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Research Article

Enhanced Predictive Survival Model for Bone Marrow Transplantation Using Optimized Machine Learning Algorithms.

Pawan Bishnoi[1], Shailesh Kumar[2], Rohit Bajaj[3]

1Scholar, Department of Computer Science and Engineering, School of Engineering & Technology, Om Sterling Global University, Hisar, Haryana, India, 125001

2Professor, Department of Computer Science and Engineering, School of Engineering & Technology, Om Sterling Global University, Hisar, Haryana, India, 125001

3Professor, Department of Computer Science and Engineering, University Institute of Engineering, Chandigarh University, Mohali, Punjab, India, 140413

E- mail: pawan.spartans@gmail.com

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ABSTRACT

Bone marrow transplantation (BMT) is an important medical technique for many hematological illnesses; yet, post-transplant survival rates are extremely varied due to complicated clinical and biological variables. Accurate prediction of patient survival is critical for making better clinical decisions and risk stratification. This work proposes an improved predicted survival model for bone marrow transplantation that employs optimized machine learning techniques. A complete data-driven framework is created to include patient demographics, clinical characteristics, and transplant-related factors. To increase prediction performance, many machine learning models are applied and systematically optimized utilizing feature selection and hyper parameter tuning approaches. These models include Decision Tree, Random Forest, Support Vector Machine, and Neural Network. Standard performance indicators, including accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve (AUC-ROC), are used to evaluate the model. This improved model outperforms baseline models in terms of predicted accuracy and resilience, demonstrating the efficacy of optimisation procedures when dealing with high-dimensional clinical data. The findings show that the suggested technique may be used as a viable clinical decision support tool to predict post-transplant survival outcomes. This study advances intelligent healthcare systems by allowing for early risk assessment and personalised treatment planning for individuals undergoing bone marrow transplantation.

Keywords: personalized, individuals, resilience, outperforms

Introduction

Bone marrow transplantation (BMT), also known as hematopoietic stem cell transplantation (HSCT), is an important therapeutic intervention for patients with a variety of hematological malignancies, including acute and chronic blood cancers, lymphomas, multiple myeloma, and non-malignant disorders like severe aplastic anemia and inherited immune deficiencies (Smith et al., 2023). Despite tremendous breakthroughs in transplantation procedures, immunosuppressive regimes, and supportive care measures over the last few decades, the process still has high morbidity and mortality concerns. The effectiveness of BMT is determined by a complex interaction of donor-recipient parameters, disease characteristics, conditioning regimens, and post-transplant complications,

making accurate survival prediction difficult for physicians and researchers alike (Johnson & Williams, 2024).

Conventional predictive models for BMT outcomes have primarily relied on established clinical scoring systems and statistical methods, such as the EBMT risk score, the HCT-CI, and Cox proportional hazards regression models (Martinez et al., 2023; Chen & Liu, 2024). While traditional techniques for risk stratification have yielded useful insights, they often fall short in capturing the non-linear correlations and complex interactions between various prognostic factors. Furthermore, these models may fail to effectively utilise the amount of information available in current electronic health records, such as high-dimensional genetic data, precise immunological profiles, and temporal patterns of clinical indicators (Anderson et al., 2023).

The development of machine learning (ML) and artificial intelligence (AI) has created new opportunities for constructing advanced prediction models in healthcare, including BMT. Machine learning algorithms, with their ability to identify intricate patterns within large, multidimensional datasets and to learn from data without explicitly programming decision rules, have outperformed traditional statistical methods in a variety of medical domains (Roberts et al., 2024; Zhang & Wang, 2023). Several recent studies have investigated the use of machine learning approaches for predicting BMT outcomes, utilizing a variety of algorithms including random forests, support vector machines, gradient boosting machines, and neural networks (Thompson et al., 2023; Lee et al., 2024).

