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A DYNAMIC MODEL FOR DIETARY AMINO ACIDS UTILISATION IN FISH LARVAE

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Background

Improvement of growth performance in fish larviculture

Determination of dietary AA requirements

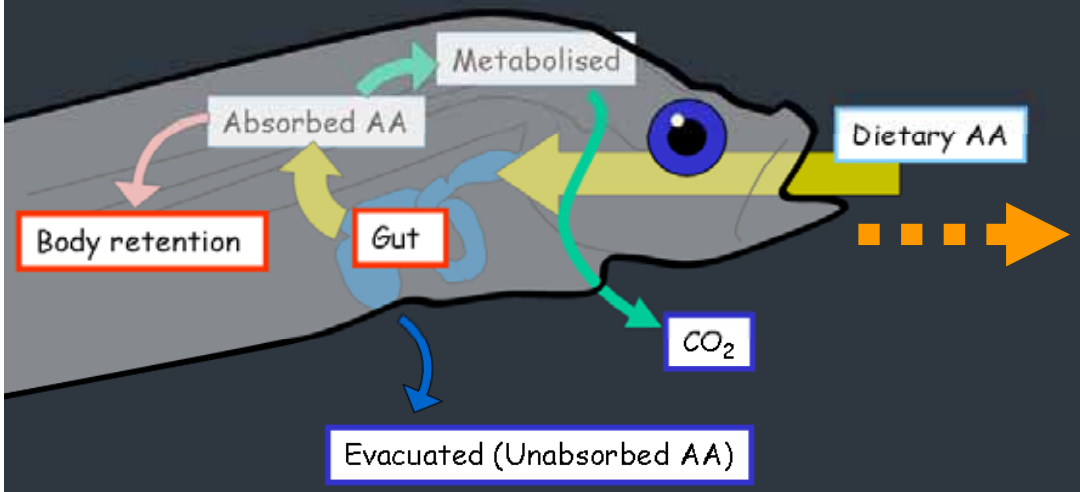
understanding AA metabolism

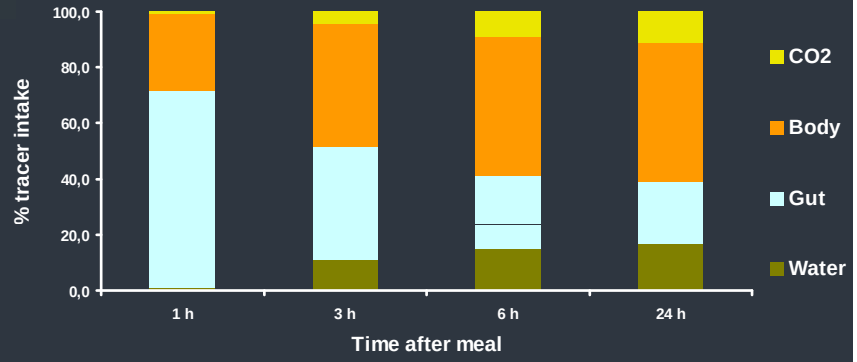
Background

Tracer studies :

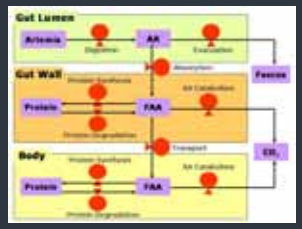
=> Better understanding of amino acid metabolism

but interpretation limited to the comparison of a number of body compartments in a few time points, and relative (not absolute) numbers





Background



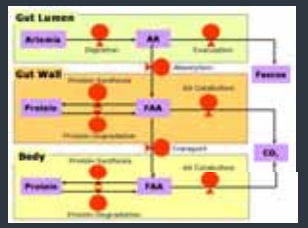
Modelling

- holistic approach to integrate knowledge on growth and metabolism
- identify most important processes and gaps in knowledge

Dynamic model => simulate metabolism and/or growth in time

Mechanistic model => processes are defined based on the underlying biochemistry & model parameters have (as much as possible) a biological meaning

Objectives



- Develop a dynamic mechanistic model that simulates AA metabolism of fish larvae.
- Assist in the interpretation of results obtained using tracer studies.
- Improve the understanding of larval digestion and absorption of dietary AA, and the postprandial AA metabolism and growth.

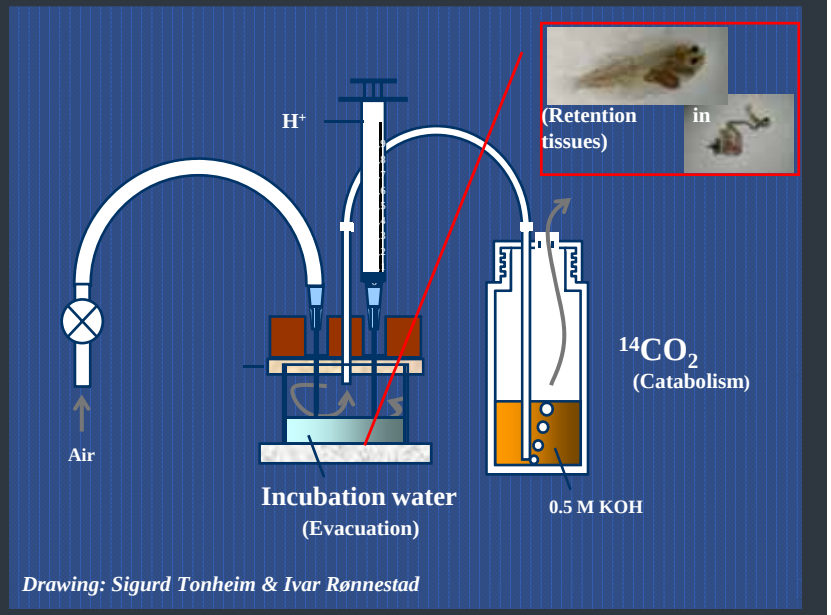
Data set to model

- Senegalese sole fed one meal of ^{14}C-labelled Artemia

12 DAH

(20-30 min.)

