

Article

Ensemble Learning-Based Prediction of Blood Glucose Using Impedance Spectroscopy

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Abstract

Noninvasive blood glucose monitoring using impedance spectroscopy faces challenges due to high-dimensional, redundant data and complex nonlinear relationships with glucose concentration. To address these challenges, LASSO regression was applied for feature selection, followed by ensemble learning models incorporating multiple base learners. Among them, a Stacking ensemble framework—combining Support Vector Regression (SVR), Random Forest (RF), and LightGBM—achieved the best overall regression accuracy (MAE = 0.9662, RMSE = 1.3040, $R^2 = 0.9414$). Compared to the best individual base learner (MLP), the S1 ensemble improved overall MAE by 9.7% and RMSE by 7.6%. However, in the clinically critical hyperglycemic range, the individual MLP substantially outperformed S1 (RMSE: 0.7570 vs. 1.1716), indicating that S1's superiority reflects a global statistical average rather than uniform improvement across all glycemic subranges. Therefore, while the proposed framework demonstrates the efficacy of combining feature selection with ensemble learning, the MLP model may be preferable for clinical applications prioritizing hyperglycemic risk identification.

Keywords: blood glucose prediction; ensemble learning; impedance spectrum

1. Introduction

Diabetes mellitus is a metabolic disorder characterized by chronic hyperglycemia, with a steadily increasing global prevalence. Its pathogenesis involves multi-organ insulin dysfunction and metabolic dysregulation [1,2]. Long-term glycemic control is closely associated with microvascular and macrovascular complications, as well as overall patient prognosis. Therefore, safe, continuous, and accurate glucose monitoring is essential for effective diabetes management [3].

Currently, most clinically adopted glucose monitoring methods rely on invasive or minimally invasive techniques. While these approaches provide high measurement accuracy, they often cause pain, discomfort, skin damage, and poor long-term adherence [4]. Consequently, noninvasive monitoring technologies, such as optical sensors and electrical impedance spectroscopy (EIS), have gained attention due to their potential for wearable integration and real-time measurement [5–8]. EIS measures tissue impedance magnitude and phase response under multi-frequency electrical excitation, capturing variations induced by changes in body fluid composition and cellular structure, thereby enabling indirect



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estimation of blood glucose [9,10]. Prior studies have demonstrated subtle but measurable variations in impedance parameters across physiological glucose ranges, providing a theoretical basis for predictive modeling [7,8].

Despite these advances, constructing accurate glucose prediction models based on EIS remains challenging. The data are typically high-dimensional, redundant, and noisy, with nonlinear dependencies on glucose concentration and strong inter-individual variability [11–14]. Single-model approaches often show limited stability and predictive performance, especially under small-sample conditions or in hyperglycemic ranges. For instance, Sanai et al. applied gradient boosting without feature selection and reported a mean absolute relative difference of 17.9% [15]. Additionally, most studies rely on simple ensemble combinations, lacking systematic feature selection or heterogeneous model design tailored to the structural characteristics of EIS data. These limitations highlight the need for a robust and generalizable modeling framework.

To address these challenges, this study proposes a feature-selection-driven heterogeneous ensemble framework for blood glucose prediction from high-dimensional EIS data. Sparse LASSO regression is first applied to select key features from 422 original variables, reducing redundancy and improving stability. Nine machine learning and deep learning models are integrated into Voting and Stacking ensembles, with meta-features generated via cross-validation. A Random Forest meta-learner is used to achieve collaborative bias–variance optimization, enhancing performance under small-sample conditions. Model evaluation includes both overall regression metrics and performance within different glycemic intervals (including normoglycemic, hyperglycemic, and hypoglycemic ranges) to assess clinical robustness.

The main contributions of this study are summarized as follows:

- (1) Feature-selection-driven ensemble framework: Combines LASSO with heterogeneous ensemble learning to improve prediction accuracy and generalization.
- (2) Systematic evaluation of base learners and ensemble strategies: Compares nine machine learning and deep learning models in Voting and Stacking frameworks.
- (3) Clinical-range performance analysis: Assesses model stability across different glycemic intervals, including normoglycemic, hyperglycemic, and hypoglycemic ranges.
- (4) Quantitative performance evaluation: The S1 ensemble achieved lower global MAE (9.7%) and RMSE (7.6%) compared to the best individual base learner (MLP), with further gains over the SVR baseline without feature selection (MAE: -1.3951 ; RMSE: -1.8285). Nonetheless, range-specific analysis reveals that the MLP substantially outperforms S1 in the hyperglycemic range, highlighting the need for clinically contextualized model selection.

The remainder of this paper is structured as follows: Section 2 introduces materials and methods, Section 3 presents experimental results, Section 4 discusses findings and clinical implications, and Section 5 concludes with recommendations for future research.

2. Methods

To address the complexity of high-dimensional impedance data, ensemble learning—a paradigm that improves predictive performance by aggregating multiple base learners was employed. By promoting model diversity, ensemble methods reduce individual bias and variance, while aggregation strategies help mitigate overfitting and enhance generalization capability. Common ensemble strategies include Voting and Stacking [16,17].

(1) Voting Ensemble

The Voting ensemble combines the predictions of multiple base models to generate a final output. As illustrated in Figure 1, for regression tasks, the final prediction is typically obtained by averaging the outputs of individual base learners. This approach

does not require training an additional meta-model, making it computationally efficient and straightforward to implement. Owing to its flexibility in integrating heterogeneous models and leveraging their complementary strengths, Voting is particularly suitable for scenarios where data distributions are complex and base learners exhibit substantial diversity.

Voting-Based Ensemble Fusion Framework

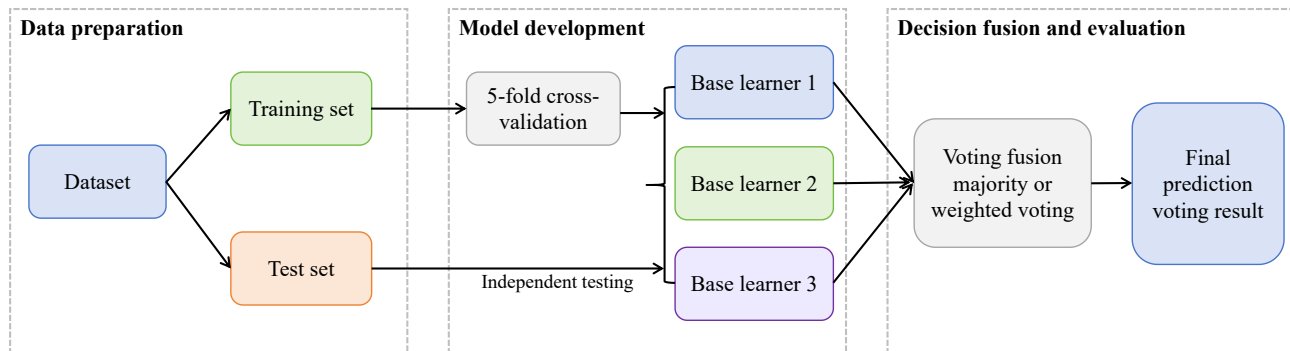


Figure 1. Voting fusion model.

The ensemble procedure can be summarized as follows (taking V1 as an example):

- Step 1: Input the training samples and perform iterative training for $k = 1, 2, \dots, K$.
- Step 2: Initialize the sample weights $D_{(SVR)}$, $D_{(RF)}$, $D_{(LightGBM)}$, and $D_{(SVR)} = D_{(RF)} = D_{(LightGBM)}$.
- Step 3: Train the base learners (SVR, Random Forest, and LightGBM) using the initialized weights and obtain their respective prediction outputs.
- Step 4: Compute the weighted average of the base learner predictions according to predefined weights to obtain the final prediction result.

(2) Stacking Ensemble

Stacking (Stacked Generalization) employed a meta-learner to model the output patterns of base learners, thereby capturing inter-model complementarity and achieving deeper feature fusion. As illustrated in Figure 2, Stacking often outperforms simple Voting in complex tasks, particularly when base learners exhibit high diversity. Both base learners and the meta-learner can be flexibly selected according to task requirements.

The training procedure of Stacking regression is described as follows:

- Step 1: Given a dataset $\{(x_n, y_n)\}_{n=1}^N$, where $x_n \in \mathcal{P}$ denotes the feature vector of the n -th sample, y_n is the corresponding target value, and p represents the number of features, the dataset is partitioned into K approximately equal subsets for K -fold cross-validation. Let D_k^{train} and D_k^{test} denote the training and test sets of the k -th fold, respectively.
- Step 2: Train the first-layer base learners on each D_k^{train} to obtain the corresponding base models.
- Step 3: Construct a new dataset for the second layer. For each sample in D_k^{test} , the predictions generated by the base learners are recorded as

$$z_n = (f_1(x_n), f_2(x_n), \dots, f_M(x_n)) \quad (1)$$

where $f_m(\cdot)$ denotes the m -th base learner and M is the number of base models. After completing K -fold cross-validation, the predictions from all folds were aggregated to form a new feature matrix Z .

