Leveraging on High-throughput Phenotyping Technologies to Optimize Livestock Genetic Improvement and Husbandry

G. J. M. Rosa^{1,2}, J. R. R. Dorea¹, A. F. A. Fernandes¹, V. C. Ferreira¹ and T. L. Passafaro¹

¹Department of Animal Sciences ²Department of Biostatistics & Medical Informatics





Unraveling genetic architecture of complex traits using multi-omics approaches

High-throughput OMICS technologies:

- Phenomics

- Genomics
- Epigenomics
- Transcriptomics
- Proteomics
- Metabolomics
- etc.

Outline

- Introduction
- Examples
 - Feed Efficiency in Group-housed Broilers
 - Dairy Cow Feed Intake Prediction Using Milk MIR
 - Pig Growth and Development
- Concluding Remarks

High-Throughput Phenotyping

- Automated data recording systems
- 24-7 shift
- Robotics and artificial intelligence
- Real time measurements; sensors
 - Image
 - Motion
 - Sound
 - Chemical composition
 - Spectroscopy
 - etc.





Precision Livestock Production

200



Novel traits, better scoring, G x E

High-Throughput Phenotyping

- Novel phenotypes
 Indicator traits
- Genetic Improvement
- Intermediate traits (DNA \rightarrow phenotype)
- Scientific Research in Animal Sciences •
- Precision Livestock Farm
 - Nutrition
 - Reproduction
 - Health surveillance
 - Welfare
 - Control of meat and milk composition and quality

High-Throughput Phenotyping

- Benefits and Challenges
- Data management and data processing
- Cost-benefit tradeoff (PLF)
- Can be disruptive; labor force (PLF)

Example 1. Feed Efficiency in Group-housed Broilers

Breeder's Equation

Expected genetic progress with phenotypic selection on a single trait y:



Indirect Selection

- Selection performed on a specific trait (indicator trait) but targeting the genetic improvement of another trait (economically important trait)
- It can only be successful if the indicator trait has a high genetic correlation with the target trait
- It may be advantageous if:
 - It produces greater genetic gain on the target trait
 - Indicator trait is less costly to measure
 - Selection of sex-limited traits, target trait difficult to measure, binary target trait, etc.



• Feed Efficiency, Feed Conversion in Broilers



DMI:ADG assessed in cages, as an indicator of feed conversion in commercial conditions (floor, social interactions, etc.)

Correlated Response

• The correlated response to selection can be predicted by:



where $r_{x,y}$ is the genetic correlation between traits x and y

Correlated Response

 The correlated response to selection can be then expressed as:

$$\mathbf{R}_{\mathbf{x} \cdot \mathbf{y}} = \mathbf{r}_{\mathbf{x}, \mathbf{y}} \left(\frac{\mathbf{S}_{\mathbf{x}}}{\mathbf{S}_{\mathbf{y}}} \right) \mathbf{h}_{\mathbf{y}} \left(\mathbf{i}_{\mathbf{y}} \right) \mathbf{S}_{\mathbf{y}}$$

 Its effectiveness, relative to direct selection, is given by:

$$\frac{\mathbf{R}_{x \cdot y}}{\mathbf{R}_{x}} = \mathbf{r}_{x,y} \cdot \frac{\mathbf{h}_{y}}{\mathbf{h}_{x}} \cdot \frac{\mathbf{i}_{y}}{\mathbf{i}_{x}} \cdot \frac{\mathbf{L}_{x}}{\mathbf{L}_{y}}$$

Example





Heritabilities:

Cages h² ≈ 0.20
 Floor h² ≈ 0.25
 → r_{x,y} ≈ 0.35

$$\frac{R_{x \cdot y}}{R_x} = r_{x,y} \cdot \frac{h_y}{h_x} \cdot \frac{i_y}{i_x} \cdot \frac{L_x}{L_y}$$

Feed Efficiency in Broilers

- Individual feed intake (DMI)
- Genetic selection for feed efficiency
- RFID on floor raised bird; social interactions
- 3,986 birds (males and females)
- 28 day trials; BW measured at beginning, middle and end of trials







Residual Feed Intake - RFI



DMI (g/d) = $\mu + \beta_1 \times ADG + \beta_2 \times Hen Flock + \beta_3 \times Sex + \beta_4 \times Trial +$ **RFI**

Using Feeding Behavior to Predict RFI



Defining Meal Criteria

AAI1993



Using Feeding Behavior to Predict RFI

Modeling Approaches:

- Logistic Regression
- Support Vector Machine
 - Linear SVM
 - Quadratic SVM
- Decision Tree
 - Boosted Trees

Model Comparison:

• 5-fold Cross-validation

Using Feeding Behavior to Predict RFI

Accuracy (%)	Modeling Approach			
	Logistic	SVM-	SVM-	Boosted
	Regression	linear	quadratic	Trees
Overall	50	60	66	64
High	87	45	65	62
Low	13	76	67	66
AUC	0.51	0.67	0.72	0.67

Health and Welfare



Healthy Animals

Animals Withdrawn from the Trial

Example 1; Conclusions

- Higher genetic gain for RFI
- Behavior seemingly associated with RFI
- Additional prediction models to be tested (modeling approaches and predictors)
- Potential for earlier detecting of health problems
- Integration of pedigree and genomic information

