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Application of the smote and backpropagation neural network (BPNN) techniques in the classification of non-alcoholic fatty liver disease (NAFLD)

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ABSTRACT

Non-alcoholic fatty liver disease (NAFLD) is a liver disorder with a high global prevalence and a significant mortality risk. However, clinical NAFLD datasets often exhibit severe class imbalance, causing machine learning models to become biased toward the majority class. This study aims to classify the mortality risk of NAFLD patients using the backpropagation neural network (BPNN) algorithm combined with the synthetic minority over-sampling technique (SMOTE). To ensure model validity, the follow-up time variable (futime) was excluded to prevent data leakage. The experiments were conducted by comparing different data split ratios (70:30, 80:20, and 90:10) as well as various hidden layer configurations and learning rates. The experimental results indicate that, without SMOTE, the model was trapped in the illusion of high accuracy (92%) while failing to detect mortality cases effectively (recall < 15%). In contrast, the application of SMOTE significantly improved the recall value, reaching 79.85% under the 80:20 data split scenario. These findings demonstrate that the integration of SMOTE and BPNN is highly effective in minimizing missed diagnoses (false negatives) in imbalanced medical datasets.

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1. INTRODUCTION

Non-Alcoholic Fatty Liver Disease (NAFLD) is a liver disorder with a very high global prevalence and encompasses a broad spectrum of clinical manifestations, ranging from cardiovascular risks in its early stages to the potential progression toward advanced fibrosis or cirrhosis, which significantly increases the risk of mortality [1]. The urgency of addressing this disease has become increasingly evident, as recent estimates indicate that NAFLD affects approximately 38% of the world's population, making it the most common liver disease today. This prevalence is projected to continue rising, particularly in developing countries, driven by dramatic changes in dietary patterns, urbanization, and the growing incidence of obesity and type 2 diabetes mellitus [2].

The greatest concern regarding NAFLD lies in its potential to develop into fatal complications such as cirrhosis and liver failure. Therefore, identifying its risk factors is of paramount importance, as the disease has been shown to result from a complex interplay of genetic predisposition, metabolic disorders (such as obesity and insulin resistance), and unhealthy lifestyle patterns [3]. This condition is further complicated by gut microbiota imbalance, which may exacerbate liver damage. Given the numerous interconnected risk factors involved, manual medical analysis becomes highly challenging, thereby necessitating the use of advanced technologies to support a more accurate diagnostic process [4].

The application of Machine Learning algorithms, particularly the Support Vector Machine (SVM), has become a prominent approach for detecting NAFLD. Nevertheless, one of the major challenges frequently encountered is class imbalance, which introduces bias into prediction outcomes.

Previous studies have demonstrated that the use of the Synthetic Minority Over-sampling Technique (SMOTE) effectively addresses this issue, achieving an accuracy of up to 78.70%, indicating that data balancing is a fundamental element in ensuring diagnostic precision [5]. Even more impressive potential has been demonstrated by the Backpropagation Neural Network (BPNN) algorithm in medical case studies involving stroke, where the integration of SMOTE significantly improved model performance, resulting in an accuracy of 96.14%. This finding suggests that the combination is considerably more effective in handling imbalanced data than other classification methods [6]. The reliability of BPNN has also been confirmed in Diabetes Mellitus classification, achieving an accuracy of 80.75%, outperforming conventional Neural Networks, which attained only 78.35%. This result further emphasizes that the Backpropagation method offers a more accurate solution for disease diagnosis problems [7].

Based on the urgency of addressing NAFLD and the technical challenge of data imbalance, which often leads to bias in automated diagnosis, this study proposes an integrative approach that combines the strengths of resampling techniques and artificial neural network algorithms. By leveraging the capability of SMOTE to reconstruct balanced data distributions and the reliability of the Backpropagation Neural Network (BPNN) algorithm in identifying complex clinical patterns, this study aims to develop a detection model that not only achieves high accuracy but also maintains optimal sensitivity toward positive cases. This objective is consistent with the perspective of [8], which emphasizes that in critical disease diagnosis, the primary priority of a model is to minimize false negative predictions in order to prevent fatalities resulting from delayed treatment. Therefore, this study is entitled "The Application of the SMOTE Technique for NAFLD Disease Classification Using the Backpropagation Neural Network (BPNN) Algorithm" as a contributory effort toward providing a precise and reliable medical decision support system.

