

Deep phenotyping of feed efficiency in individual dairy cattle using longitudinal and average feed quality data

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1. Background

- Feed-efficiency is a composite trait that is likely to be influenced by several physiologic processes which are difficult to record.
- Deep phenotypes are inner, invisible components of feed efficiency that might be more useful than phenotypes as selection criteria in animal breeding.
- A pilot study estimated nine deep phenotypes for 937 cows using the mechanistic LiGAPS-Dairy model and a genetic algorithm, but used average feed quality (FQ) for crude protein and feed digestibility (Van der Linden *et al.* 2022).

2. Objective

To assess whether deep phenotyping improves by using individual, longitudinal FQ data compared to average FQ data.

3. Materials/Methods

- Datasets: 't Gen farm, Lelystad farm
- Multiparous Holstein cows (n =110) with ≥ 5 weekly records for FQ and ≥ 10 weekly records for milk production, feed intake, body weight selected from each dataset.
- LiGAPS-Dairy simulated feed intake, live weight, and milk yield in such a way that first energy and protein towards maintenance, physical activity, and gestation are met before they are mobilized for milk production and growth.
- Objective function is the sum of errors between simulated and measured milk production, feed intake and body weight (Fig. 1).
- Genetic algorithm optimized nine deep phenotypes which correspond to a set of nine parameters in the LiGAPS-Dairy by minimizing the objective function value (Fig. 1).

