AOMM™ SCIENCE · WHITE PAPER 02

Also in this series: White paper 01 — Validation

Comparing AOMM™ and MATLAB metabolic calculations.

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The objective of this study is to validate the AOMM™ non-OMM indices against an independent mathematical pipeline implemented in MATLAB.

Dataset and methods

Dataset

The validation framework utilizes a dataset which includes 999 individual records. For each subject, the dataset provides unique identification, demographic and anthropometric characteristics (age at visit, BMI, weight), and plasma glucose, insulin and C-peptide, temporal tracking across a 120-minute OGTT. The physiological kinetic curves include a baseline sample (t = –10 min) and five sampling points at 0, 30, 60, 90, and 120 minutes.

Preprocessing

The preprocessing phase involves unit standardization with AOMM™, which requires plasma glucose expressed in mg/dL, insulin in µU/mL, and C-peptide both in ng/mL and pmol/L for different index calculations. While the raw glucose and insulin profiles were already provided in the required standard units, the C-peptide values were originally reported in ng/mL. Consequently, these values were also converted into pmol/L by multiplying them by 331.

Methods

To systematically verify the mathematical formulas implemented by the AOMM™ software, an independent validation pipeline was developed in MATLAB, evaluating five distinct parameter groups.

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1. Static fasting indices

$$\text{HOMA-IR} = \frac{G_0 \cdot I_0}{405}$$

$$\text{HOMA-}\beta = \frac{360 \cdot I_0}{G_0 - 63}$$

$$\text{QUICKI} = \frac{1}{\log_{10}(I_0) + \log_{10}(G_0)}$$

Where G_0 represents fasting glucose and I_0 denotes fasting insulin, both measured at the baseline of the test (t = 0 min).

2. Dynamic empirical indices

$$\text{Matsuda ISI} = \frac{10{,}000}{\sqrt{G_0 \cdot I_0 \cdot \bar{G} \cdot \bar{I}}}$$

$$\text{IGI} = \frac{I_{30} - I_0}{G_{30} - G_0}$$

$$\text{Matsuda disposition index} = \text{IGI} \cdot \text{Matsuda ISI}$$

$$\text{C-peptide index} = \frac{\text{CP}_{30} - \text{CP}_0}{G_{30} - G_0}$$

$$\text{ISSI-2} = \frac{\text{AUC}_I}{\text{AUC}_G} \cdot \text{Matsuda ISI}$$

Here, $\bar{G}$ and $\bar{I}$ denote the mean concentration of glucose and insulin across the OGTT, while G_t, I_t and CP_t represent the glucose, insulin, and C-peptide concentrations recorded at time point t (C-peptide in pmol/L). Additionally, the composite IGI/HOMA-IR ratio index was computed.

3. Incremental area under the curve (iAUC)

$$\begin{aligned}\text{iAUC}_G = {} & 15(G_0 + G_{30}) + 15(G_{30} + G_{60}) \\ & + 15(G_{60} + G_{90}) + 15(G_{90} + G_{120}) - 120 \cdot G_0\end{aligned}$$

$$\begin{aligned}\text{iAUC}_I = {} & 15(I_0 + I_{30}) + 15(I_{30} + I_{60}) \\ & + 15(I_{60} + I_{90}) + 15(I_{90} + I_{120}) - 120 \cdot I_0\end{aligned}$$

$$\begin{aligned}\text{iAUC}_{\text{CP}} = {} & 15(\text{CP}_0 + \text{CP}_{30}) + 15(\text{CP}_{30} + \text{CP}_{60}) \\ & + 30(\text{CP}_{60} + \text{CP}_{120}) - 120 \cdot \text{CP}_0\end{aligned}$$

Trapezoidal rule over 0–120 min; C-peptide in pmol/L.