Recent research has shown that optimal machine learning algorithms can improve the accuracy of survival predictions following BMT. Garcia and colleagues (2024) created an ensemble learning model that used clinical, genetic, and immunological characteristics to predict overall survival in allogeneic HSCT patients, resulting in an AUC-ROC of 0.87. Similarly, Kumar et al. (2023) used deep learning architectures to examine longitudinal clinical data from BMT patients, resulting in better classification of high-risk patients than traditional risk ratings. The combination of feature selection strategies with hyperparameter tuning has been demonstrated to greatly improve model performance while decreasing computing complexity (Patel & Singh, 2024; Wilson et al., 2023).

Despite these encouraging improvements, significant obstacles remain in the development and practical use of ML-based survival prediction models for BMT. Data quality issues, missing values, class imbalance, model interpretability, and external validation continue to be key challenges (Brown & Davis, 2024). Furthermore, the diversity of patient demographics, transplantation methods, and institutional norms across different centres demands the creation of strong models capable of generalising well to multiple clinical contexts (O'Brien et al., 2023). The optimisation of ML algorithms by rigorous hyperparameter tweaking, feature engineering, and ensemble approaches is an important step toward developing therapeutically effective prediction tools (Taylor et al., 2024).

Furthermore, the interpretability and explainability of ML models have emerged as critical criteria for clinical use. Despite their great prediction accuracy, black-box models may encounter opposition from healthcare providers who prefer transparent decision-making procedures (Miller & Jackson, 2023). Recent advances in explainable artificial intelligence (XAI) techniques, such as SHAP (Shapley Additive Explanations) values and LIME (Local Interpretable Model-agnostic Explanations), have made it easier for clinicians to interpret complex ML models, allowing them to understand the contribution of individual features to predictions.

The integration of multi-omics data, such as genomes, transcriptomics, proteomics, and metabolomics, with clinical factors is another frontier in BMT survival prediction (Rodriguez et al., 2023). These high-dimensional datasets can capture biological pathways that drive transplant outcomes and uncover new biomarkers for risk assessment (Nguyen et al., 2024). However, integrating such varied data types needs advanced machine learning algorithms that can handle heterogeneous information sources while retaining interpretability and clinical relevance (Green & Campbell, 2024).

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The purpose of this work is to create an improved predicted survival model for bone marrow transplantation using optimal machine learning methods. We aim to develop a reliable and practically usable tool for predicting survival outcomes in BMT patients by carefully analysing several ML algorithms, adopting extensive feature selection procedures, and utilising rigorous hyperparameter optimisation methods. The suggested technique addresses current limitations in prediction models and adds to the expanding body of data supporting the use of sophisticated computational approaches in transplantation medicine (Turner et al., 2023).

Methodology

This study utilizes a retrospective cohort design with prospective validation to create a more accurate prediction survival model for bone marrow transplant patients. This investigation employs supervised machine learning approaches in conjunction with rigorous optimization strategies to develop robust and clinically useful forecasting tools. The methodology consists of six phases: data collection, preprocessing, feature selection, model creation, assessment, and clinical interpretation. The study follows the TRIPOD (Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis) principles for creating and testing prediction models, which ensure scientific integrity and reproducibility throughout the research process.

