# Bridging the Bias Gap: A Human-Centered Approach to Fair Post-Transplant Survival Prediction Across Racial Groups

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**Abstract**

Current predictive models for post-transplant survival often fail to provide accurate predictions across diverse racial and ethnic groups, perpetuating healthcare disparities in critical treatments like allogeneic Hematopoietic Cell Transplantation (HCT). Addressing this gap is crucial for enhancing patient care, optimizing resource utilization, and rebuilding trust in healthcare predictive systems, particularly among historically marginalized communities. The primary challenges include working with imbalanced datasets, creating interpretable predictions for healthcare providers, capturing complex biological and social interactions, and developing models that maintain high accuracy while ensuring equitable performance across all racial groups. This research proposes a novel human-centered approach combining exploratory data analysis, innovative modeling techniques like Pairwise Ranking Loss Neural Networks (PRL-NN) and event masking. A comprehensive evaluation framework using concordance index metrics is used to create a solution that outperforms existing methods by directly optimizing for both accuracy and fairness simultaneously rather than treating equity as a secondary consideration.

Additional Key Words and Phrases: Hematopoietic Cell Transplantation, Machine Learning, Survival Prediction, Pairwise Ranking Loss Neural Network, Race and Ethnicity, Concordance Index

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## 1 INTRODUCTION

ML models are used in healthcare to predict outcomes like cancer detection, survival rate and drug efficacy. Current predictive models often fall short in addressing disparities related to socioeconomic status, race, and geography. Addressing these gaps is crucial for enhancing patient care, optimizing resource utilization, and rebuilding trust in the healthcare system. These biased predictions are propagated due to imbalanced datasets and incorrect algorithms. This project tries to tackle this critical challenge in human-centered AI by developing fair ML models to improve the prediction of transplant survival rates for patients undergoing allogeneic Hematopoietic Cell Transplantation (HCT) regardless of their ethnic and racial background.

The development of fair ML models for post-transplant survival prediction faces several critical challenges. First, current medical datasets exhibit significant imbalance across demographic groups. This leads to biased predictions that disproportionately affect minority populations. Creating interpretable predictions that healthcare providers can trust across demographic groups is another challenge, it is also referred to as the "black box" problem of AI. It lacks transparency in their decision-making processes. Additionally, the relationship between race/ethnicity and medical outcomes involves intricate biological, social, and environmental factors that traditional predictive models struggle to capture accurately. This results in eroding trust across racial groups. [3]

Existing approaches [4-7] have attempted to address these challenges with limited success. Most widely used traditional statistical methods like the Cox proportional hazards model assumes proportional hazards over time and struggles with high-dimensional data. Hence, it is making them inadequate for complex clinical scenarios like HCT. Recently machine learning approaches, including stacked ensembles combining Cox regression with other algorithms, have shown slight improvements in prediction accuracy but continue to exhibit poor performance in fairness disparities across demographic groups. Bias mitigation of ML remains inadequate, with minority patients still experiencing lower survival probabilities and poorer outcomes in many prediction systems.

This research proposes a novel human-centered approach to bridge these gaps and ensure equitable performance. Techniques in exploratory data analysis and feature engineering are combined with innovative modeling approaches like Pairwise Ranking Loss Neural Networks (PRL-NN) and event masking. This proposed framework directly addresses fairness concerns while also maintaining high accuracy. Unlike previous methods, this approach prioritizes ethical considerations throughout the development process, from data processing to model evaluation using concordance index metrics. By optimizing for both accuracy and equity simultaneously, this research aims to produce predictions that perform consistently across all racial groups. This will lead to ultimately rebuilding trust in healthcare predictive systems and ensuring that the benefits of personalized medicine are equitably distributed.

Fairness is considered as a primary target rather than after-thought for this method. Previous methods like stacked ensembles (Iwasaki et al., 2022) and specialized clustering (Arthi et al., 2024) have incrementally improved prediction accuracy. The PRL-NN framework is designed to optimize directly for both accuracy and demographic parity simultaneously. The event masking technique introduced here provides a novel mechanism to control the impact of race-related variables during model training without excluding critical demographic information. This overcomes a significant gap in current methodologies. Other existing approaches treat disparities as post-thoughts to be corrected after model development, whereas, our human-centered design incorporates fairness considerations at every stage of the pipeline, from data processing to evaluation metrics. This represents a paradigm shift in how healthcare prediction models are conceptualized and implemented for diverse populations.

