

# Exploring Nutritional Influence on Blood Glucose Forecasting for Type 1 Diabetes Using Explainable AI

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# Motivation:

- Predicting BGLs due to various factors beyond insulin infusions, including meal intake, physical activity, sleep patterns, and emotional states. This paper focus on **insulin infusions and meal intake**.
- The BGLs prediction models in the literature, **lack interpretability**, rendering them as black boxes for ML scientists, healthcare practitioners, and patients.

# Related Works

**TABLE I**  
PREDICTION PERFORMANCE COMPARISON IN CURRENT LITERATURE. PH  
[PREDICTION HORIZON], RMSE [ROOT MEAN SQUARED ERROR]

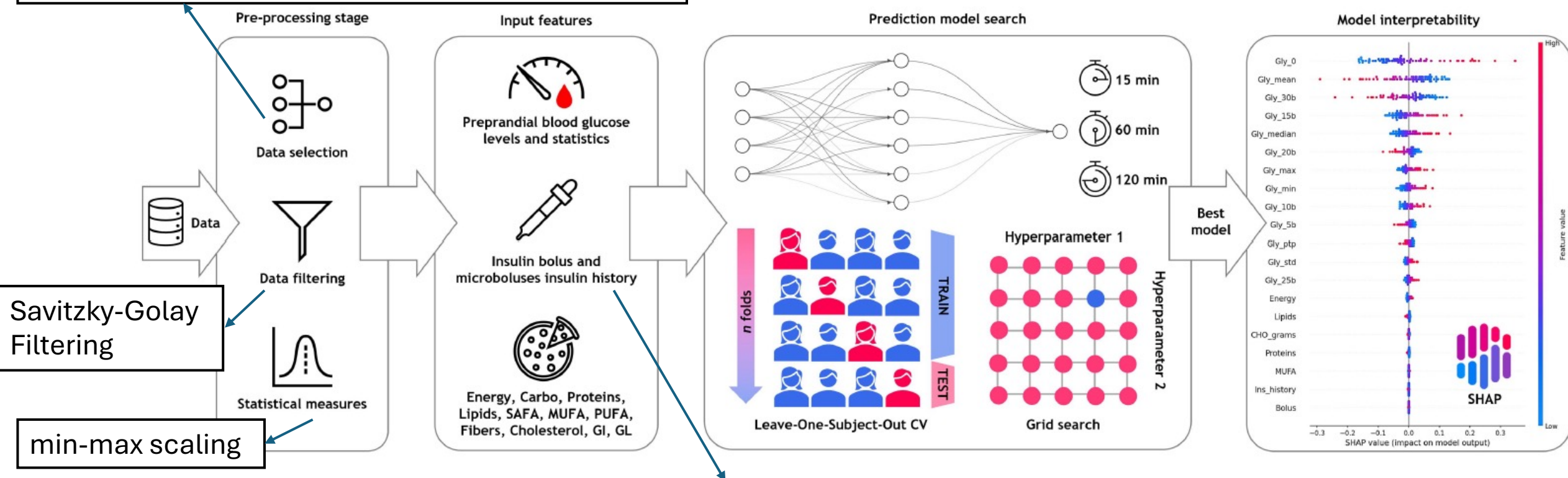
<b>Study</b>	<b>Type of inputs</b>	<b>PH (min)</b>	<b>RMSE (mg/dL)</b>
Annuzzi et al. [10]	CGM data, statistical attributes, insulin, meal related information	30	$8.0 \pm 0.6$
		60	$21.3 \pm 1.6$
Daniels et al. [21]	CGM data, insulin, physiological signals, meal intake	30	$18.8 \pm 2.3$
		60	$31.8 \pm 3.9$
		120	$47.2 \pm 4.6$
Alfian et al. [23]	CGM data, statistical attributes	30	$6.6 \pm 2.4$
		60	$15.3 \pm 5.9$
Jaloli et al. [27]	CGM data, insulin, carbohydrates	30	$9.8 \pm 1.2$
		60	$18.3 \pm 2.8$
Li et al. [31]	CGM data, insulin, carbohydrates	30	$19.3 \pm 2.8$
		60	$31.8 \pm 3.5$