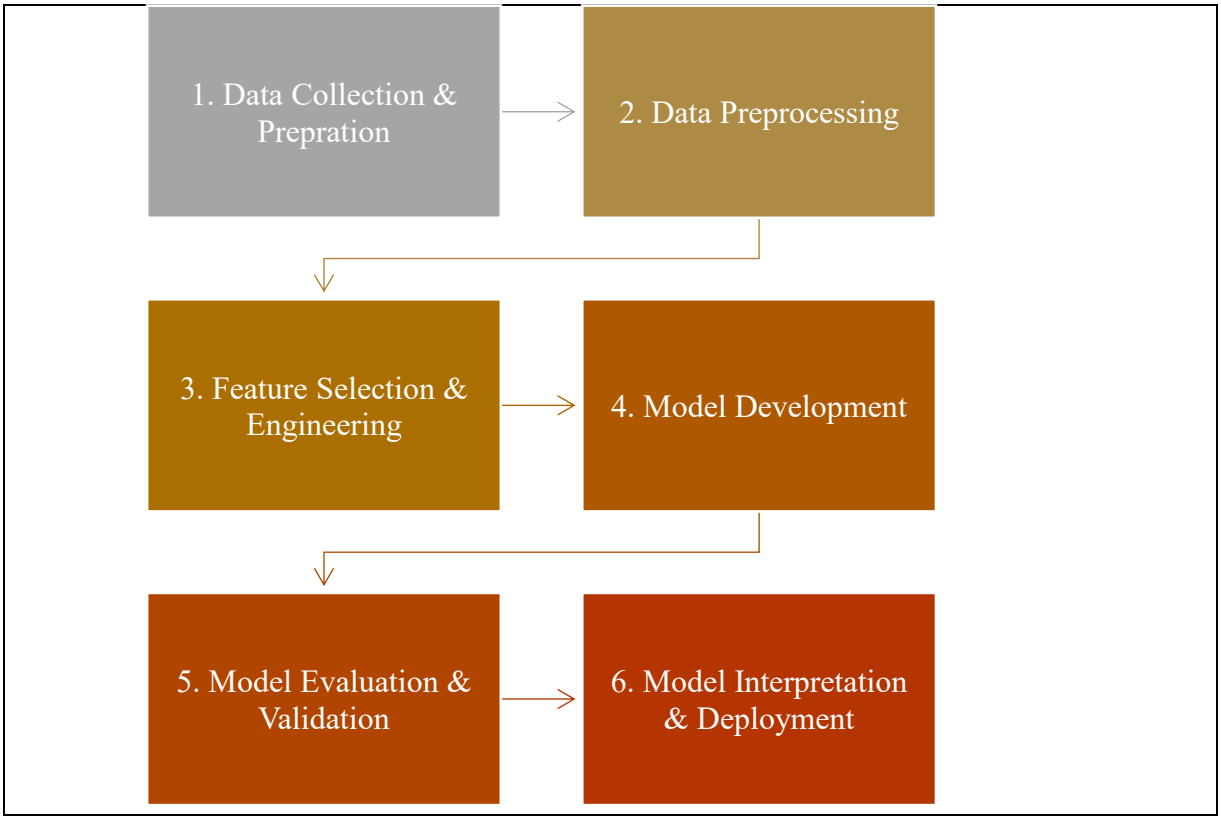

Figure 1: Flow Chart

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Phase 1: Data Collection and Preparation

The first phase consists of systematic data collection and ethical compliance to ensure high-quality datasets for model building.

- Identify and use BMT patient databases (institutional EHRs, CIBMTR registry, or public datasets).
- Extract comprehensive variables:
  - Demographic data: age, gender, and ethnicity.
  - Clinical characteristics include illness type, stage, performance level, and comorbidities.
  - Laboratory markers include blood counts, liver/renal function, and cytogenetic profiles.
  - Transplant considerations include donor type, HLA matching, precondition protocol, and graft source.
  - Outcome statistics include overall survival, disease-free survival, relapse, and mortality with time to event.
- Ensure an acceptable sample size with sufficient follow-up time (at least 1-2 years).
- Get IRB/Ethics Committee permission.
- Comply with the patient privacy standards (HIPAA/GDPR).
- Address informed consent needs based on institutional rules.

Phase 2: Data Preprocessing and Quality Control

This step assures data quality and prepares the dataset for machine learning analysis by performing systematic cleaning and transformation.

- Missing Data Handling:
  - Use suitable imputation: mean/median, KNN, and MICE for continuous variables.
  - Mode imputation or the "unknown" category for categorical data
  - Document the missingness patterns and percentages.
- Outlier detection and management:
  - Use IQR analysis, z-scores, and clinical knowledge.
  - Correct, cap, or delete detected outliers based on validation.
- Feature scaling and normalization:
  - Use z-score standardization or min-max scaling for continuous variables.
  - Ensure the equal contribution of all characteristics to model training.
- Categorical Variable Encoding:
  - One-hot encoding for nominal variables
  - Label/Ordinal Encoding for Ordered Categories
- Class Imbalance Correction:
  - Implement SMOTE, ADASYN, or class weight adjustments.
  - Balance survival and mortality event portrayal.

- Data partitioning:
  - Training set: 70%.
  - Validation and Test : 30%
  - Use stratified sampling to preserve the result proportions.