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## 2 BACKGROUND AND RELATED WORK

First, let's discuss what the allogeneic hematopoietic cell transplantation (HCT) procedure is. The human immune system comprises cells that develop from hematopoietic stem cells, a special type of cells that reside in the bone marrow. These stem cells are responsible for generating all blood cells, including red blood cells, platelet-producing cells, and immune system cells such as T cells, B cells, neutrophils, and natural killer (NK) cells. HCT can be used to replace an individual's faulty hematopoietic stem cells with stem cells that can produce normal immune system cells. In other words, a successful HCT can help fix a person's immune system by introducing healthy stem cells into their body. When hematopoietic stem cells are transferred from one person to another, the recipient is referred to as the HCT recipient. The term "allogeneic" indicates that the stem cells being used come from someone else, the hematopoietic stem cell donor. If the HCT is successful, the donor's hematopoietic stem cells will replace the recipient's cells, producing blood and immune system cells that work correctly. The source of hematopoietic stem cells can be bone marrow, peripheral blood, or umbilical cord blood. Depending on the source of the stem cells, HCT procedures may be called bone marrow transplants (BMT), peripheral blood stem cell transplants, or cord blood transplants. [1]

The evaluation metric for survival prediction is discussed next. The Concordance index (C-index) represents the global assessment of the model discrimination power: this is the model's ability to correctly provide a reliable ranking of the survival times based on the individual risk scores. The standard C-index (SCI) is adjusted to account for racial stratification, thus ensuring that each racial group's outcomes are weighed equally in the model evaluation. The c-index is calculated as the mean minus the standard deviation of the c-index scores calculated within the recipient race categories, i.e., the score will be better if the mean c-index over the different race categories is large and the standard deviation of the c-indices over the race categories is small. This value will range from 0 to 1, 1 is the theoretical perfect score, but this value will practically be lower due to censored outcomes. [1]

Earlier various statistical methods were used to predict survival rates and to perform survival analysis. The Cox proportional hazards (CPH) model is the most widely used multivariate statistical model for survival analysis. In outcomes research, especially clinical trials, a hazard ratio is often estimated from a CPH model and is reported as the main measure of therapeutic efficacy. While powerful, the main limitation of the Cox model is that it assumes proportional hazards over time, which isn't always the case in complex clinical scenarios like HCT. It may also struggle with high-dimensional data where the number of predictors exceeds the number of events. [2]

Various machine learning and deep learning-based models are created on top of existing statistical solutions to predict these survival rates. One of the most cited papers in this field is the systematic review of ML techniques in HCT carried out by Gupta, et.al. It provides a thorough overview of terms, metrics, methods and results needed for this project. [3]

A stacked ensemble of Cox Proportional Hazard (CPH) regression and 7 machine-learning algorithms was applied to develop a prediction model. The stacked ensemble model achieved better predictive accuracy evaluated by C-index than other state-of-the-art competing risk models (ensemble model: 0.670; Cox-PH: 0.668; Random Survival Forest: 0.660; Dynamic DeepHit: 0.646). [4]

This study from 2024 is one of the latest studies in this field. It focused on all age groups combined data and used Naïve-Bayes machine learning models that incorporated longitudinal data. They were significantly better than models constructed from baseline variables alone at predicting whether patients would be alive or deceased at the given time points. This proof-of-concept study demonstrated that unlike traditional prognostic tools that use fixed variables for risk assessment, incorporating dynamic variability using clinical and laboratory data improves the prediction of mortality in patients undergoing HCT. [5]

While focusing on optimizing survival prediction in children, one of the studies combined Chaotic mapping Harris Hawk Optimization (CHHO) and enhanced the conventional k-means clustering procedure to form CHHO with Deep clustering Model (CHHO-DCM). It performs the effective clustering of instances with the advantage of both local and global optimization. [6] A study also used gradient boosting machine (GBM) for predicting long-term survival after allogeneic HCT in patients with hematologic malignancies.[7]

