Table 1
Model evaluation parameters of the digestion model for growing pigs, presenting goodness of fit of observed (obs) v. predicted (pred) postprandial time of peak (TOP, h) and area under the curve[2] (AUC, % of ingested) of nutrients absorbed from the intestine.

Nutrient	Variable	Obs (SD)	Pred (SD)	R-sq	RMSPE[1] (%)	ECT[1] (%)	ER[1] (%)	ED[1] (%)	CCC[1]	Cb[1]
Glucose	TOP	56 (20)	44 (15)	0.25	39	31	4	65	0.38	0.8
	AUC	63 (20)	69 (30)	0.41	39	6	52	42	0.58	0.9
Amino acids	TOP	58 (34)	61 (11)	0.03	60	1	3	96	0.09	0.6
	AUC	63 (13)	83 (2)	0.03	40	69	0	27	-0.02	0.1
Protein	AID	70 (5)	78 (5)	0.67	12	88	0	12	0.34	0.4
Fat	AID/AFD	82 (15)	86 (4)	0.30	16	6	8	86	0.27	0.5

[1] RMSPE = root mean square prediction error (as % of observed mean), ECT = error of overall bias, ER = error due to deviation of the regression slope from unity, ED = error due to disturbance (i.e. random error), CCC = Lin's concordance correlation coefficient, Cb = bias correction faction, AID = apparent ileal digestibility, AFD = apparent faecal digestibility.
[2] Area under the curve calculated based on observed sampling time (varying from 5 to 12h).

the passage of digesta solids and liquids from the stomach was modelled as a function of nutrient solubility and by diet viscosity, diet solubility, and feed intake. Results were evaluated against independent literature data on nutrient absorption from studies with (portal) blood measurements in pigs (12 studies, 32 dietary treatments for glucose; 8 studies, 15 dietary treatments for amino acids).

Results and Discussion
Model evaluation focussed on the prediction of glucose and amino acid absorption kinetics (Table 1). The predicted time of peak (44 ± 15 *vs.* 56 ± 20 min after meal) and extent (69 ± 30 *vs.* 63 ± 20% of intake) of glucose absorption after a meal, compared with observed values, were adequate (RMSPE = 39%). For amino acids, the mean, but not the variation in time of peak could be predicted (61 ± 11 *v.* 58 ± 34 min, RMSPE = 60%). Although net portal appearance is the closest estimation for amino acid absorption from the gut, the absorption kinetics of amino acids can be affected by gut metabolism, which is not represented in the model. The extent of small intestinal protein digestion was slightly over-predicted (70 ± 5 *v.* 78 ± 5 %, RMSPE = 12%), while variation among diets and ingredients was well predicted. To improve model calibration, a more extensive observational dataset is required. Ideally, such a dataset should cover data regarding the net portal appearance of amino acids in pigs fed diets, including 'slow' and 'fast' *in vitro* degradable protein sources, and also includes passage kinetics of digesta and the extent of ileal protein digestibility.

Conclusion and implications
In conclusion, results show SNAPIG can predict variation in nutrient digestion kinetics in pigs fed diets varying in feed ingredient composition and physicochemical properties. The use of SNAPIG enables the identification of knowledge gaps in pig nutrition concerning feedstuff properties and its consequences on digestion kinetics. To further improve the evaluation of both feed nutritional value and pig growth, a post-absorptive metabolism model was also developed. The coupled digestion and metabolism model (called DyNAMPIG) will allow such evaluation.

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15. Behavioural analysis of the fasting substrate conversion for energy utilization in growing pigs using within-day kinetics in the DyNAMPig model

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Introduction
Homeostasis of metabolite pools in pigs is challenged when confronted with a rapid post-absorptive influx of nutrients. Physiological mechanisms that buffer this influx are key in overcoming this challenge, e.g. by storing excess absorbed glucose as glycogen. On the other hand, utilization of these body stores for energy in between meals ensures energy is available during fasting by providing oxidizable substrates (glucose, fatty acids). With our current development of an *in-silico* nutrient-based post-absorptive metabolism model using within-day kinetics (DyNAMPig), a representation of these mechanisms is included to accommodate predictions of the post-absorptive metabolic fate of nutrients in growing pigs. Here, we present a showcase of the conversion of body stores to metabolite pools in between meals.

