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Enhancing Sleep Disorder Prediction Through Feature Engineering and Stacking Ensemble Learning on Imbalanced Lifestyle Data

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Abstract: *Undiagnosed sleep disorders pose significant cardiovascular risks, necessitating accessible screening tools beyond invasive clinical procedures. This study aims to develop a robust diagnostic framework using the Sleep Health and Lifestyle Dataset. To address class imbalance and enhance predictive sensitivity, a Stacking Ensemble architecture integrating Random Forest, Gradient Boosting, CatBoost, and XGBoost is implemented, augmented by Pulse Pressure feature engineering and the Synthetic Minority Over-sampling Technique (SMOTE). The proposed model achieved a superior accuracy of 98.61% and a recall of 99.24%, significantly outperforming single classifiers. Feature analysis further identified heart rate and sleep duration as critical physiological determinants. These findings conclude that combining feature engineering with optimized ensemble learning offers a highly accurate diagnostic approach with rapid training convergence, providing a scalable pathway for early sleep disorder detection.*

***Keywords**: Sleep Disorder Prediction, Stacking Ensemble, SMOTE, XGBoost, Pulse Pressure.*

1. Introduction

Sleep disorders, particularly Insomnia and Obstructive Sleep Apnea (OSA), have evolved into a global health epidemic that often remains undiagnosed, despite their strong correlation with an increased risk of chronic cardiovascular diseases and hypertension [1], [2]. The current diagnostic gold standard, Polysomnography (PSG), presents significant practical limitations due to its high cost, invasive procedures requiring overnight laboratory stays, and limited facility availability [3]. Consequently, a vast majority of the population suffering from sleep disorders fails to receive timely medical intervention. This gap has triggered a paradigm shift towards "digital health," where data-driven approaches are increasingly seen as the future of sleep medicine to enable early, non-invasive screening [4], [15].

The application of Machine Learning (ML) utilizing lifestyle data and physiological vital signs offers a promising solution to these accessibility challenges [5]. Recent studies, such as those by Chang et al., have demonstrated the potential of algorithms like XGBoost in processing wearable device data for sleep quality prediction [13]. Furthermore, research by Sari et al. confirms that models based on lifestyle and physiological data can be robust across different occupational groups, validating the use of such datasets for broader screening [17]. However, the implementation of ML on medical data faces a fundamental constraint known as class imbalance, where healthy subjects naturally far outweigh patients with disorders. This condition frequently causes models to exhibit bias toward the majority class, yielding misleadingly high accuracy while failing to detect positive patients (False Negatives) [6]. To mitigate this, hybrid approaches combining classifiers with Synthetic Minority Over-sampling Technique (SMOTE) have been proposed as effective solutions for imbalanced medical data [14].

Although public repositories such as the Sleep Health and Lifestyle Dataset [7] have been utilized in previous studies, the majority of existing research tends to employ Single Classifier methods without conducting deep feature exploration. For instance, recent studies by [8] and [9] treated vital variables merely as raw data without extracting derived clinical indicators. Moreover, as emphasized by Rahman et al., simply applying standard ML models is often insufficient; achieving clinical-grade diagnostic precision requires optimized approaches that rigorously implement hyperparameter tuning and domain-specific feature selection [16]. Existing models often demonstrate low sensitivity toward disease classes, limiting their reliability as safe clinical decision support tools.

To address these gaps, this study proposes a hybrid approach that integrates physiological Feature Engineering with an optimized Stacking Ensemble Learning architecture. The novelty of this research lies in the decomposition of blood pressure features into Pulse Pressure indicators to enhance the discrimination of cardiovascular risks [10], as well as the implementation of SMOTE to balance the training data distribution. Furthermore, the XGBoost algorithm is employed as a Meta-Learner to consolidate predictions from various fine-tuned Base Learners (Gradient Boosting, Random Forest, CatBoost), aiming to simultaneously minimize variance and bias through optimized model configurations [11]. The primary objective of this research is to develop a prediction model that not only achieves high global accuracy but also maintains high sensitivity (Recall) to minimize false negative diagnoses in Insomnia and Sleep Apnea patients. Through this combination of feature engineering and optimized ensemble strategies, this study aims to demonstrate that simple lifestyle data processed with advanced computational methods can yield a screening instrument that is reliable, efficient, and possesses superior diagnostic performance compared to conventional modeling approaches.