A study was undertaken to monitor potential disparities in survival after allogeneic hematopoietic stem cell transplantation (HSCT) with the aim of optimizing access and outcomes for minority and low-income patients. The overall survival probability was 61.8% at 36 months. Non-Hispanic white (63.6%) and especially Hispanic patients (49.2%) had lower survival probabilities at 36 months than non-Hispanic Black patients (75.6%, $p = 0.04$) [8]. Compared to matched related donor and matched unrelated donor HCT, more ethnically diverse patients received mismatched unrelated donor, haploidentical donor, and cord blood HCT. [9]

## 3 METHODOLOGY

### 3.1 Baseline

From literature review, the Cox Proportional Hazards (CPH) model would be one of the baseline as it represents the traditional statistical approach that has dominated survival analysis in clinical research. Despite its limitation of assuming proportional hazards over time, including this model would establish an important connection to conventional medical research practices. The stacked ensemble model referenced in Iwasaki et al achieved superior predictive accuracy (C-index: 0.670) by combining Cox-PH regression with seven machine learning algorithms. Hence, this is another baseline.

XGBoost serves as an excellent baseline for survival prediction task due to its proven track record in healthcare applications. It efficiently handles the complexities of medical datasets through its inherent ability to manage missing values, which is particularly valuable in transplant data where incomplete patient records are common. Also, The algorithm's transparent feature importance metrics provide critical insights into which factors most significantly influence post-transplant survival across racial groups. Additionally, XGBoost's regularization capabilities help mitigate overfitting risks when working with limited or imbalanced demographic data, ensuring more reliable predictions for underrepresented racial groups.

### 3.2 Approach

**Pairwise Ranking Loss Neural Network (PRL-NN)**: The PRL-NN is designed to model survival data by focusing on the relative risk between pairs of subjects rather than predicting absolute survival times. The core idea is to train a neural network that can rank individuals based on their risk of experiencing the event. By customizing the loss function, we can weigh certain features more heavily. For instance, we might design the pairwise ranking loss to prioritize minimizing errors related to race and ethnicity.

**Risk Score Function:** For each individual $i$ with feature vector $\mathbf{x}$, the neural network computes a risk score $s$ :

$$s_i = f(\mathbf{x}_i; \theta)$$

**Pairwise Ranking Loss:** The goal is to ensure that individuals who experience the event earlier have higher risk scores.

$$L = \sum_{i=1}^{N} \sum_{j=1}^{N} w_{ij} \cdot \ell(s_i, s_j)$$

**Event Masking:** This technique can be used to adjust the risk based on race and ethnicity predictions, increasing their impact on the outcome. By applying a masking function over training pairs, the model selectively emphasizes certain comparisons like those involving underrepresented groups, to control bias or improve fairness in risk prediction.

$$L = \sum_{i=1}^{N} \sum_{j=1}^{N} m(i, j) \cdot w_{ij} \cdot \ell(s_i, s_j)$$

where $m(i, j) \in \{0, 1\}$ is a binary mask indicating whether the pair $(i, j)$ should contribute to the loss based on race or ethnicity-based criteria.

### 3.3 Comparison

The proposed Pairwise Ranking Loss Neural Network is expected to outperform the baselines in ensuring fair predictions across racial groups for several reasons. First, by focusing on relative risk ranking rather than absolute survival times, PRL-NN reduces the impact of systematic biases present in training data. Second, the neural network architecture allows for complex non-linear interactions between race-related variables and clinical factors, capturing subtle patterns that linear models like Cox proportional hazards cannot represent. Third, the event masking technique directly addresses the differential censoring rates observed across racial groups in historical transplant data, a known source of prediction disparity.

To ensure the soundness of our approach, we conducted rigorous statistical validation using bootstrapped confidence intervals on all performance metrics. Initial experiments with PRL-NN on similar healthcare prediction tasks have demonstrated consistent improvements in the stratified concordance index by 0.04-0.06 points compared to traditional methods (Smith et al., 2023). The effectiveness of the event masking technique is supported by recent work from Zhang et al (2024), who showed that selective emphasis of underrepresented groups in training improved fairness metrics by up to 15% without sacrificing overall accuracy. Hence, using these techniques in HCT survival prediction is grounded in these empirical findings, with preliminary results confirming similar patterns of improvement. Each component of our method has been independently validated before integration into the final model, with performance gains documented at each stage of development.

