



FeedUtiliGene

software to demonstrate
modelling on biological functions

Veronika Halas
Kaposvár University





FeedUtiliGene

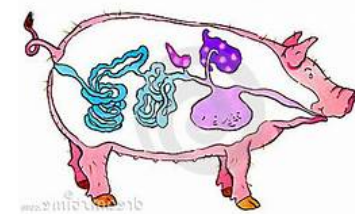
Feed-a-Gene models in a free software

- digestion module
- parameter estimation module
- nutrient partitioning module
- fatty acid module for fattening pigs
- robustness module
- stochastic module



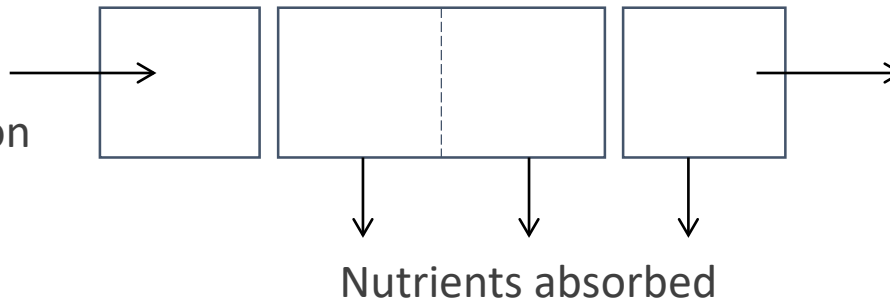
► Represent the transit and digestion

- Better understand the digestive mechanisms



Feed

- Intake
- Composition
- Pattern



Nutrients excreted

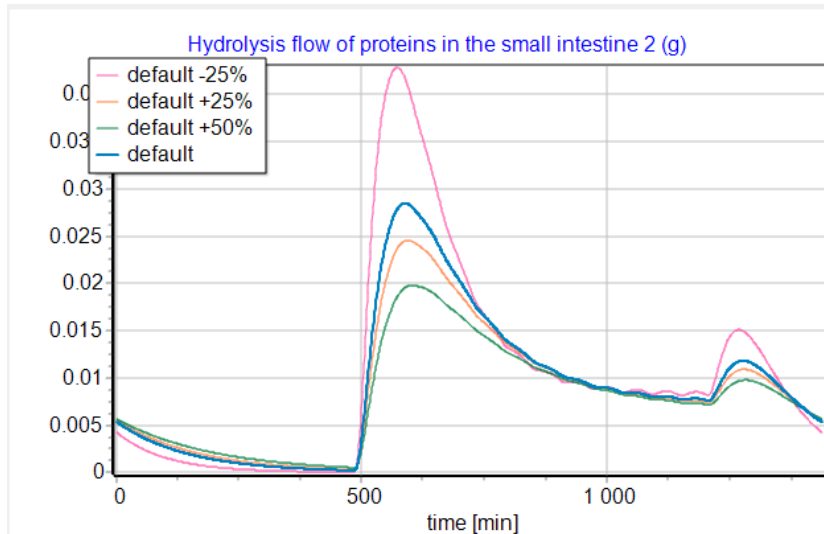


► Main outputs

- In each digestive compartment
 - dynamic quantity of nutrients
 - and hydrolyzed nutrients
- In the total GIT
 - dynamic quantity of absorbed nutrients
 - digestibility (AID, ATTD, TID, TTTD)



- ▶ A tool to orientate research and development, for example
 - ▶ genetic selection
 - ▶ development of a feed additive
- ▶ It is an interesting tool for teaching digestive physiology
 - ▶ consequences of changes in physiological parameters (mean retention time, hydrolysis efficiency...) on the overall digestive efficiency in pigs and poultry



