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Session 33

Characterizing animal response to environmental challenges: new traits of more efficient animals

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Farm animals are constantly facing perturbations due to changing environmental and farm conditions. Characterization of the animal's response when it is facing perturbations that influence performance and health is of main concern to ensure sustainable livestock production. Indeed, a better understanding of the adaptation mechanisms used by the animal to cope with challenges (through resistance and resilience) is a prerequisite to propose adequate farm management strategies. Several experimental studies have been conducted to investigate the influence of the environment on animal performance. Mathematical models can be used consider and to quantify the systemic aspects of the animal's response to a perturbation. Existing models of farm animal performance have accounted to a limited extent for environmental perturbations. With novel monitoring technologies, it is now possible to evaluate the impact of these perturbations on the animal in real time and with a high frequency. We propose a mechanistic model to describe the influence of a generic perturbation of unknown origin on feed intake of growing pigs. The model is based on two sub-models: InraPorc, a model to describe the performance of the growing pig in a standard environment, and the well-known spring-and-damper system used in physics to describe the behavior of a system in presence of an external force. The InraPorc model was used to describe the phenotypic performance of the animal in the absence of acute perturbing factors. The spring-and-damper system included two parameters to characterize the adaptive response of animals when facing a perturbation. The main interest of this characterization is to define new standards to rank animals based on feed efficiency together with their adaptive capacity, and to identify potential correlation between performance and robustness traits. We can then propose model-derived traits for genetic selection of more efficient and robust animals. Currently, the model is able to simulate the performance of animals facing with a single perturbation. Future development of the model will include successive perturbations of known or unknown origin. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement no. 633531.

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Theatre 7

Modelling individual uncertainty and population variation in phenotypical traits of livestock

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Characterising between-animal variation and its population-level consequences is key to effective livestock management and selective breeding. The aim may be to predict trait development (e.g. performance) from early growth or estimate unobserved traits (e.g. maximum growth or maturity parameters). A usual sequence of steps is: (1) to develop a mathematical model of chosen animal-level traits; (2) to estimate individual parameters across a sample of animals; (3) to estimate a population distribution of parameters; (4) to generate a population distribution of traits by simulating the model across distribution 3. The challenge is in the parameter estimation given typical limitations. We use a Bayesian inference methodology to estimate the population distribution of predicted traits. The approach: (i) accounts for individual-level uncertainty in parameters (2) due to their correlation and data limitations, e.g. short growth span or infrequent records, and (ii) does not invoke distributional assumptions and estimation of variance-covariance parameters (3). We present results derived from individual data with usual limitations. Results include distribution of growth parameters within breeds and across species (pigs, chicken, rabbits); they extend the literature by showing the extent of uncertainty and variation in parameters and by comparing variation not only across species but against that within breeds. We show distributions of protein and lipid growth parameters and metabolic heat production (HP) estimated across animals and species and predicted distributions of dynamic body composition. Literature body composition estimates usually condition on input of average HP data; by estimating both jointly, their individual-level correlation is included and no metabolic data is needed. HP estimates distributed about 0.7 MJ/kg/d in pigs in line with literature, and body fat content variation was much larger than that of body protein. We suggest this approach has general application in model parameterisation and prediction of trait development in populations using limited individual data. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement no. 633531.