Example 2. Dairy Cow Feed Intake Prediction Using Milk MIR



Milk Mid-infrared Spectra





dry matter intake

mid-infrared (MIR) spectroscopy

Dorea JRR, Rosa GJM, Weld KA and Armentano LE. Mining data from milk infrared spectroscopy to improve feed intake predictions in lactating dairy cows. J. Dairy Sci. 101: 5878-5889, 2018. Experimental Data

- Improve intake predictions
- Hard to measure in practical conditions Feed efficiency
 - 310 cows from 5 trials
 - 1276 observations of DMI, behavior (visit duration), milk yield, BW, milk spectra
 - Milk spectra: 1060 wavelengths





Milk Mid-infrared Spectra

- Milk spectra: 1060 wavelengths
- CV > 5%: 362 wavelengths



Markov Blanket

- Dimension reduction techniques
- Bayesian Network; Markov Blanket (MB):
 - MB of a variable X is the smallest set MB(X) containing all variables carrying information about X that cannot be obtained from any other variable
 - In a DAG, this is the set of all parents, children, and spouses of X.
 - Milk spectra MB: 33 wavelengths



Data Analysis; Models

- Approaches: Partial Least Squares (PLS) and Artificial Neural Network (ANN)
 - 1) Milk yield, BW0.75, DIM
 - 2) Milk yield, BW0.75, DIM, and 362 WL
 - 3) Milk yield, BW0.75, DIM, and 33 WL (MB)
 - 4) Milk yield, BW0.75, DIM, Fat, Protein + Lactose
 - 5) Milk yield, BW0.75, DIM, 33 WL, Visit duration
 - 6) Milk, DIM, and 33 WL (MB)
 - 7) 362 WL (WL)
 - 8) 33 WL (MB)





Data Analysis; Model Validation

• Validation: Independent datasets





Milk components vs raw spectra: better performance with ANN



 Variable selection through MB improved model performance, decreasing RMSEP



 Model including MY + DIM + BW + Milk spectra (33 WL; BN) + Behavior (VD) presented accurate and precise predictions

Example 2; Conclusions

- ANN on reduced WL set (with BN) improved prediction quality
- Superiority of ANN indicates potential nonlinear relationships between DMI and WL
- Superiority of models including raw spectra compared with milk components (fat, protein, and lactose) indicates that other unknown compounds may be important
- Validation of model predictions should be carefully conducted

Example 3. Pig Growth and Development

Computer Vision in Livestock



- Others

Prediction of Pig Weight

- Data 700 pigs
- Weight across different ages
- Leg and back scores





Real-Time Monitoring: Growth

- Periodic measurements:
 - Direct assessment of animals growth
 - Assess intra-group variability
 - Management improvement
 - Prohibitive
 - Labor and cost
 - Animal welfare (stress)

Data Acquisition

- Recordings of groups of pigs were made on the test date (nursery and off test)
- Sensor positioned on top of the area before to the scale
- Pigs were contained under the sensor for a variable amount time
- Males and females

Segmentation Algorithm



Features Extracted

- Feature extraction:
 - Body Measurements:
 - Area Volume Length Width Height



Shape Descriptors:
 Eccentricity
 Back curvature linear coefficient
 Polar Fourier Descriptors



Image Selection

- Variables from a random image
- Image with max area
- Image with max length
- Image with max volume
- Average across all images
- Median across all images
- Truncated average removing 20% of data for each animal
- Truncated average of the subset on 3rd quantile

Statistical Analyses

Linear model:

- For all the reduced datasets 10 permutations on a 5-fold cross-validation were used to access the quality of the predictions
- Stepwise regression with AIC as model selection criterion was applied



Histogram of live body weight (kg) distribution for nursery and off-test pigs with relative means and variation

• Analysis including nursery data



A) Box plots for Mean absolute error (MAE) as percentage of the average body weight. B) Coefficient of determination (R²) of the different models on the test data across the cross validation.

• Analysis without nursery data



A) Box plots for Mean absolute error (MAE) as percentage of the average body weight. B) Coefficient of determination (R²) of the different models on the test data across the cross validation.

Example 3; Conclusions

- Fully automated system for online extraction of body measurements with 3D camera
- Goal: implementation of a CVS for the acquisition of biometric traits and body weight on commercial farms
- Lower MAE with the truncated average and truncated median on the 3rd quartile
- Incorporation of sex and line in the models did not improve predictions

Concluding Remarks

- Technologies always improving; lower cost
- Data storage and data management
- Machine learning and artificial intelligence techniques
- Cost-benefit for breeding programs and for commercial applications

Acknowledgements







Lab Members

Alexandre Cominotte Arthur Fernandes Camila U. Braz Dr. Camus Adoligbe Cansu Tekin • Claudia Koda 🍙 Dr. Joao R. R. Dorea Dr. Juan Jiang Ligia Cavani 🔴 Ligia Moreira Lucio F. M. Mota Nayanny Guimaraes Dr. Nora Bello **Tiago Bresolin** Tiago Passafaro Dr. Toshihiro Okamura Vera C. Ferreira Dr. Yalda Zare



