A DSS tool (software) integrating the models developed in Tasks 3.1 to 3.4 for different livestock species and categories

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FEED-A-GENE

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

Deliverable D3.7

A DSS tool (software) integrating the models developed in Tasks 3.1 to 3.4 for different livestock species and categories (M60)

Due date of deliverable: M60

Actual submission date: M60

Start date of the project: March 1st, 2015 **Duration:** 60 months

Organisation name of lead contractor: KU

Revision: V1

Dissemination level	
Public – PU	**X**
Confidential, only for members of the consortium (including Commission Services) – CO	
Classified, as referred to in Commission Decision 2001/844/EC - Cl	

Access to the software

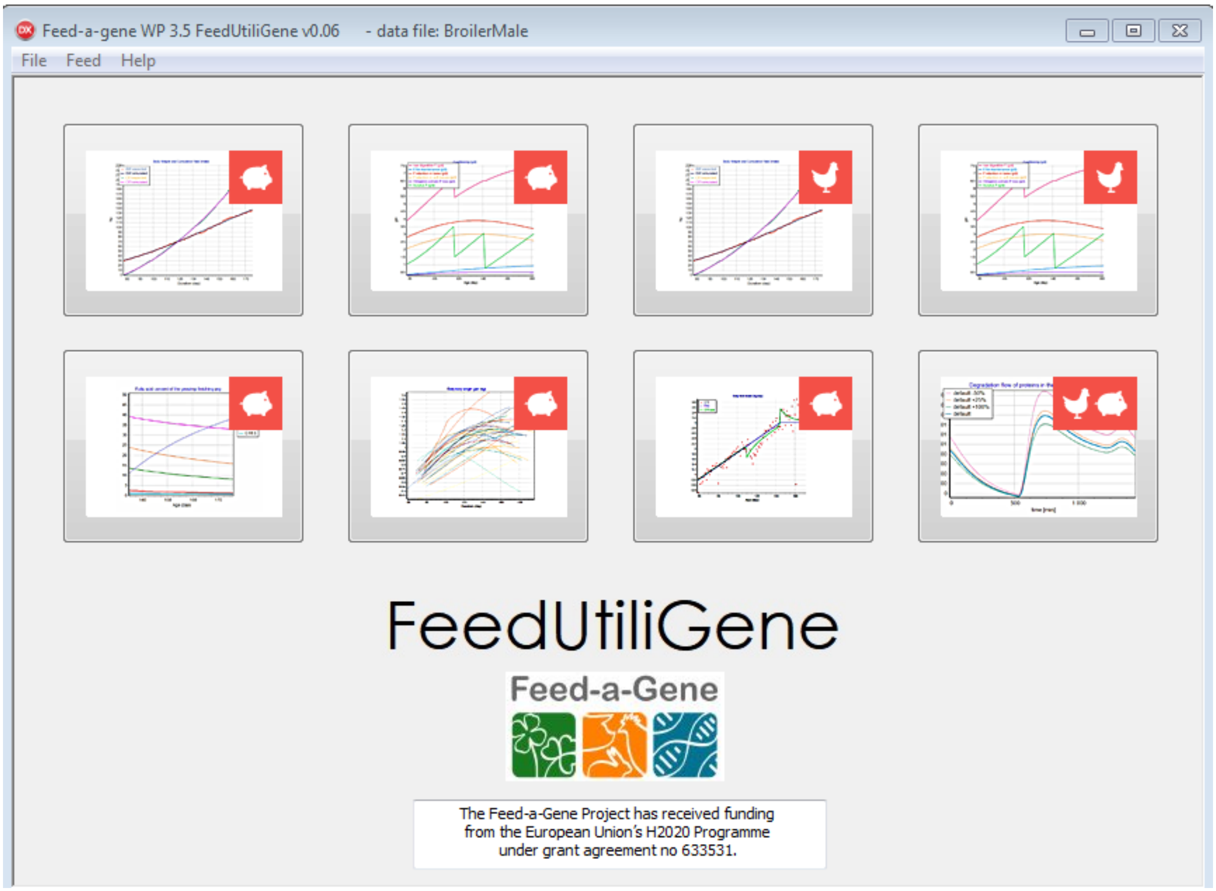
A number of mathematical models are available to predict, characterise an animal or a group of animals, or to improve our understanding of underlaying mechanisms of animal production. In general, these models are not easily accessible for end-users. Although described and published in scientific journals, these models typically are written in specific programming languages and the source code of the model is not always published with the publication. Consequently, most of the conceptual models cannot be evaluated and used by non-expert users. It is therefore essential that models adhere to the Open Science concept and that tools (and the source code) are made available to allow end-users to work with these models.