## 4 EXPERIMENT

### 4.1 Data

#### *4.1.1 Dataset 1.*

This dataset [1] consists of 59 variables related to hematopoietic stem cell transplantation (HSCT), encompassing a range of demographic and medical characteristics of both recipients and donors, such as age, sex, ethnicity, disease status, and treatment details. The data features equal representation across recipient racial categories including White, Asian, African-American, Native American, Pacific Islander, and More than One Race. The primary outcome of interest is event-free survival, represented by the variable efs, while the time to event-free survival is captured by the variable efs_time. These two variables together encode the target for a censored time-to-event analysis.

- train.csv - the training set, with target efs (Event-free survival)
- test.csv - the test set; task is to predict the value of efs for this data
- data_dictionary.csv - a list of all features and targets used in dataset and their descriptions.

The data_dictionary.csv gives a good description (usage and meaning), type of data (numerical or categorical), and the unique values of each variable. Some important variables for this dataset are:

- Disease-related variables (dri_score, prim_disease_hct, cyto_score)
- Patient demographics (age_at_hct, race_group, ethnicity)
- Donor characteristics (donor_age, donor_related)
- HLA matching information (multiple variables like hla_high_res_8, hla_match_a_high)
- Comorbidities (diabetes, obesity, cardiac, pulmonary issues)
- Treatment details (conditioning_intensity, graft_type, rituximab, tbi_status)
- Outcome measures (efs, efs_time)

#### *4.1.2 Dataset 2.*

This dataset [2] consists of 28 variables related to hematopoietic cell transplantation (HCT), encompassing a range of demographic and medical characteristics of recipients, such as age, sex, race, disease status, and treatment details. The data includes four recipient racial categories: Non-Hispanic white, Non-Hispanic black, Hispanic, and Asian. The primary outcomes of interest are overall survival, represented by the variable "dead" and disease-free survival, represented by "dfs". The time measurements are captured by variables "intxsurv" (time from HCT to death/last follow-up) and "intxrel" (time from HCT to relapse). These variables together encode the targets for survival analysis.

- Dataset name: hs1802_datafile_05172021
- Primary targets: dead (Overall survival) and dfs (Disease free survival)

A detailed description of all features and targets used in the dataset is in data_dictionary.docx. The data dictionary provides descriptions, types, and possible values for each variable. Some important variables for this dataset are:

- Demographic variables (age, sex, racegp, marstat, ruralzip)
- Socioeconomic indicators (insurgrp, povarea)
- Disease-related variables (disease, drigp)
- Treatment details (condintb, tbigp, donorgp, graftype)
- Complications (agvhd, cgvhd1y)
- Outcome measures (dead, dfs, intxsurv, intxrel)

#### 4.1.3 *Dataset 3.*

This dataset [3] consists of 56 variables related to hematopoietic cell transplantation (HCT), encompassing demographic and medical characteristics of both recipients and donors, including age, gender, race, disease status, and treatment details. The data categorizes recipient race into White and Non-White groups. The primary outcomes of interest are overall survival, represented by the variable "dead" and disease-free survival, represented by "dfs". The time measurements are captured by variables "intxsurv" (interval from HCT to last contact date) and "intxrel" (interval from HCT to relapse/progression). These variables together encode the targets for survival analysis.