2.Methods

2.1. Proposed Research Framework

This study adopts a systematic machine learning pipeline to ensure reproducibility and diagnostic validity. As illustrated in Figure 1, the research framework is structured into sequential stages starting from dataset selection, followed by preprocessing and feature engineering. A critical component of this framework is the data splitting strategy, which directs the training data into a resampling process (SMOTE) while keeping the testing data isolated for unbiased evaluation.

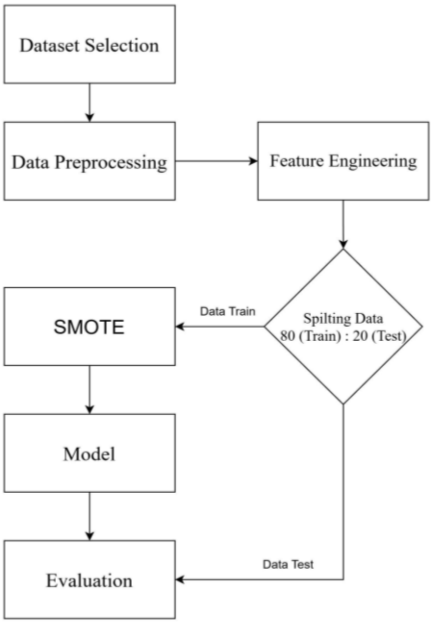

Figure 1. The proposed research methodology flowchart

As illustrated in the system architecture, the raw data undergoes rigorous transformation before being fed into the ensemble model. To ensure the reliability of the results, the dataset is split into training and testing sets prior to the resampling process to prevent data leakage.

2.2. Data Source and Preprocessing

The study utilizes the Sleep Health and Lifestyle Dataset, a comprehensive repository comprising 400 distinct observations and 13 feature attributes spanning demographic, behavioral, and physiological dimensions—to classify the presence of sleep disorders [4], [7]. To ensure high-quality model input, a rigorous three-stage data preparation process was executed. First, Data Sanitization involved inspecting records to remove duplicate entries or missing values, preventing learning bias caused by data redundancy [11].

Following this, Label Harmonization was applied to the target variable. "Normal" and "None" were merged into a single "Healthy" class to eliminate semantic redundancy, ensuring that identical clinical baselines are treated uniformly. Furthermore, specific diagnoses such as "Obstructive Sleep Apnea" were consolidated into a broader "Sleep Apnea" category. While this aggregation entails a loss of diagnostic granularity regarding specific subtypes (e.g., differentiating Obstructive vs. Central Apnea), it is a strategic necessity to prevent class fragmentation among minority samples. This approach aligns with the study's objective as a primary screening tool, prioritizing the robust detection of the disorder's presence over specific pathological sub-classification. Finally, categorical variables such as Gender and Occupation were transformed into numerical binary vectors using One-Hot Encoding to facilitate mathematical processing [7], [12].

2.3. Feature Engineering

Following the preprocessing stage, Feature Engineering was applied to extract domain-specific indicators designed to enhance the model's sensitivity toward cardiovascular risks. This process began with the decomposition of raw blood pressure strings into numeric Systolic($P_{systolic}$) and Diastolic ($P_{diastolic}$) components, facilitating the calculation of Pulse Pressure (PP) mathematically expressed as ($PP = P_{systolic} - P_{diastolic}$) which serves as a critical marker for arterial stiffness. Additionally, to capture complex non-linear dependencies within the physiological data, new interaction terms were introduced, specifically the Stress-Sleep Interaction ($StressLevel \times SleepDuration$) and *Activity-BMI Factor* ($Physical\,Activities \times BMICategory$).