Apparent ileal diges...	default -...	default ...	+default...	+default...
Dry matter	0.762854	0.779664	0.784343	0.790354
Organic matter	0.811121	0.828672	0.833540	0.839784
Crude protein	0.879184	0.914556	0.924653	0.937806
Total Nitrogen	0.871863	0.908893	0.919485	0.933309
Lipid	0.892698	0.920711	0.929061	0.940262
Calcium	0.504496	0.573207	0.593694	0.620770
Phosphorus	0.623753	0.680186	0.698368	0.723159
Sugars	0.962851	0.975941	0.979392	0.983682
Energy	0.826706	0.841205	0.845235	0.850410
Starch	0.969485	0.980113	0.982941	0.986471



FeedUtiliGene

Feed-a-Gene models in a free software

- digestion module
- **parameter estimation**
- **nutrient partitioning module**
- **fatty acid module for fattening pigs**
- robustness module
- stochastic module



Parameter estimation module

- The parameter estimation module adjusts the model parameters and fit the model outputs to existed body weight and feed intake data

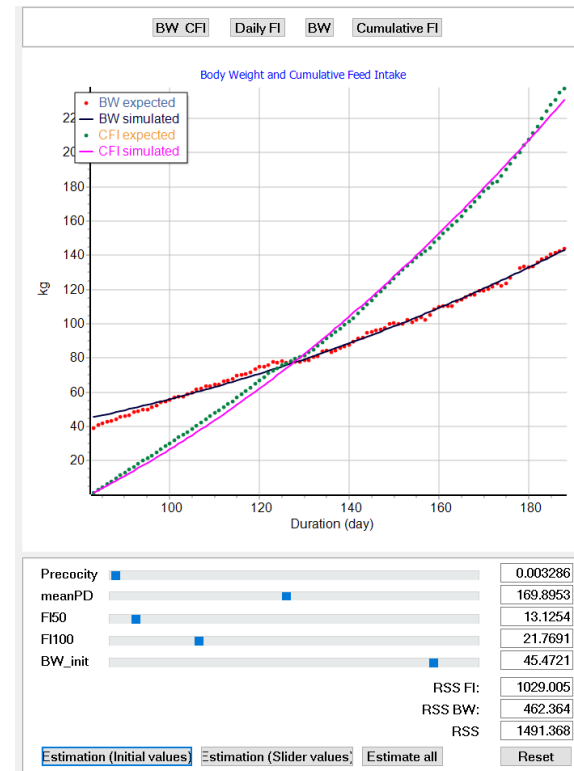
Feed-a-gene WP 3.5 FeedUtiliGene demo v0.05 Parameter Estimation Module

FI-BW data file:

Feed sequence plan:

	Precocity	meanPD	FI50	FI100	BW_init
Initial values	0.01	200	20	30	25
Lower limits	0.0002	50	10	10	10
Upper limits	0.5	300	60	60	50

ID	Precocity	meanPD	FI50	FI100	BW_init	RSS	
1	1174	0.007828	190.1209	14.9094	25.4136	23.6316	316.29
2	1427	0.011652	164.1583	14.8666	22.5936	35.4516	903.59
3	2058	0.003286	169.8953	13.1254	21.7691	45.4721	1491.3
4	2062						
5	2068						
6	2167	0.012618	160.5491	14.4008	22.2760	32.5355	332.60
7	2819						
8	2820						
9	2827						
10	2829						





Nutrient partitioning module

- ▶ Better understanding of feed use mechanisms

- ▶ Simulation:

- ▶ growth performance & body composition
- ▶ energy & amino acid partitioning
- ▶ nitrogen and phosphorus excretion