2. MATERIAL AND METHODS

This study was conducted through a systematic framework based on the principles of Knowledge Discovery in Databases (KDD), in which the transformation of raw data into a predictive model was carried out in a structured manner, starting from the acquisition of secondary NAFLD data to performance evaluation. The initial phase focused on improving data quality through comprehensive preprocessing, including critical feature selection by eliminating the futime attribute to mitigate the risk of data leakage, imputing missing values, and applying Min-Max normalization. Subsequently, a data balancing strategy was implemented using the Synthetic Minority Over-sampling Technique (SMOTE) specifically on the training dataset to reconstruct the asymmetric class distribution before partitioning the data into training and testing subsets. In the final stage, the Backpropagation Neural Network (BPNN) algorithm was employed to capture complex feature patterns, and its performance was validated using a confusion matrix, with particular emphasis on the sensitivity (Recall) metric to ensure the reliability of medical diagnosis.

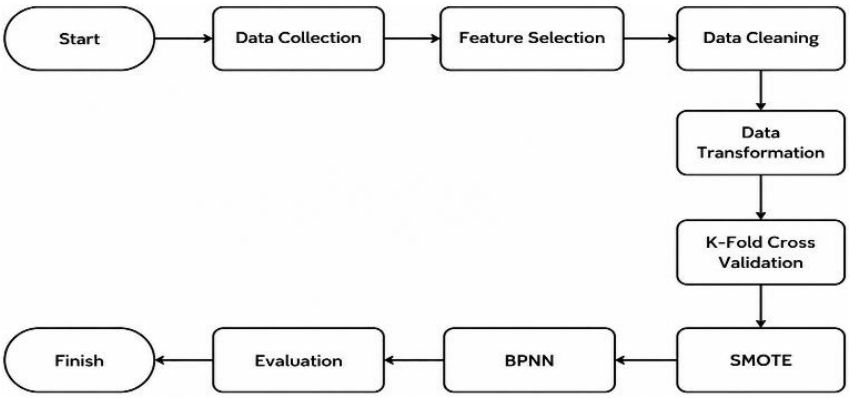

Figure 1. Research methodology.

2.1. Data Collection

The data collection process in this study employed a secondary dataset acquired from the public Kaggle repository, focusing specifically on patients with Non-Alcoholic Fatty Liver Disease (NAFLD). The dataset consists of longitudinal observational records that capture patients' metabolic conditions and clinical endpoints, with mortality serving as the primary outcome of interest. The dataset consists of 17,549 observations and 10 variables representing the clinical records of the study subjects. As shown in Table 1, the raw data contain diverse numerical characteristics and several missing values, indicated by the notation "NA" in a number of records. These conditions underscore the importance of a comprehensive preprocessing stage to ensure data quality and suitability prior to model development.

Table 1. Dataset.

	Id	Age	Male	⋯	Case.id	Futime	Status
3631	1	57	0	⋯	10630	6261	0
8458	2	67	0	⋯	14817	624	0
6298	3	53	1	⋯	3	1783	0
…	…	…	…	…	…	…	…
1522	17564	59	0	⋯	16164	5081	0
5764	17565	61	0	⋯	17276	3627	1
6658	17566	69	1	⋯	2017	2744	0

The dataset comprises 10 variables, including one unnamed index variable, eight clinical feature variables, and one target variable. The Unnamed: 0 attribute represents the original row index generated by the source database system. The id and case.id attributes are used as administrative identifiers for subjects and clinical cases. The main predictor variables consist of age, male, weight, height, and bmi, whereas futime denotes the follow-up duration. The status attribute serves as the binary classification target. Detailed descriptions of all variables are provided in Table 2.

Table 2. Data structure.

Variable name	Data type	Description
Unnamed: 0	Numeric	Original row index from the source database.
Id	Nominal	Unique subject identifier.
Age	Numeric	Age at study enrollment.
Male	Binary	Sex (0 = Female, 1 = Male).
Weight	Numeric	Body weight (kg).
Height	Numeric	Body height (cm).
Bmi	Numeric	Body Mass Index (BMI).
Case.id	Nominal	Matched NAFLD case identifier.
Futime	Numeric	Follow-up duration until death or last visit.
Status	Binary	Mortality status (0 = Alive, 1 = Deceased).

2.2. Feature Selection

Feature selection is an essential stage in the initial data processing phase, aiming to identify variables that genuinely contribute to the prediction outcomes. This process began by removing administrative variables, including the original index number (Unnamed: 0), patient identification code (id), and case identification code (case.id) from the dataset. These variables were excluded because they merely serve as data identifiers and have no medical relevance to patient mortality risk.