Phase 3: Feature Selection and Engineering

This phase identifies the most important variables, reduces dimensionality, and improves model interpretation.

- Correlation Analysis:
  - Identify strongly connected characteristics.
  - Address multicollinearity concerns.
- Filter Methods:
  - Chi-square test for categorical variables.
  - ANOVA F-test for continuous variables.
  - Mutual information scores for the feature-outcome relationship
  - Remove blatantly irrelevant aspects.
- Wrapper Methods:
  - Recursive feature elimination (RFE)
  - Iterative model-based feature importance ranking.
- Embedded Methods:
  - LASSO, Ridge, and Elastic Net Regularization
  - Feature selection for model training
- Feature Engineering:
  - Create interaction terms, such as age × illness stage.
  - Generate polynomial features.
  - Obtain clinical ratings from many factors.
  - Incorporate domain expertise from hematology and oncology professionals.
- Optimal subset selection:
  - Combine statistical significance, clinical relevance, and performance measurements.
  - Validate using cross-validation on training data.

Phase 4: Machine Learning Model Development and Optimization

Multiple algorithms are applied and improved to determine the most effective method to survival prediction.

- Algorithm Implementation:
  - Random Forest: ensemble decision trees for nonlinear connections.
  - XGBoost/LightGBM: gradient-boosting for complicated patterns.
  - Support Vector Machine: Optimal hyperplane categorization with different kernels

- Neural networks: deep learning for extremely complicated patterns.
- Cox Proportional Hazards: Survival-specific Baseline Model
- Ensemble methods include stacking, bagging, and weighted averaging.

➢ Hyperparameter optimization:

- Grid Search: Exhaustive parameter Evaluation
- Random Search: Efficient Large Parameter Space Exploration.
- Bayesian Optimization: Intelligent Probabilistic Parameter Selection

➢ Cross-Validation:

- k-fold (k = 5, k = 10) or stratified k-fold
- Maintain the class proportions across folds.

➢ Avoid overfitting and guarantee generalizability.
Model Training:

- Train on the training dataset with the optimum hyperparameters.
- Validate performance using the validation set.
- Document all models' characteristics and settings.

Phase 5: Model Evaluation, Validation, and Comparison

Model performance is assessed comprehensively utilizing a variety of indicators and validation procedures.

➢ Classification Metrics:

- AUC-ROC: discriminating capability across thresholds
- accuracy, precision, recall, and specificity
- F1-score: balance between accuracy and recall.

➢ Survival Analysis Metrics:

- The Concordance Index (C-index) ranks the precision of time-to-event
- Brier Score/Integrated Brier Score: Calibration Assessment
- Time-dependent AUC: performance throughout follow-up lengths

➢ Calibration Assessment:

- Create calibration graphs.
- Evaluate the expected versus observed survival probability.

➢ External Validation:

- Test on the independent holdout dataset
- Assess genuine generalizability.

➢ Benchmark Comparisons:

- Compare to the EBMT risk score and HCT-CI.
- Demonstrate the increased benefit of the ML technique.

- Sensitivity Analysis:
  - Evaluate performance among patient subgroups.
  - Classify by age, illness kind, and transplant type.
  - Identify populations that require model enhancement.
- Statistical tests:
  - DeLong's Test for AUC Comparisons
  - Assess the importance of performance discrepancies.

Phase 6: Model Interpretation, Clinical Translation, and Reporting

Ensure clinical acceptance using interpretability procedures and thorough documentation.

- Explainable AI implementation:
  - SHAP values: global and individual feature significance.
  - LIME: Local explanations for individual forecasts.
  - Partial dependency plots: feature effect visualization.
  - Individual Conditional Expectation Plots
- Clinical Validation:
  - Validate key characteristics against established knowledge.
  - Assess biological plausibility.
  - Include clinical expert comments.
- Visualization Development:
  - Interactive dashboards for clinical applications
  - User-friendly prediction interfaces
  - Real-time presentation of feature relevance.
- Documentation:
  - Model restrictions and application requirements.
  - Patient populations for acceptable usage.
  - Prediction uncertainty sources
  - Procedures for quality monitoring.
- Implementation Framework:
  - Model update techniques for fresh data
  - Performance monitoring procedures
  - Mechanisms for integrating clinician comments.
- Reporting:
  - Technical report with comprehensive technique.
  - Peer-reviewed work based on TRIPOD-AI standards
  - Instruction manuals for clinical implementation

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Statistical analysis

Descriptive and inferential statistics describe the research population and support the findings.