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4. Other glycemic indices

$$G_{60} = G(60)$$

$$G_{\text{peak}} = \max(G)$$

$$t_{\text{peak}} = t(\max(G))$$

$$G_{\text{range}} = \max(G) - \min(G)$$

$$G_{120} = G(120)$$

5. T1D progression indices

$$\text{Index}_{60} = 0.3695 \cdot \ln(\text{CP}_0) + 0.0165 \cdot G_{60} - 0.3644 \cdot \text{CP}_{60}$$

$$\text{DPTRS} = 1.571 \cdot \ln(\text{CP}_0 + 1) + 0.115 \cdot G_{120} - 0.193 \cdot \frac{\text{CP}_{60}}{\text{CP}_0} + 0.0019 \cdot \text{age} + 1.5 \cdot \ln(\text{BMI})$$

C-peptide in ng/mL.

Results

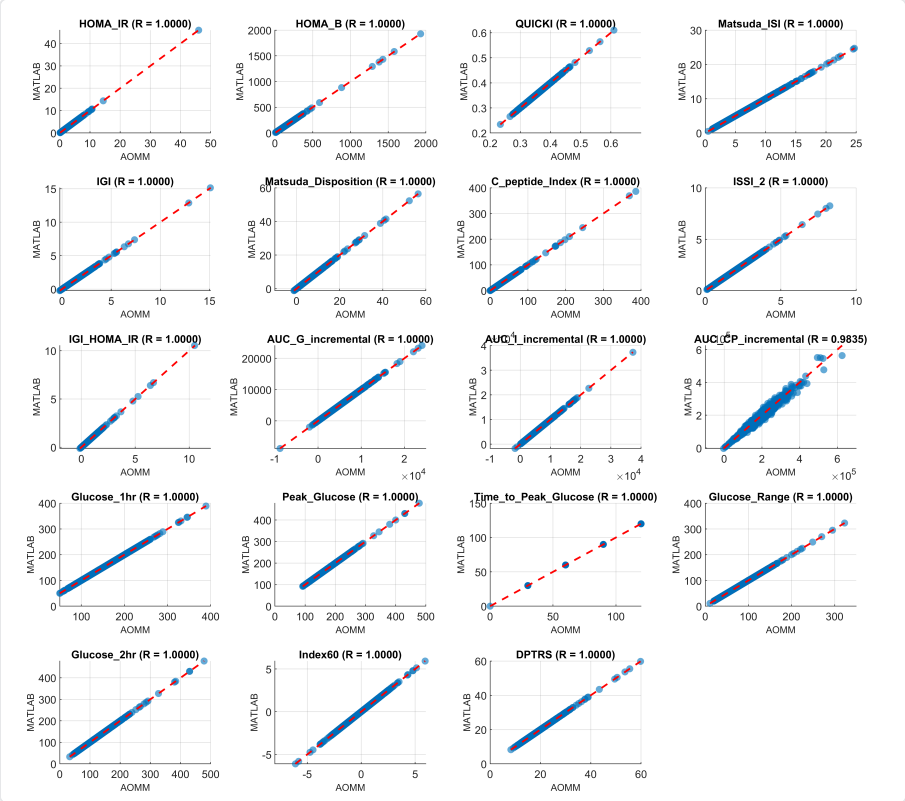


Figure. AOMM™ (x-axis) versus MATLAB (y-axis) for each of the 19 parameters (n = 999 records); red dashed line: identity (y = x).

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The level of agreement between the two methodologies was evaluated using correlation scatter plots, plotting AOMM™ reference values on the horizontal axis (x-axis) against the MATLAB calculations on the vertical axis (y-axis), with the theoretical identity line (y = x) superimposed in red. In this graphical framework, a perfect linear convergence of the 999 data points along the identity line, paired with a Pearson correlation coefficient of R = 1, mathematically proves that both methods calculated the parameters identically.

18 of the 19 evaluated parameters demonstrated this perfect mathematical agreement (R = 1), with all subject coordinates falling precisely along the red reference line. Only the incremental C-peptide AUC showed small deviations from the identity line (R = 0.9835): while the correlation remains strong, a minor scatter is visible, particularly at higher values. This slight variation is likely due to differences in how the two systems handle the numerical trapezoidal integration across the 60-to-120-minute time gap, or minor variations in baseline subtraction.

Acknowledgements

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Validation material

The validation material for this study is publicly available on GitHub: github.com/SimonNanoMath/aomm-validation-public.

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