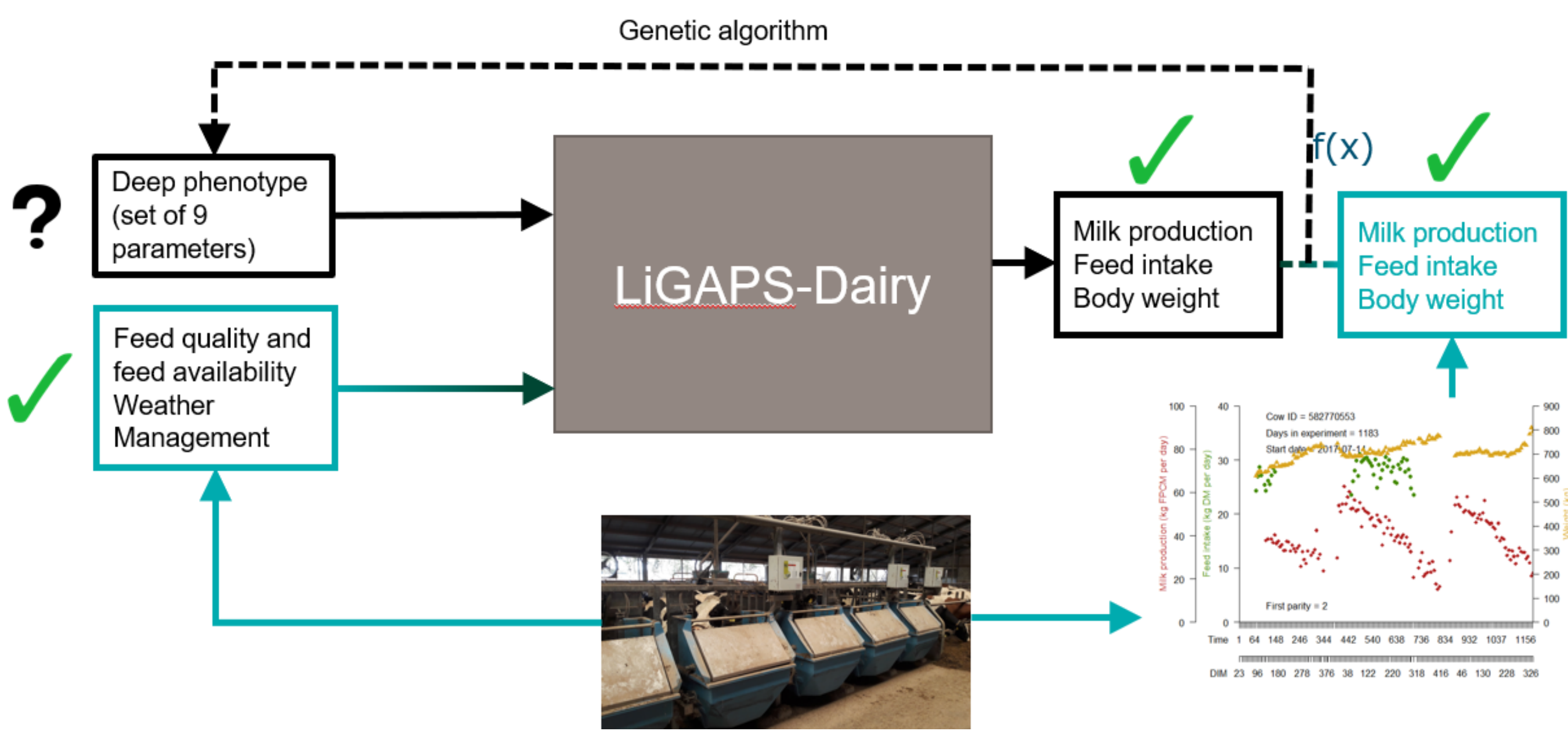


Figure 1: Deep phenotyping model where LiGAPS-Dairy simulates milk production, feed intake, body weight taking account of deep phenotypes, feed quality/quantity, weather and indoor herd management. Nine deep phenotypes are optimized using genetic algorithm which minimizes the sum of errors between simulated and measured phenotypes.

- Deep phenotyping model was run under four scenarios (Run)
 - Run 1: one average FQ value from the pilot project
 - Run 2: One average FQ value from datasets
 - Run 3: One average FQ value per cow
 - Run 4: Individual longitudinal FQ data and interpolated values for missing FQ data.

References

Van der Linden, A., Schopen, G. C. B., Gredler-Grandl, B., de Jong, G., Sol, M., van der Beek, S., & Veerkamp, R. F. (2022). Lifetime feed efficiency and deep phenotypes from scarce feed intake records using the mechanistic LiGAPS-Dairy model. *Proceedings of 12th World Congress on Genetics Applied to Livestock Production (WCGALP)*, 280–283. https://doi.org/10.3920/978-90-8686-940-4_58

4. Results and discussion

- Deep phenotyping improved from Run 1 to Run 4 in 't Gen data while less improvement was seen in Lelystad (Table 1). At some instances, Lelystad cows were recorded as high feed-efficient cows having feed efficiency (milk yield/feed intake); $FE > 5$. An initial test run for a few Lelystad cows excluding $FE > 5$ records showed a similar trend as observed in 't Gen dataset, while a final run including all cows is still in progress. Thus, the lower improvement in deep phenotyping in Lelystad can be attributed to some erroneously recorded milk yield or feed intake records.
- Crude protein (CP) content in Lelystad = 142 grams/kg dry matter (DM), 't Gen = 204 grams/kg DM, and pilot study = 166 grams/kg DM. Model fitness improved in Run 1 (Table 1) for Lelystad cows, since high feed efficient cows ($FE > 5$) were provided with a high CP diet.
- Cows in 't Gen had higher average maintenance requirements, a lower energy efficiency for milk synthesis and a lower protein efficiency for milk synthesis than cows in Lelystad (Table 2). Thus, cows in 't Gen were less efficient than in Lelystad.

Table 1: Objective function value for four model runs in 't Gen and Lelystad datasets. The closer to zero, the better the fit between simulated and measured phenotypes.

Dataset	Run 1 Average FQ from pilot	Run 2 Average FQ from dataset	Run 3 Average FQ per cow from dataset	Run 4 Individual FQ from dataset
't Gen	-147.40	-72.23	-70.93	-53.87
Lelystad	-88.45	-97.30	-98.79	-95.83

Table 2: Comparison of nine deep phenotypes between Lelystad and 't Gen farm data using individual, longitudinal FQ data (Run 4). The values indicate the average value of deep phenotypes for 't Gen (110 cows) and Lelystad (87 cows) after excluding cows with objective function value < -150 .

Variables	Units	Lelystad Run 4	't Gen Run 4
Net energy requirements for maintenance	kJ NE/kg ^{0.75} /day	333.01	377.16
Maximum intake capacity	Fill units/kg ^{0.75} /day	114.05	118.16
Maximum body weight	kg	673.80	636.44
Woods curve parameter 1 (scaling factor)	kg	30.78	29.10
Woods curve parameter 2 (increase pre-peak)	-	0.15	0.16
Woods curve parameter 3 (decrease post-peak)	-	0.003	0.003
Net energy efficiency for milk	%	88	72
Protein efficiency for milk	%	73	53
Protein requirements per unit net energy	g per kJ NE	1.99	2.03

5. Conclusions

- Overall deep phenotyping improved in 't Gen when using individual, longitudinal FQ data compared to average herd FQ data, while deep phenotyping in Lelystad showed less improvement due to inclusion of FE records > 5 .
- On average 't Gen cows were less efficient than Lelystad cows.

