EAAP
European Federation of Animal Science

Artificial intelligence-driven plasma metabolomics identifies metabolic signatures of FEED EFFICIENCY IN BEEF CATTLE

Alanne T. Nunes[1]*, Camila A. Faleiros[1], Mirele D. Poleti[1], Yamilé López-Hernández[2], David S. Wishart[2], Heidge Fukumasu[1]

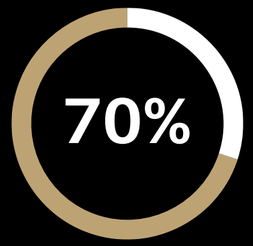
[1]University of São Paulo, Brazil
[2]University of Alberta, Canada

Beef cattle production plays a critical role in global food security and national economies, particularly in Brazil, the world's leading beef producer and exporter.

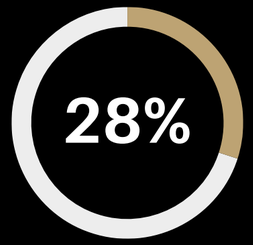
USDA (2025); ABIEC (2025)

Why feed efficiency matters and why it is hard to predict

RELEVANCE

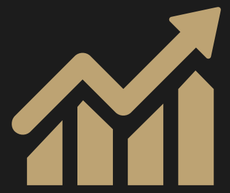


Major production cost



Reduction in CH_4 emissions

RESIDUAL FEED INTAKE



Observed - expected dry matter intake

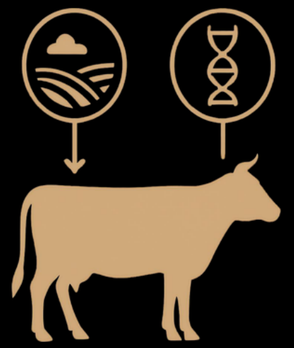
DMI = MBW + ADG + RFI

56 to 70 days

BIOLOGICAL COMPLEXITY

Moderate heritability

Polygenic phenotype



Difficult to find robust biomarkers

1 Feed intake

2 Digestion

3 Metabolism

4 Activity

5 Thermoregulation

Herd, Oddy and Richardson (2004)

Metabolomics offers a powerful path to unlock the biology of feed efficiency, but its real impact depends on validated biomarkers generated through large-scale studies.

Nunes et al. (2024)

Hypothesis

Distinct plasma metabolomic signatures enable discrimination between cattle with high and low feed efficiency.

Objectives

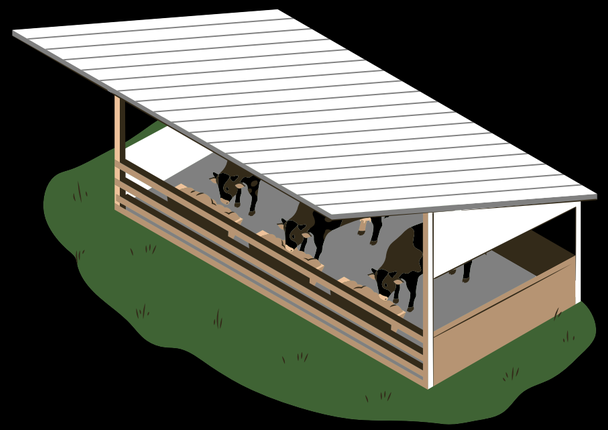
Define divergent feed-efficiency phenotypes

Identify plasma metabolic signatures

Evaluate their discriminative potential

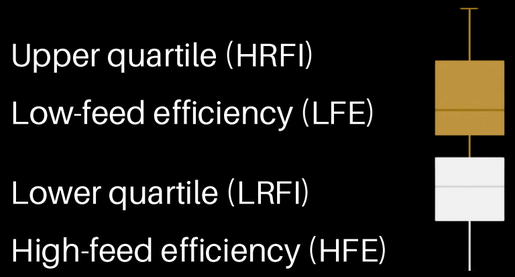
Study design

1 Phenotypic data and sample collection



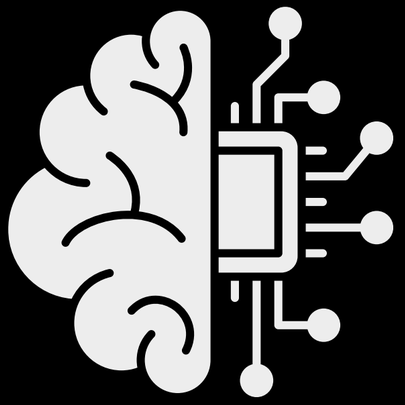
360 animals, 5 cohorts
Nellore, Angus and crossbred cattle
Plasma collection before the feedlot trial