In addition to removing administrative attributes, the most critical step in this phase was the elimination of the futime (follow-up time) variable, which contains information regarding the duration until a patient's death or last follow-up. Retaining this variable would introduce data leakage, allowing the model to implicitly access future information during training. Kapoor and Narayanan (2023) classify the use of future-derived features as a form of feature leakage, a severe methodological flaw that can produce overly optimistic performance estimates while failing to generalize to real-world applications [9]. Therefore, to ensure scientific validity, the futime variable was excluded from the training process. Consequently, the final model utilized only five primary features—age, sex, weight,

height, and Body Mass Index (BMI)—which were considered objective indicators for representing patients' health conditions.

2.3. Cleaning Data

Data quality plays a critical role in the performance of predictive models, as incomplete observations may compromise classification accuracy. Preliminary analysis identified missing values in three key clinical attributes: weight, height, and Body Mass Index (BMI). To preserve valuable patient information and avoid reducing the sample size, the Mean Imputation technique was applied, replacing missing entries with the mean value of each respective feature. This approach was chosen to maintain data integrity and ensure that the dataset was adequately prepared for subsequent modeling procedures.

2.4. Data Tranformation

The data transformation stage aims to convert the dataset into a format compatible with the requirements of data mining algorithms. One of the essential techniques applied in this phase is normalization using the Min-Max Scaler, which rescales data values into the interval between 0 and 1. This procedure ensures consistency across feature scales without distorting the original information, thereby preventing certain variables from dominating the learning process due to differences in numerical ranges and ultimately contributing to improved machine learning performance [10].

$$X_{norm} = \frac{X - X_{min}}{X_{max} - X_{min}} \quad (1)$$

In this study, data normalization was performed using the Min-Max Scaling method based on Equation (1), which maps the original data values into a uniform range between 0 and 1. This step was particularly important because preliminary observations of the raw data (Before Normalization) revealed substantial disparities in value ranges across attributes. For example, in the first sample, the age and BMI features had values on a scale of tens (57 and 23.0, respectively), whereas the futime feature exhibited a much larger magnitude, reaching thousands (6,261). Without normalization, the Backpropagation Neural Network (BPNN) algorithm would tend to assign excessive importance to features with larger numerical scales, potentially biasing the learning process and distorting model performance.

After applying normalization (After Normalization), these disparities were successfully eliminated. This is illustrated in the first data sample, where the value of age (57) was transformed to 0.4875, BMI (23.0) to 0.1488, and futime (6,261) to 0.8613. Consequently, all features contributed on a comparable scale within the artificial neural network, promoting a more stable, objective, and reliable model performance.

2.5. K-Fold Cross Validation

During the model evaluation stage, this study employed 10-fold cross-validation as a validation technique to obtain more stable and representative performance estimates. This method partitions the transformed dataset into ten subsets (folds) of approximately equal size. In each iteration, nine folds are used as the training set, while the remaining fold serves as the testing set. The process is repeated ten times until every fold has been utilized exactly once as the testing set. This approach was selected to minimize bias resulting from a single data partition and to enhance the model's generalization capability on unseen data [11].

The dataset, consisting of 17,549 samples with a distribution of 16,185 instances in class 0 (alive, 92.23%) and 1,364 instances in class 1 (deceased, 7.77%), was comprehensively validated using this mechanism. In the SMOTE scenario, the resampling process was applied exclusively to the training data within each fold to prevent data leakage and to ensure that the testing data preserved the original class distribution of the population.

2.6. SMOTE

The Synthetic Minority Over-sampling Technique (SMOTE) is defined as an oversampling method that increases the number of instances in the minority class by generating synthetic samples based on existing minority data [12]. Introduced by Chawla et al. in 2002, this technique provides an

effective alternative for addressing class imbalance problems [13]. Previous studies have applied SMOTE to medical datasets, such as stroke prediction, where stroke cases constituted the minority class [14].

To address the significant class imbalance in the training data, this study employed SMOTE to generate synthetic instances for the minority class. The technique was applied exclusively to the training set and not to the testing set, a crucial methodological step to prevent data leakage and preserve the validity of model evaluation on real-world data. Through this resampling process, the class distribution within the training data was successfully balanced, enabling the model to learn patterns from both classes with equal representation and reducing bias toward the majority class.