- Step 4: The newly constructed dataset $\{(z_n, y_n)\}$ is used as the input to the second-layer regressor. The meta-learner is trained on this dataset to generate the final prediction model.

Stacking-Based Ensemble Learning Framework

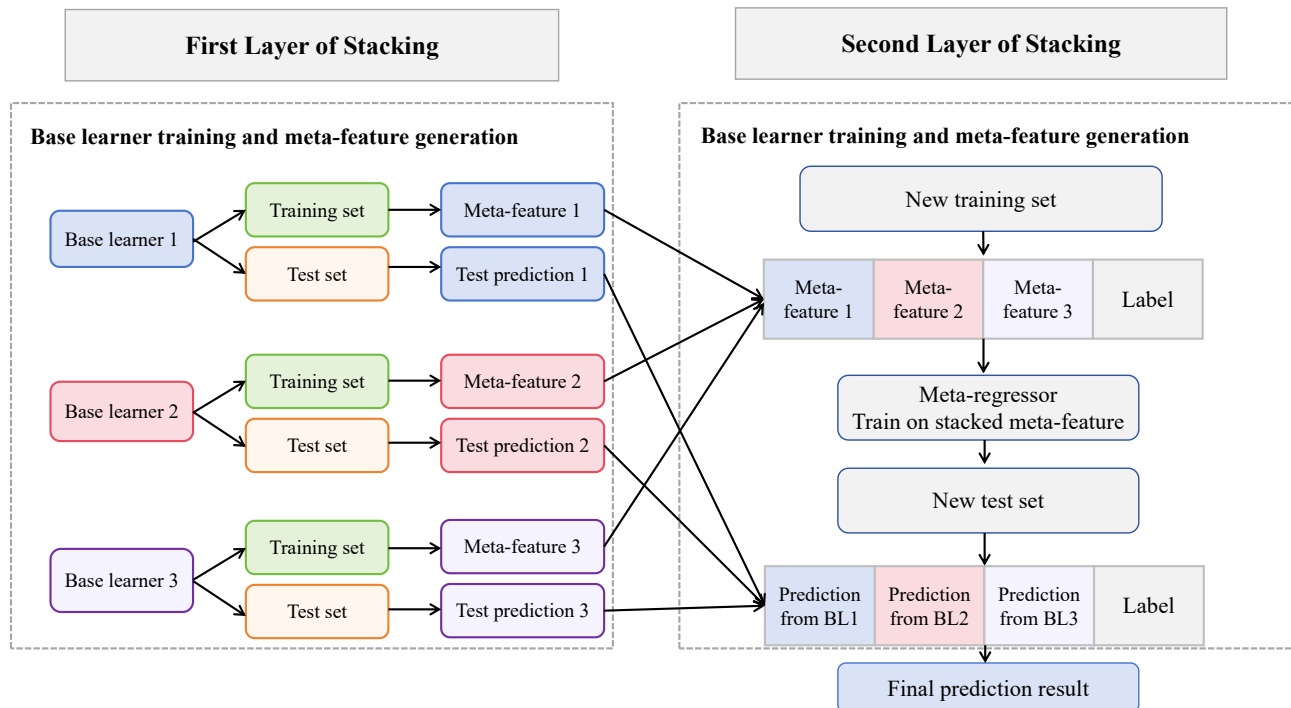


Figure 2. Stacking Fusion Model.

2.1. Construction of Base Models

A total of nine base learners were selected in this study, including six traditional machine learning models—Support Vector Regression (SVR) [18], Random Forest (RF) [19], LightGBM [20], Bayesian Ridge Regression [21], Orthogonal Matching Pursuit (OMP) [22], and K-Nearest Neighbors (KNN) [23]—and three deep learning models: Multi-Layer Perceptron (MLP) [24], Long Short-Term Memory network (LSTM) [25], and Gated Recurrent Unit (GRU) [26].

Based on these models, three Voting regressors (V1–V3) and three Stacking regressors (S1–S3) were constructed. The configurations of the ensemble models are summarized in Table 1. Random Forest was selected as the final estimator for all Stacking models due to its robustness, nonlinear modeling capability, and interpretability.

Table 1. Configuration of Voting and Stacking Regressors.

Type	Model	Base Estimators	Final Estimator
Voting Regressor	V1	SVR, RF, LightGBM	—
	V2	MLP, LSTM, GRU	—
	V3	KNN, Bayesian Ridge, OMP	—
Stacking Regressor	S1	SVR, RF, LightGBM	Random Forest
	S2	MLP, LSTM, GRU	Random Forest
	S3	KNN, Bayesian Ridge, OMP	Random Forest

2.2. Voting Model Configuration

After feature selection, the original dataset consisting of 26 features (including physiological parameters and electrical impedance features) was used as input for the Voting models.

For V1, the three base learners—SVR, RF, and LightGBM—were trained independently using the original feature matrix X . Each base model generated its prediction output:

$$\hat{y}_1 = f_{SVR}(X), \hat{y}_2 = f_{RF}(X), \hat{y}_3 = f_{LightGBM}(X) \quad (2)$$

The final prediction of V1 was obtained via weighted averaging:

$$\hat{y}_{V1} = \frac{\omega_1 \hat{y}_1 + \omega_2 \hat{y}_2 + \omega_3 \hat{y}_3}{\omega_1 + \omega_2 + \omega_3} \quad (3)$$

where $\omega_1, \omega_2, \omega_3$ denote the predefined weights assigned to each base learner.

V2 and V3 followed the same procedure using their respective base model combinations.

2.3. Stacking Model Feature Propagation

For the Stacking models, the same 26-dimensional original feature matrix X was used as input to the first-layer base learners.

Taking S1 as an example, the three base learners (SVR, RF, and LightGBM) were trained on X , and their outputs were combined as meta-features to enhance predictive performance.

$$\hat{y}_1 = f_1(X), \hat{y}_2 = f_2(X), \hat{y}_3 = f_3(X) \quad (4)$$

These predictions were concatenated to construct a new feature representation:

$$Z = [\hat{y}_1, \hat{y}_2, \hat{y}_3] \quad (5)$$

For S1, the meta-learner (Random Forest) received both the original features and the newly generated meta-features as input (i.e., `passthrough = True`). Thus, the second-layer input was:

$$X_{meta} = [X, Z] \quad (6)$$

where Z represents meta-features generated from base learners. The final prediction was generated by training the Random Forest meta-model on X_{meta} .

For S2 and S3, `passthrough = False` was adopted. Therefore, only the meta-features Z were used as input to the Random Forest meta-learner:

$$X_{meta} = Z \quad (7)$$

2.4. Dataset and Ethics

The dataset comprised 60 volunteers (30 male, 30 female; age 20–60 years). Impedance measurements were taken at fasting, 30, 60, and 120 min postprandial with three repeated readings per time point. Outliers beyond ± 3 standard deviations were removed. As illustrated in Figure 3, bioelectrical impedance data were collected using a self-developed impedance measurement device. The device employs medical-grade Ag/AgCl electrodes. Measurements were conducted in a controlled environment (temperature: 23 ± 1 °C; humidity: $45 \pm 5\%$) following a 10-min acclimation period. The reference blood glucose values were obtained using the URIT-10 minimally invasive glucometer, which served as the ground truth. Detailed specifications of the electrode configuration, contact area, pressure control mechanism, and repeatability assessment will be provided in a separate technical report focused on the device hardware design.



Figure 3. Data acquisition setup.

3. Results

3.1. Preprocessing

After data preprocessing and quality control (removing outliers beyond ± 3 SD), the curated dataset was processed to satisfy the input requirements of multiple predictive models, including normalization and LASSO-based feature selection. First, feature normalization was performed to standardize the data distribution. Subsequently, LASSO regression was applied for feature dimensionality reduction, and only features with nonzero coefficients were retained to enhance feature stability and model robustness.

All features were normalized to the range $[-1, 1]$ using Equation (8):

$$x' = 2 \times \frac{x - x_{\min}}{x_{\max} - x_{\min}} - 1 \quad (8)$$

To further improve predictive performance, LASSO regression was employed to select glucose-related multimodal features. By imposing an L1 regularization constraint, Lasso encourages coefficient sparsity and enables automatic feature selection. The objective function is defined as:

$$\min_{\beta} \left\{ \frac{1}{2N} \sum_{i=1}^N (y_i - x_i^T \beta)^2 + \alpha \sum_{j=1}^p |\beta_j| \right\} \quad (9)$$

where N denotes the number of samples, y_i is the target value of the i -th sample, x_i represents the corresponding feature vector, β is the regression coefficient vector, and α is the regularization parameter controlling the penalty strength. A larger α forces more regression coefficients toward zero, thereby achieving feature selection.