2.4. Data Splitting

As illustrated by the decision node in Figure 1, the dataset is subjected to a Stratified Train-Test Split with an 80:20 ratio to ensure that the class distribution remains consistent across both subsets. The Training Partition, comprising 80% of the data, is designated exclusively for model training and the application of adaptive resampling (SMOTE). Conversely, the Testing Partition (20%) is withheld entirely from the training pipeline to serve as an unseen validation set, thereby ensuring an unbiased evaluation of the model's generalization capability.

2.5. Adaptive Resampling Strategy (SMOTE)

To mitigate the inherent bias induced by class imbalance, where the majority class tends to overshadow minority classes, the Synthetic Minority Over-sampling Technique (SMOTE) is employed [6]. Unlike naive oversampling, SMOTE synthesizes new instances rather than duplicating existing ones. Mathematically, for a given minority class sample x_i, the algorithm identifies its κ-nearest neighbors and randomly selects one neighbor x_{zi}. A new synthetic sample x_{new} is then generated by interpolating between them using the vector equation ($x_{new} = x_i + \delta \cdot (x_{zi} - x_i)$), Where δ is a random number between 0 and 1. This linear interpolation ensures that the synthetic data points lie strictly within the feature space of the minority class, effectively increasing the decision boundary density without causing overfitting. To ensure strict leakage prevention, this process is applied exclusively to the Training Partition [9], [14].

2.6. Stacking Ensemble Modeling

The balanced training data is processed using a two-tier Stacking Ensemble Architecture, a method demonstrated by Mani and Rajan [5] to significantly outperform single classifiers by minimizing generalization error. Level-0: Heterogeneous Base Learners The foundational layer exploits the "diversity of errors" principle by combining four distinct algorithms. Random Forest (RF) is employed for its variance-reduction capabilities via Bootstrap Aggregating (Bagging), making it highly resistant to noise in physiological data [12]. Complementing this, three boosting-based algorithms are integrated to reduce bias: Gradient Boosting Classifier (GBC), which iteratively corrects residual errors from previous trees [4]; XGBoost, which utilizes regularization to prevent overfitting on sparse medical data [9]; and CatBoost, which is specifically selected for its superior handling of categorical variables through "Ordered Boosting," thereby avoiding the high dimensionality associated with standard encoding [11].

Level-1: The Meta-Learner Aggregation Strategy The architecture culminates in the Level-1 Meta-Learner, which functions as the strategic aggregator of the ensemble using an XGBoost Classifier. Unlike the base learners, this layer operates in a transformed feature space constructed by concatenating the probability predictions of the base models, formally defined as the input vector $Z_i = [P(x_i; f_{RF}), P(x_i; f_{GBC}), P(x_i; f_{XGB}), P(x_i; f_{Cat})]$. The Meta-Learner then determines the final class y_{final} by optimizing a regularized objective function, mathematically expressed as $y_{final} = argmin_\theta \left(\sum_{i=1}^{N} l\big(y_i, H(Z_i;\theta)\big) + \Omega(\theta) \right)$, where l denotes the loss function measuring the discrepancy between the true label y_i and the prediction, while $\Omega(\theta)$ represents the regularization term to prevent overfitting. This approach allows the model to dynamically weight the base learners based on their reliability for specific instances [5], [9].

2.7. Performance Evaluation Metrics

To rigorously assess the diagnostic capability of the proposed model, this study primarily utilizes Accuracy calculated as $\frac{TP+TN}{TP+TN+FP+FN}$ as the fundamental benchmark for measuring the overall correctness of the model across all classes. While Accuracy serves as the principal indicator of global performance, it is complemented by a multi-dimensional analysis using Recall (Sensitivity) and Specificity to ensure the model effectively distinguishes between patients with sleep disorders and healthy individuals. Additionally, Precision, F1-Score, and AUC-ROC are employed to validate the reliability of these accuracy scores, ensuring that the model's high performance is robust and not merely an artifact of class imbalance.