Material and methods
Principles for nutrient partitioning were adapted from the pig growth model developed by Halas et al. (2004) and modified to accommodate within-day kinetics of nutrient metabolism. Body components (protein, fat) and metabolites (glucose, glycogen, fatty acids, acetyl-CoA

and amino acids) are represented as eleven whole-body pools connected by fluxes their respective deposition, breakdown, storage and partitioning. Fluxes use Michaelis-Menten kinetics to represent the inhibition and affinity aspects of nutrient partitioning. Parameters describing the rate and type of within-day nutrient utilization are currently calibrated to indirect calorimetry data.

Results and discussion

Substrate conversion rates for (A) body fat mobilization, (B) glycogenolysis and (C) amino acid degradation for either energy or gluconeogenesis, over a two-day period of a pig fed a restricted diet (30% and 70% of total daily feed intake in a morning and afternoon meal respectively) are shown in Fig. 1. Presented values are to be fine-tuned in the current calibration. In general, all three substrate utilizations are responding according to expectations, being low following the influx of nutrients during and immediately after meals and increasing in periods of fasting. The majority of energy during fasting periods is provided by lipolysis, consistent with *in vivo* observations. Glycogen utilization precedes lipolysis, which increases in time as glycogen stores start to become depleted. Amino acid degradation is negatively correlated with glycogenolysis, implying that glucose homeostasis is achieved by increasingly utilizing amino acids as a source of glucose when there is insufficient influx of glucose via either a meal or glycogenolysis.

Conclusion and implications

Providing sources of energy during fasting for pigs using storage pools is a promising new direction for the modelling of nutrient utilization in pigs using within-day kinetics. It allows modelling the effects of variation in nutrient absorption kinetics, and provides a basis for the incorporation of more biological processes in whole-animal models. Further calibration of these mechanisms to within-day energy utilization data is required to ensure overall partitioning of nutrients adheres to *in vivo* data.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.anscip.2022.07.406.

References

Halas, V., Dijkstra, J., Babinszky, L., Verstegen, M.W.A., Gerrits, W.J.J., 2004. Modelling of nutrient partitioning in growing pigs to predict their anatomical body composition. 1. Model description. The British Journal of Nutrition 92 (4), 707–723.

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16. Mechanistic modelling of turkey growth in response to genotype and nutrition using Michaelis-Menten kinetics

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Introduction

Concurrently, the poultry industry is aiming to increase productivity and efficiency to meet global demand for food while societal concerns demand slowing the rate of bird growth due to ethical concerns (Olschewsky et al., 2021). Mechanistic modelling offers an alternative or supplementary tool to conducting costly animal experiments, by allowing hypothesis testing before implementing changes to address these complexities. The most recent fully reported mechanistic model for turkeys was published in 2011 and focused on the exponential growth phase of turkeys in response to genotype and nutrition (Rivera-Torres et al., 2011b). Over 10 years later, significant changes in growth and nutrition have been made, and thus the objective of this work was to update this growth and metabolism model. A new mechanistic model for turkeys is presented, using Michaelis-Menten kinetics to replace exponential kinetics to describe nutrient transactions, and updated 'pythonic' libraries to effectively predict growth and body composition in response to genotype and nutrition.

Materials and Methods

A mechanistic model was created based on the previous model structures described in Rivera-Torres et al. (2011b), and the flow diagram describing the model is presented in Fig. 1. Model development was performed in Python. The model describes the transfer of digested nutrients into intermediary metabolites (amino acids, AA; glucose, Gl; fatty acids, FA; acetyl-coA, Ay) which are then used for protein and lipid metabolism in the viscera and carcass as well as anabolism in the feathers. Acetyl-coA is produced from the catabolism of AA, Gl, and FA, and consumed for maintenance transactions. Protein retention represents the difference between anabolic and catabolic fluxes in the carcass, viscera, and anabolic fluxes in feather pools.

Advancements made to the model were (1) implementation of more stable Michaelis-Menten kinetics to describe metabolite fluxes (based on genetic potential and substrate availability), and (2) defining new genetic parameters. The equation's *Vmax* described the genetic potential or maximal value for the reaction rate (also influenced by age), and the denominator represents the limiting or activating effects of substrate concentrations. Fitting was done using the LMFIT library to compare model predictions to observed data, with a Levenberg-Marquardt fitting method (Newville et al., 2014). The new parameters fitted (*Vmax*, *km*, exponent '*n*') to a default dataset corresponded to data taken from Rivera-Torres et al. (2011b).