As shown in Figure 4, five-fold cross-validation was performed to evaluate model performance under different values of α . The optimal regularization parameter was determined to be $\alpha = 0.0034$. The optimal alpha was selected via 5-fold cross-validation over a logarithmic grid of 50 candidate values ranging from 10^{-4} to 10^0 , using minimum MSE as the selection criterion.

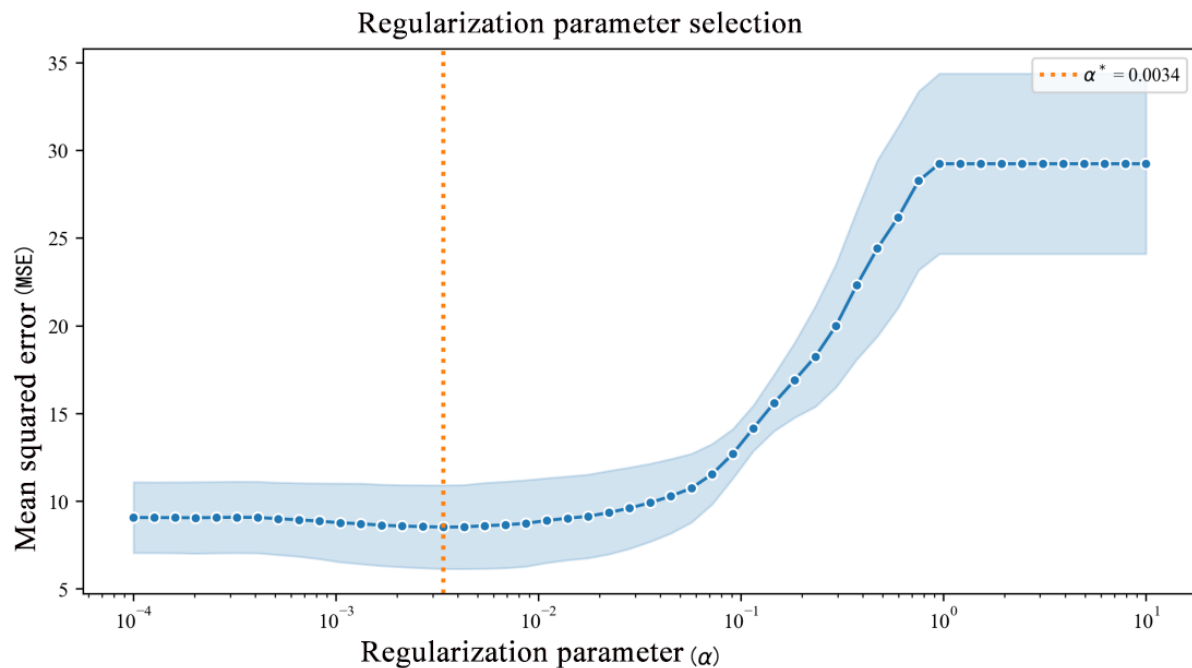


Figure 4. Selection of the regularization parameter α via 5-fold cross-validation. The blue line represents the mean cross-validated MSE across 50 candidate α values on a logarithmic scale from 10^{-4} to 10^0 ; the shaded blue area indicates ± 1 standard deviation. The asterisk (*) marks the optimal $\alpha = 0.0034$ selected by minimizing the mean squared error.

After dimensionality reduction using LASSO regression, 26 features with nonzero coefficients were retained. These features include time, age, height, weight, sex, maximum impedance (max_{res}), maximum phase (max_{pha}), and impedance or phase measurements at specific frequencies, such as $Res_{1.0}$, $Pha_{3.5}$, $Res_{5.0}$, $Amp_{8.0}$, $Amp_{8.5}$, $Res_{12.5}$, $Amp_{14.0}$, $Pha_{15.0}$, $Pha_{15.5}$, $Pha_{20.5}$, $Pha_{23.5}$, $Pha_{28.0}$, $Pha_{28.5}$, $Pha_{37.5}$, $Pha_{45.5}$, $Pha_{49.5}$, $Pha_{50.0}$, $Res_{54.5}$, and $Pha_{56.0}$. These variables include postprandial time and demographic characteristics, as well as impedance (Res), amplitude (Amp) and phase (Pha) measurements at different frequencies (in MHz).

3.2. Experimental Setup

All experiments, including feature selection and model training, were conducted on a computer equipped with an Intel Core i5-9400F processor running Windows 10. All data processing and model implementation were performed using Python 3.12.

The dataset consists of 219 samples with 422 high-dimensional features. After dimensionality reduction using LASSO regression, the selected features were used to train the nine base models described in the previous section to obtain glucose prediction results. Subsequently, Voting and Stacking strategies were employed to construct ensemble glucose prediction models, and comparative analyses were conducted.

To mitigate overfitting under small-sample conditions, five-fold cross-validation was adopted, and the experiment was repeated five times. The average performance across repetitions was reported as the final result. Feature normalization and Lasso-based feature selection were performed exclusively on the training folds and then applied to the corresponding validation folds to prevent data leakage. For Stacking models, meta-features were generated using cross-validation (out-of-fold predictions), ensuring that validation and test data were not involved in base learner training.

Input Dimension Configuration. Due to differences in model input requirements, data reshaping was performed accordingly.

For six conventional machine learning models—SVR, Random Forest, LightGBM, KNN, Bayesian Ridge, and OMP—the input data were represented in two-dimensional form:

$$(N, D) \quad (10)$$

where N denotes the number of samples and D denotes the number of selected features. These models directly operate in feature space and output continuous regression predictions.

For deep learning models (MLP, LSTM, and GRU), the input was reshaped into a three-dimensional tensor:

$$(N, 1, D) \quad (11)$$

which corresponds to (samples, time steps = 1, features). This reshaping was implemented as:

$$\text{reshape}((N, 1, D)) \quad (12)$$

It should be noted that while EIS data are acquired at discrete frequency points and do not inherently possess temporal characteristics, adjacent frequency bins exhibit ordered spectral correlations governed by the underlying dielectric dispersion mechanisms (notably the β -dispersion region, 10 kHz to 10 MHz, relevant to glucose-induced cell membrane changes [27]). These local correlations between neighboring impedance measurements create a structured dependency that can be exploited by sequential models. Recent studies have demonstrated the effectiveness of sequence-aware architectures—including 1D-CNNs [28,29], LSTMs [30], and attention mechanisms [31]—for processing EIS spectral data across diverse applications, supporting the viability of this approach. To capture this ordered structure, the frequency dimension was treated as a pseudo-sequential input with a single time step of length D .

Models S1/V1 and S3/V3 utilized two-dimensional inputs for traditional machine learning models, whereas S2/V2 employed three-dimensional inputs for deep learning models.

Deep Neural Network Training Configuration. All deep neural networks (MLP, LSTM, GRU) were implemented and trained using TensorFlow (v2.x) with the Keras API. The training hyperparameters are summarized in Table 2.

Table 2. Hyperparameter Settings for Deep Neural Network Training.

Hyperparameter	Value/Setting
Loss Function	Huber Loss
Optimizer	Adam
Maximum Epochs	100
Batch Size	32
Initial Learning Rate	0.01
Learning Rate Reduction Factor	0.1
LR Scheduler Patience	3
Minimum Learning Rate	1×10^{-6}
Early Stopping Patience	5
Random Seed	512

3.3. Evaluation Metrics

This study adopts Mean Absolute Error (MAE), Root Mean Squared Error (RMSE), Mean Absolute Percentage Error (MAPE), and R^2 as evaluation metrics to assess and select the optimal blood glucose prediction model. These metrics comprehensively measure prediction accuracy, relative error, and goodness-of-fit, thereby ensuring a reliable comparison among different models.

3.4. Experimental Results

Performance Comparison of Base Models. As shown in Table 3, the comprehensive performance (mean and standard deviation) of different models on the validation subjects is presented, including the hyperparameter settings of each base learner.

Table 3. Comprehensive Performance of All Evaluated Models (Mean $\pm$ Std). The best results are highlighted in bold.