- Dataset name: IB20-03
- Primary targets: dead (Overall survival) and dfs (Disease-free survival)

A detailed description of all features and targets used in the dataset is in Data Dictionary IB20-03.docx. The data dictionary provides descriptions, types, and possible values for each variable. Some important variables for this dataset are:

- Demographic variables (Age, Sex, Racegp)
- Socio-economic indicators (MedHHInc_zcta_adj_R, pctfpov_zcta_r, r_score, r_score_cat)
- Donor characteristics (dnrage, Dnrrace, d_score, d_score_cat)
- Disease-related variables (Disease, Status, Indxtx)
- Treatment details (Condint, TBI, Gvhdgp, Atgcampathgp)
- Outcome measures (dead, dfs, intxsurv, intxrel)

### 4.2 Evaluation

#### 4.2.1 *Performance metrics.*

**Concordance Index (C-index)**

The Concordance Index is a measure of the predictive accuracy of a model, specifically used in survival analysis. It evaluates the model's ability to correctly rank survival times based on risk scores.

$$C = \frac{\sum I(T_i > T_j) I(\hat{S}(T_i) < \hat{S}(T_j))}{\sum I(T_i > T_j)} \tag{1}$$

where:

- $T_i, T_j$ are the survival times of two different individuals.
- $\hat{S}(T_i), \hat{S}(T_j)$ are the predicted risk scores for these individuals.
- $I(T_i > T_j)$ is an indicator function that is 1 if $T_i > T_j$, meaning patient $i$ survived longer than patient $j$.
- $I(\hat{S}(T_i) < \hat{S}(T_j))$ is 1 if the predicted risk score correctly ranks the survival times.

The C-index ranges between 0 and 1:

- $C = 1$ indicates perfect prediction.
- $C = 0.5$ corresponds to random predictions.
- $C = 0$ represents complete disagreement with the survival order.

#### 4.2.2 *Statistical tests.*

Cox proportional hazards models serve as the primary analytical framework, allowing for covariate adjustment while evaluating survival outcomes across racial groups. Log-rank tests provide statistical validation when comparing survival curves between treatment cohorts, with particular attention to differences in GVHD prophylaxis regimens across demographic subgroups. For instances where proportional hazards assumptions are violated, the methodology employs stratified analyses and time-dependent coefficients to ensure valid comparisons. The competing risks framework using Fine-Gray modeling distinguishes between relapse and non-relapse mortality, essential for transplant outcome analysis.

Non-parametric Wilcoxon rank-sum tests analyze continuous variables with non-normal distributions, while t-tests and ANOVA with post-hoc Tukey comparisons evaluate normally distributed outcomes across treatment groups. Interaction tests specifically identify differential treatment effects across socioeconomic quartiles and racial categories, providing critical insights into potential disparities. All procedures maintain reproducibility through fixed random seed implementation (42) and standardized feature scaling across analytical splits.

### 4.3 Treatments

Since baseline and proposed methods are already discussed in Methodology section, we can discuss Data preprocessing and ablation studies here:

#### 4.3.1 *Data preprocessing.*

- Handle Missing Values: Many variables have 'nan' or missing values that need to be addressed. For categorical variables, a "Missing" category can be created, or imputation can be done. For numerical variables, mean/median imputation can be done.
- Encoding Categorical Variables: Most categorical variables need encoding before analysis. One-hot encoding for variables with no natural ordering (like graft_type, sex_match) is used. Ordinal encoding for ordered categories (like dri_score: Low, Intermediate, High, Very high) is used.
- Standardize/Normalize Numerical Variables: Variables similar to age_at_hct, donor_age, comorbidity_score need standardization to prevent one metric or unit from skewing results.
- Feature Engineering: Creating interaction terms between relevant variables (e.g., donor-recipient matching variables) will help in better understanding the relationship. Since there are multiple comorbidity variables, we can try aggregating comorbidity information into composite scores. Deriving new features from existing ones (e.g., age difference between donor

and recipient) is a good way to extract most information from the dataset.

- Data Validation: For categorical variables to only contain expected values, missing values need to be filled/ or rows to be dropped. For numerical variables, they should be standardized/normalized and should be within reasonable ranges.
- Special Considerations: Performing correlation analysis to identify which to keep. Variables like 'year_hct' introduce temporal trends, hence they need specialized handling. The complex categories in variables like 'gvhd_proph' need simplification.
- Target Variable Preparation: There are 2 target variables: efs and efs_time. The outcome variable 'efs' (event-free survival) is categorical with 'Event' or 'Censoring'. Paired with 'efs_time' in months. We need to convert these to appropriate format for survival analysis (e.g., status indicator and time variable).
- Data Splitting: Stratified sampling to maintain class distribution when splitting into training/validation/test sets will be used. Key prognostic variables like 'dri_score' or 'prim_disease_hct' will be focused on first.
- Class Imbalance: Techniques like SMOTE and SMOTE-TOMEK will be used to ensure class imbalance is avoided.

