



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

**INRAE**

**SMARTER Final meeting**  
22<sup>nd</sup> May 2023



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

Uruguay



854 Merino/ 237 Dohne/ 290 Corriedale

Meat sheep

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  
<sup>15</sup>N

**Faeces**

NIRS

**Milk**

Fatty acids

**GHG**

CH<sub>4</sub>, CO<sub>2</sub>

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)



Fatty acids  
in milk

RFI	FCR	FI
<b>0.48</b>	<b>0.70</b>	
<b>NS</b>	<b>0.82</b>	



Backfat thickness  
GHG (CH<sub>4</sub>, CO<sub>2</sub>, O<sub>2</sub>)  
PCA (MW, ADG, GHG)

<b>0.09</b>	<b>0.07</b>	
<b>0.28</b>	<b>0.35</b>	
		<b>0.82</b>



Backfat thickness  
Microbiota 16S  
Metabolomics plasma  
NIRS faeces  
<sup>15</sup>N in plasma

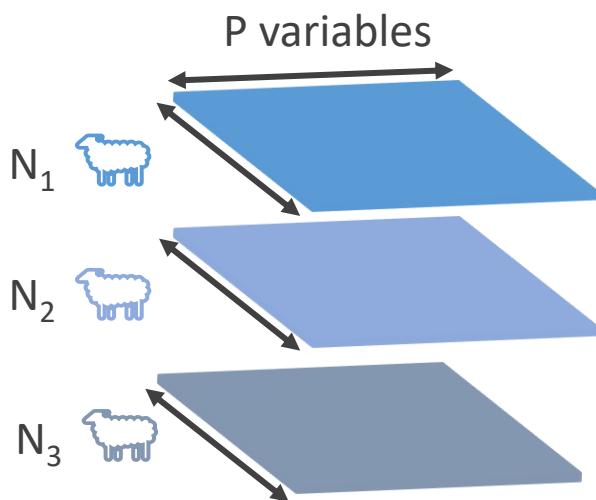
<b>0.02</b>	<b>0.06</b>	
<b>0.07</b>	<b>0.40</b>	<b>0.59</b>
<b>0.10</b>	-	<b>0.20</b>
<b>0.01</b>	<b>0.15</b>	<b>0.19</b>
<b>0</b>	<b>0.67</b>	-



Q. Le Graverand  
PhD

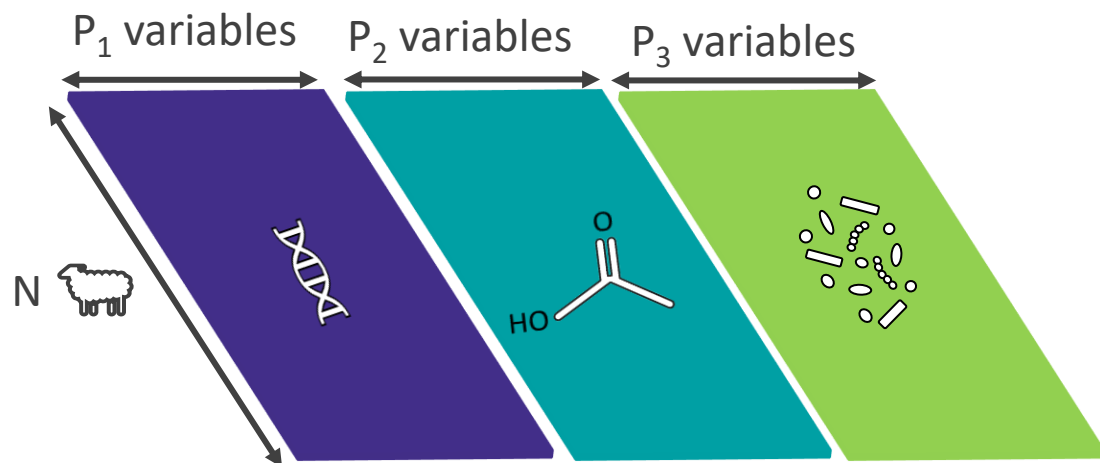
## 2 types of integration (mixOmics)

### P-integration (mint.sPLSR)



Integrate different **studies**  
(years)