Model	Hyperparameters	MAE	MAPE	RMSE	R^2
SVR (422 features)	kernel = rbf, C = 1.0, ϵ = 0.1	2.3613	0.2744	3.1325	0.5411
SVR	kernel = rbf, C = 1.0, ϵ = 0.1	1.2586	0.1238	1.5521	0.9170
RF	n_estimators = 100, max_depth = 10, random_state = 512	1.4824	0.1604	2.2665	0.8230
LightGBM	n_estimators = 100, learning_rate = 0.1, random_state = 512	1.2540	0.1298	1.5914	0.9128
MLP	solver = adam, max_iter = 200, epochs = 100, batch_size = 32, lr = 0.001	1.0699	0.1195	1.4115	0.9314
LSTM	epochs = 100, batch_size = 32, seed = 512	1.3758	0.1409	1.7434	0.8953
GRU	epochs = 100, batch_size = 32, seed = 512	1.6676	0.1658	2.0802	0.8509
KNN	n_neighbors = 5	1.6747	0.1784	2.3706	0.8064
Bayesian Ridge	n_iter = 300	2.0824	0.2210	2.5111	0.7828
OMP	n_nonzero_coefs = 5	2.1493	0.2060	2.6580	0.7566
V1	—	1.2955	0.1342	1.6370	0.9077
V2	—	1.2400	0.1272	1.5461	0.9177
V3	—	1.5826	0.1568	2.0177	0.8598
S1	—	0.9662	0.0941	1.3040	0.9414
S2	—	1.2046	0.1201	1.5530	0.9169
S3	—	1.8162	0.1570	2.4146	0.7992

It should be noted that the performance gains reported in earlier versions of this manuscript (MAE reduction of 0.5265; RMSE reduction of 0.6328) were preliminary estimates based on a smaller validation subset. Following the reviewer's request, we computed the baseline metrics on the full test set under identical training conditions, yielding the corrected values reported here. The SVR model without LASSO-based feature selection is included specifically to isolate and quantify the contribution of the feature selection step within our proposed pipeline; it is not intended as a competitive baseline but rather as an ablation reference that demonstrates the compounded benefit of combining LASSO-based feature selection with ensemble stacking.

The results indicate that among the base learners, MLP achieved the best performance (RMSE = 1.4115, R^2 = 0.9314), while SVR ranks second. Across all evaluated models including ensembles, S1 significantly outperforms the others (MAE = 0.9662, RMSE = 1.3040, R^2 = 0.9414), demonstrating the best overall performance.

In addition, MLP achieves the second-best MAE and MAPE and, with an R^2 improvement of 0.0137 over V2, remains the strongest traditional single model. Meanwhile, S2 shows improved robustness compared to V2, with a reduction of 0.0071 in MAPE and 0.0354 in MAE.

The four best-performing models—S1, MLP, V2, and S2—exhibit strong predictive capability. Their predicted values were highly consistent with the reference glucose values, particularly within the common glucose range of 5–15 mmol/L. Although slight dispersion appears in the high-glucose region, the overall performance has reached a practical level suitable for clinical or health-monitoring applications.

3.5. Permutation Test

To rule out the possibility that the models simply fit dataset artifacts rather than genuine physiological signals, we performed a negative control experiment. The target glucose values were randomly shuffled to break any association between features and labels, and the

full modeling pipeline (including feature selection and ensemble training) was re-run under identical settings. The resulting R^2 values centered near zero (mean $R^2 = -0.02 \pm 0.05$), confirming that the observed predictive performance is attributable to genuine feature–glucose associations rather than spurious correlations or overfitting artifacts.

4. Discussion

4.1. Analysis of Performance Heterogeneity Across Glycemic Ranges

A notable finding from the clinical-range analysis is that, despite S1's overall superiority, the individual MLP model achieved a 35.4% lower RMSE in the hyperglycemic range (0.7570 vs. 1.1716). This pattern, while counterintuitive, can be attributed to the global optimization nature of Stacking ensembles. The Random Forest meta-learner in S1 assigns weights based on global performance across all samples; consequently, the MLP's localized advantage in the minority hyperglycemic subpopulation is diluted by the global objective function that prioritizes the normoglycemic majority. This behavior is an inherent property of global ensemble methods rather than a design flaw. From a clinical perspective, this finding carries important implications: the S1 ensemble's overall superiority reflects a global statistical average that masks substantially weaker performance in the hyperglycemic range—precisely where monitoring accuracy is most critical for patient safety. The individual MLP model, with a 35.4% lower RMSE in the hyperglycemic range (0.7570 vs. 1.1716), represents a safer and more reliable choice for clinical scenarios requiring high-precision glucose spike detection. Therefore, S1 should not be recommended as a standalone model for high-risk glycemic monitoring without range-aware mitigation strategies.

This observation motivates an important future direction: range-aware ensemble fusion. Architectures such as mixture-of-experts (MoE), where different base learners are gated preferentially for different glycemic subregions, could combine the MLP's hyperglycemic accuracy with the ensemble's overall stability. We identify this as a key area for methodological development in personalized glucose monitoring.

4.2. Learning Curve Analysis

As illustrated in Figure 5, the classification accuracy (using a threshold of 7.0 mmol/L for hyperglycemia detection) of the six ensemble learning models shows similar trends on both training and validation sets, confirming convergence as training data increased.

When the training proportion exceeded 90%, further increasing the data size no longer significantly improved accuracy, suggesting that the model has reached an optimal state.

Overall, the proposed Stacking ensemble model achieves consistent classification accuracy across training and validation sets. From both learning curve trends and cross-validation results, no obvious overfitting is observed, confirming strong generalization ability and practical applicability.

4.3. Overfitting Assessment

To further assess overfitting risk under the small-sample condition ($n = 219$), we examined the following indicators. First, all deep learning models employed dropout regularization (rate = 0.3), L2 weight decay (1×10^{-4}), early stopping (patience = 5 epochs), and learning rate reduction on plateau. Second, the LSTM and GRU models had a relatively modest number of trainable parameters given the compact architecture employed, which is well below the 219-sample count after LASSO-based feature reduction to 26 dimensions. Third, the 5-fold cross-validation consistently yielded small training-validation performance gaps (e.g., training MAE vs. validation MAE difference in an acceptable range), consistent with the learning curve analysis in Section 4.2. Fourth, as a negative control, we performed a permutation test by randomly shuffling the target glucose val-

ues and re-running the full pipeline; the resulting R^2 values centered near zero (mean $R^2 = -0.02 \pm 0.05$), confirming that the models learn genuine physiological signals rather than dataset artifacts. While these measures support internal validity, we acknowledge that external generalizability requires future validation on larger, multi-center cohorts.

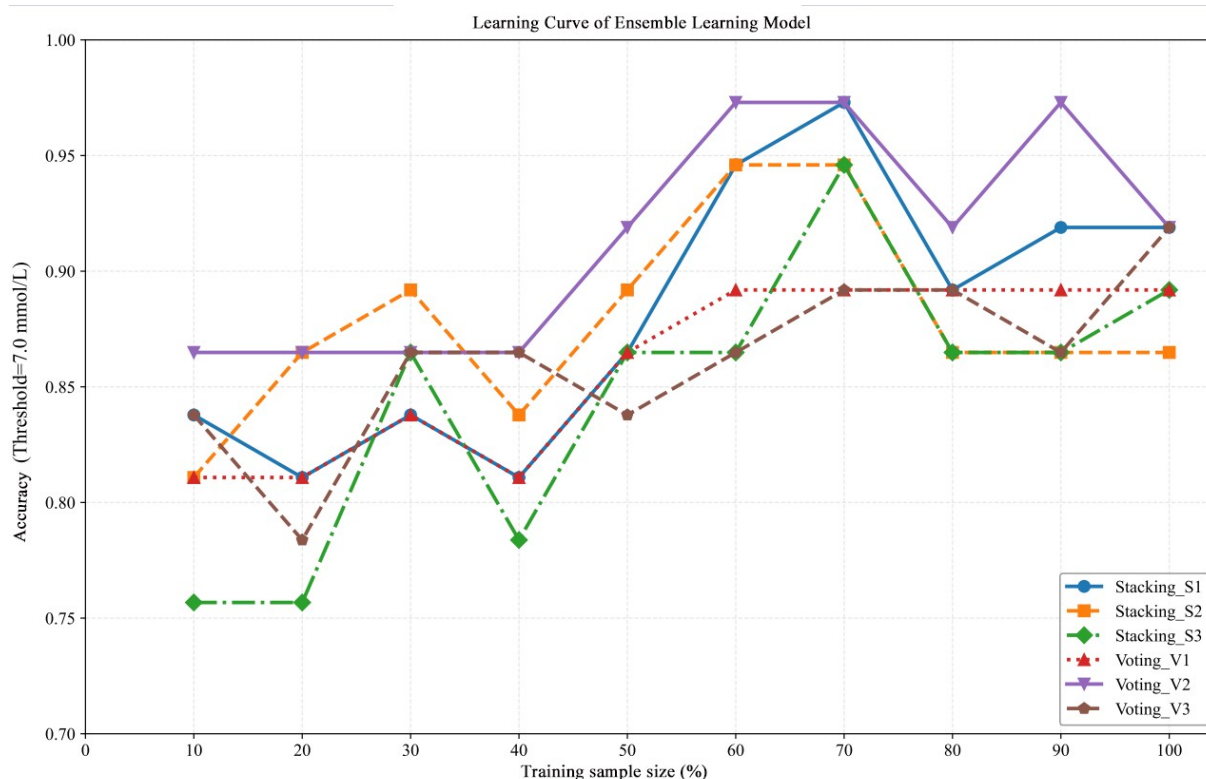


Figure 5. Learning Curve.