1, 3, 6 or 24h incubation



Morais et al. (2004)

Data set to model

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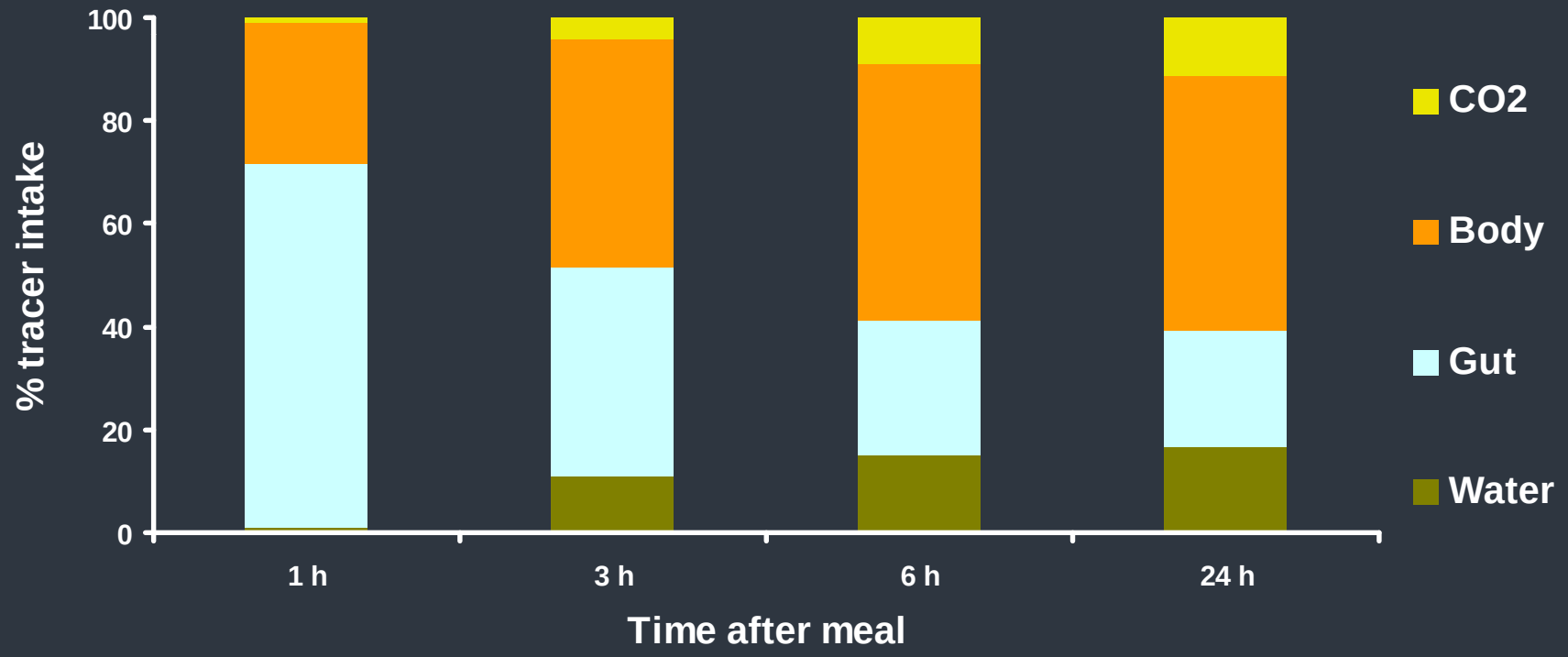
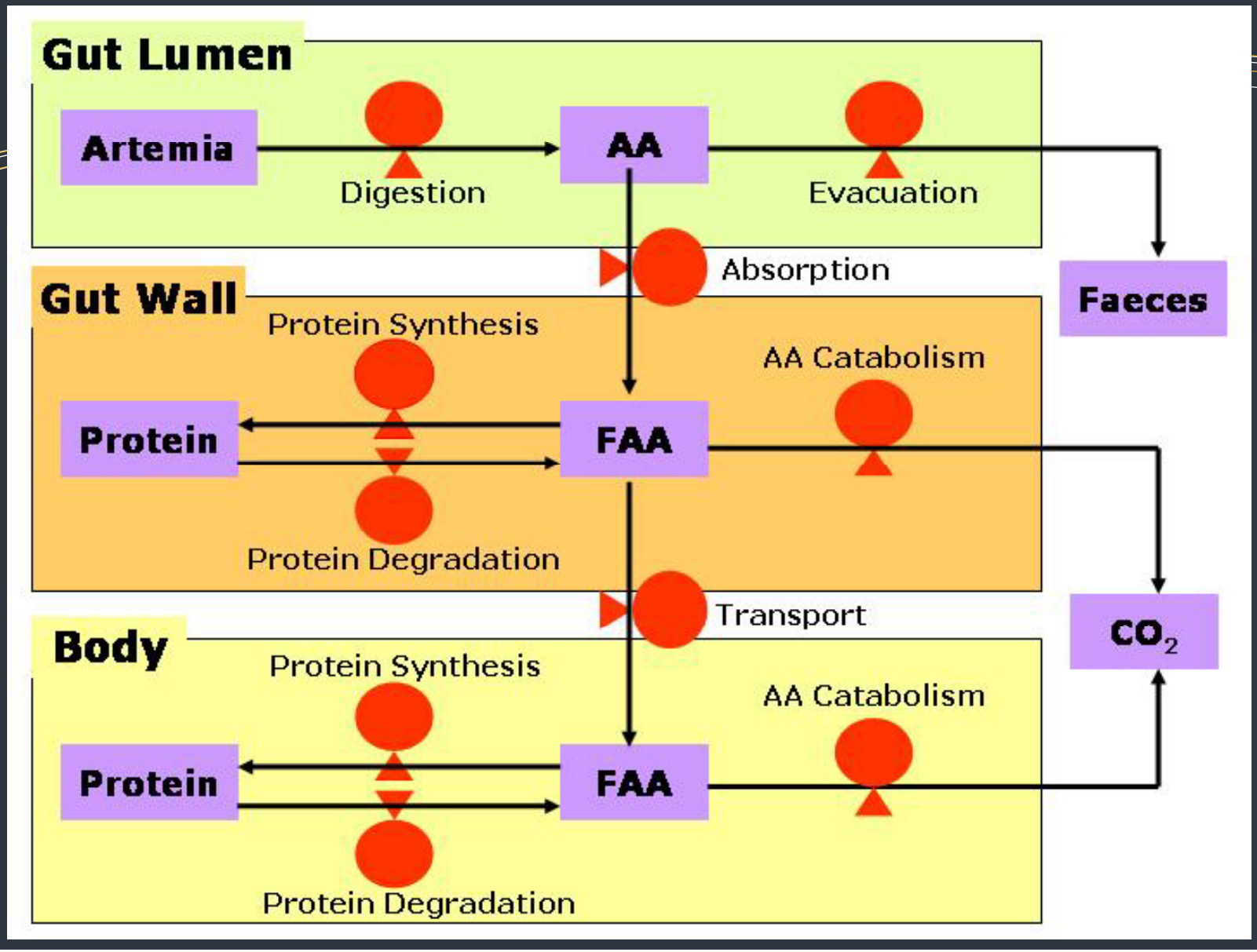