2.7. BPNN

Backpropagation Neural Network (BPNN) is a supervised learning algorithm based on a multilayer neural network architecture, where the prediction error obtained during the forward propagation phase is propagated backward to adjust the connection weights and minimize the overall loss function [15]. The network architecture comprises three primary layers: an input layer, one or more hidden layers, and an output layer, all of which interact during the training process. The hidden layer is particularly important because it enables the network to capture complex nonlinear relationships and achieve lower prediction errors than simpler single-layer neural networks or architectures without hidden layers [16].

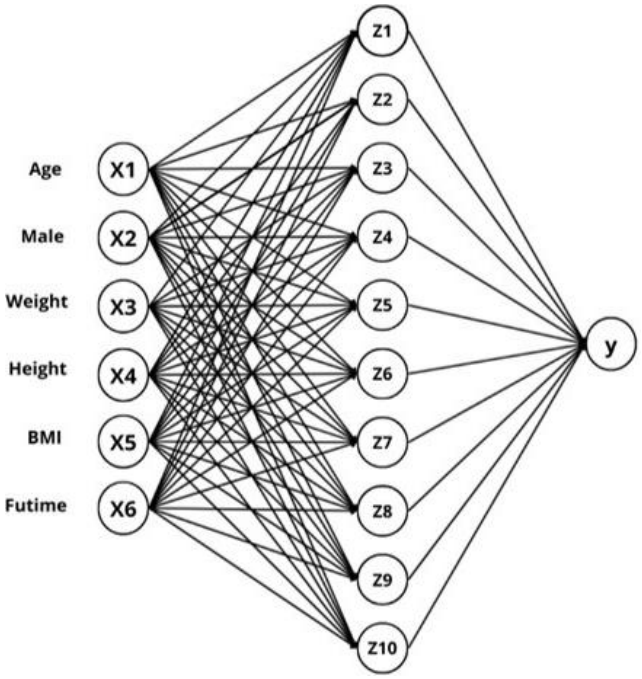

Figure 2. 6-10-1 architecture.

2.8. Evaluation

To ensure that the proposed network architecture achieves optimal convergence and minimizes prediction errors, this study did not rely on a single static configuration but instead explored several parameter variations. The experimental design was intended to investigate the effects of network capacity and learning speed by varying the number of neurons in the hidden layer (8, 10, and 12 neurons) and the learning rate values (0.001, 0.01, and 0.1). The selection of these parameters was based on previous findings indicating that the hidden layer configuration determines the network's ability to learn underlying patterns and generalize effectively to previously unseen data [17]. Meanwhile, the learning rate is considered one of the most critical hyperparameters in neural network training, as it directly influences the speed and stability of convergence toward an optimal solution with progressively lower prediction errors [18]. Through this systematic comparison, the parameter

combination that yields the best evaluation performance in terms of both accuracy and sensitivity is selected as the final model configuration for precise NAFLD status classification.

Accuracy measures the proportion of correctly classified instances to the total number of instances and is defined as follows:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (2)$$

Precision measures the proportion of positive predictions that are actually correct. The equation for Precision is given as follows:

$$Precision = \frac{TP}{TP+FP} \quad (3)$$

Recall measures the model's ability to identify all positive instances in the dataset. The equation for Recall is expressed as follows:

$$Recall = \frac{TP}{TP+FN} \quad (4)$$

The F1-Score is the harmonic mean of Precision and Recall, and is calculated using the following equation:

$$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (5)$$

In both scenarios, the model performance was further explored by varying several parameters, including the number of neurons in the hidden layer (8, 10, and 12 neurons) and the learning rate values (0.001, 0.01, and 0.1).

Table 3. Evaluation.

Evaluation aspect	Description
Classification method	Backpropagation neural network (BPNN)
Data balancing technique	SMOTE
Hidden layer	8, 10, dan 12
Learning rate	0.001, 0.01, dan 0.1
Data validation method	10-fold cross-validation (k = 10)
Evaluation objective	This study aims to optimize the classification performance of the backpropagation neural network (BPNN) by comparing the baseline model with the model incorporating SMOTE. Performance evaluation is conducted using accuracy, precision, recall, and F1-score metrics within a 10-fold cross-validation framework (k = 10). The experiments also investigate variations in the number of hidden-layer neurons (8, 10, and 12) and learning rates (0.001, 0.01, and 0.1) to determine the optimal model configuration.

3. RESULTS AND DISCUSSIONS

This section delivers a rigorous presentation and critical analysis of the experimental findings obtained from the Backpropagation Neural Network (BPNN) model. To ensure objective performance evaluation and mitigate systematic bias, a stratified 10-Fold Cross-Validation framework was executed across two distinct methodology tracks: the baseline paradigm (Without SMOTE) and the balanced paradigm (With SMOTE integrated inside individual training folds). The predictive capacities are rigorously quantified using Accuracy, Precision, Recall, and F1-Score metrics to ascertain the optimal architectural configuration for Non-Alcoholic Fatty Liver Disease (NAFLD) mortality risk prediction.