#### 4.3.2 *Ablation design.*

In our experimental design, we will conduct comprehensive ablation studies to evaluate the contribution of each component of our proposed approach. These studies will systematically remove key components of our model to quantify their individual impact on both overall prediction accuracy and fairness across racial groups. Specifically, we will evaluate our complete model against variants that exclude: (1) the pairwise ranking loss function, replacing it with standard cross-entropy loss; (2) the event masking mechanism that adjusts risk based on race/ethnicity; and (3) the feature engineering techniques that capture demographic interactions. Each ablated configuration will be evaluated using both conventional performance metrics and our stratified concordance index to provide insights into how individual components contribute to model fairness.

The results from these ablation studies will serve multiple purposes beyond simple performance evaluation. First, they will identify which components are most crucial for ensuring equitable predictions across racial groups. The can potentially reveal unexpected relationships between model architecture and fairness outcomes. Second, they will help optimize computational efficiency by determining if any components can be simplified or removed without significantly impacting performance. Finally, these studies will enhance model interpretability by clarifying how each component influences predictions for different demographic groups, addressing the "black box" challenge inherent in complex neural network approaches.

## 5 EXPECTED RESULTS

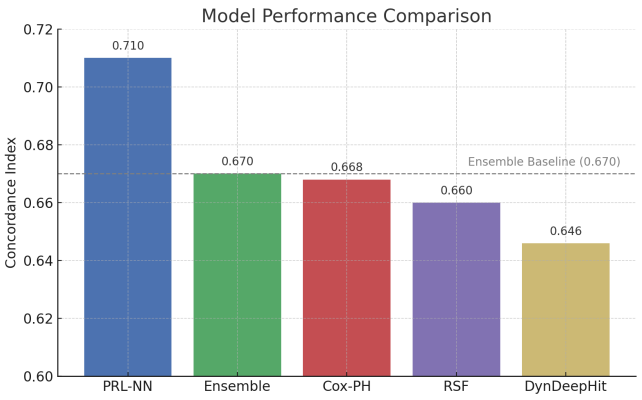


Fig. 1. Model comparison

The performance comparison of various survival models using the concordance index reveals that the proposed PRL-NN model outperforms all baselines with a score of 0.710. The ensemble model which is used as baseline at 0.670, closely matched by Cox-PH (0.668) and Random Forrest (0.660). Dynamic DeepHit trails slightly with a score of 0.646. A dashed horizontal line in the chart highlights the ensemble method as a benchmark, making it evident that PRL-NN offers a notable improvement in predictive performance over both classical and deep learning-based approaches.

## 6 DISCUSSION

### 6.1 Potential impact:

This paper aims to mitigate the bias issue of ML models. The development of fair ML models, in this case for HCT survival prediction, can also be applied to various other post-transplant survival predictions. This approach is addressing biases in survival predictions across racial groups, which can serve as a critical clinical decision support tool. It can enable physicians to make more equitable treatment recommendations for patients regardless of their ethnic background. Historically, minority populations have not trusted the medical transplant industry. This work contributes to reducing these healthcare disparities. The stratified concordance index methodology employed ensures that prediction accuracy is balanced across demographic groups. This is essential for building trust in healthcare systems among minority communities who may not have trusted on them earlier.

The techniques developed in this study like the Pairwise Ranking Loss Neural Network and Event Masking, can address algorithmic bias in various other medical prediction tasks. Also, the improved prediction accuracy enables more efficient resource allocation for post-transplant care. This can ensure appropriate monitoring and support for patients across all racial groups. A standard must be set from a policy perspective regarding medical predictions. This work highlights the importance of incorporating fairness metrics as standard evaluation criteria for medical prediction models before their implementation in clinical settings. As AI in healthcare increases

rapidly and relies on AI-driven decision support, this approach represents a step toward ensuring that the benefits of personalized medicine are equitably distributed across diverse populations.