Morais et al. (2004)

Model Description



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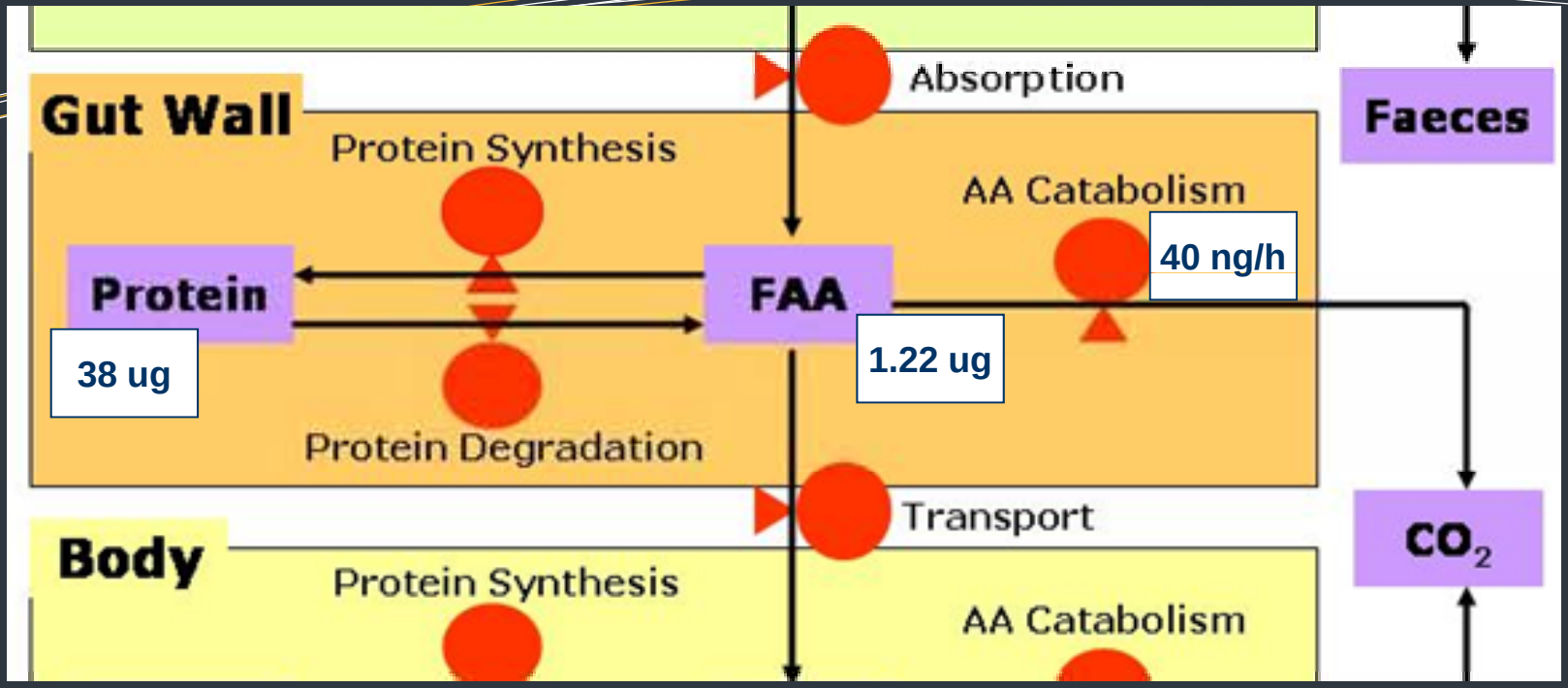


Example of equations:

Gut wall protein synthesis = KsGut * Excess FAA in gut + Basal Ks

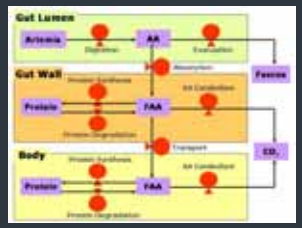
Gut wall AA catabolism = KcatGut * Excess FAA in gut + Basal AA cat