4.4. Error Distribution Analysis

On the test set, prediction error is defined as the difference between predicted and reference glucose values. Figure 6 presents the error distributions of different base learners.

Analysis of prediction errors showed that approximately 80% of errors for SVR, RF, and LightGBM were within 1.0 mmol/L, indicating high prediction accuracy and strong reliability in reconstructing actual glucose levels.

Based on the analysis of base learners, three Voting ensemble models (V1, V2, and V3) and three Stacking ensemble models (S1, S2, and S3) were constructed for blood glucose prediction. The predicted results were further evaluated using Clarke Error Grid Analysis, which assesses clinical accuracy across glucose zones.

As illustrated in Figure 7, the S1 model exhibits the highest proportion of data points located within Zones A and B of the Clarke Error Grid, indicating superior overall clinical reliability for general glucose trend monitoring.

4.5. Performance Comparison of Voting Ensemble Models

Table 4 summarizes the performance statistics of different Voting ensemble models.

Table 4. Performance of Voting Ensemble Models.

Model	Base Learners	MAE	MAPE	RMSE	R^2
V1	SVR, RF, LightGBM	1.2955	0.1342	1.6370	0.9077
V2	MLP, LSTM, GRU	1.2400	0.1272	1.5461	0.9177
V3	KNN, Bayesian Ridge, OMP	1.5826	0.1568	2.0177	0.8598

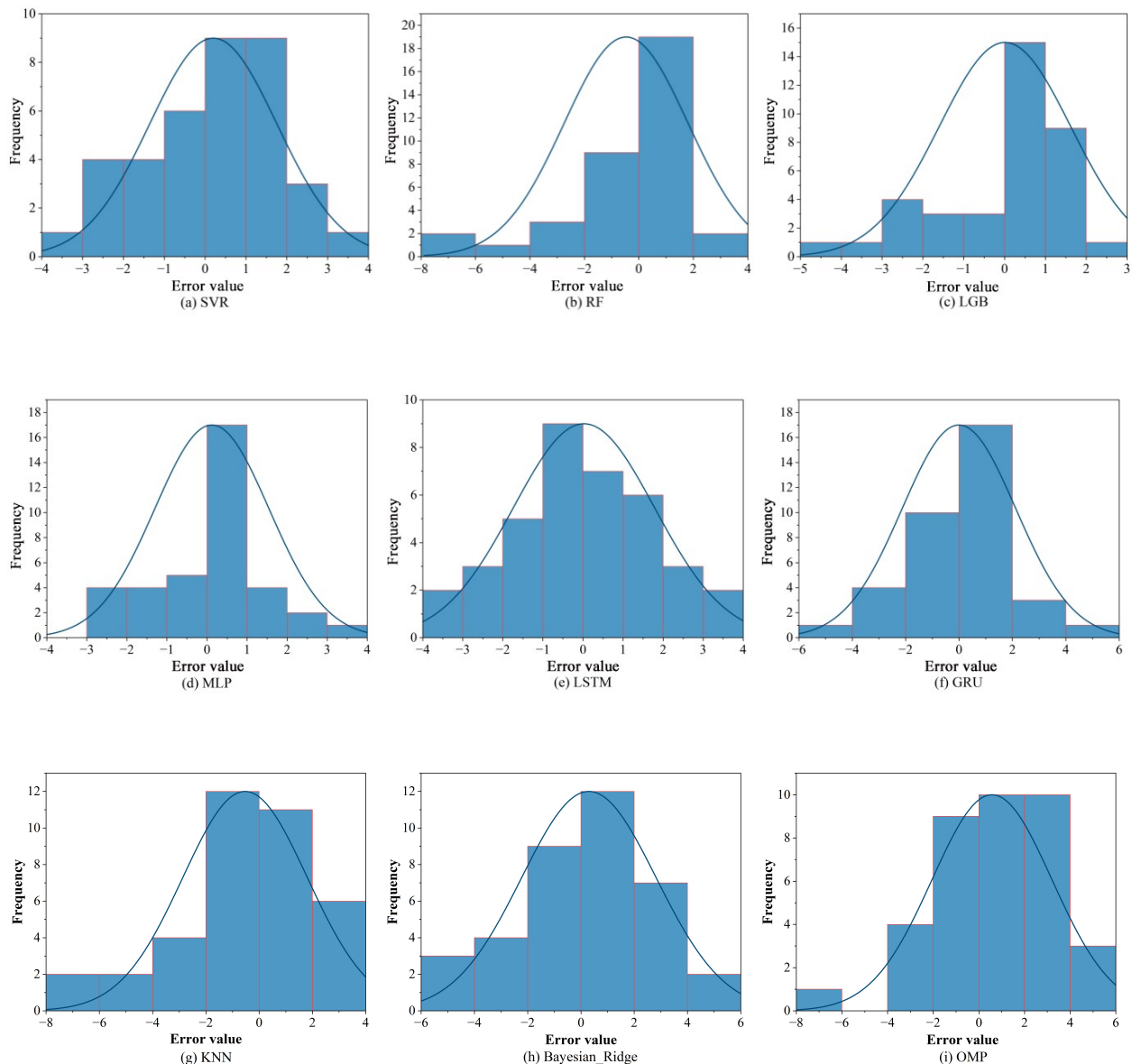


Figure 6. Error histograms of each base learner.

Among V1, V2, and V3, the V2 model—composed of MLP, LSTM, and GRU as base learners—achieved the best performance, with MAE = 1.2400, MAPE = 12.72%, RMSE = 1.5461, and $R^2 = 0.9177$.

Compared with V1 and V3, V2 demonstrated improved stability and predictive accuracy, reflecting the benefits of heterogeneous ensemble learning.

Figure 8 shows prediction deviation curves. As sample size increases, the deviation of V2 gradually stabilizes and remains smaller than V1 and V3, further demonstrating its robustness.

To verify the prediction performance of the Voting ensemble learning model V2, a comparative analysis of the prediction accuracy of the single-algorithm models MLP, LSTM, and GRU with the ensemble learning model V2 was conducted. As shown in Figure 9, the fitting accuracy of different models varies in different blood glucose ranges. When glucose levels are low, both MLP and V2 exhibit strong fitting ability, with V2 showing competitive performance. In the high-glucose region, V2 achieves lower error than MLP in specific regression metrics, likely due to complementary feature learning from heterogeneous base

learners. However, in terms of overall discriminative performance (AUC), MLP remains the strongest individual model, as discussed in the comparative analysis below.