# Novelty:

- Impact of input features on BGLs prediction using Explainable AI
- Features used for the BGL prediction model are:
  - BGL values,
  - Insulin administered during mealtime
  - Meal-related attributes
- Develop three distinct prediction models, with PHs of 15 min, 60 min, and 120 min

# Proposed method

- BGL values measured each 5 min from 30 min before the meal until the mealtime
- 15- step sliding window for smoothing the BGLs trends



## Insulin Measurement:

Micro boluses administered by the AP system in the 3h before the meal were summed to obtain a single quantity that takes into account the amount of basal insulin.

# Method

- Proposed 3 Feed Forward Neural Networks (FFNN) to investigate the influence of specific features on BGLs prediction for different PHs (15 min, 60 min, and 120 min) after a meal
- The FFNNs took as input features:
  - **30 min window of BGLs (Gly\_30b - Gly\_0) along with associated statistical attributes:** minimum (Gly\_min), maximum (Gly\_max), mean (Gly\_mean), standard deviation (Gly\_std), peak-to-peak difference (Gly\_ptp), median (Gly\_median), kurtosis (Gly\_kurt), and skewness (Gly\_skew)
  - **Information regarding the insulin dosages:** – manually-administered bolus (MB) of insulin (Bolus) at mealtime; – cumulative sum of micro boluses delivered by the closed-loop system worn by patients in the three-hour interval preceding the meal (Ins\_history), as an absolute measure of the system's insulin delivery
  - **Meal-related information:** – energy intake (Energy); – carbohydrates (Carbo), glycemic index (GI), glycemic load (GL); – Proteins; – Fibers; – Lipids, monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), saturated fatty acid (SAFA), Cholesterol.

# Method

- Three separate models were derived, specifically tailored to predict at distinct PHs: 15 min, 60 min, and 120 min.
- Each model was validated by using Leave-One-Subject-Out Cross-Validation (LOSO-CV) strategy.

TABLE II  
SEARCH SPACE ADOPTED DURING THE GRID SEARCH FOR TUNING  
HYPERPARAMETERS

Tuned Hyperparameters	Search Space
number of hidden layers	{1, 2, 3}
number of neurons in each layer	{8, 16, 32, 64, 128}
optimization algorithm	{Stochastic Gradient Descent (SGD) [55], Adam [56]}
activation function	{Rectified Linear Unit (ReLU) [57], hyperbolic tangent function (tanh), Variable Activation Function (VAF) [58]}
learning rate	{0.0001, 0.0005, 0.001, 0.005, 0.01}
weight decay parameter (penalty L2)	{0.0001, 0.001, 0.01}

# Method

- SHAP is a method to explain individual predictions, providing relevance scores to each input feature. This methodology utilizes Shapley values, derived from coalitional game theory, to attribute the contribution of each feature to the final prediction. The basic principle of SHAP technique is to decompose the model output into the cumulative impacts of individual features.
- For complex models such as DNNs, the adopted SHAP method (i.e., Kernel SHAP) relies on weighted linear regression to compute the importance of each feature.



# Method

$$g(z') = \phi_0 + \sum_{j=1}^M \phi_j z'_j, \quad (2)$$

where  $z'_j$  denotes the presence (1) or absence (0) of the feature  $j$ ;  $\phi_j$  is the Shapley value representing the relative feature contribution; and  $\phi_0$  is the base value when all input features are absent (0).