Model Calibration

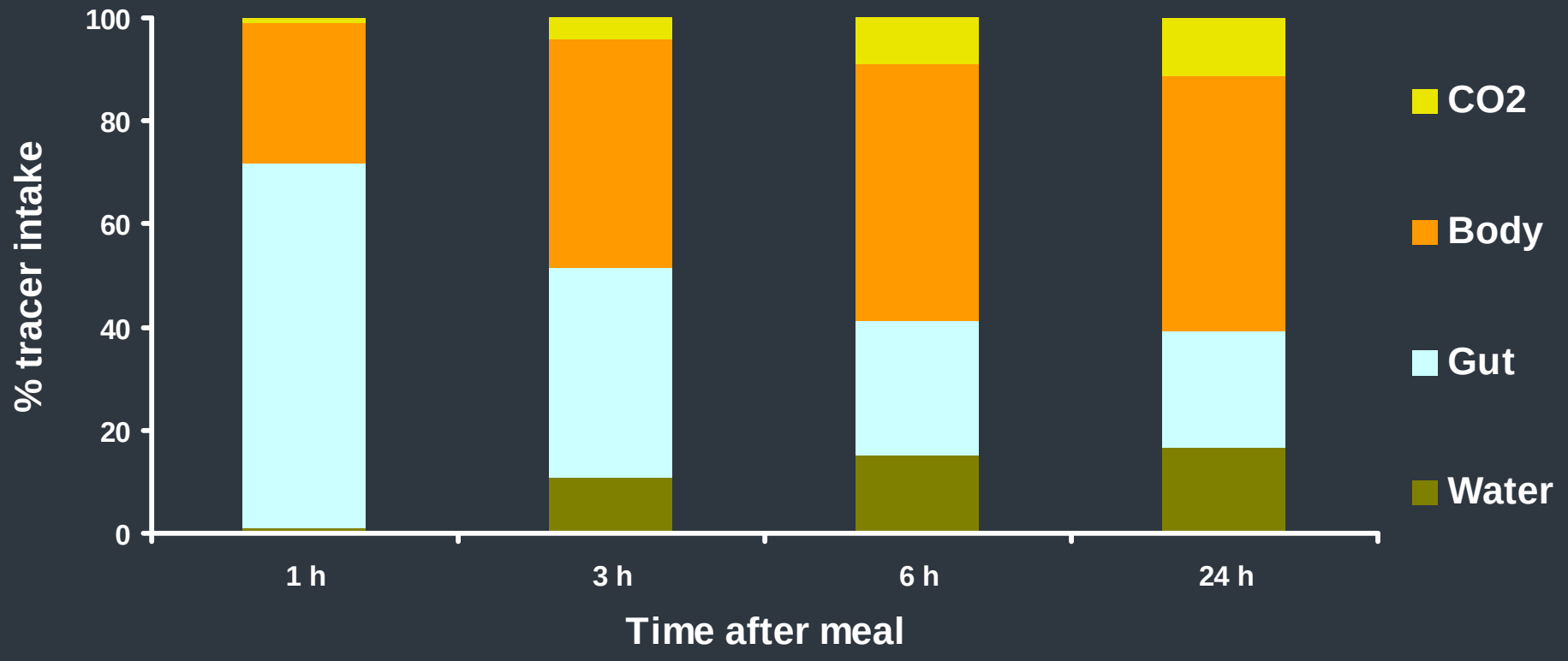
Parameters from bibliography:

- **Initial size of FAA and protein pools in sole (fasted) and *Artemia***

Model Calibration



Data from Morais et al (2004):



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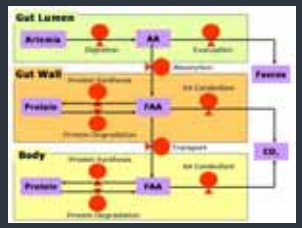


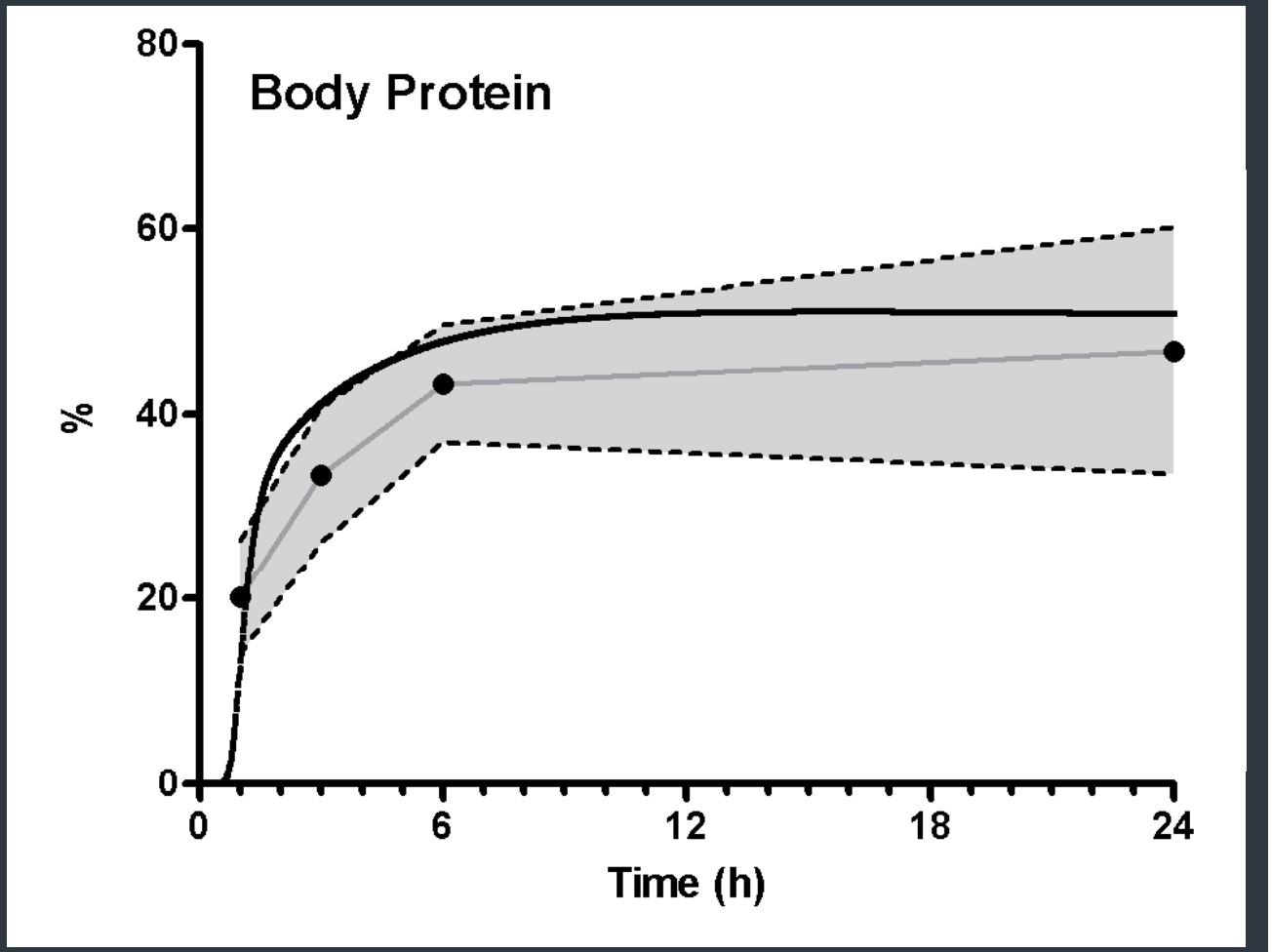
Parameters to be calibrated with model:

Parameter	Unit
Basal AA Catabolism rate	ng/h
Delay onset of Digestion	min
Rate of Digestion & absorption	min^{-1}
Gut AA catabolism rate	min^{-1}
Gut Protein Synthesis rate	min^{-1}
No of Artemia fed	n
Protein degradation rate	ng/h

Model Calibration

Using Powersim Studio 7

- Lines are simulated values
- Points (and shaded area) are mean values (and 95% confidence intervals) from Morais et al. (2004)



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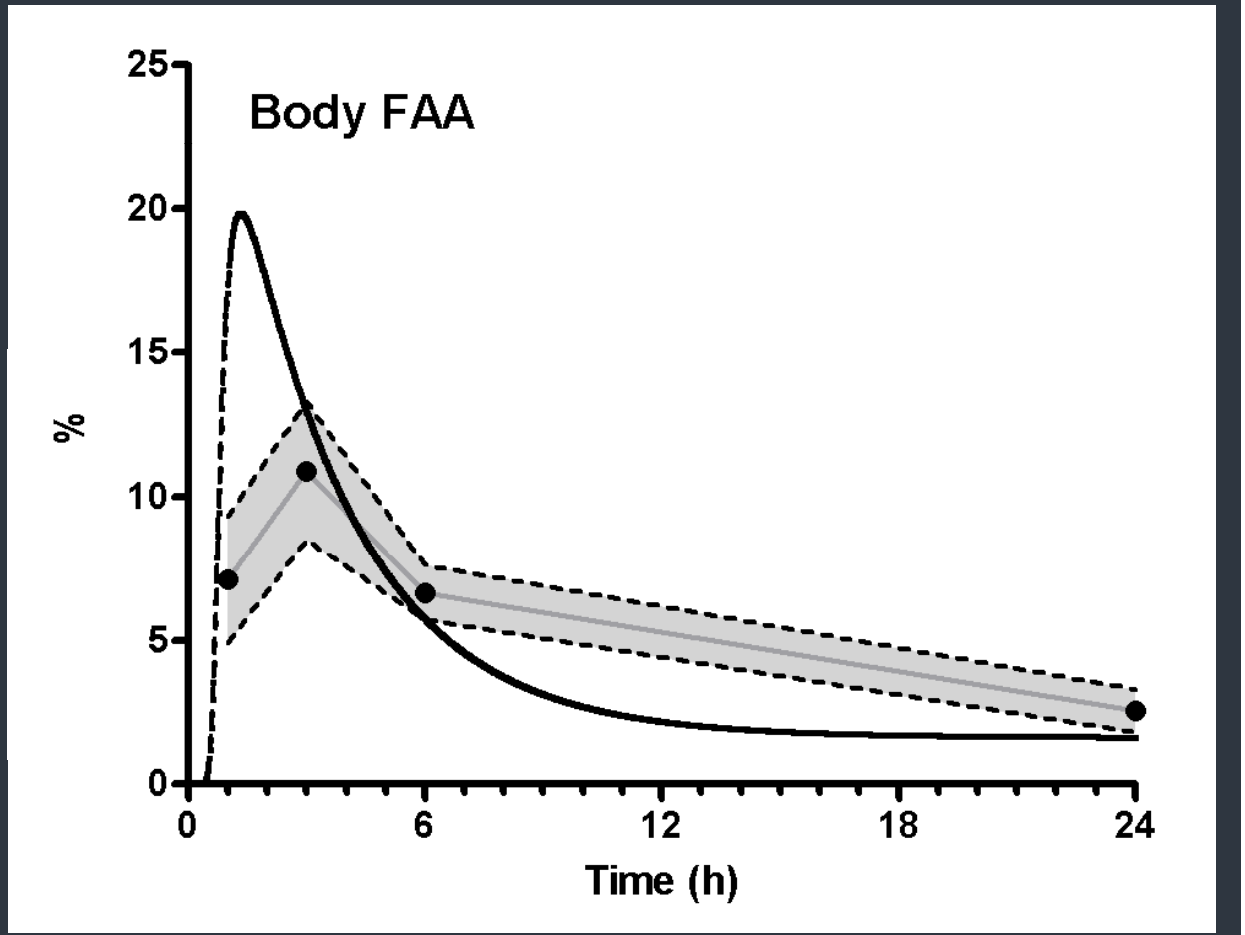

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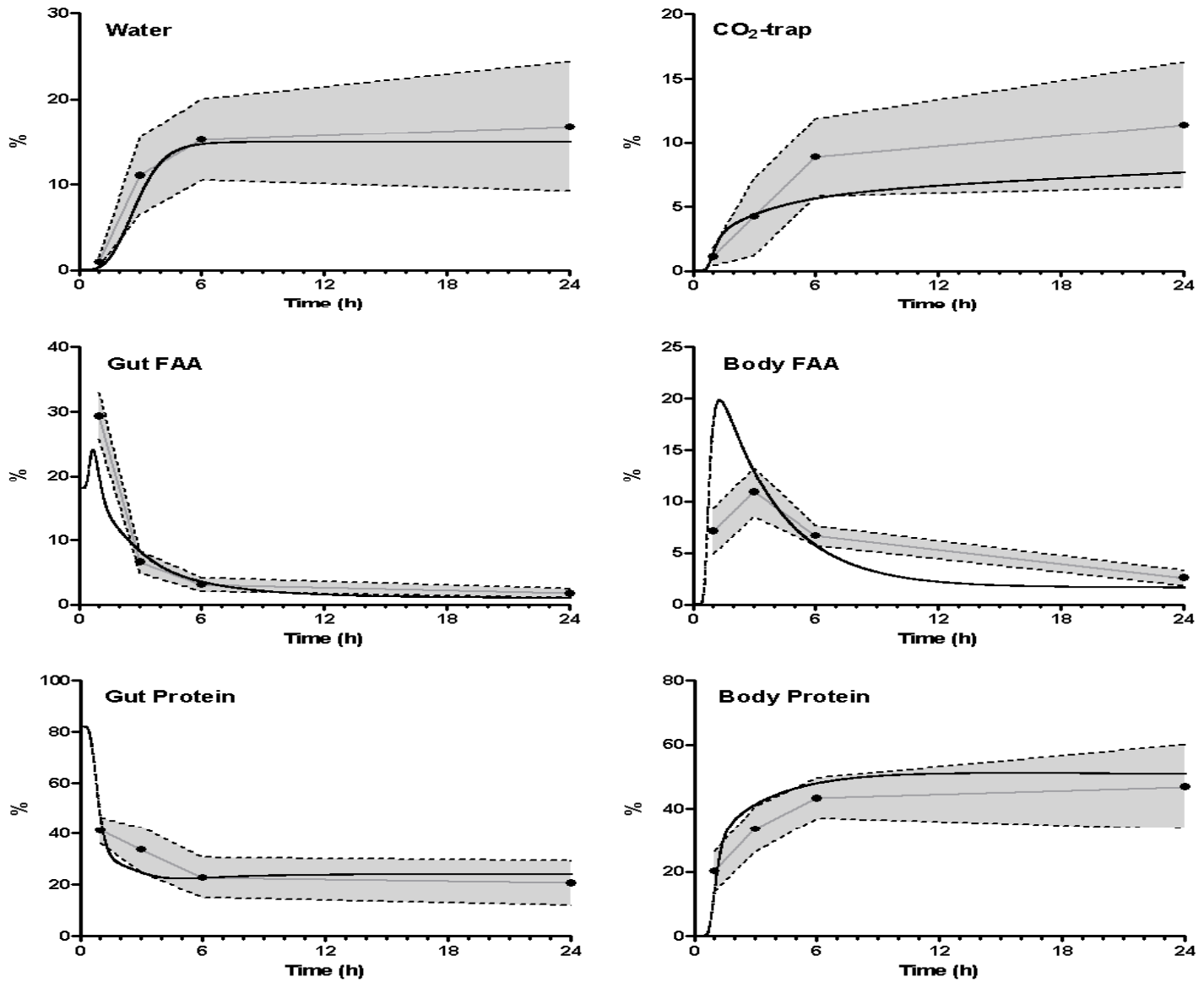