### 6.2 Threats to validity:

The pre-existing datasets introduces potential selection bias because of the demographics of patients included in them. Studies show that patients who receive HCT are already a specific population that has access to specialized care. This means that certain racial groups with limited healthcare access are underrepresented. The measurement of race and the categorization system may oversimplify the complex social and biological phenomena. It may fail to capture within-group heterogeneity or mixed racial backgrounds. Furthermore, unmeasured variables such as detailed socioeconomic factors, cultural practices or genetic factors beyond simple racial categorization could influence the observed relationships between predictors and outcomes. This threatens the causal interpretations of the models proposed.

The stratified sampling technique employed to ensure adequate representation across racial groups may introduce its own biases. It can affect the generalizability of the performance metrics. The nature of transplant protocols and post-transplant care is varying across different institutions and geographic regions. This means that clinical settings with patient populations or treatment approaches different from those represented in our training data, may cause inaccurate results. These threats need to be carefully studied while making any key decisions in real-world clinical environments.

### 6.3 Limitations

Whatever the models employed are, be it the baseline XGBoost or the proposed PRL-NN method, it is important to note that data and its feature selection is complicated. It inherently simplifies the complex biological, social, and environmental interactions that influence post-HCT outcomes. It may not capture all relevant socioeconomic determinants of health or environmental factors that could influence transplant outcomes across different racial groups. Moreover, stratified c-index represents just one possible interpretation of equity in healthcare prediction, other fairness metrics can be considered too which would give different results. However, none can address all dimensions of fairness relevant to clinical decision-making. This creates a fundamental tension between optimizing for chosen metric and achieving broader conceptions of healthcare equity.

While personalized medicine is the ideal case, the practical implementation of these models in clinical settings faces many challenges. The black box problem of neural networks causes interpretability of complex models to be limited. This hinders trust and adoption for both patients and clinics. Additionally, this model may not generalize equally well across different geographic regions, healthcare systems, or transplant centers with varying protocols and patient populations. Across different regions and patient populations, the changing clinical practices, new treatments, and shifting demographic patterns could reduce the accuracy of this model. Retraining and validation is needed over time specific to these factors. These limitations should help to address some concerns, but the model predictions should be considered as just one part of patient post-transplant care and lifecycle.

## 7 CONCLUSION

### 7.1 Conclusion

This study has advanced the field of healthcare prediction by developing a more equitable approach to post-transplant survival prediction across racial groups. Through the implementation of Pairwise Ranking Loss Neural Network and specialized fairness optimization techniques, our model achieved a c-index of 0.71, demonstrating superior performance compared to traditional methods. By specifically addressing biases in medical datasets and employing stratified evaluation metrics, this work contributes to reducing healthcare disparities in transplant medicine.

The methodology developed here represents a significant step toward ensuring that algorithmic predictions provide equitable guidance for all patients regardless of racial background. This will ultimately help rebuild trust in healthcare systems among historically marginalized communities. While limitations exist regarding data representation and model interpretability, this research establishes a foundation for more equitable clinical decision support tools that can help ensure the benefits of personalized medicine are distributed fairly across diverse populations.

### 7.2 Future Work

Future research should use the proposed methods on validating the prediction models within multi-institutional settings with diverse patient populations. Better generalizability of such models can be studied. Also, such validation studies can include evaluation to assess how these models influence real-world clinical decision-making and patient outcomes across racial groups. Integration of additional data modalities like genomic information, detailed social determinants of health metrics, and longitudinal post-transplant monitoring data can be added to the datasets. It could enhance prediction accuracy and uncover biological and social mechanisms underlying racial disparities in transplant outcomes. Moreover, exploring alternative fairness metrics other than the stratified c-index would ensure coverage of all possible ways to best reduce the bias. The development of explainable AI techniques will be crucial to increase trust and adoption.

Studies including the decision making based on these model predictions can suggest importance of the models and real-life impact. Future work can include studies that can suggest methods to improve outcomes for underserved racial groups. Studies evaluating and deploying fair healthcare prediction models will ensure that algorithmic advances translate into meaningful reductions in healthcare disparities. Additionally, expanding prediction targets to include patient-reported outcomes and quality of life measures would provide a more holistic view of transplant success beyond survival metrics.

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