Digital phenotypes predicted via machine learning and their use in genomic evaluations

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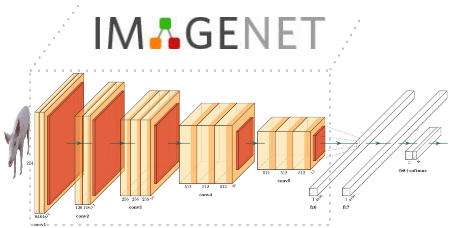
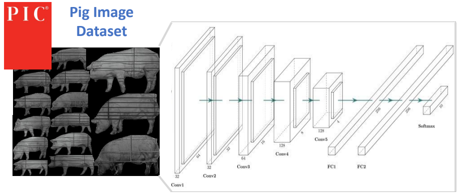
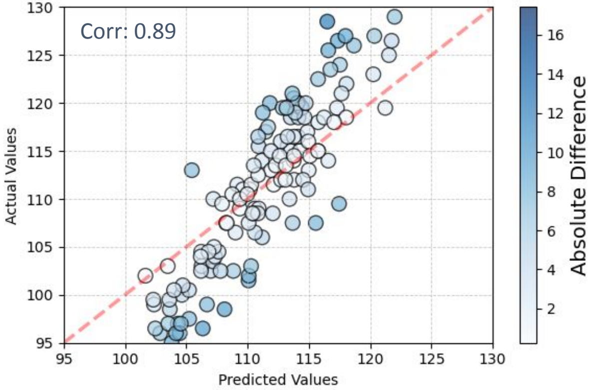
Summary: Methods & Results



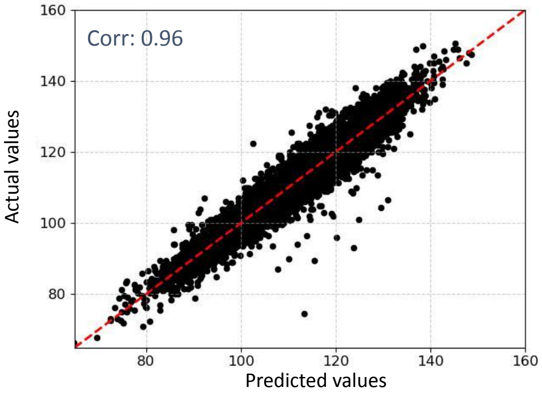


Mixed model equation to estimate fixed and random effects

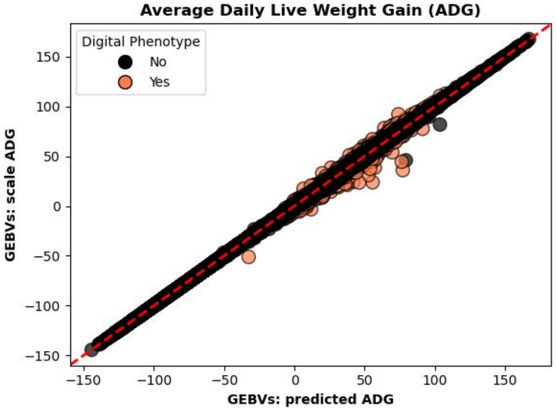
$$\begin{bmatrix}\hat{\beta}\\ \hat{u}\\ \hat{a}\end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + H^{-1}\frac{\sigma_e^2}{\sigma_u^2} & Z'W \\ W'X & W'Z & W'W + I\frac{\sigma_e^2}{\sigma_a^2}\end{bmatrix}^{-1} \begin{bmatrix} X'y\\ Z'y\\ W'y\end{bmatrix}$$



Actual vs. predicted: Body weight



Actual vs. predicted: Body weight



GEBVs: scale ADG vs. digital predicted ADG

Conclusions

- ❖ We successfully used deep learning to extract features and predict phenotype
- ❖ Pre-trained models provide meaningful feature extraction
- ❖ Digital phenotyping yields insights for genomic prediction

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