2 Residual feed intake determination



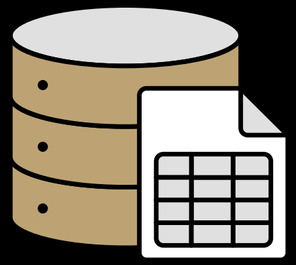
3 Metabolomics analyses

LC-MS/MS and DFI-MS
TMIC MEGA assay



4 Machine learning analyses

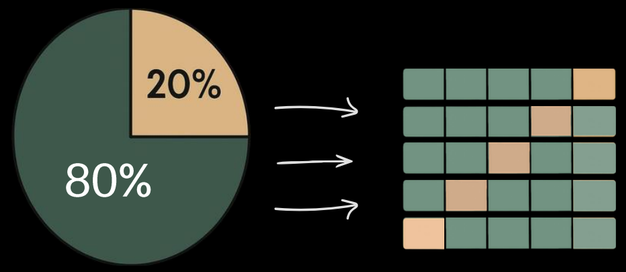
Modeling strategy

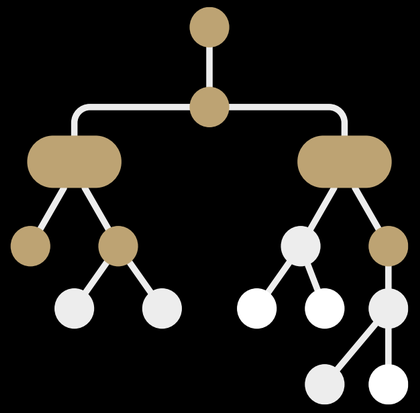


Metabolomics dataset preprocessing

<LOD and >ULOQ handling
Missingness filtering and imputation
Log10 transformation and normalization