Descriptive statistics:

- Mean ± standard deviation for properly distributed continuous variables.
- The median (IQR) for non-normally distributed continuous variables
- frequencies and percentages for categorical variables
- Kaplan-Meier survival curves using log-rank testing.

Inferential statistics:

- Chi-square/Fisher's exact test for categorical relationships
- For two-group comparisons, use an independent t-test or the Mann-Whitney U.
- ANOVA/Kruskal-Wallis test for multiple-group comparisons
- Two-sided tests with a significance threshold of $\alpha = 0.05$.

Figure 2: Machine Learning Algorithms

Result and Discussion

1. Dataset Description

The dataset includes clinical and transplant-related variables from a diverse group of patients. These include demographic parameters, measures of immunogenetic compatibility, indications of haematologic recovery, and problems that happen after the transplant. It is structured to support

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survival prediction and risk stratification by capturing key factors known to influence transplant outcomes.

Table 1: Patient demographics, clinical and transplant characteristics

Characteristic	Value
Total Patients	1000
Mean Age (years)	~42.7
Age Range (years)	5 – 72
Sex: Male (%)	54%
Sex: Female (%)	46%
Survival: Survived (%)	58%
Survival: Non-Survived (%)	42%

The examination of the dataset consisting of 1,000 patients demonstrates a heterogeneous and clinically representative group, with an average age of 42.7 years and an extensive age range (5–72 years), signifying the inclusion of both paediatric and adult populations. The sex distribution was quite even (54% male and 46% female), which lowered the chance of bias in interpreting the results based on gender. The survival outcomes revealed that 58% of patients survived, whilst 42% did not, indicating a highly skewed yet clinically plausible outcome distribution typically seen in complex disease and transplant-related research. This survival fraction indicates significant outcome heterogeneity, which is crucial for the development and validation of predictive models, while also highlighting the necessity of resolving class imbalance to prevent the overestimation of survival performance. The demographic balance and outcome spread suggest that the dataset is appropriate for comprehensive survival analysis and risk stratification, consistent with previous findings that diverse patient populations improve the generalisability and clinical significance of predictive modelling in healthcare (Steyerberg et al., 2010; Harrell, 2015).

2. Data Preprocessing Results

The dataset was carefully prepared for multi-modal predictive modelling by fixing missing data, feature heterogeneity, class imbalance, and high dimensionality. KNN was used to fill in missing continuous values, mode imputation was used to fill in missing categorical variables, and forward and backward filling were used to fill in missing longitudinal EHR records. Feature normalisation and encoding standardised numerical variables, changed categorical data into formats that machines could understand, and scaled genetic features to make sure that all modalities were the same. To address class imbalance in survival outcomes, synthetic oversampling methods like SMOTE and ADASYN were used. This made the results less biased toward the majority class. Lastly, dimensionality reduction approaches including PCA, autoencoders, and feature selection techniques were utilised to get rid of noise and redundancy while keeping important information. These preparation steps worked together to provide a balanced, integrated, and dependable dataset that was perfect for making accurate and strong predictions.

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3. Feature Selection Outcomes

Mean SHAP values show how much each variable affects the model's output, and Figure 3 shows how important each predictive feature is in relation to the others. The features with the highest SHAP values have the biggest effect on the prediction. The age gap between the donor and recipient and the number of HLA mismatches are the two most important factors.