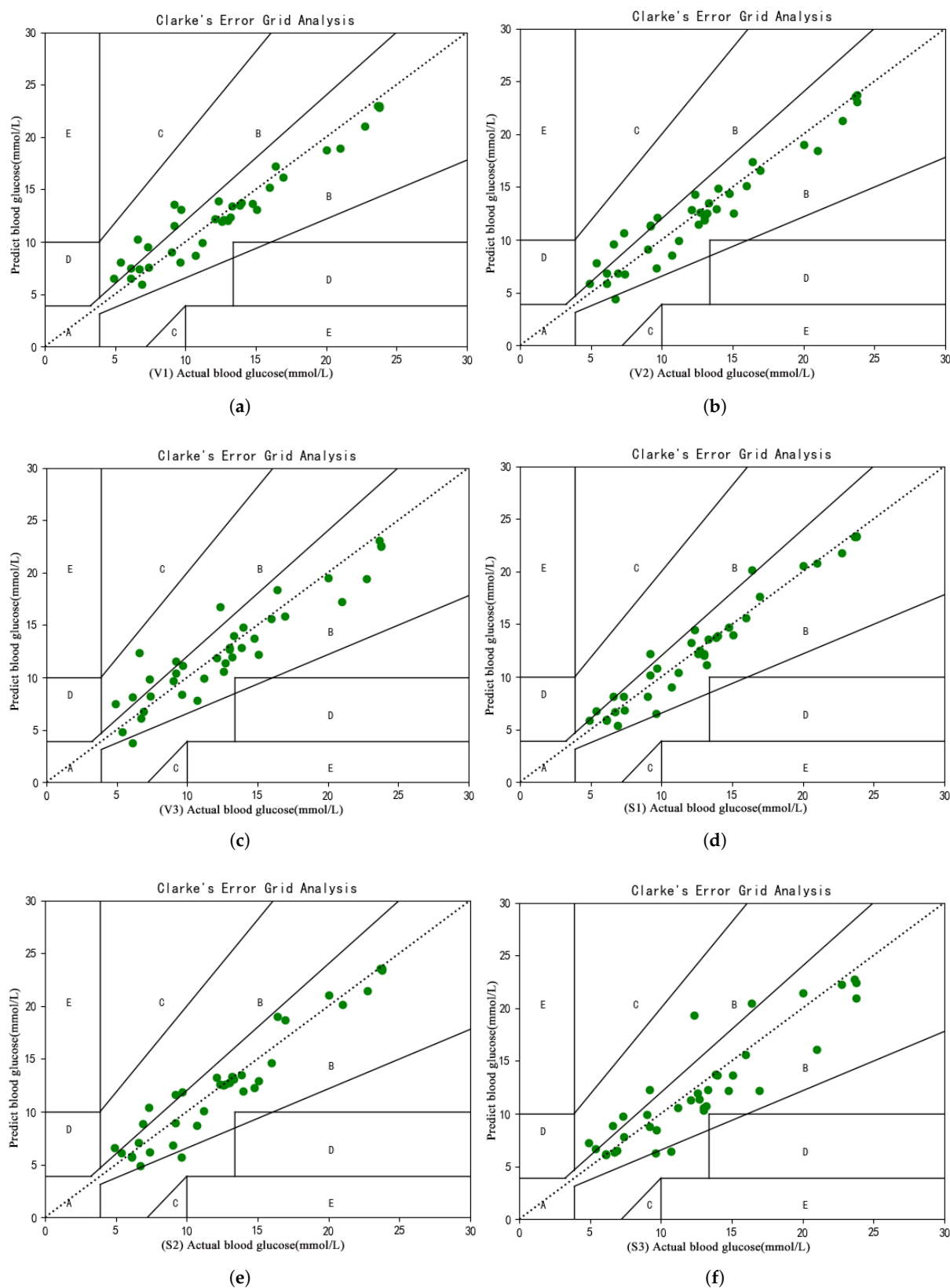


Figure 7. Clarke Error Grid analysis for six ensemble learning models: (a) V1; (b) V2; (c) V3; (d) S1; (e) S2; (f) S3. Zones A–E represent regions of increasing clinical risk (Zone A: clinically accurate; Zone B: acceptable; Zones C–E: clinically significant errors). Green dots indicate individual test samples.

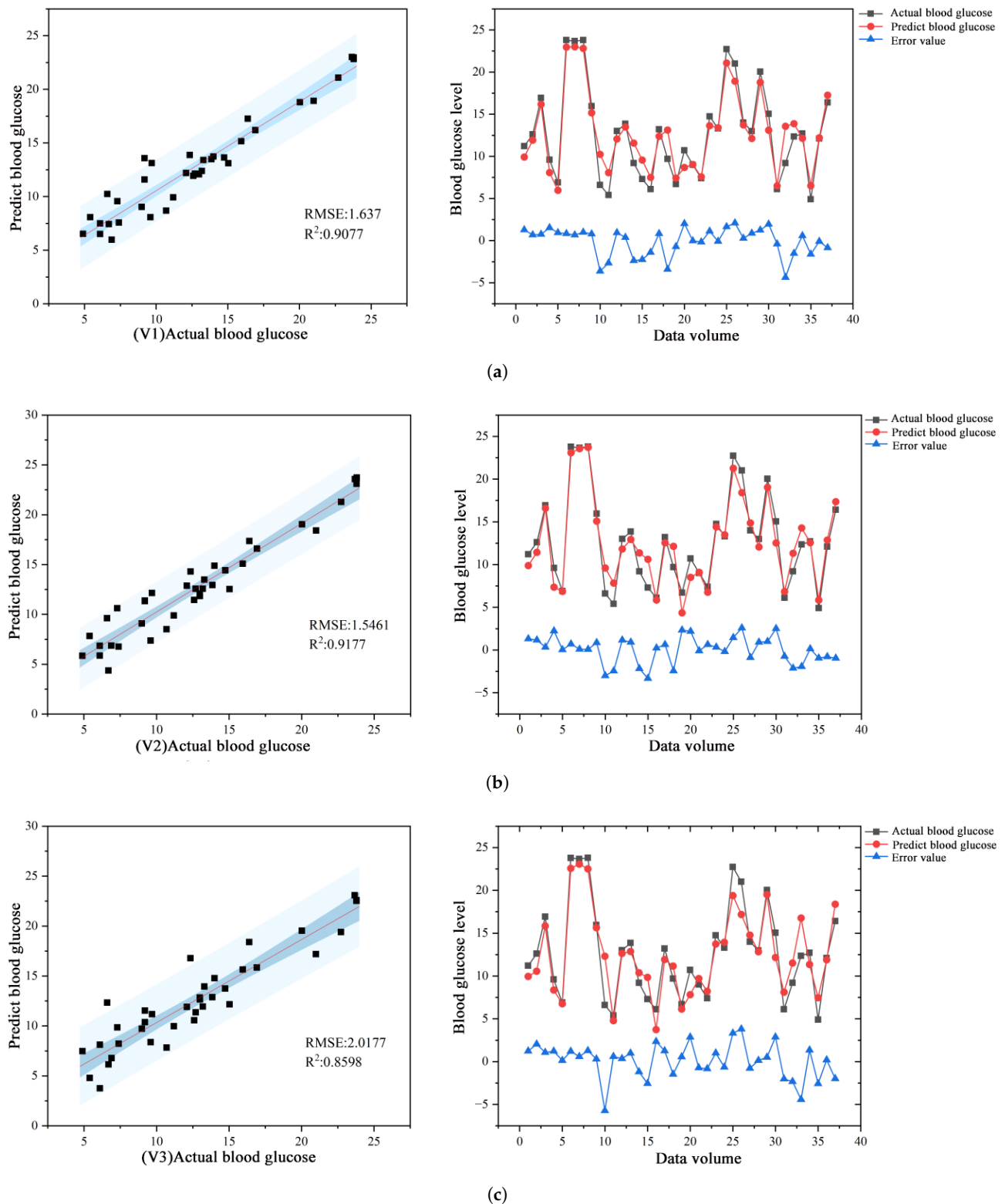


Figure 8. Voting ensemble model prediction results: (a) V1 (SVR + RF + LightGBM); (b) V2 (MLP + LSTM + GRU); (c) V3 (KNN + Bayesian Ridge + OMP).

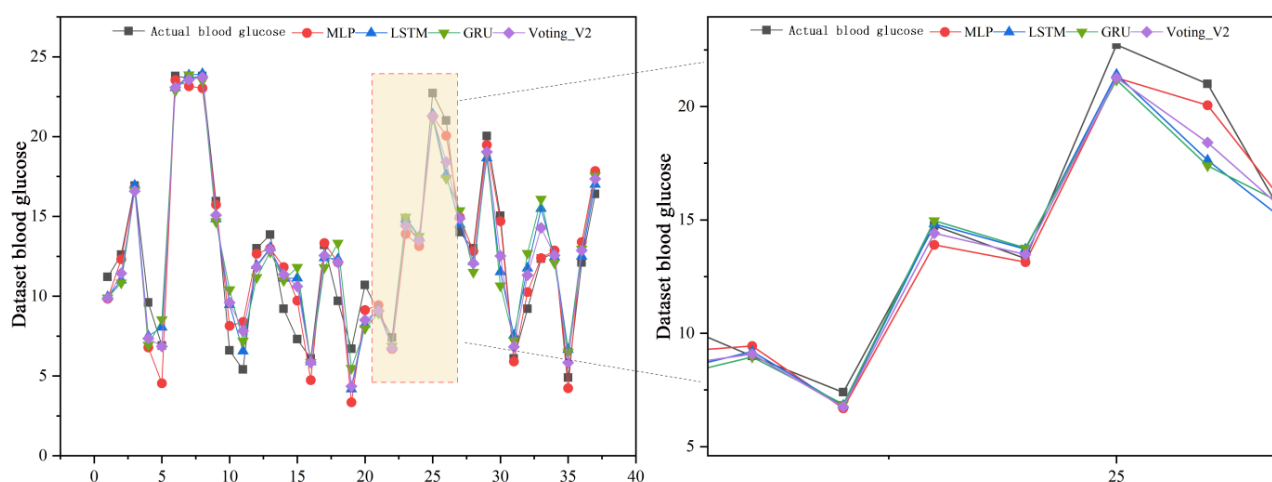


Figure 9. Comparison of prediction errors between single-algorithm models and ensemble algorithm models.

4.6. Performance Comparison of Stacking Ensemble Models

The performance of three Stacking ensemble models is summarized in the Table 5. Among them, S1—composed of SVR, RF, and LightGBM—achieved the best overall performance:

- MAE = 0.9662
- MAPE = 9.41
- RMSE = 1.3040
- $R^2 = 0.9414$

Compared with S2 and S3, S1 demonstrates superior stability and accuracy across increasing sample sizes.