- To estimate the global relevance of each input on the model's outcome, it is possible to compute the absolute Shapley values of feature  $j$  were averaged across the data.

$$I_j = \frac{1}{n} \sum_{i=1}^n \left| \phi_j^{(i)} \right| \quad (3)$$

# Results

<b>PH (min)</b>	<b>RMSE (mg/dL) (mean <math>\pm</math> std)</b>	<b>Selected Hyperparameters</b>
15	2.53 $\pm$ 0.43	number of hidden layers = 2 number of neurons = {32,16} optimization algorithm = Adam activation function = tanh learning rate = 0.0001 L2 penalty = 0.001 batch size = 32
60	24.74 $\pm$ 4.27	number of hidden layers = 3 number of neurons = {32,16,8} optimization algorithm = Adam activation function = tanh learning rate = 0.0001 L2 penalty = 0.01 batch size = 32
120	50.15 $\pm$ 7.70	number of hidden layers = 3 number of neurons = {32,16,8} optimization algorithm = Adam activation function = tanh learning rate = 0.0001 L2 penalty = 0.01 batch size = 16

# Results

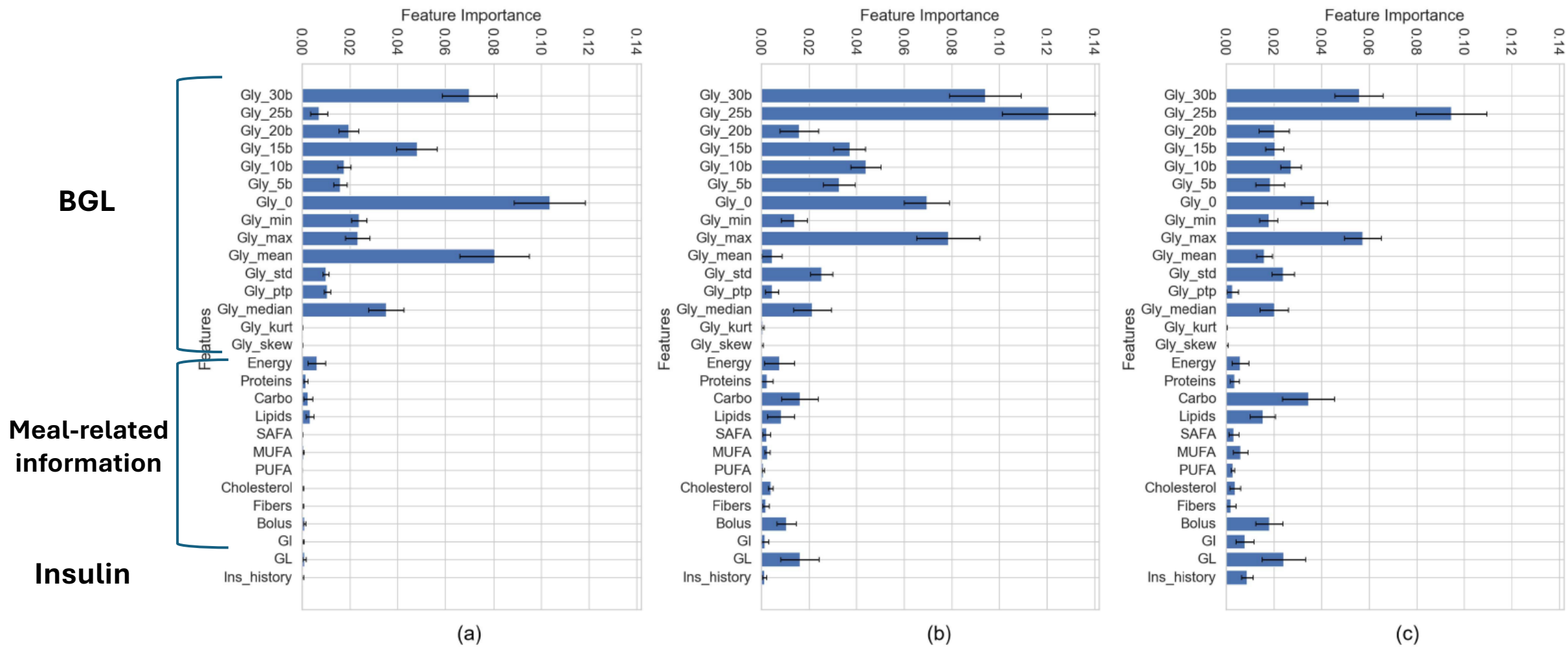


Fig. 2. Boxplots for feature importance analysis at (a) 15 min, (b) 60 min, and (c) 120 min after mealtime. Each feature bar corresponds to the

