assaf ewes

Meat sheep

Uruguay

854 Merino/ 237 Dohne/ 290 Corriedale

France

277 Romane

Feed Efficiency traits to predict

Residual Feed Intake RFI	**Feed Conversion Ratio FCR**	Feed Intake FI

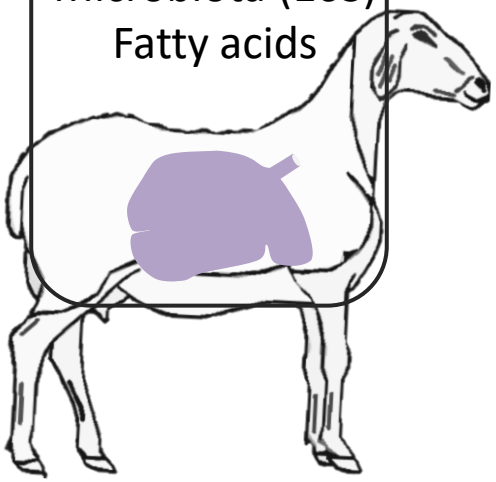
Proxies tested :

Farm records

Bodyweight - ADG
Ultrasound
(Backfat Thickness)

Rumen fluid

Microbiota (16S)
Fatty acids



Blood

Metabolomics
Genomics
^{15}N

Faeces

NIRS

Milk

Fatty acids

GHG

CH_4, CO_2

Variety of approaches :

1- Relationships between FE traits and proxies : **correlations ($FE_{measured}$ & proxies)**

2- Prediction of FE from proxies :

3- Integration of different groups of proxies :

} ***correlations ($FE_{predicted}$ & $FE_{measured}$)***

with or without cross-validations

correlations ($FE_{measured}$ & *proxies)*

correlations ($FE_{predicted}$ & $FE_{measured}$) without cross-validations

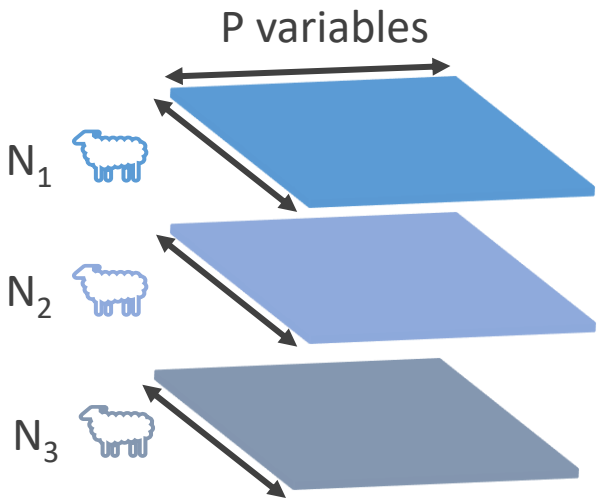
(Maximum value)

	RFI	FCR	FI
Fatty acids in milk	0.48	0.70	
	NS	0.82	
Backfat thickness	0.09	0.07	
GHG (CH_4, CO_2, O_2)	0.28	0.35	
PCA (MW, ADG,GHG)			0.82
Backfat thickness	0.02	0.06	
Microbiota 16S	0.07	0.40	0.59
Metabolomics plasma	0.10	-	0.20
NIRS faeces	0.01	0.15	0.19
^{15}N in plasma	0	0.67	-

2 types of integration (mixOmics)