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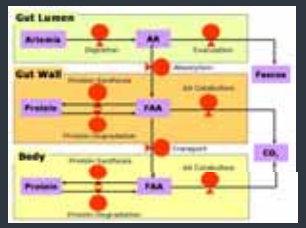


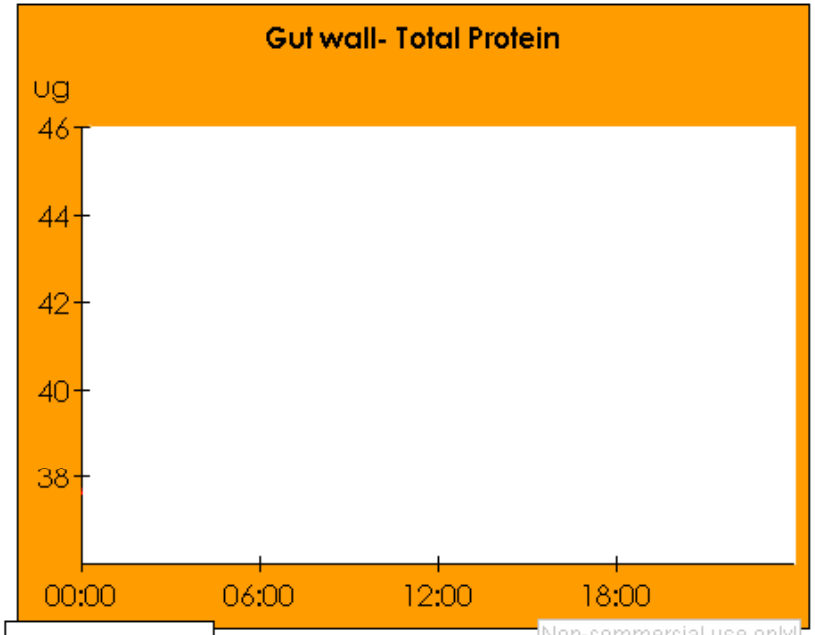
Parameters calibrated with model:

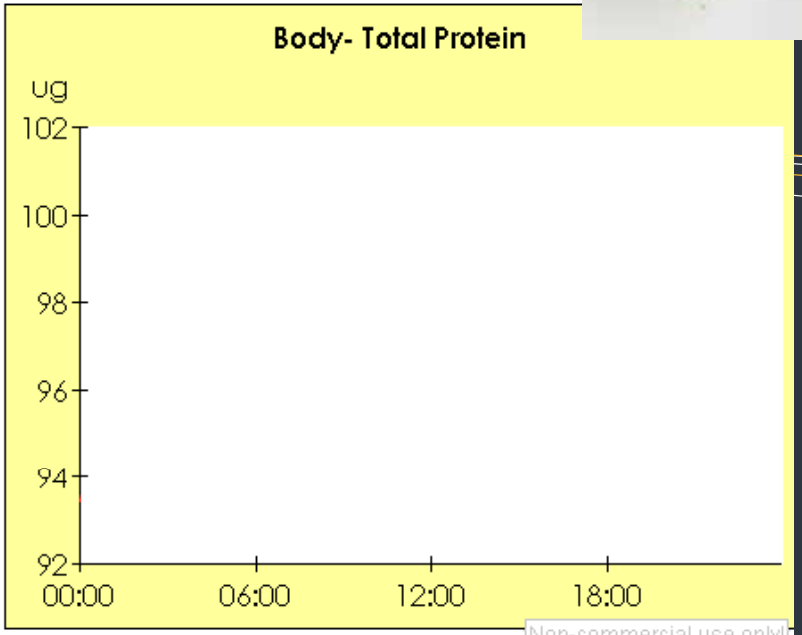
Parameter	Unit	Mean	CV(%)
Basal AA Catabolism rate	ng/h	502.6	18.6
Delay onset of Digestion	min	0.032	3.3
Rate of Digestion & absorption	min^{-1}	0.539	3.9
Gut AA catabolism rate	min^{-1}	0.010	8.1
Gut Protein Synthesis rate	min^{-1}	0.161	2.0
No of Artemia fed	n	15.0	1.1
Protein degradation rate	ng/h	25.5	0.7