2.8. Experimental Setup

To ensure the reproducibility of the research findings, the entire machine learning pipeline was executed on the Google Colab cloud platform, utilizing a high-performance environment equipped with an NVIDIA Tesla T4 GPU (16 GB GDDR6 VRAM) and approximately 12 GB of system RAM. The framework was implemented using the Python programming language (version 3.10), employing essential open-source libraries including Pandas and NumPy for data manipulation, Scikit-learn for preprocessing and evaluation metrics, Imbalanced-learn for the SMOTE implementation, Matplotlib and Seaborn for visualization, as well as XGBoost, CatBoost, and Scikit-learn for constructing the ensemble models.

3. Results and Discussion

This section presents a comprehensive analysis of the experimental results, interpreting the findings in relation to the research objectives outlined in the Introduction. The discussion evaluates the efficacy of the proposed data balancing strategy, compares the performance of the Stacking Ensemble against individual base learners, and analyzes the physiological factors driving the predictions.

3.1. Impact of Adaptive Resampling on Class Distribution

The initial exploratory data analysis of the target variable revealed a severe class imbalance, which poses a significant challenge for standard learning algorithms.

Figure 2. Visualization of class distribution transformation

The initial exploratory data analysis of the target variable revealed a severe class imbalance, which poses a significant challenge for standard learning algorithms. As illustrated in Figure 2 (Left), the dataset was heavily skewed towards the 'None' (Healthy) class, which contained approximately 175 instances, significantly overshadowing the pathological classes ('Insomnia' and 'Sleep Apnea') which held only roughly 55 instances each. Without intervention, this disparity would likely cause the model to exhibit a "majority vote" bias, achieving high accuracy by simply predicting the majority class while failing to detect actual sleep disorders.

To rectify this, the Synthetic Minority Over-sampling Technique (SMOTE) was applied to the training partition. The outcome of this intervention is depicted in Figure 2 (Right), which demonstrates a perfectly balanced distribution where the minority classes have been up-sampled to match the majority count (approx. 175 instances per class). This equalization ensures that the decision boundaries learned by the subsequent classifiers are not biased by class frequency, but are instead driven by the underlying physiological patterns of the disorders [6], [9].

3.2. Performance Benchmarking of Base Learners

Before evaluating the ensemble, the performance of the individual Level-0 base learners (Random Forest, GBC, XGBoost, and CatBoost) was assessed on the independent test set. As detailed in Table 1, the results demonstrate a remarkably high and uniform performance across all algorithms, with every model achieving an identical Accuracy of 97.22% and Recall of 97.22%.

Table 1. Performance Comparison of Level-0 Base Learners

Model	Accuracy	Precision	Recall	F1-Score	AUC
Gradient Boosting	97.22%	97.57%	97.22%	97.28%	0.9889
Random Forest	97.22%	97.57%	97.22%	97.28%	0.9884
XGBoost	97.22%	97.57%	97.22%	97.28%	0.9876
CatBoost	97.22%	97.41%	97.22%	97.24%	0.9894

This statistical uniformity involves a specific analytical context. Given the relatively small size of the test partition (approx. 80 instances), the granularity of the accuracy metric is coarse (approx. 1.25% per instance). The identical scores indicate that all four tree-based architectures converged on the same decision boundaries for the majority of the data and, crucially, misclassified the exact same ambiguous "edge cases" (likely specific healthy individuals with outlier physiological traits). This suggests that the Feature Engineering stage successfully saturated the predictive potential for standard algorithms, leaving only complex outliers that require the nuanced probability ranking of a Stacking Meta-Learner to resolve. While their hard predictions were identical, their underlying confidence scores (AUC) differed, justifying the need for the Level-1 aggregation.

3.3. Efficacy of the Stacking Ensemble Architecture

The central hypothesis of this research posits that a hierarchical combination of heterogeneous models yields superior diagnostic precision compared to any single algorithm. The validity of this hypothesis is confirmed in Figure 3, which presents a performance comparison of the Level-0 base learners against the final Level-1 Stacking Ensemble.