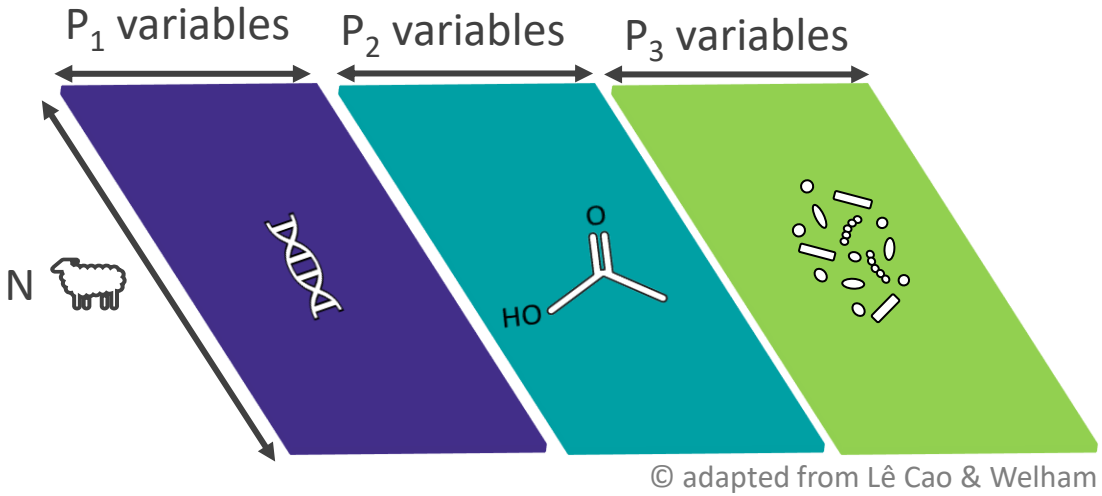
Q. Le Graverand
PhD

P-integration (mint.sPLSR)



Integrate different **studies** (years)

N-integration (block.sPLSR)

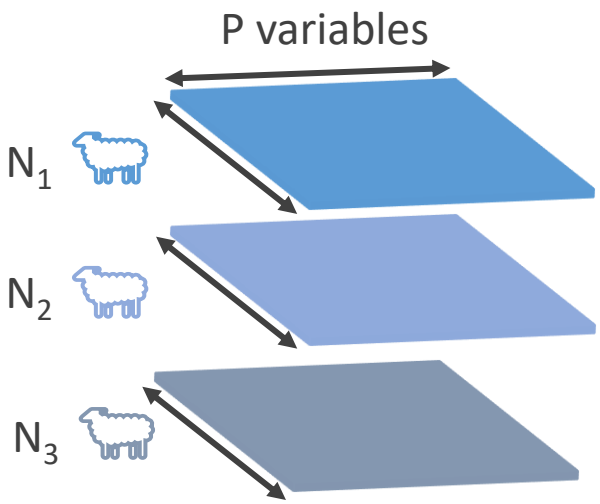


© adapted from Lê Cao & Welham

Integrate different **variables** (omics)

P-Integration with cross-validation – single omics predictions

P-integration (mint.sPLSR)



Integrate different **studies** (years)

Farm records

Bodyweight - ADG
Ultrasound
(backfat Thickness)

Rumen fluid

Microbiota (16S)
Fatty acids

Faeces

NIRS

Blood

Metabolomics
Genomics
^{15}N

Integration with a new ensemble strategy

Cross-validation: training (60%), validation (30%) and testing sets (10%)