3.1. Performance Analysis of Baseline Model (Without SMOTE)

This subsection evaluates the classification efficacy of the BPNN model trained without the intervention of data-balancing mechanisms. The extreme class asynchrony inherent in the NAFLD clinical registry fundamentally skewed the network's optimization path. The empirical performance distribution across the 10 cross-validation folds for the baseline scenario is systematically detailed in Table 4.

Table 4. 10-fold cross validation results without SMOTE.

Fold	Accuracy	Precision	Recall	F1-score
Fold 1	92.19%	49.12%	20.59%	29.02%
Fold 2	92.71%	56.45%	25.74%	35.35%
Fold 3	92.82%	63.16%	17.65%	27.59%
Fold 4	92.08%	47.06%	17.65%	25.67%
Fold 5	92.59%	57.89%	16.18%	25.29%
Fold 6	93.33%	81.25%	18.98%	30.77%
Fold 7	94.02%	75.81%	34.31%	47.24%
Fold 8	92.88%	64.29%	19.71%	30.17%
Fold 9	92.82%	62.79%	19.71%	30.00%
Fold 10	93.33%	65.57%	29.41%	40.61%
Average	92.88%	62.34%	21.99%	32.17%

The empirical indicators documented in Table 4 demonstrate that the baseline model achieved a deceptively high average global Accuracy of 92.88% and a robust Precision of 62.34%. However, this heightened accuracy presents a classic manifestation of the accuracy paradox. Because the clinical dataset is disproportionately dominated by the majority class (survived patients), the neural network converges toward a suboptimal local minimum that favors majority-class classification. This mathematical bias is substantiated by the poor average Recall metric of 21.99%. The results conclusively indicate that the network failed to map the critical clinical representations of the minority cohort, thereby misclassifying approximately 78% of high-risk patient mortalities. Consequently, deploying a baseline model without mitigating class imbalance poses severe risks in clinical decision support environments due to the unacceptable rate of False Negatives.

3.2. Performance Analysis of Balanced Model (With SMOTE Inside Fold)

To counteract the severe classification skew observed in the baseline configuration, the second scenario integrates the Synthetic Minority Over-sampling Technique (SMOTE) to re-establish class equilibrium. Crucially, to preserve validation integrity and ensure absolute isolation from data leakage, SMOTE oversampling was executed strictly on the training partitions within each fold iteration, ensuring that the respective validation partitions remained structurally authentic and unmanipulated. The comprehensive evaluation metrics for this cross-validated balancing approach are systematically tabulated in Table 5.

Table 5. 10-fold cross validation results with SMOTE inside fold.

Fold	Accuracy	Precision	Recall	F1-score
Fold 1	77.09%	19.77%	63.97%	30.21%
Fold 2	73.68%	17.79%	66.18%	28.04%
Fold 3	77.89%	18.81%	55.88%	28.15%
Fold 4	78.86%	20.10%	58.09%	29.87%
Fold 5	83.59%	25.80%	59.56%	36.00%
Fold 6	77.78%	20.92%	66.42%	31.82%
Fold 7	77.38%	21.49%	71.53%	33.05%
Fold 8	74.30%	18.60%	67.88%	29.20%
Fold 9	74.07%	18.70%	69.34%	29.46%
Fold 10	80.84%	23.12%	63.24%	33.86%
Average	77.55%	20.51%	64.21%	30.96%

The statistical evidence summarized in Table 5 illustrates that incorporating SMOTE within the cross-validation boundaries fundamentally restructured the network's predictive capabilities. Although the average global Accuracy underwent an anticipated trade-off, descending to 77.55%, and Precision dropped to 20.51%, the model's diagnostic sensitivity regarding the minority risk cohort exhibited an extensive escalation. The average Recall advanced significantly from 21.99% to 64.21%, implying that the balanced network identified nearly threefold the number of authentic clinical mortalities relative to the baseline configuration. While the F1-Score experienced a minor down-shift to 30.96% owing to the precision penalty, the operational stability and clinical safety of the model improved markedly.

To provide a concise and clear visual synthesis of the structural changes in model performance, a direct comparison of the evaluated metrics across the two 10-fold cross-validation tracks is illustrated in Figure 3.