After about 9 million iterations

Using Powersim Studio 7

Model Output





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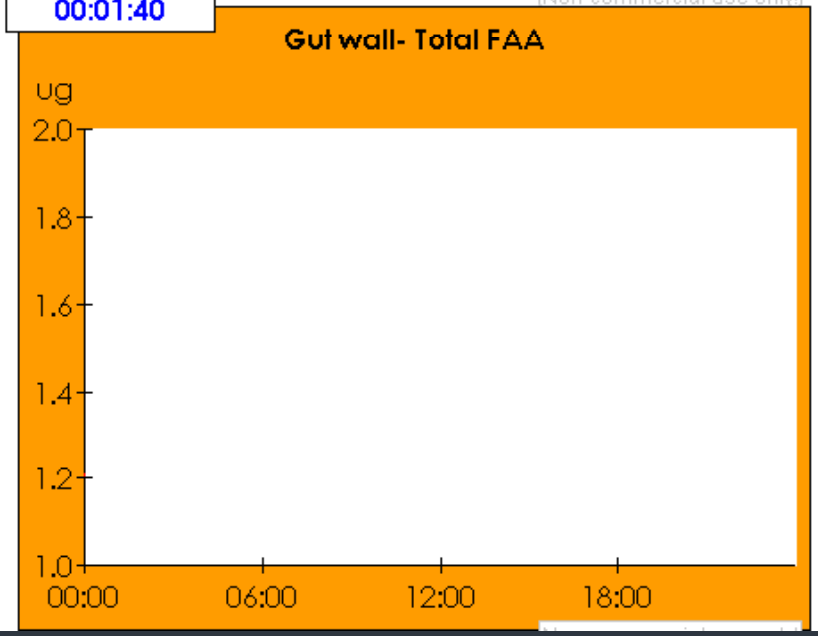

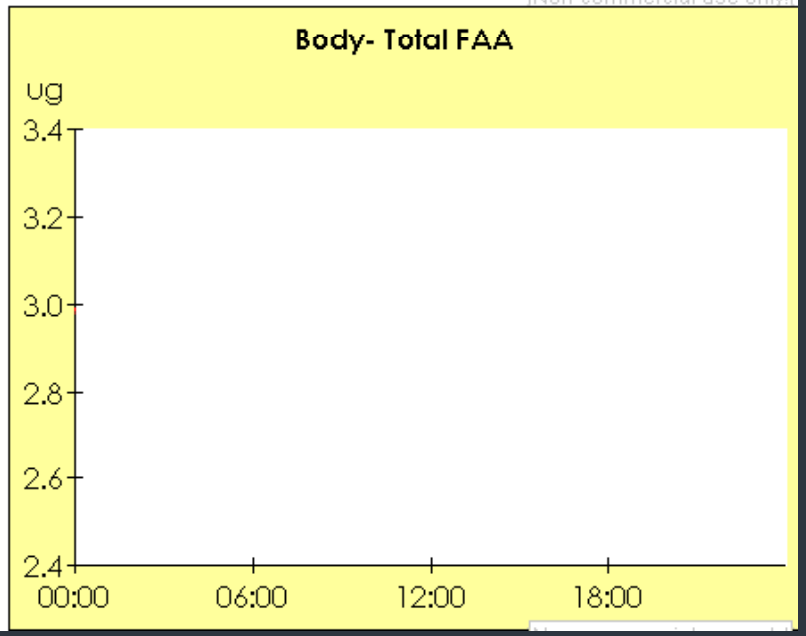

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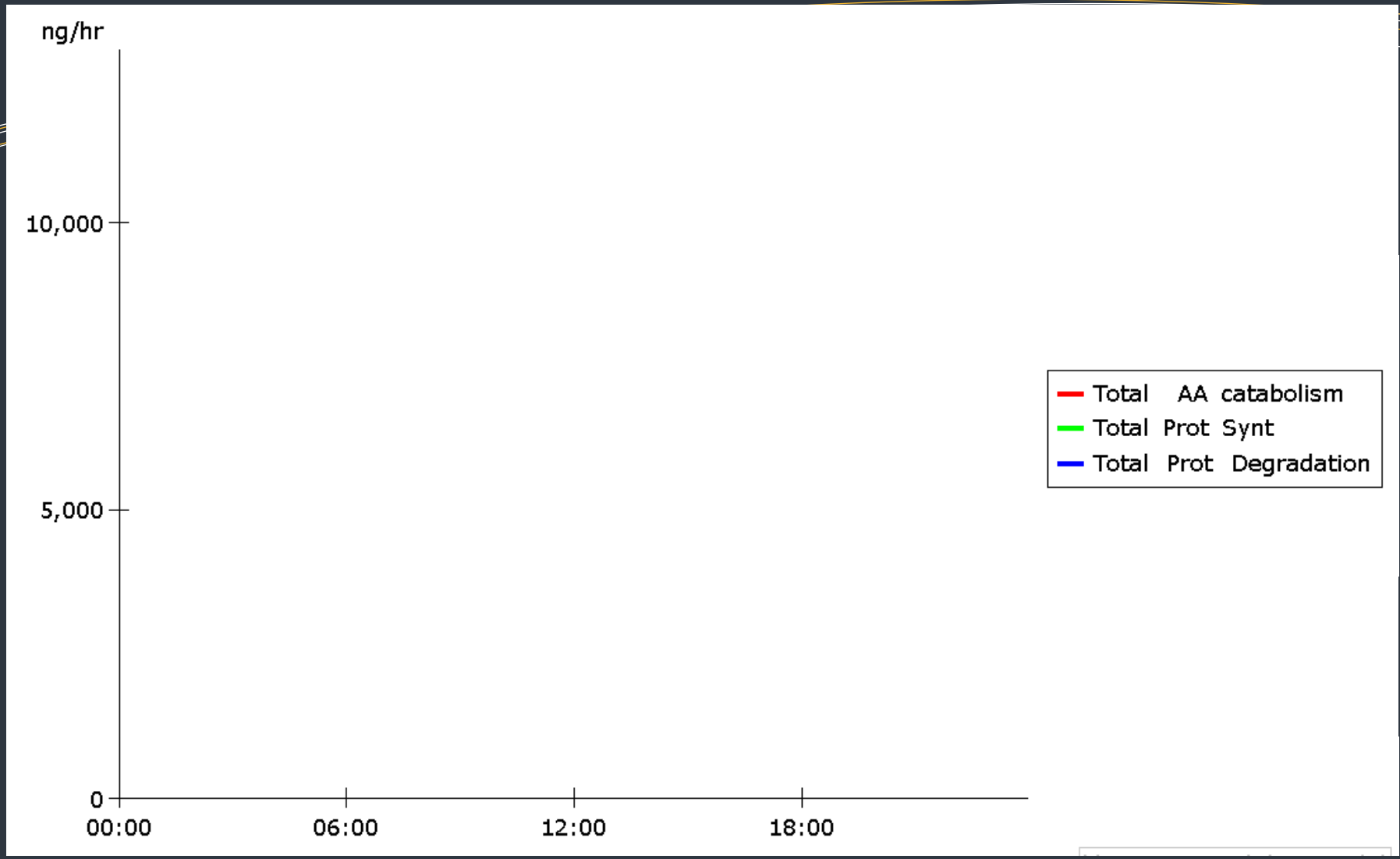
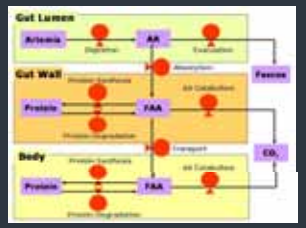
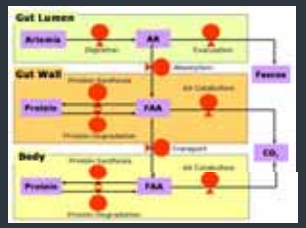