# Results

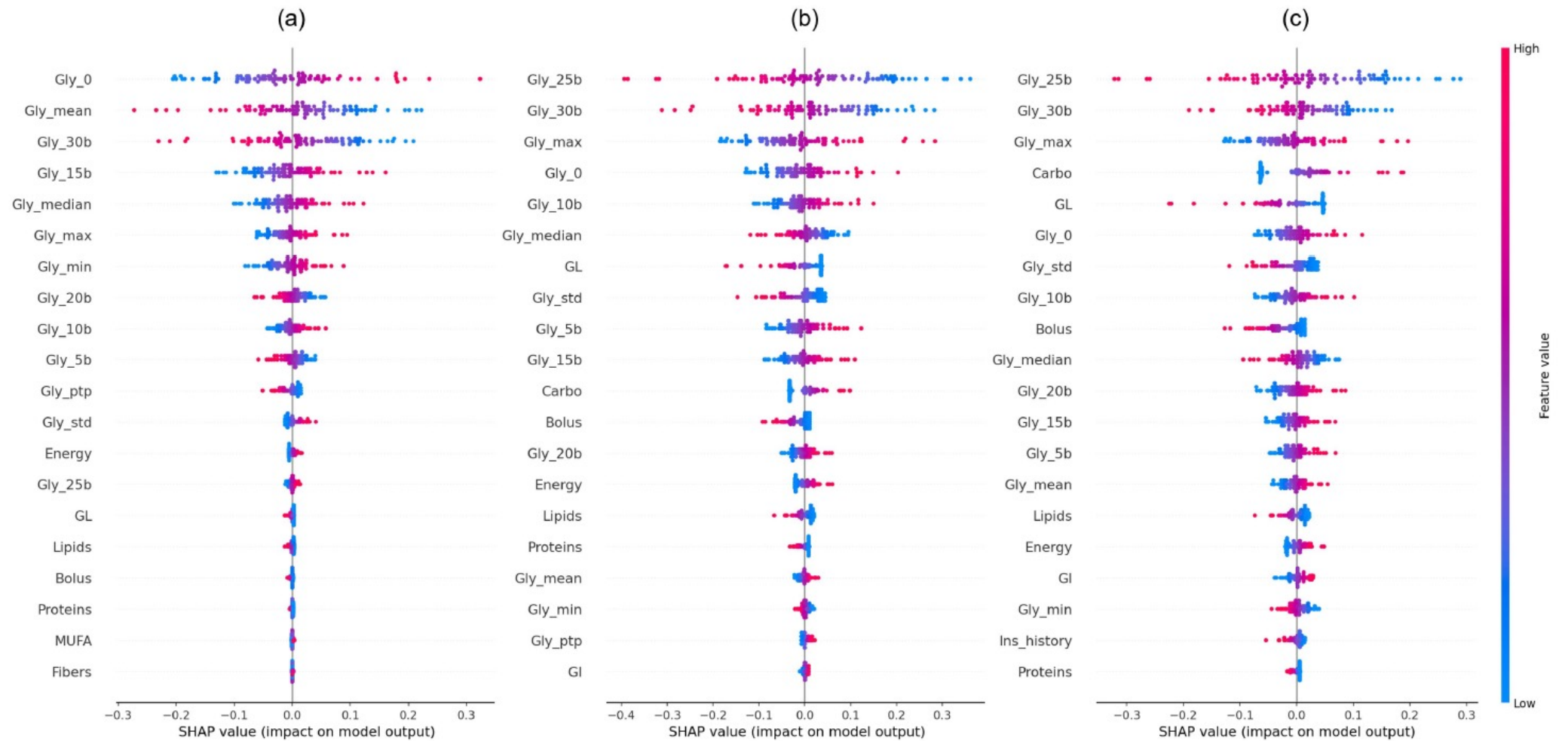


Fig. 3. Best-fold summary plots of SHAP values at (a) 15 min, (b) 60 min, and (c) 120 min after mealtimes for a single subject. Features are listed