The objective of the work was to provide models predicting feed use mechanisms and animal variation and to integrate those Feed-a-Gene models into a software. The developed software is a support tool facilitating the understanding how the models developed in Feed-a-Gene work. The models are described in different project deliverables and in scientific publications.

The software tool is composed of eight modules, which can be accessed using the buttons on the main screen:

- Parameter estimation of the growing pig model
- The fitted growing pig model
- Parameter estimation of the poultry model
- The fitted poultry model
- The fatty acid model
- Stochasticity of the fitted growing pig model
- Modeling Response to Perturbations
- Modeling digestibility

The software is provided with a number of sample datasets, but user can also import their own data for use with the models.



FeedUtiliGene

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Figure 1. User-interface of the FeedUtiliGene software tool.

Parameter estimation of the growing pig model (top 1st button)

This module estimates model parameters of the InraPorc model for growing pigs (van Milgen *et al*. (2008). Animal Feed Science and Technology 143:387-405; http://doi.org/10.1016/j.anifeedsci.2007.05.020) based on observed feed intake and body weight data. The module estimates two parameters describing feed intake and three parameters describing protein deposition in a batch procedure for a number of animals. The outcome of this module is used in the other modules.

The fitted growing pig model (top 2nd button)

This module uses information from the previous module. It expands on the concepts developed in the InraPorc model by accounting for the effect of ambient temperature on animal performance and by the inclusion of a phosphorus partitioning model. The module is described in detail in Deliverable D3.3 ("A simulation model to predict the post-digestion nutrient use in monogastric animals").

Parameter estimation of the poultry model (top 3rd button)

This module is an adaptation of the parameter estimation module for pigs and estimates model parameters of the poultry model based on observed feed intake and body weight data of individual chickens or of the mean body weight in the pen. The module estimates two parameters describing feed intake and three parameters describing protein deposition in a batch procedure for a number of animals or pens. The outcome of this module is used in the fitted poultry module.

The fitted poultry model (top 4th button)

This module uses information from the previous module. It predicts the body weight and the nutrient partitioning in poultry (Dukhta *et al*. (2018). Acta Agraria Debreceniensis; https://ojs.lib.unideb.hu/actaagrar/article/view/1640) with the same approach as in InraPorc. It accounts for the effect of ambient temperature on chicken performance and is extended by a phosphorus partitioning model. The module is described in detail in Deliverable D3.3 ("A simulation model to predict the post-digestion nutrient use in monogastric animals").

The fatty acid model (lower 1st button)

This module also uses the parameter estimation module and the concepts of the model are described in Deliverable D3.3 ("A simulation model to predict the post-digestion nutrient use in monogastric animals"). It accounts for the partitioning of dietary fatty acids and the *de novo* fatty acid synthesis and it illustrates the dynamics of whole-body fatty acid retention and composition in growing pigs.

Stochasticity of the fitted growing pig model (lower 2nd button)

This module estimates the variation in nutrient utilization in growing pigs. It also uses information from the parameter estimation module. It shows the correlation among model parameters for a population of pigs, and it uses a resampling technique to estimate the uncertainty in different response traits. The technique is described in deliverable D3.5 ("A model to predict the variation in nutrient utilisation for different purposes (i.e., growth, gestation, milk and egg production) in monogastric animals") and in Filipe and Kyriazakis (2019). Frontiers in Genetics 10:727; https://doi.org/10.3389/fgene.2019.00727.

Modelling the response to Perturbations (lower 3rd button)

This module allows modelling the feed intake response of animals to perturbations of known or unknown origin to quantify robustness traits such as resistance and resilience. The model has been described in detail in deliverable D3.4 (A 'Robustness' simulation model to predict short and long-term animal responses to fluctuations in nutrient supply and in environmental conditions) and in Nguyen-Ba *et al*. (2020). Animal 14:253-280; https://doi.org/10.1017/S1751731119001976.

Modelling digestibility (lower 4th button)

This stand-alone module is described in deliverable D3.2 ("A simulation model to evaluate the digestive use of compound feeds and nutrients in monogastric animals"), and it allows to assess the effect of different digestion traits (e.g., retention time, rates of hydrolysis and absorption) on the dynamics of digestion and on ileal and faecal nutrient digestibility in pigs and poultry.

The decision support system provides a tool to end-users to run simulations by changing inputs and to test different scenarios. The end-users of this tool are mainly advisory personnel with a background in nutrition and/or genetics or students.

The software is available from: https://www.ke.hu/download/FeedUtiliGene.zip

Instruction for download:

Once downloaded, unzip the downloaded file into a folder of your choice and start the executable file.

Teams involved:

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