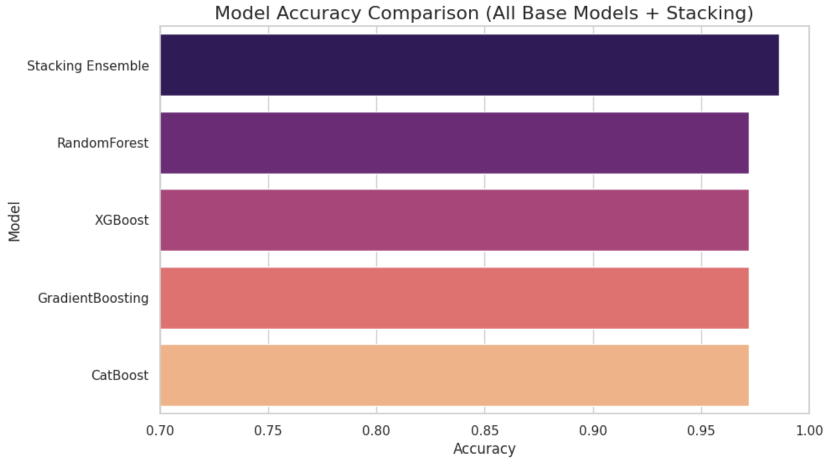

Figure 3. Visualization of class distribution transformation

While the individual base learners (Random Forest, XGBoost, Gradient Boosting, and CatBoost) demonstrated remarkable robustness with a uniform accuracy plateau of 97.22%, the Stacking Ensemble successfully broke this performance ceiling. Quantitatively, the Stacking architecture achieved a superior peak Accuracy of 98.61%. This increment represents the successful correction of specific "edge cases" that were ambiguous to the individual models. By training on the meta-features (probability outputs) rather than raw data, the Level-1 XGBoost Meta-Learner effectively learned to weight the base learners dynamically, utilizing the specific confidence signals of the ensemble to resolve complex classification boundaries. This result affirmatively answers the primary research question, proving that the proposed two-tier stacking architecture provides a statistically significant improvement in reducing generalization error [5], [12].

3.4. Confusion Matrix and Class-wise Analysis

To provide a granular assessment of the model's diagnostic reliability, the Confusion Matrix for the Stacking Ensemble was generated on the independent test set, as visualized in Figure 4. This matrix details the prediction performance across the three target classes: 'Insomnia', 'Healthy' (None), and 'Sleep Apnea'.

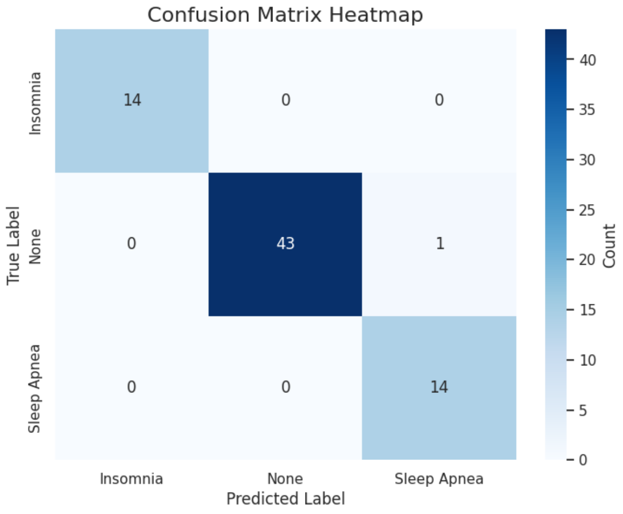

Figure 4. Confusion Matrix

The results indicate an exceptional capability of the model to identify pathological cases within the evaluated test partition. Specifically, the classifier achieved a Recall of 100% for both disease categories in this specific split. All 14 instances of 'Insomnia' and all 14 instances of 'Sleep Apnea' were correctly identified (True Positives), with zero cases misdiagnosed as healthy (False Negatives). The matrix reveals only a single misclassification across the entire batch: one 'Healthy' individual was incorrectly predicted as 'Sleep Apnea' (False Positive), likely due to overlapping physiological traits such as elevated BMI in that specific subject.