100× | Training | Validation | Testing

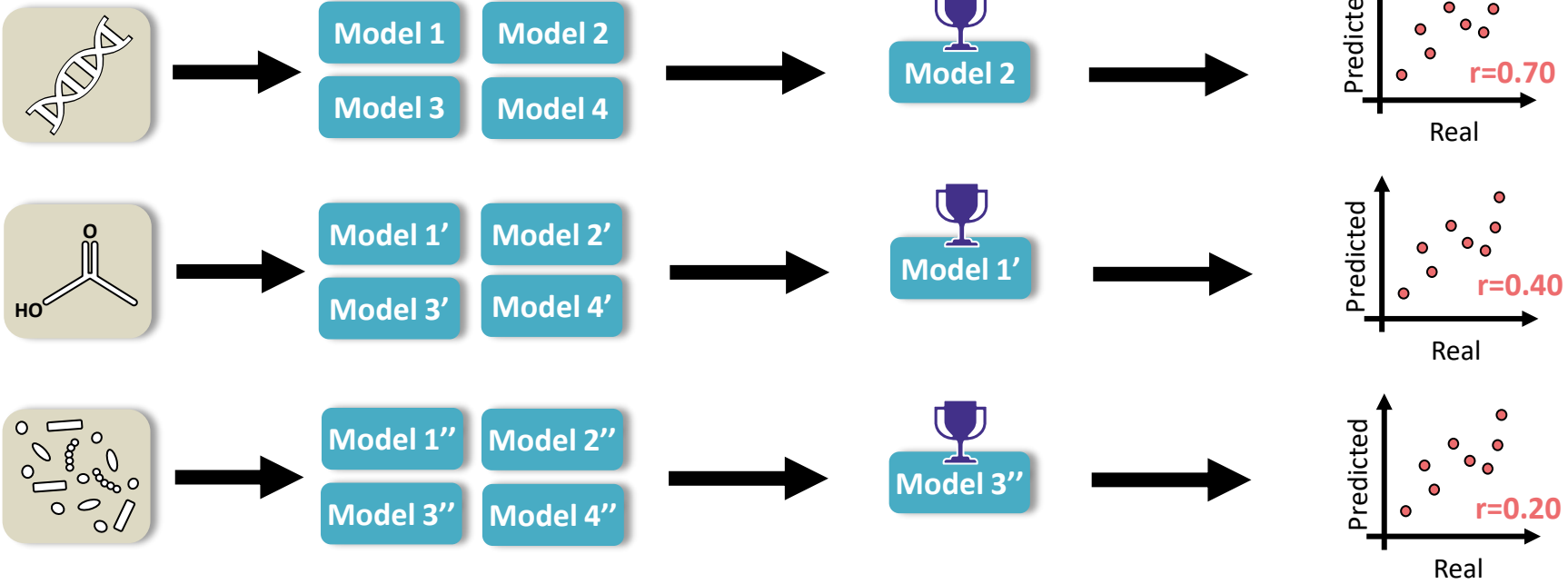
Separate omics blocks

Try different mint.sPLSR hyperparameters

Select best hyperparameters

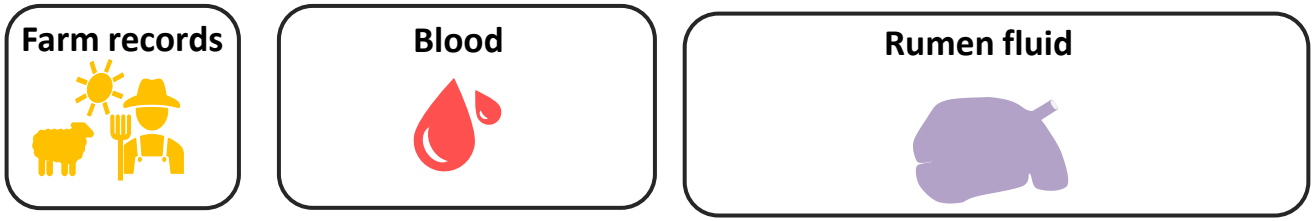
Evaluate

P-integration



P-Integration with cross-validation – single omics predictions

Cross-validation: training (60%), validation (30%), testing (10%) - Repeated 100 times

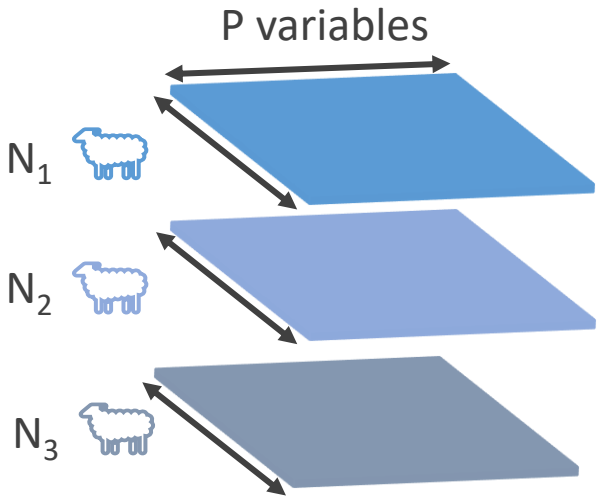


	Mint.sPLSR					
	Fixed effects & covariates	Genetics	Metabo-lomics	LFA	VFA	Microbiota 16S
Feed Intake	0.85 (0.04)	0.54 (0.11)	0.51 (0.12)	0.39 (0.12)	0.42 (0.13)	0.46 (0.14)
Residual Feed Intake	0.34 (0.11)	0.46 (0.13)	0.33 (0.13)	0.20 (0.15)	0.08 (0.17)	0.23 (0.14)

Average pearson correlations (and standard deviation) between predictions and real values