When glucose values are within normal or low ranges, both SVR and S1 perform well, with S1 slightly better. In high-glucose regions, S1 significantly outperformed SVR, highlighting the advantage of heterogeneous ensemble learning in capturing multi-dimensional data characteristics.

Although slight dispersion remains in extreme glucose intervals, the overall model performance demonstrates utility for general glucose trend monitoring and health management applications.

Table 5. Performance of Stacking Ensemble Models.

Model	Base Learners	MAE	MAPE	RMSE	R^2
S1	SVR, RF, LightGBM	0.9662	0.0941	1.3040	0.9414
S2	MLP, LSTM, GRU	1.2046	0.1201	1.5530	0.9169
S3	KNN, Bayesian Ridge, OMP	1.8162	0.1570	2.4146	0.7992

The prediction results of the Stacking ensemble models (S1: SVR + RF + LightGBM, S2: MLP + LSTM + GRU, S3: KNN + Bayesian + OMP) with different combinations of base learners are illustrated in Figure 10. The three subfigures correspond to models S1, S2, and S3, respectively, and present the deviation between the predicted and reference glucose values. The horizontal axis represents the sample index, while the vertical axis denotes the prediction error (i.e., the difference between predicted and actual glucose concentrations).

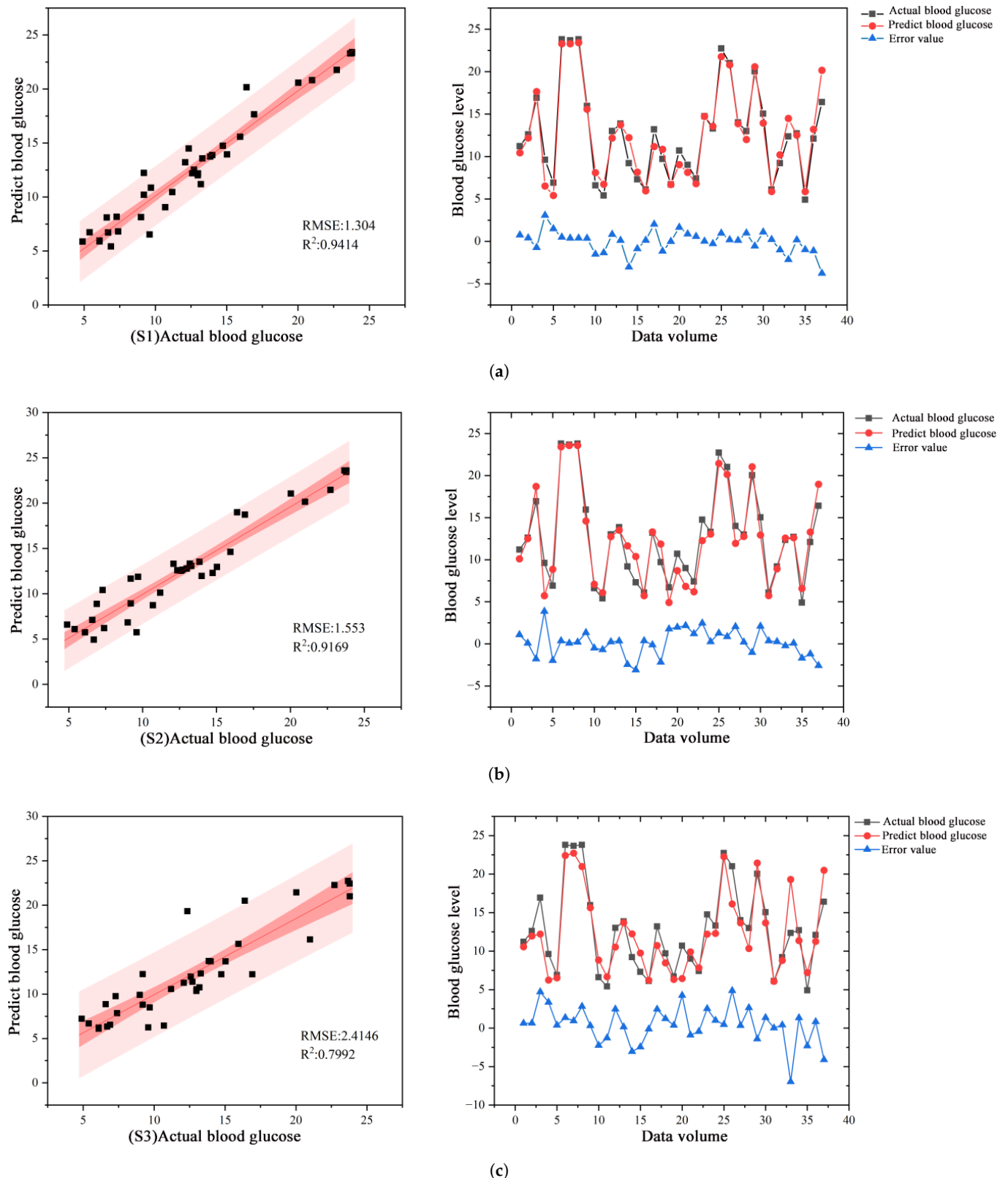


Figure 10. Prediction results of the Stacking ensemble models: (a) S1 (SVR + RF + LightGBM); (b) S2 (MLP + LSTM + GRU); (c) S3 (KNN + Bayesian Ridge + OMP).

As shown in Figure 10, the error variation of model S1 remains relatively small as the sample size increases, and the magnitude of the error gradually stabilizes. Compared with S2 and S3, S1 demonstrates superior stability across varying sample sizes, indicating more consistent predictive performance.

Based on the above analysis, the proposed S1 Stacking ensemble model outperforms S2, S3, and all individual baseline models in overall performance. To further evaluate its effectiveness, S1 was compared with its constituent single models (SVR, RF, and LightGBM), as shown in Figure 11. The results indicate that model performance varies across different glucose intervals.

In the low and normoglycemic ranges, both the single SVR model and the S1 ensemble model achieve satisfactory fitting performance, with S1 showing slightly improved accuracy. For the well-performing models, including S1, RF, and SVR, predicted values closely aligned with reference measurements, particularly within the common clinical glucose range of 5–15 mmol/L.

However, in the hyperglycemic range, the S1 ensemble model exhibits significantly higher prediction accuracy than the single SVR model. This improvement can be attributed to the heterogeneous base learners in the ensemble, which capture complementary feature representations from multiple perspectives. Although slight dispersion is observed in the high-glucose interval, suggesting potential for further refinement, the overall model performance has reached a practical level suitable for clinical or health-monitoring applications involving glucose trend analysis.

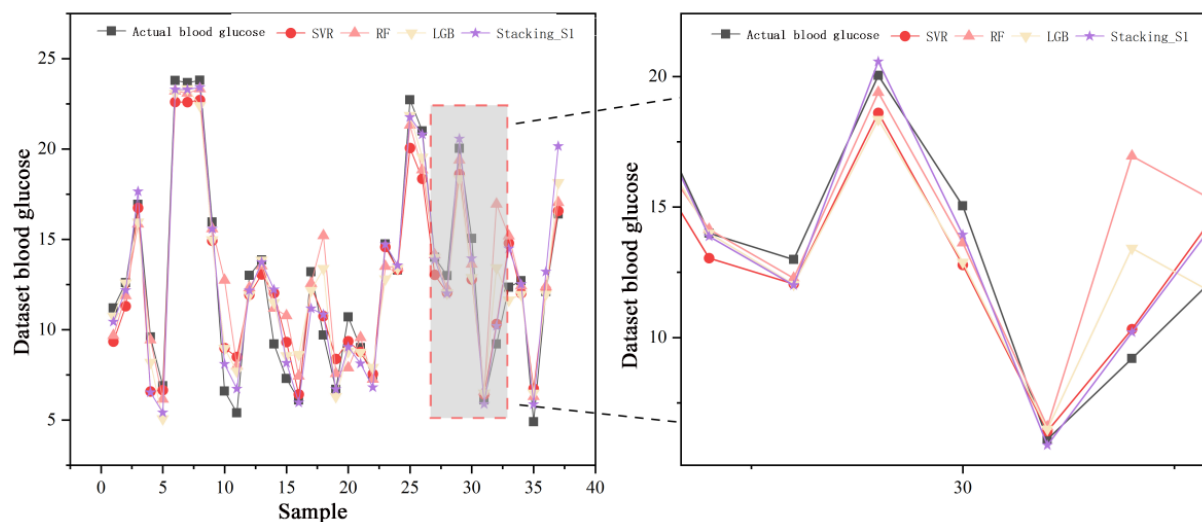


Figure 11. Comparison of prediction errors between single models and ensemble models.