Conclusions



- Food has a major contribution to the FAA pool composition - Rates of protein synthesis and AA Catabolism show a major increase after the meal
- Peak for this postprandial metabolism occurs only 1 hour after the meal, and the rates returning to “basal” values 3 hours after the meal.
- This suggests a rapid handling of Artemia protein by larvae, and supports the need for feeding sole larvae at a high frequency (every 3-4 hours) in order to fully use its growth potential.
- Model Mechanistic nature => can be used with different AA tracers, and also for other fish species.

Future work

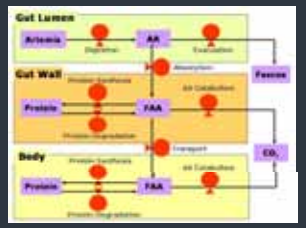


- Model several meals / days of feeding
- Model effects of few meals vs. continous feeding
- Test (validate) with different experiments / ages / species
- Simulate metabolism of individual AA

  => estimation of requirements
  => better understanding of AA
- Integrate AA metabolism with energetics and growth

  => better understanding of growth process
  => defining feeding strategies
  => growth predictions

Thank you!!



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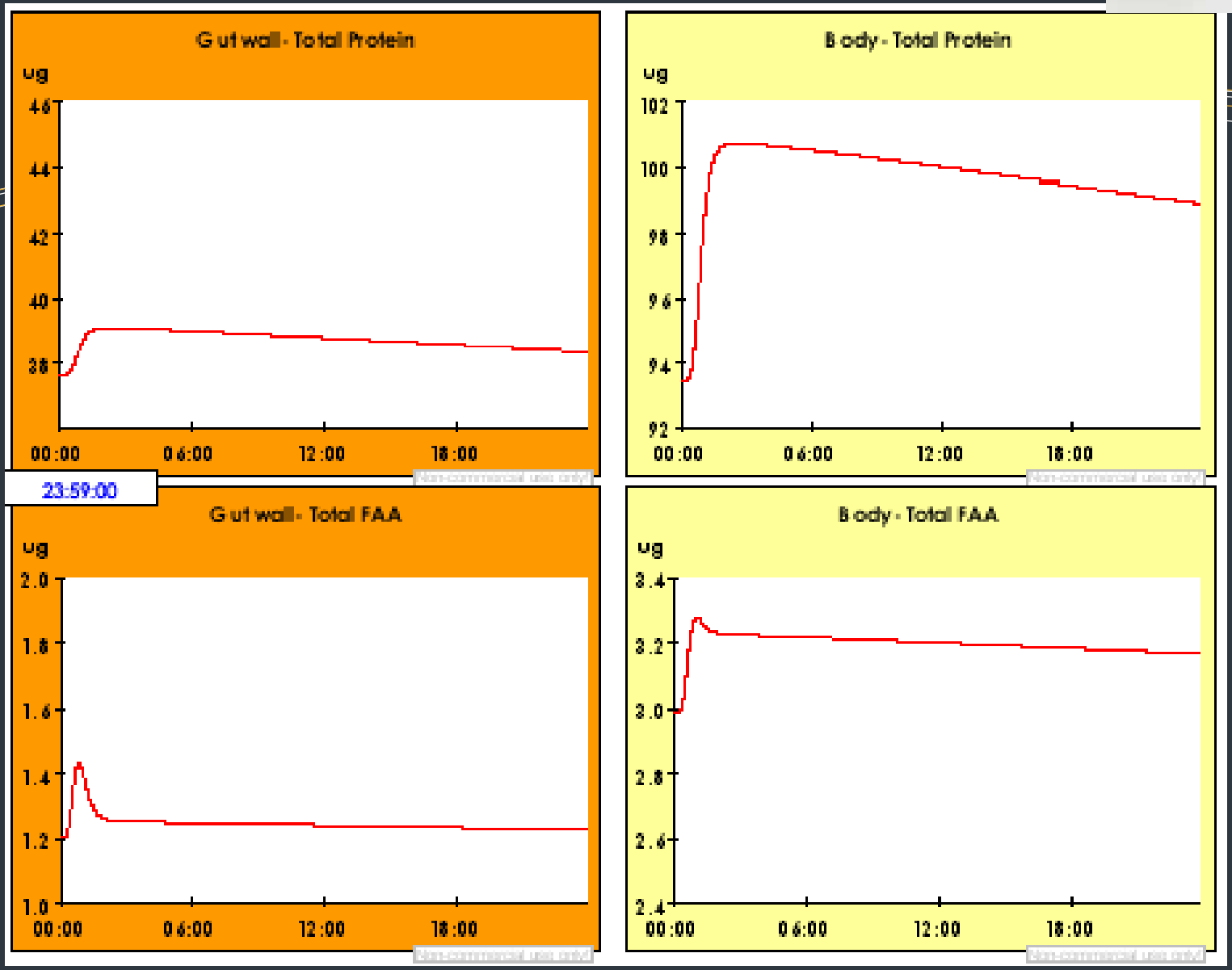

Model Output