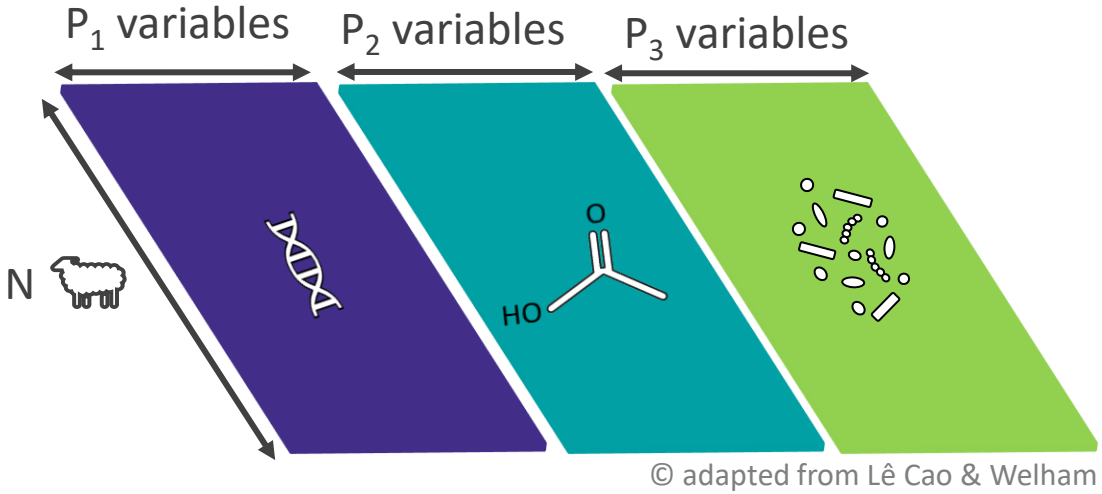
2 types of integration (mixOmics)

P-integration (mint.sPLSR)



Integrate different **studies** (year)

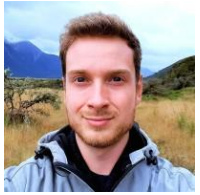
N-integration (block.sPLSR)



Integrate different **variables**

What about NP-integration ?

As mixOmics function is not working, another ensemble strategy is investigated !

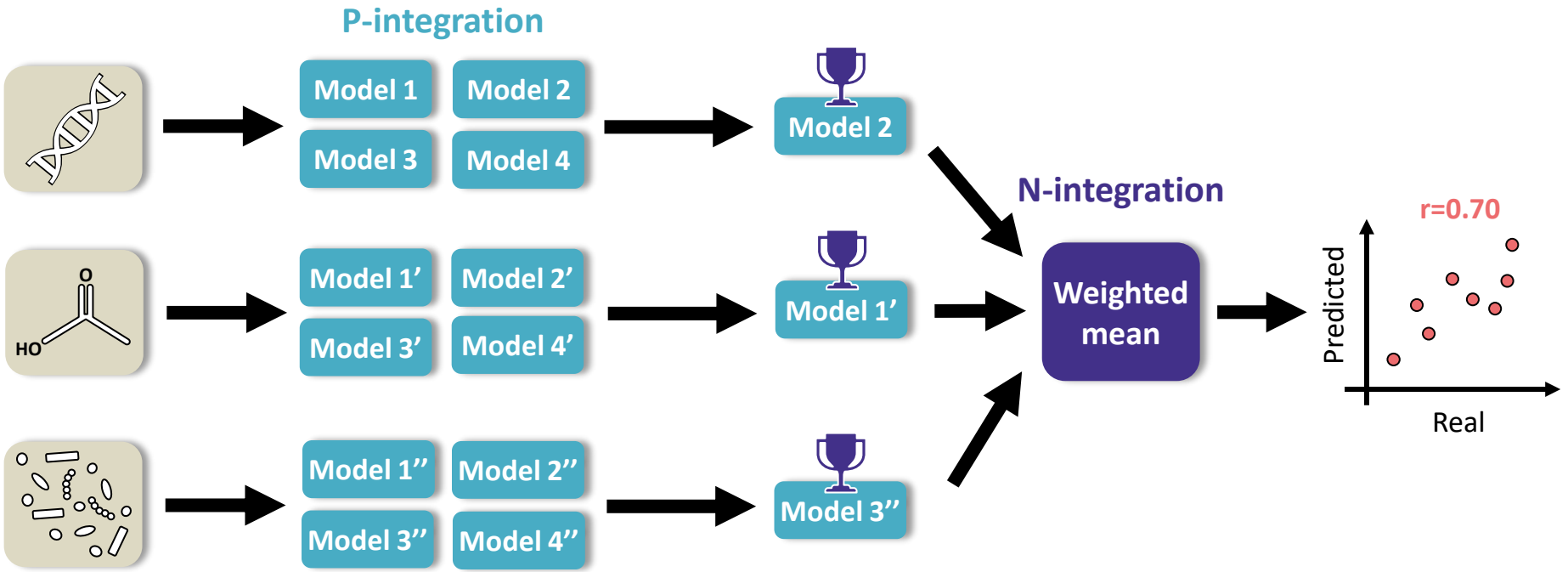


Integration with a new ensemble strategy

Cross-validation: training (60%), validation (30%) and testing sets (10%)