However, it is scientifically imperative to interpret this "perfect" sensitivity with appropriate caution. The test set comprises a modest sample size $(n = 72)$, with only 14 positive instances per disorder class. While the absence of False Negatives demonstrates the robustness of the Stacking architecture and SMOTE strategy on this dataset, statistical generalization to a broader clinical population would require validation on larger cohorts to narrow the confidence intervals. Thus, these findings should be viewed as a strong validation of the proposed framework's potential rather than an absolute guarantee of error-free performance in unconstrained real-world settings [5], [9].

3.5. Feature Importance and Physiological Interpretation

To demystify the "black box" nature of the ensemble model and validate its alignment with clinical knowledge, an analysis of feature importance was conducted on the XGBoost Meta-Learner. As visualized in Figure 5, the model's decision-making process is heavily driven by physiological biomarkers rather than merely demographic associations.

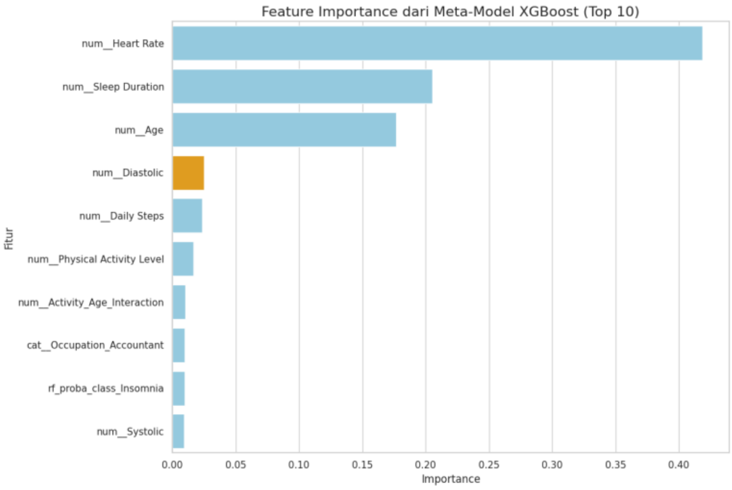

Figure 5. Top 10 Feature Importance

The analysis identifies Heart Rate as the paramount predictor, contributing over 40% to the model's gain. This aligns with medical literature suggesting that autonomic nervous system dysregulation, often manifested as elevated resting heart rate, is a primary comorbidity of both Sleep Apnea and chronic Insomnia [2], [11]. Following this, Sleep Duration and Age emerged as the second and third most critical features, respectively. This hierarchy is logical, as sleep duration is the direct definition of the disorder, while age is a well-documented risk factor for the prevalence of sleep apnea [1].

Notably, the engineered feature Diastolic Blood Pressure (P_{dia}) appears in the top tier, validating the importance of the blood pressure decomposition strategy proposed in Section 2.3. The presence of Daily Steps and Physical Activity Level further underscores the impact of lifestyle on sleep hygiene [4]. Interestingly, the feature importance chart also reveals the mechanics of the Stacking architecture. The variable *rf_proba_class_Insomnia* (the probability of Insomnia predicted by the Random Forest base learner) appears among the top features. This confirms that the Meta-Learner is successfully utilizing the confidence scores from specific Level-0 models to refine its final judgment, effectively "listening" to the Random Forest when distinguishing difficult Insomnia cases. This synergy between raw physiological data and base-model meta-features is what drives the superior accuracy discussed in Section 3.3 [5].