Train-test split and CV model tuning



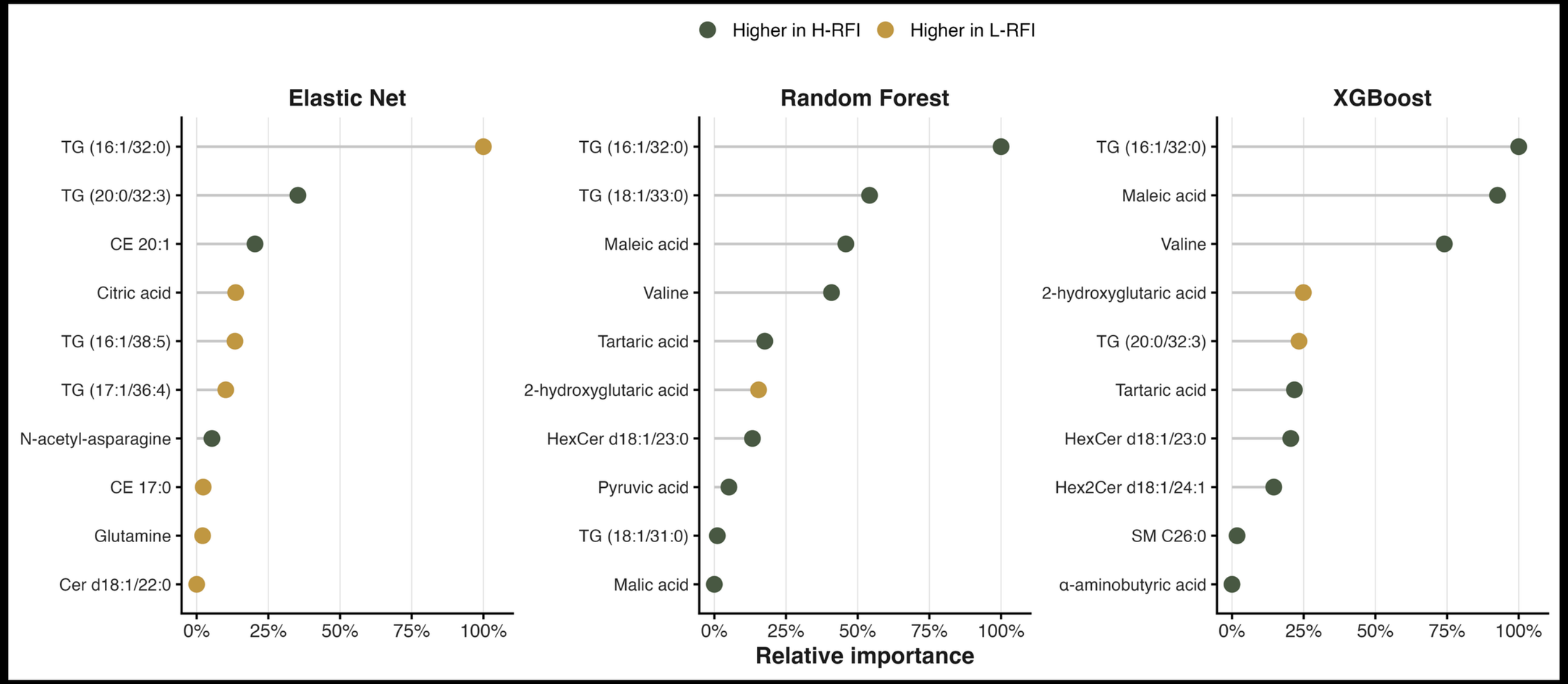


Model comparison

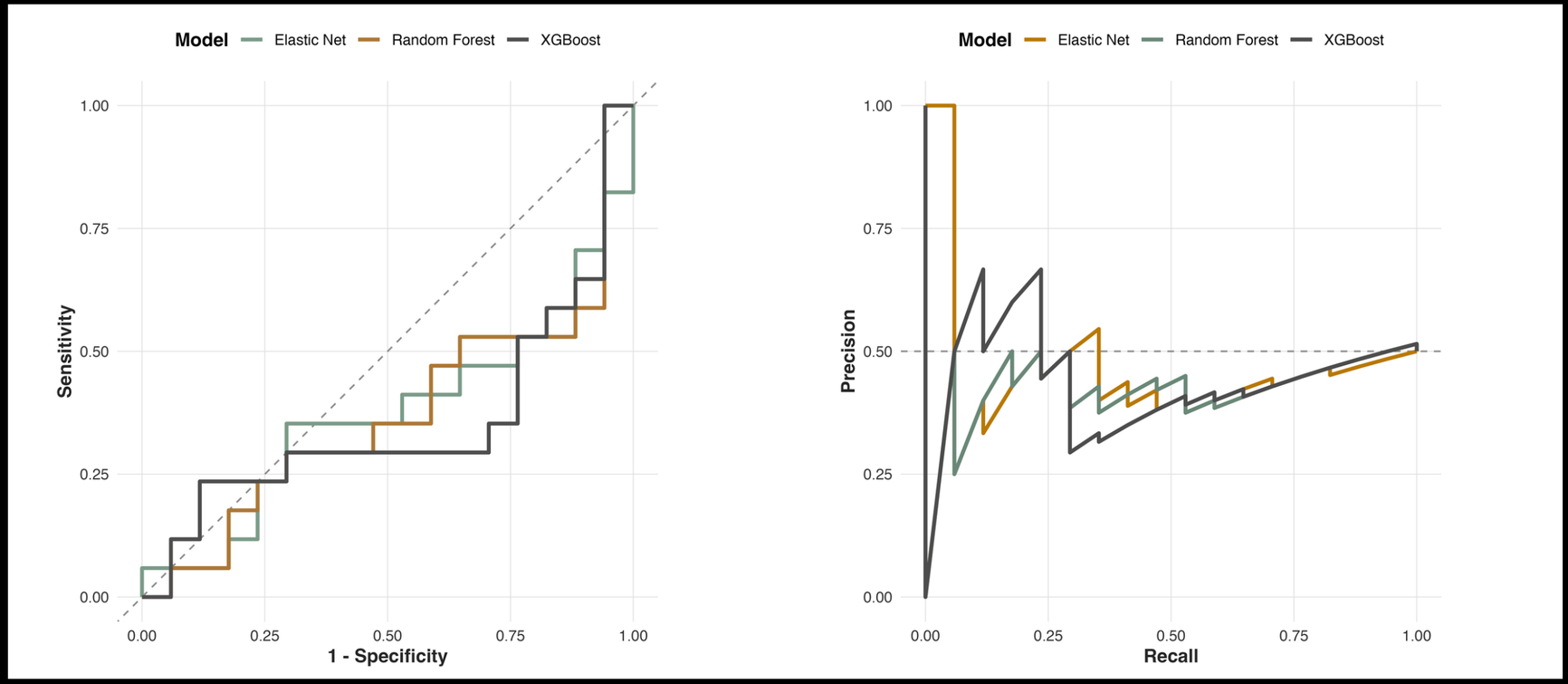
Elastic Net, Random Forest, and XGBoost

Independent test evaluation

Independent hold-out test set
ROC-AUC and Brier score



Metabolites selected by each model



Independent test performance was limited

Low feed efficiency (H-RFI)

Higher lipid-related metabolites
triacylglycerols, cholesteryl esters, sphingolipids

Higher energy-related metabolites
succinate, pyruvate and hexose

Suggests altered lipid handling and post-absorptive energy metabolism

VS

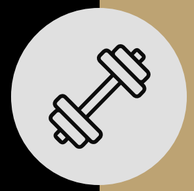
High feed efficiency (L-RFI)

Higher amino acid-related metabolites
methionine, tyrosine and N-acetyl-tryptophan

Higher microbial/host co-metabolites
hippuric acid, p-hydroxyhippuric acid and indoxyl sulfate

Suggests rumen microbiome–host metabolic contribution

Strengths



Well-defined phenotype
Multiple supervised models
Independent hold-out test set
Cross-model consensus biomarkers

Limitations

Separation was modest
No external validation yet
Biomarker reproducibility across populations still unknown
Heterogeneous population: increased biological variability

Take-home message

01

AI-guided targeted plasma metabolomics

identified metabolic signatures associated with feed efficiency

02

Independent test performance was modest

results should be interpreted as exploratory

03

Cross-model consensus metabolites

suggests biologically meaningful differences in energy metabolism, amino acid turnover, and lipid handling, which help uncover the biology of feed efficiency

04

External validation

Is needed before proposing biomarkers for feed efficiency selection

THANK YOU!

Questions?

+55 19 99922-2434

www.loctusp.com.br

alanne.nunes@usp.br