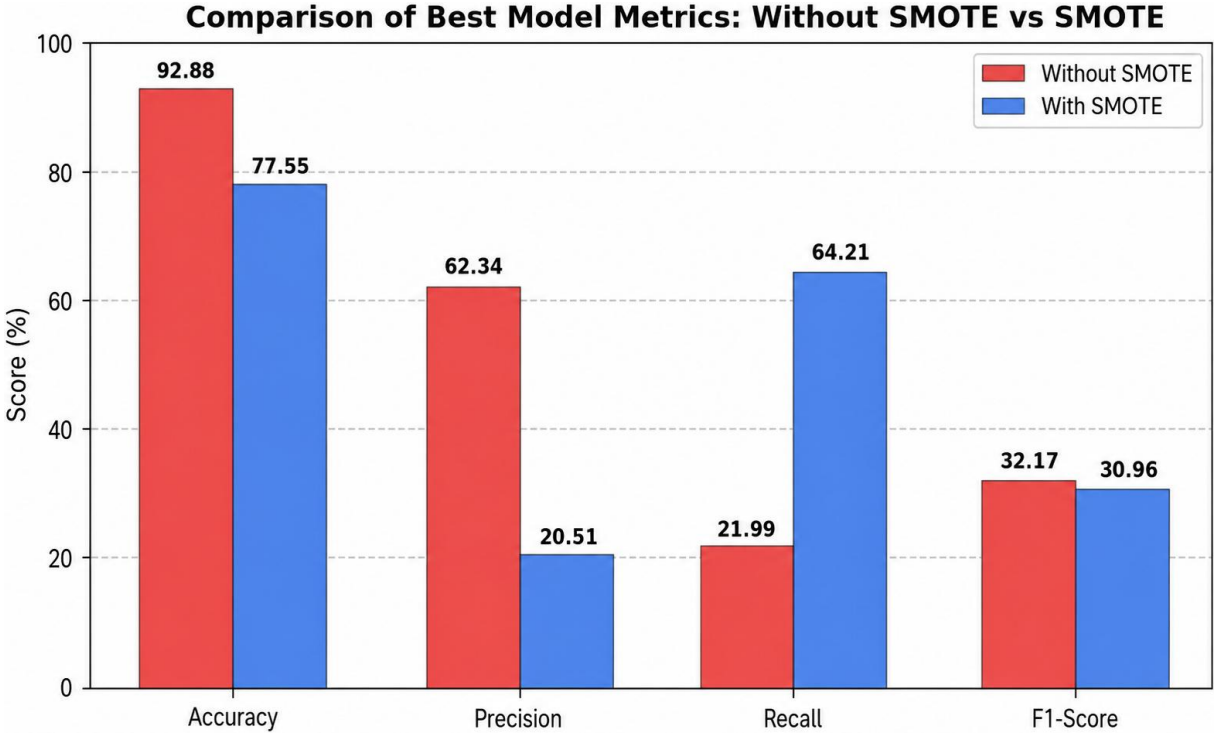

Figure 3. Comparison with smote and without SMOTE.

4. CONCLUSION

This study successfully evaluated the classification performance of a Backpropagation Neural Network (BPNN) model combined with a 10-Fold Cross-Validation scheme to predict mortality risks in Non-Alcoholic Fatty Liver Disease (NAFLD) patients. The experimental results demonstrated that resolving severe class imbalance is highly paramount for clinical decision-making.

The baseline model (Without SMOTE) exhibited a stark manifestation of the accuracy paradox, achieving a deceptively high average global accuracy of 92.88% but failing critically in clinical utility due to a low average Recall of 21.99%. Conversely, integrating the Synthetic Minority Over-sampling Technique (SMOTE) strictly within the cross-validation folds successfully alleviated this classification bias. Although it introduced an expected trade-off by lowering the average Accuracy to 77.55% and Precision to 20.51%, the model's sensitivity towards the critical minority class improved dramatically, with the average Recall advancing to 64.21%. This almost threefold increase in diagnostic sensitivity signifies that the balanced network is substantially more capable of detecting high-risk mortality cases.

In conclusion, implementing SMOTE internally within individual cross-validation folds provides a structurally sound and reliable predictive framework that eliminates the risk of data leakage. For medical data mining applications, prioritizing a higher Recall metric over global accuracy

is scientifically and ethically justified, as it minimizes life-threatening False Negatives. Future research may explore hyperparameter optimization or hybrid ensemble techniques to recover the dropped Precision while maintaining high model sensitivity.

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