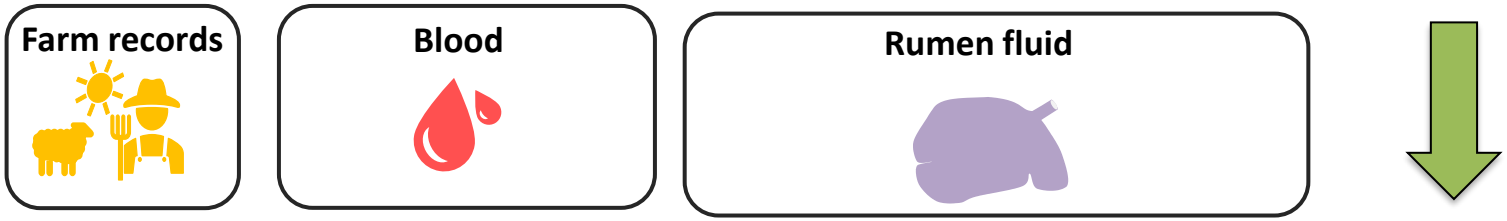
100× | Training | Validation | Testing

Separate omics blocks | Try different mint.sPLSR hyperparameters | Select best hyperparameters | Combine models | Evaluate



Integration with a new ensemble strategy

Cross-validation: training (60%), validation (30%) and testing sets (10%)

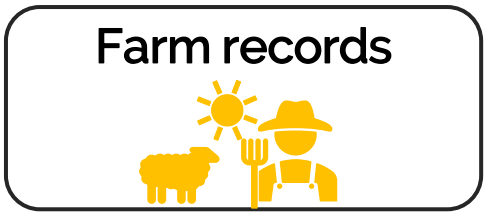


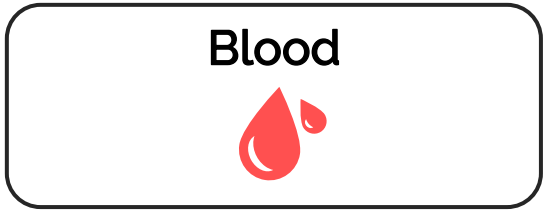
	Mint.sPLSR						Ensemble integration
	Fixed effects & covariates	Genetics	Metabo-lomics	LFA	VFA	Microbiota 16S	All
Feed Intake	0.85 (0.04)	0.54 (0.11)	0.51 (0.12)	0.39 (0.12)	0.42 (0.13)	0.46 (0.14)	0.83 (0.05)
Residual Feed Intake	0.34 (0.11)	0.46 (0.13)	0.33 (0.13)	0.20 (0.15)	0.08 (0.17)	0.23 (0.14)	0.55 (0.11)

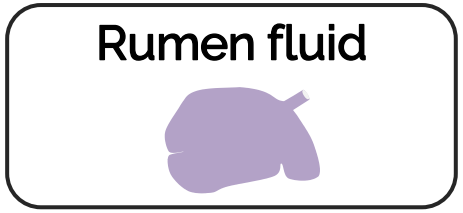
Average pearson correlations (and standard deviation) between predictions and real values

Data contributions in the ensemble model

Relative contributions = relative weight while averaging predictions







	Fixed effects & covariates	Genetics	Metabolomics	LFA	VFA	Microbiota 16S
Feed intake	40.9%	17.4%	14.3%	7.8%	9.3%	10.4%
Residual feed intake	20.3%	39.9%	21.1%	5.7%	3.3%	9.7%

- Host genetics: high contribution (partly due to the divergent lines)
- Rumen: not the best sampling location to predict feed efficiency :
  - blood metabolomics performed better !

Take-home messages

- Feed Intake is easier to predict than FE traits – particularly RFI

- Even if the rumen is a key to ruminant nutrition, rumen data are not good predictors (moreover, difficult to access)
  -> Blood (or milk?) metabolome seemed to predicted better

- GHG and faeces still need to be evaluated with cross-validation models

- “Omics by omics” RFI prediction is not sufficient: different groups of traits must be integrated to obtain a suitable prediction

Merci de votre attention