### N-integration (block.sPLSR)



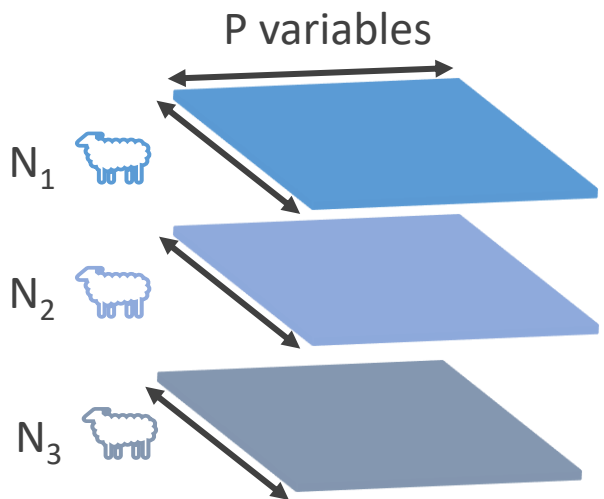
© adapted from Lê Cao & Welham

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)

**Faeces**

NIRS

**Rumen fluid**

Microbiota (16S)  
Fatty acids

**Blood**

Metabolomics  
Genomics  
<sup>15</sup>N



## Integration with a new ensemble strategy

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

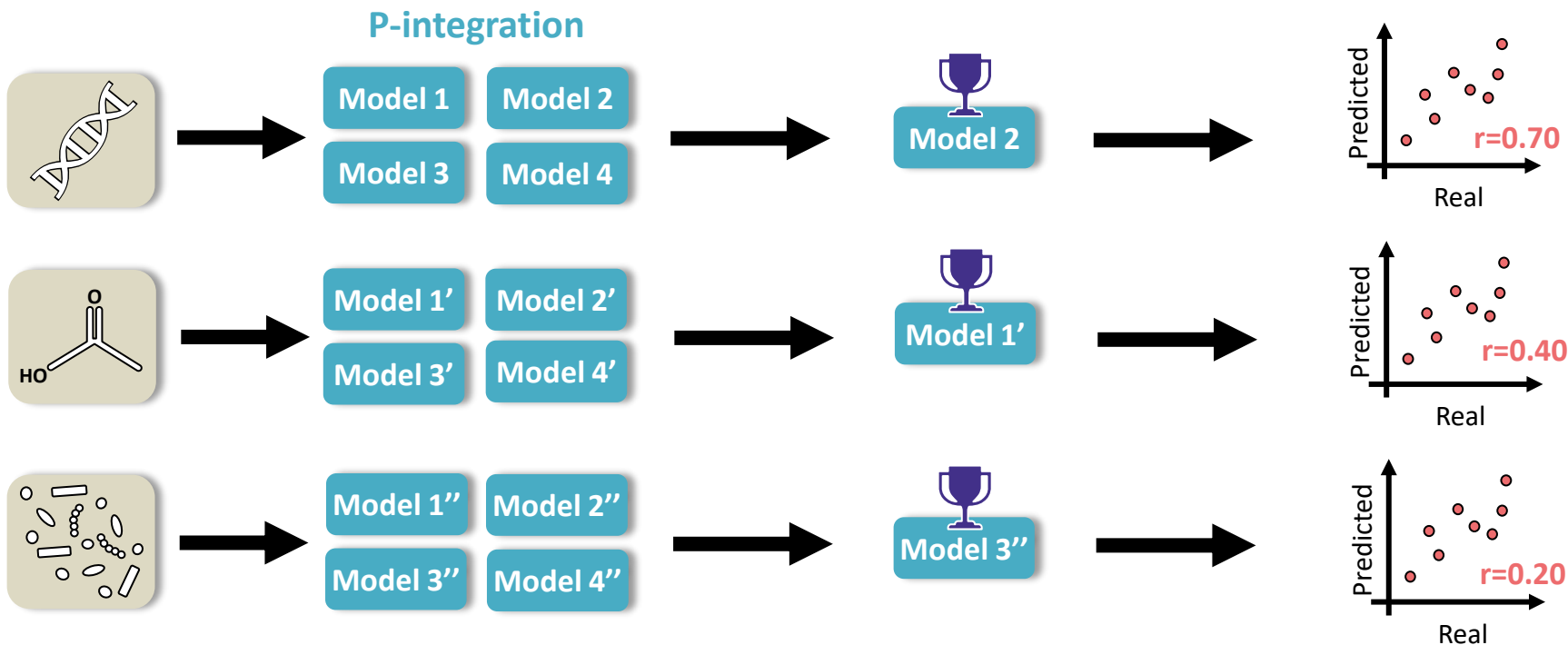


Separate omics blocks

Try different mint.sPLSR hyperparameters

Select best hyperparameters

Evaluate

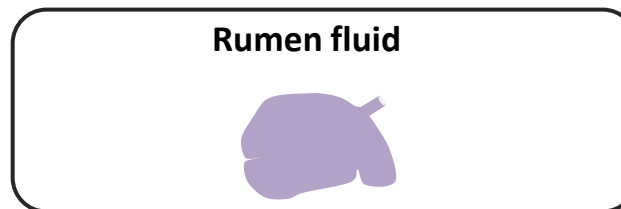
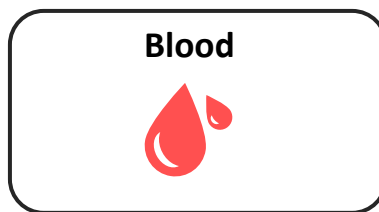