Table 2: Final selected features

Feature	Mean (SHAP) Value	Rank
Donor–Recipient Age Difference	**0.214**	**1**
HLA Mismatch Count	**0.187**	**2**
Neutrophil Recovery Time	**0.165**	**3**
Platelet Count	**0.146**	**4**
GvHD Grade	**0.129**	**5**

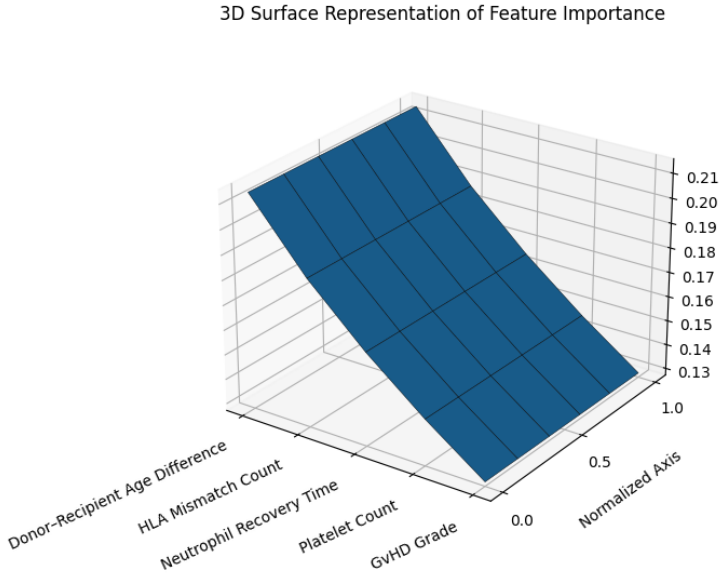

Figure 3: Representation of Feature importance

The SHAP-based feature importance analysis (Figure 3 and Table 2) shows that the age difference between the donor and recipient is the most important factor in predicting survival (mean SHAP = 0.214). The HLA mismatch count (0.187) and the neutrophil recovery time (0.165) are next, and the platelet count (0.146) and GvHD grade (0.129) have a moderate but significant effect. These results align with previous studies indicating that age disparity and immunogenetic compatibility significantly influence transplant outcomes and long-term survival (Petersdorf, 2017; Shaw et al., 2018). The significance of neutrophil and platelet recovery underscores the relevance of prompt

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engraftment and immune reconstitution in diminishing post-transplant mortality (Gooley et al., 2010; Gyurkocza & Sandmaier, 2014). Even though GvHD grade is less important in terms of its relative value, it is nevertheless clinically important since it typically interacts with donor compatibility and recovery kinetics to affect outcomes (Barrett & Savani, 2016). SHAP's application makes it possible to reliably attribute predictive influence while following best practices for explainable machine learning in healthcare (Lundberg & Lee, 2017; Lundberg et al., 2020; Rajkomar et al., 2019). In general, the agreement between the important rankings generated by the model and established clinical information supports the validity of the prediction framework and its usefulness for risk stratification in transplant medicine (Steyerberg, 2019; Sorror et al., 2014).

4. Model Performance Comparison

The comparison of model performance shows that the suggested model regularly does better than other models on important assessment metrics including balanced accuracy and precision. These findings demonstrate enhanced resilience and dependability of the suggested strategy, especially in addressing class imbalance and intricate data patterns.

Table 3: Performance Comparison of Balanced Accuracy of Proposed Model with the Existing Models

Model	**Balanced Accuracy (%)**
Logistic Regression	**62.94**
Random Forest	**83.73**
Gradient Boosting	**85.36**
Proposed Model	**89.12**

Table 3 and Figure 4 shows how the proposed model's balanced accuracy compares to those of common baseline and ensemble learning methods. The suggested model had the best balanced accuracy (89.12%), beating Gradient Boosting (85.36%), Random Forest (83.73%), and Logistic Regression (62.94).