# Results

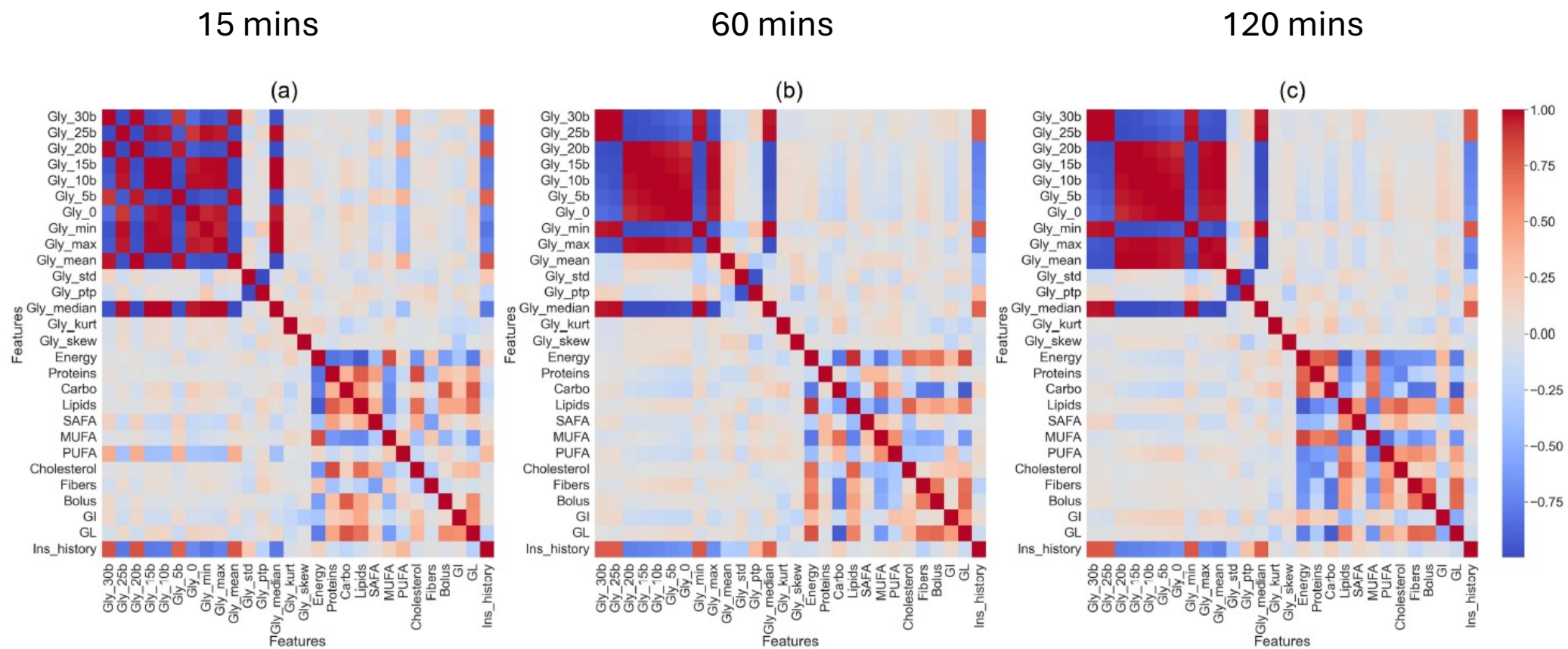


Fig. 4. Best-fold correlation matrices between SHAP values corresponding to each feature pair at (a) 15 min, (b) 60 min, and (c) 120 min after