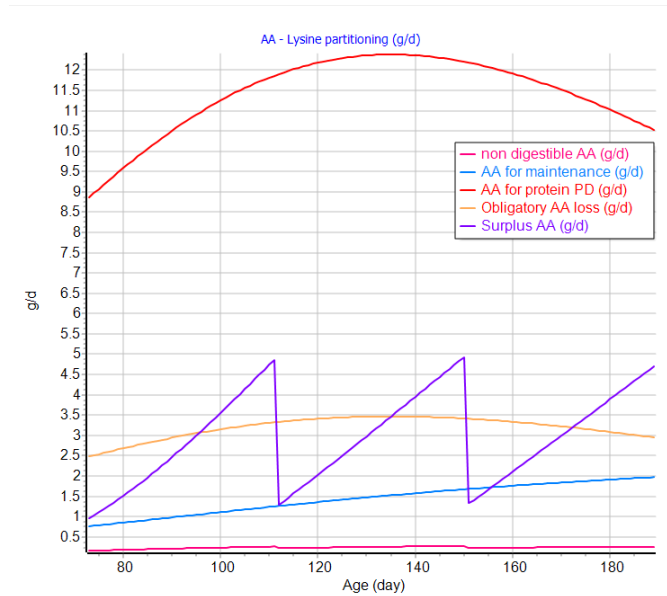
Upon different ambient temperature

- ▶ Estimation:

- ▶ digestible amino acid and P requirement

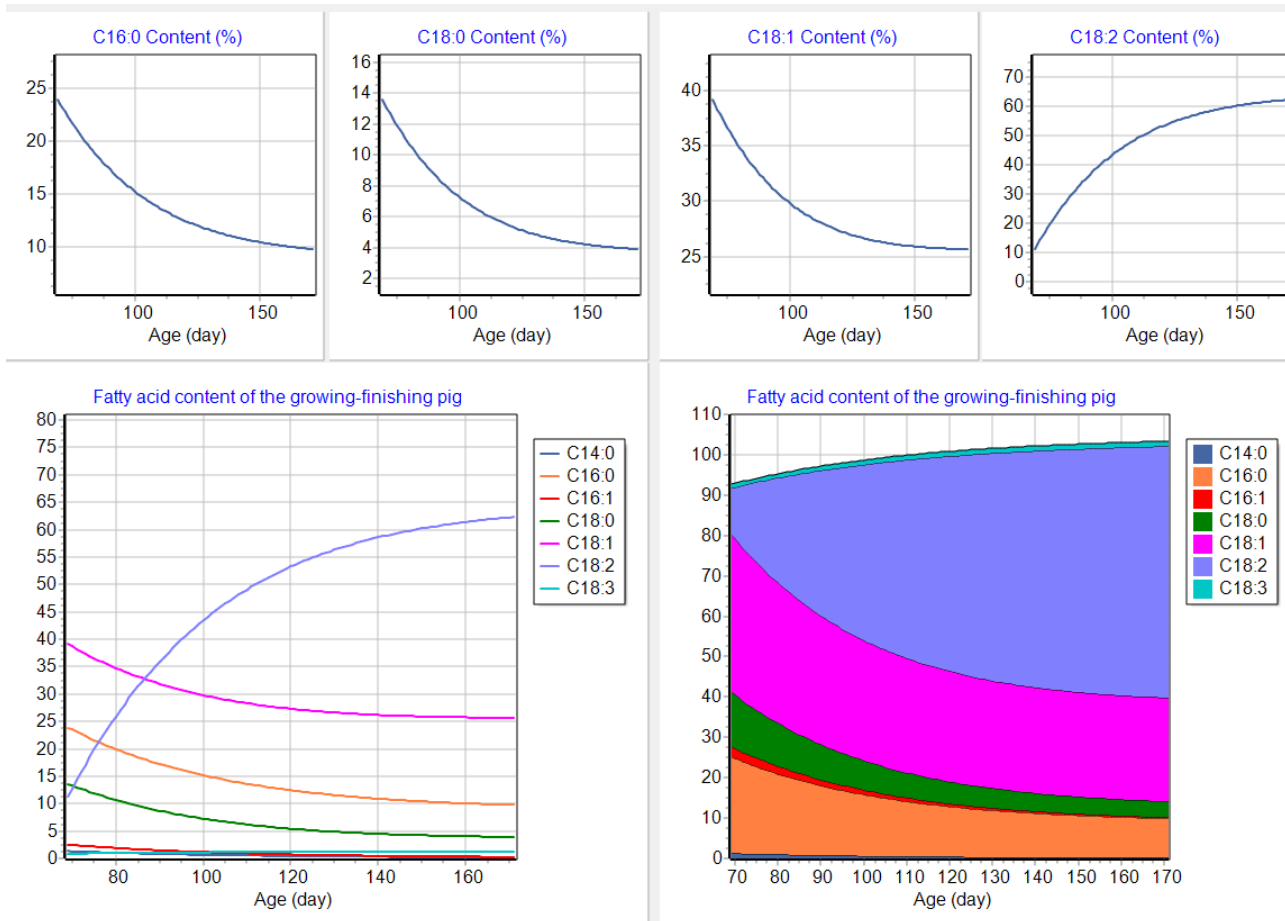
- ▶ Recommendation:

- ▶ optimal feeding strategy to minimize N and P footprint





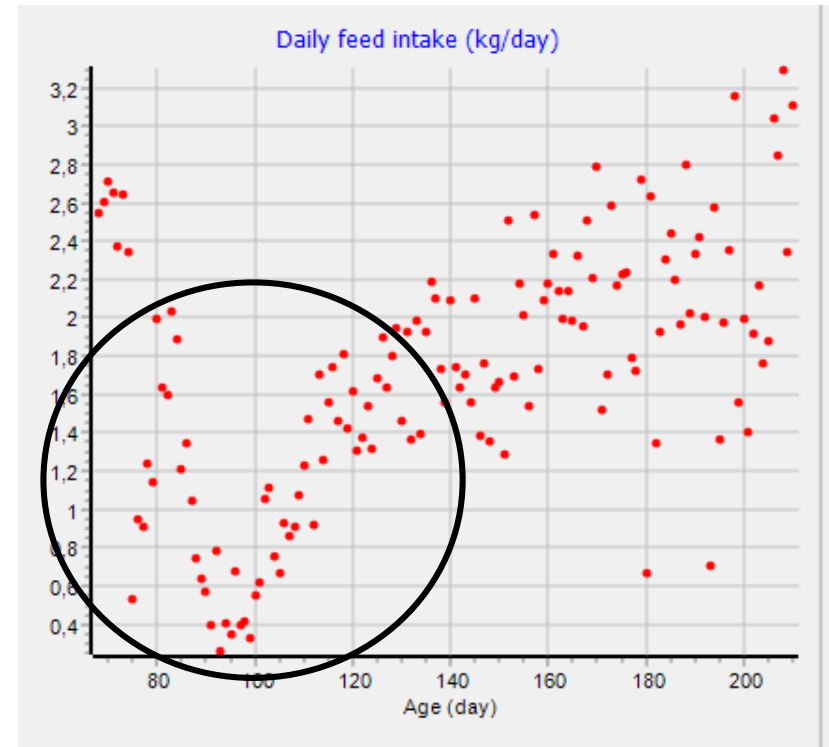
- Estimates the fatty acid composition of the pig as affected by the level and source of dietary fat.





- ▶ Daily FI can be detected automatically and frequently
- ▶ Adaptation of the animals are different

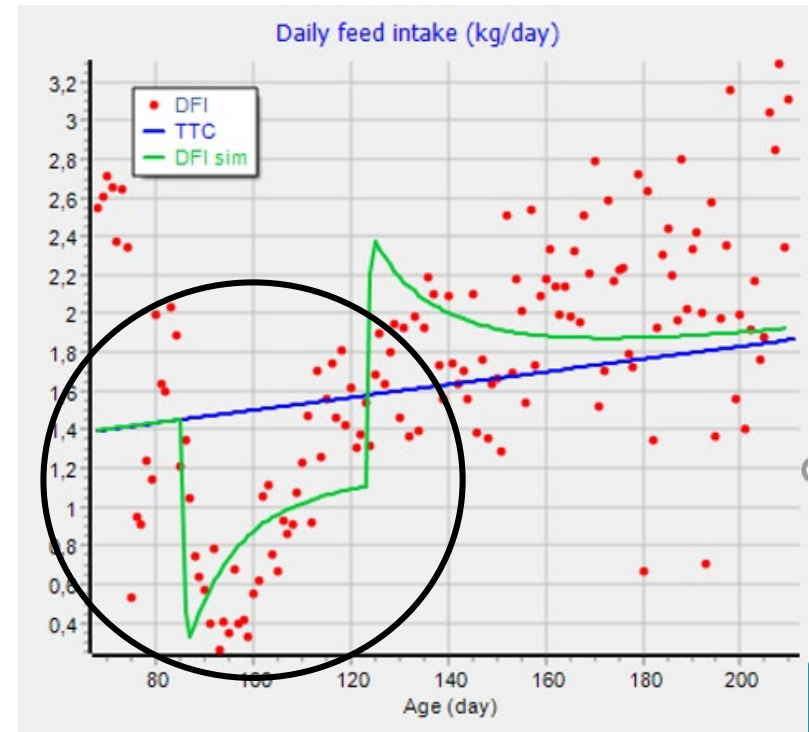
Is it possible to detect perturbations that impair feed intake and growth?