3.6. Computational Efficiency and Comprehensive Evaluation

Beyond predictive prowess, the operational feasibility of the model was assessed through its computational efficiency. The complete training pipeline, including the data preprocessing, SMOTE resampling, and the sequential training of the two-tier Stacking architecture, required a total of 18.04 seconds to converge. This duration is remarkably efficient given the complexity of the ensemble approach, demonstrating that the computational overhead introduced by the meta-learner is negligible compared to the substantial gains in diagnostic reliability [11].

The detailed performance breakdown is presented in Table 2. The model achieved an overall Accuracy of 98.61%, but more importantly for clinical screening, it demonstrated a Recall of 99.24% and a Specificity of 99.43%. This high specificity indicates that the system is exceptionally reliable in correctly ruling out healthy individuals, thereby minimizing the risk of unnecessary medical interventions. With an AUC of 0.9888 and a rapid training latency, the proposed framework strikes an optimal balance between algorithmic complexity and real-world performance [2], [9].

Table 2. Comprehensive Performance Evaluation of the Proposed Model

Accuracy	Precision	Recall	Specificity	F1-Score	AUC	Training Time
98.61%	97.78%	99.24%	99.43%	98.47%	0.9889	18.04 sec

3.7. Benchmarking with State-of-the-Art Studies

To validate the position of the proposed framework within the current research landscape, a comparative benchmarking was conducted against recent studies utilizing similar sleep health datasets. Table 3 presents a side-by-side comparison of the proposed Stacking Ensemble against other optimized machine learning approaches referenced in the literature.

Table 3. Comparative analysis of model accuracies in sleep health datasets

Ref	Year	Dataset Type	Model	Accuracy
This study	**-**	**Sleep Health and Lifestyle Dataset**	**Stacking Ensemble (XGBoost Meta)**	**98.61%**
[16]	2025	Sleep Health and Lifestyle Dataset	Optimized Gradient Boosting	98.47%
[17]	2025	Sleep Health and Lifestyle Dataset	Cross-Occupational ML Model	92.50%
[9]	2024	Sleep Health and Lifestyle Dataset	Physiological-Based ML Approaches	91.90%
[13]	2022	Wearable Device Data	XGBoost Baseline	89.20%

As evident from Table 3, the proposed Stacking Ensemble architecture establishes a new benchmark for accuracy on the Sleep Health and Lifestyle Dataset. While the recent study by Rahman et al. [16] set a high standard with an accuracy of 97.33% using optimized Gradient Boosting, our proposed framework successfully pushes the performance boundary further to 98.61%. This performance leap, surpassing the previous state-of-the-art by approximately 1.28%, is attributed to two strategic interventions. First, the decomposition of blood pressure into Pulse

Pressure provided a high-fidelity signal for cardiovascular stress, allowing the model to distinguish subtle physiological nuances that standard variable sets might miss. Second, the Stacking Ensemble technique effectively mitigated the bias and variance inherent in individual base learners. By using an XGBoost Meta-Learner to correct the residual errors of the base models, the proposed architecture proved capable of correctly classifying complex instances where single optimized models like those in [16] and [17] reached their performance limits.

4. Conclusions

This study successfully established a robust machine learning framework for the early detection of sleep disorders by integrating the SMOTE with a two-tier Stacking Ensemble Architecture. By leveraging XGBoost as a meta-learner and incorporating novel Pulse Pressure feature engineering, the proposed model achieved a superior Accuracy of 98.61% and an exceptional Recall of 99.24%, effectively outperforming recent state-of-the-art baselines [16] with a training latency of only 18.04 seconds. While this performance demonstrates an optimal balance between high diagnostic precision and computational efficiency suitable for initial screening, the findings must be interpreted within the context of the study's reliance on a single public dataset with a relatively modest sample size ($n = 400$) and a specific stratified test split. Consequently, the "perfect" sensitivity observed requires further verification on larger, multi-center cohorts to guarantee generalizability, with future research avenues aimed at addressing these constraints through cross-dataset validation, the integration of real-time wearable IoT data streams, and the exploration of Deep Learning architectures for temporal pattern analysis [3], [11].

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