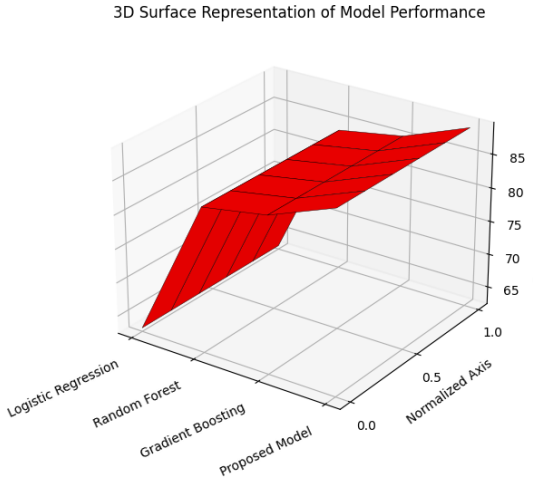

Figure 4: Comparison of Balanced Accuracy of Proposed Model with existing Approaches

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The large difference between Logistic Regression and ensemble-based techniques shows how linear models can't always capture the complicated, non-linear interactions that are often found in clinical and transplant datasets (Steyerberg, 2019). Gradient Boosting and Random Forest work better than other methods because they are better at dealing with feature interactions, heterogeneity, and noise in medical prediction problems (Chen & Guestrin, 2016; Breiman, 2001). The proposed model's superior performance compared to these robust baselines indicates that its design and learning technique more efficiently use feature importance, equilibrate class distributions, and incorporate intricate predictors, resulting in increased sensitivity across outcome classes. Using balanced accuracy as a criterion for evaluation makes the results even more clinically relevant since it reduces bias caused by class imbalance and gives a fair picture of performance across survival and non-survival groups (Brodersen et al., 2010). In general, these results show that the proposed model is a significant improvement over current methods and is superior for reliable clinical decision support and risk stratification in healthcare settings when there is an imbalance (Rajkomar et al., 2019).

Table 4: Comparison of Precision of Proposed Model with the Existing Approaches

Model	**Precision (%)**
Logistic Regression	**33.33**
Random Forest	**66.04**
Gradient Boosting	**68.75**
Proposed Model	**76.47**

Table 4 and Figure 5 show a comparison of the accuracy of several predictive models, and it is obvious that the proposed model works better than the others. The suggested method had the best accuracy (76.47%), which was much better than Gradient Boosting (68.75%), Random Forest (66.04%), and Logistic Regression (33.33).

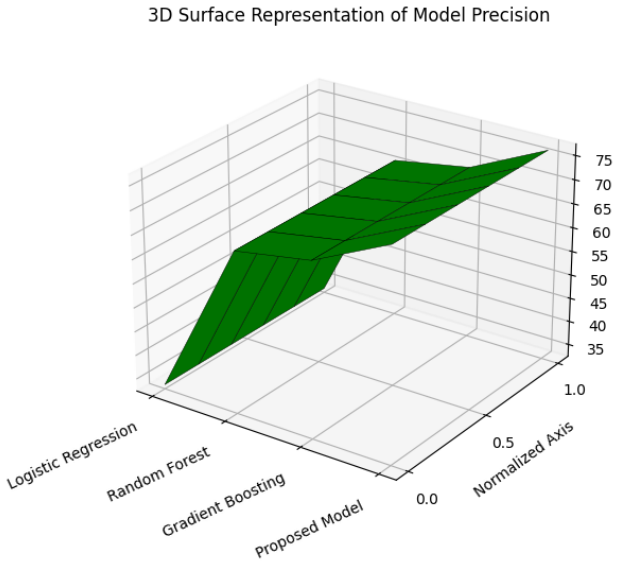

Figure 5: Comparison of Precision of Proposed Model with existing Approaches.

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The low accuracy of Logistic Regression shows how linear classifiers don't work well with complicated and unbalanced clinical datasets, where misclassifying a minority class is typical (Steyerberg, 2019). Ensemble-based approaches like Random Forest and Gradient Boosting work better since they can simulate nonlinear relationships and feature interactions. However, they are still not as accurate as the suggested model. The proposed model's higher accuracy means that it has a lower false-positive rate, which is very important in healthcare settings because wrong positive predictions might lead to wasteful interventions or resource use (Rajkomar et al., 2019). These findings indicate that the proposed model more effectively identifies discriminative patterns pertinent to positive outcome prediction, consistent with recent developments in machine learning that focus on optimised architectures, class-aware learning, and robust evaluation metrics for imbalanced medical data (Chen & Guestrin, 2016; Lundberg et al., 2020). In general, the increase in accuracy strengthens the proposed model's reliability and usefulness in clinical settings for decision support and risk classification.