## P-Integration with cross-validation – single omics predictions

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



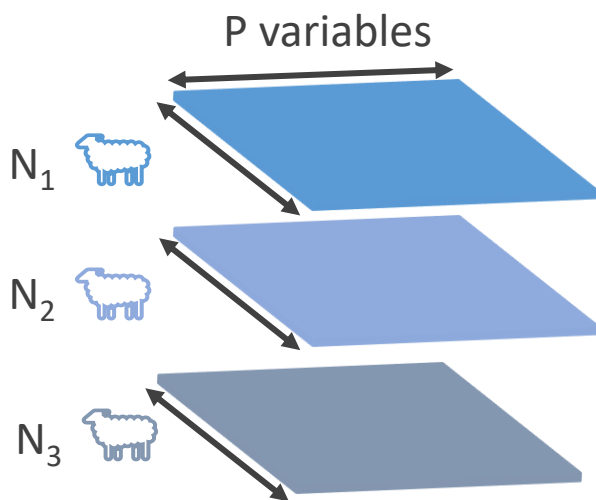
Mint.sPLSR						
	Fixed effects & covariates	Genetics	Metabo-lomics	LFA	VFA	Microbiota 16S
Feed Intake	0.85 (0.04)	0.54 (0.11)	0.51 (0.12)	0.39 (0.12)	0.42 (0.13)	0.46 (0.14)
Residual Feed Intake	0.34 (0.11)	0.46 (0.13)	0.33 (0.13)	0.20 (0.15)	0.08 (0.17)	0.23 (0.14)

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



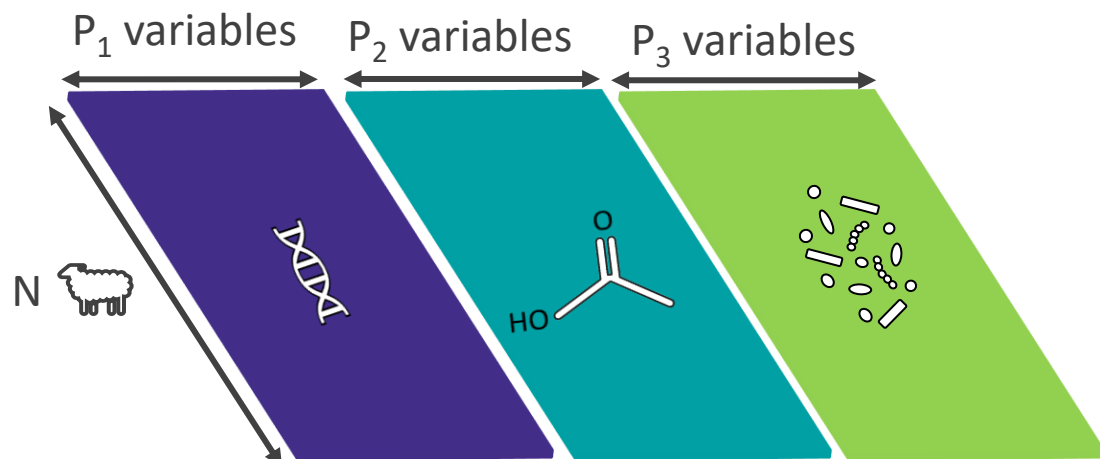
## 2 types of integration (mixOmics)

### P-integration (mint.sPLSR)



Integrate different **studies** (year)