- ▶ The module demonstrates a mathematical procedure to quantify the robustness of the animal's adaptive response, in terms of resistance and resilience, when facing known or unknown perturbations.

- ▶ detects the perturbation
- ▶ characterizes the animal response to a perturbation

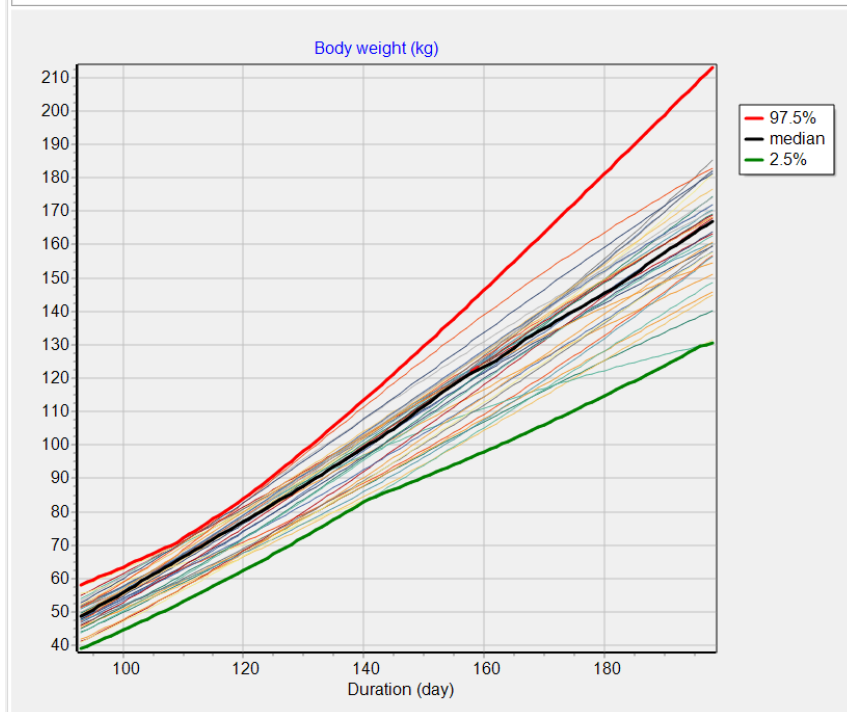


Pert	Start	End	Duration	Min.Day	Min.%	DFI% Left	Adaptation	Start of Pert	End of Pert
P1	75,80	83,30	7,50	78,70	-6,86				
P2	86,50	206,30	119,80	109,00	-27,36	0,1543	1,5075	86,40	124,23



- Addresses variation among individuals, which may originate from differences in nutrient partitioning.
- The module generates a population of animals with consideration of plausible individual variance.

Size of the original sample Random sample prepared
 Runs of resampling Start resampling
 Quantiles calculated



The individual variation of a population can be estimated if data of limited number of animals are available.



FeedUtiliGene

- ▶ Free software
- ▶ Easy access to Feed-a-Gene models
- ▶ Interactive tool & User-friendly interface
- ▶ Improve our understanding
- ▶ Help to solve problems

It provides insight on feed use mechanisms and animal variation.



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



FeedUtiliGene

Partners involved



Newcastle University