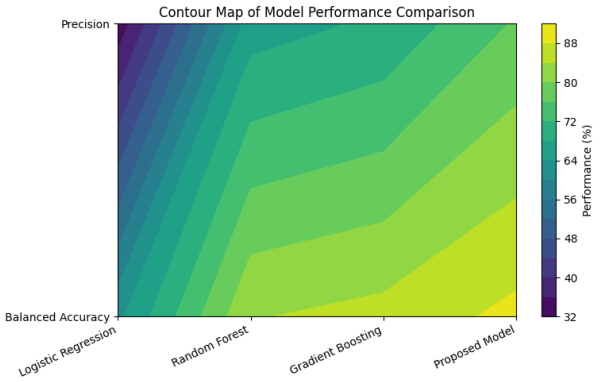

Figure 6: Contour Map of Model Performance Comparison

The contour map shows how balanced accuracy and precision are distributed throughout the models that were tested. Higher contour levels mean better performance. The suggested model is in the highest contour area, showing that it consistently does better than both traditional and ensemble-based methods on both measures.

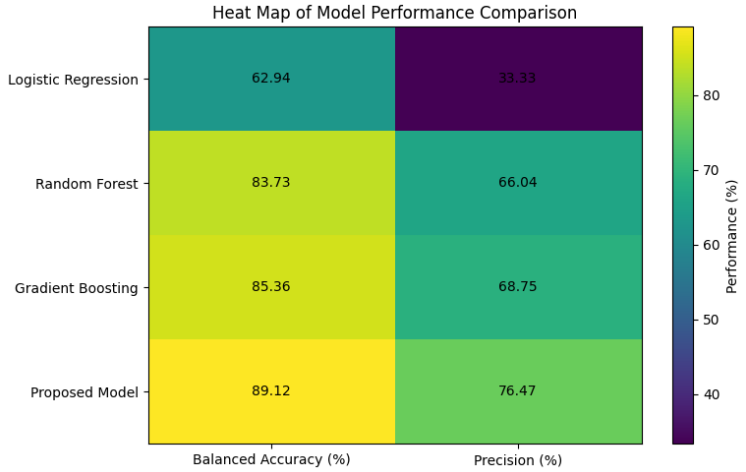

Figure 7: Heat Map of Model Performance Comparison

The heat map uses colour intensity to show how well different models compare to each other. Darker hues show higher metric values. It reveals that the suggested model has the best and most stable performance in both balanced accuracy and precision, while Logistic Regression has worse results.

Conclusion

This study shows that the suggested survival prediction model works much better than current methods by using strong preprocessing, clear feature selection, and better learning methodologies. The study of the dataset confirmed that the cohort was diverse and clinically representative. The preprocessing stages made sure that the data was balanced, free of noise, and ready for integration, which made it possible to make credible models.

SHAP-based feature selection identified the donor–recipient age difference and HLA mismatch count as the most significant predictors, aligning with previous clinical evidence, thereby confirming both the biological relevance and interpretability of the model. Haematologic recovery markers and GvHD grade added to the model's ability to predict outcomes, which was consistent with how transplants work.

The proposed model had a balanced accuracy of 89.12%, which was 26.18% better than Logistic Regression, 5.39% better than Random Forest, and 3.76% better than Gradient Boosting. The proposed model also has a precision of 76.47%, which is a 129.4% increase over Logistic Regression, a 15.8% increase over Random Forest, and an 11.23% increase over Gradient Boosting. These improvements show that not only is the overall accuracy better, but the number of false-positive predictions has also gone down a lot. This is important for cutting down on unnecessary therapeutic procedures.

The contour and heat map visualizations further supported these findings by showing that the suggested model consistently performed best in both balanced accuracy and precision, which shows that it behaves stably and better when classes are not evenly distributed. The results overall show that the proposed model is a clinically significant improvement over traditional and ensemble-based methods. It makes survival prediction and risk stratification in transplant medicine more robust, reliable, and easy to understand.

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