### N-integration (block.sPLSR)



© adapted from Lê Cao & Welham

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%)*



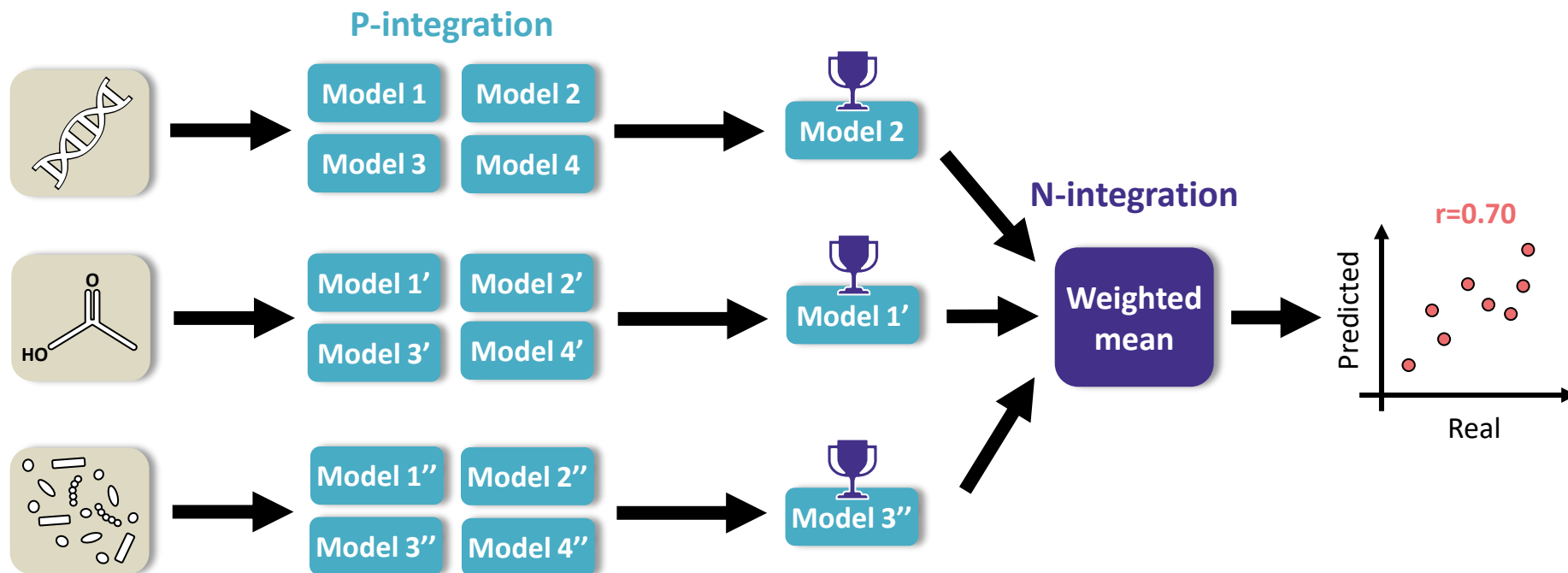
Separate omics blocks

Try different mint.sPLSR hyperparameters

Select best hyperparameters

Combine models

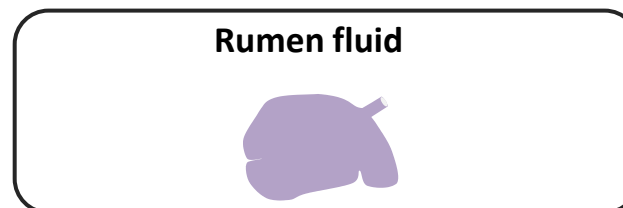
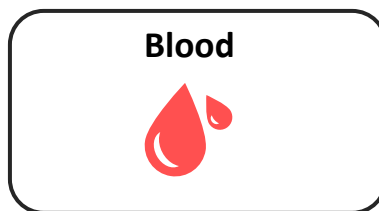
Evaluate





## Integration with a new ensemble strategy

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

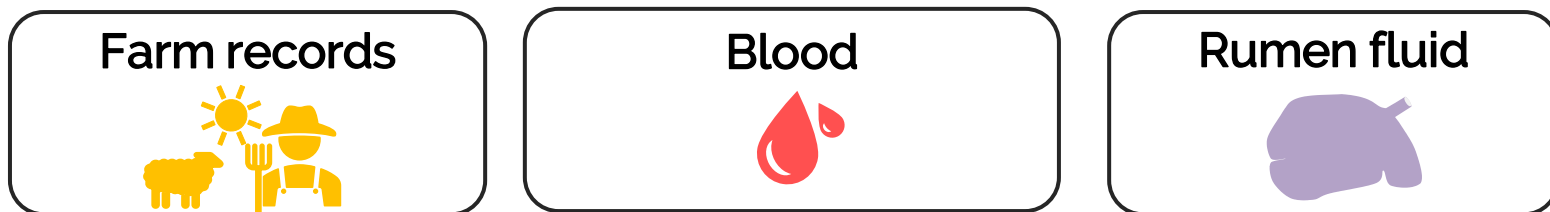


	Mint.sPLSR						Ensemble integration
	Fixed effects & covariates	Genetics	Metab-omics	LFA	VFA	Microbiota 16S	All
Feed Intake	<b>0.85</b> (0.04)	<b>0.54</b> (0.11)	<b>0.51</b> (0.12)	<b>0.39</b> (0.12)	<b>0.42</b> (0.13)	<b>0.46</b> (0.14)	<b>0.83</b> (0.05)
Residual Feed Intake	<b>0.34</b> (0.11)	<b>0.46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