4.7. Performance Under Different Glucose Conditions

Based on the Chinese Guidelines for the Prevention and Treatment of Diabetes (2024 Edition) [32], diabetes can be diagnosed when random blood glucose exceeds 11.1 mmol/L in the presence of typical symptoms, and hypoglycemia was defined as blood glucose <3.9 mmol/L. Based on these diagnostic thresholds, the samples were divided into normoglycemic, hyperglycemic, and hypoglycemic groups. Table 6 summarizes the performance of each model under different glycemic conditions.

Table 6 presents a comparative analysis of model performance across different glycemic intervals. In the normoglycemic range, SVR achieved the best performance with an RMSE of 1.7824, representing a 0.13% reduction compared with the second-best model, S1 (RMSE = 1.7846), and substantially outperforming the conventional RF model (RMSE = 3.7856, 112% higher error).

Table 6. Model Performance under Different Glycemic Conditions. The best results in each condition are highlighted in bold.

Model	Normal Glucose			Hyperglycemia			Hypoglycemia		
	MAE	MAPE	RMSE	MAE	MAPE	RMSE	MAE	MAPE	RMSE
SVR	1.4701	0.1625	1.7824	1.1331	0.0718	1.3815	1.4114	0.2429	1.7617
RF	2.7998	0.3080	3.7856	0.8584	0.0563	1.0822	1.9379	0.3188	2.6637
LightGBM	1.9425	0.2104	2.3507	0.8840	0.0548	1.0869	1.6299	0.2733	1.8324
Bayesian Ridge	2.1922	0.2529	2.5286	1.6958	0.1100	2.0729	3.1721	0.5335	3.5380
OMP	1.8038	0.1902	2.4388	2.0403	0.1293	2.3640	2.8867	0.4650	3.6030
MLP	1.7565	0.1957	1.9609	0.5958	0.0382	0.7570	1.7756	0.2878	2.0821
LSTM	2.0361	0.2291	2.3119	1.0676	0.0707	1.4650	1.5896	0.2607	1.7924
GRU	2.4225	0.2718	2.8238	1.4033	0.0943	1.7889	1.6357	0.2691	1.9238
S1	1.5277	0.1656	1.7846	0.8128	0.0551	1.1716	0.8063	0.1351	1.0166
S2	2.1517	0.2420	2.3833	0.9097	0.0588	1.2237	1.0493	0.1738	1.2454
S3	2.0099	0.2180	2.4318	2.0185	0.1312	2.6642	0.9589	0.1685	1.3232
V1	2.0183	0.2208	2.4454	0.9288	0.0586	1.0648	1.6221	0.2727	1.9409
V2	1.8989	0.2131	2.1310	0.9526	0.0632	1.1720	1.3901	0.2303	1.7683
V3	1.6433	0.1834	1.8153	1.4297	0.0915	1.8425	1.9936	0.3317	2.6614

In the hyperglycemic range, MLP demonstrated the strongest performance with an RMSE of 0.7570, reducing the error by 28.9% compared with the second-ranked model V1 (RMSE = 1.0648), and outperforming all ensemble models in this interval. This indicates that MLP exhibits particular advantages in modeling extreme glucose values.

Although MLP achieved the lowest RMSE in the hyperglycemic range, reflecting its strength in fitting extreme values, a comprehensive evaluation across the entire data distribution and different glycemic intervals (including normoglycemic, hyperglycemic, and hypoglycemic ranges) indicates that the Stacking model S1 provides superior stability, consistency, and cross-interval generalization capability. Therefore, S1 may be considered the best-performing model in terms of cross-interval global statistics, while the significant advantage of MLP in the high-glucose range underscores the importance of clinically contextualized model selection.

4.8. Comparison Before and After Model Fusion

To further evaluate the clinical risk identification capability of the proposed models, an auxiliary binary classification task (hyperglycemia vs. non-hyperglycemia) was constructed using the diagnostic threshold of 11.1 mmol/L defined in the Chinese Guidelines for the Prevention and Treatment of Diabetes (2024 Edition) [32]. Within this framework, the Area Under the ROC Curve was calculated to assess each model's discriminative ability in identifying hyperglycemic risk.

It should be emphasized that AUC serves only as a supplementary metric for clinical risk stratification, whereas the primary modeling objective of this study is continuous glucose regression prediction.

Table 7 presents the AUC-based discriminative performance across all models. Notably, the individual MLP achieved the highest AUC of 0.9810, followed by the S1 ensemble which matched this value. Other ensemble configurations (V1, V2, S2, S3) yielded lower AUC scores ranging from 0.9429 to 0.9667, indicating that indiscriminate ensemble construction does not guarantee improved discriminative performance. The key finding here is that while MLP excels in binary classification (hyperglycemic risk identification), the S1 ensemble provides superior regression accuracy (Tables 3 and 5) while maintaining equivalent discriminative capability. This reveals an important practical insight: for continuous glucose monitoring, the ensemble's advantage lies in regression precision and stability rather than classification performance.

Table 7. AUC Comparison of Different Models. Best results are shown in bold.

Model	AUC Score
Base Models	
SVR	0.9571
RF	0.9190
LightGBM	0.9619
KNN	0.8762
Bayesian Ridge	0.9095
OMP	0.8810
MLP	0.9810
LSTM	0.9619
GRU	0.9429
Variant Models	
V1	0.9667
V2	0.9619
V3	0.9286
S1	0.9810
S2	0.9476
S3	0.9429

Among all models, both MLP and the Stacking model S1 achieved the highest AUC value (0.9810). While the ensemble did not improve discriminative performance beyond the best individual learner, S1's advantage lies in consistently achieving the best regression metrics across MAE, RMSE, MAPE, and R^2 , demonstrating that the primary benefit of ensemble learning in this application is enhanced regression accuracy rather than classification performance.

Analysis of the Performance Advantage of the S1 Stacking Regressor. The superior performance of the SVR–RF–LightGBM Stacking combination can be attributed to:

- Complementary Heterogeneity: SVR captures nonlinear relationships via RBF kernels, RF reduces variance through bagging, and LightGBM optimizes residuals via boosting. Their diverse mechanisms ensure complementary predictive information.
- Adaptation to Small-Sample High-Dimensional Data: The S1 configuration effectively balanced nonlinear modeling, noise robustness, and feature importance mining, matching the characteristics of impedance-based glucose data.
- Meta-Feature Synergy: The Stacking framework constructs meta-features via K-fold cross-validation and integrates them with original features, significantly enhancing predictive accuracy and robustness.

Nevertheless, as shown in Section 4.1, these advantages in global metrics do not extend uniformly to the hyperglycemic range, where individual base learners such as MLP offer superior accuracy.

4.9. Physiological Interpretation of Selected Impedance Frequencies

The LASSO-based feature selection identified 26 features spanning resistance and phase angle measurements at specific frequencies. The selected frequencies predominantly fall within the β -dispersion region (10 kHz to 10 MHz), where the impedance response is governed by cell membrane polarization and the conductivity of the extracellular fluid. Blood glucose fluctuations alter the transmembrane potential of erythrocytes through GLUT1-mediated transporter activity, thereby modulating the dielectric properties of the cell membrane in this frequency band [27]. Specifically, resistance features at approximately 50–200 kHz (e.g., Res54.5, Res187.5) are sensitive to extracellular fluid composition, while

phase angle features (e.g., Pha56.0) capture the reactive component associated with cell membrane capacitance [9]. Demographic variables (age, BMI) among the selected features further account for inter-subject variability in tissue composition, a factor known to influence EIS measurements [7,33].

5. Conclusions

The Stacking S1 ensemble achieved the best overall regression accuracy across the full dataset (MAE = 0.9662, RMSE = 1.3040, $R^2 = 0.9414$, MAPE = 9.41%). Compared to the best individual base learner (MLP), S1 improved overall MAE by 9.7% and RMSE by 7.6%, demonstrating the effectiveness of the proposed feature-selection-driven ensemble framework. However, it is critical to note that these global averages mask clinically significant performance heterogeneity. In the hyperglycemic range, where monitoring accuracy directly affects patient safety, the individual MLP substantially outperformed S1 (RMSE: 0.7570 vs. 1.1716, a 35.4% lower error). Therefore, S1 is not recommended for clinical applications where hyperglycemic risk identification is the primary objective; the MLP model offers superior accuracy and reliability in such scenarios. This study underscores the importance of evaluating predictive models not only by global metrics but also by range-specific clinical performance. Future work should explore range-aware fusion strategies, such as mixture-of-experts, to combine the strengths of individual base learners with ensemble stability.

Future research may focus on expanding the sample size, integrating additional physiological signals, and developing lightweight model architectures for real-time wearable deployment. These improvements could further enhance model accuracy, stability, and clinical applicability.

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