

Article

Predicting 1-Year Mortality in Patients with Non-ST Elevation Myocardial Infarction (NSTEMI) Using Survival Models and Aortic Pressure Signals Recorded During Cardiac Catheterization

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Abstract

Despite successful revascularization, patients with non-ST elevation myocardial infarction (NSTEMI) remain at higher risk of mortality and morbidity. Accurately predicting mortality risk in this cohort can improve outcomes through timely interventions. This study for the first time predicts 1-year all-cause mortality in an NSTEMI cohort using features extracted primarily from the aortic pressure (AP) signal recorded during cardiac catheterization. We analyzed data from 497 NSTEMI patients (66.3 ± 12.9 years, 187 (37.6%) females) retrospectively. We developed three survival models, the multivariate Cox proportional hazards, DeepSurv, and random survival forest, to predict mortality. Then, used Shapley additive explanations (SHAP) to interpret the decision-making process of the best survival model. Using 5-fold stratified cross-validation, DeepSurv achieved an average C-index of 0.935, an IBS of 0.028, and a mean time-dependent AUC of 0.939, outperforming the other models. Ejection systolic time, ejection systolic period, the difference between systolic blood pressure and dicrotic notch pressure (DesP), skewness, the age-modified shock index, and myocardial oxygen supply/demand ratio were identified by SHAP as the most characteristic AP features. In conclusion, AP signal features offer valuable prognostic insight for predicting 1-year all-cause mortality in the NSTEMI population, leading to enhanced risk stratification and clinical decision-making.

Keywords: non-ST elevation myocardial infarction (NSTEMI); mortality; aortic pressure; survival analysis; artificial intelligence



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1. Introduction

Acute myocardial infarction (AMI) remains a leading cause of mortality and morbidity [1], despite advances in percutaneous coronary intervention (PCI) and pharmacotherapy. AMI is primarily classified into two subtypes: ST elevation myocardial infarction (STEMI) and non-ST elevation myocardial infarction (NSTEMI). NSTEMI results from a partial blockage of coronary arteries (in the majority of cases), and the diagnosis is based on history, electrocardiogram (ECG) abnormalities, and increased levels of troponin, a cardiac-specific biomarker.

For patients with AMI, the management and clinical outcomes differ between STEMI and NSTEMI cases. STEMI patients are treated with either primary PCI (preferred) or

thrombolytic therapy as soon as possible from symptom onset. NSTEMI patients are recommended to be investigated by coronary angiography and revascularization within 48–72 h from presentation, unless they have ongoing chest pain and hemodynamic instability. The incidence of STEMI is decreasing, while the NSTEMI incidence has been rising [2,3]. Compared to patients with STEMI, those with NSTEMI tend to be older, have a greater number of cardiovascular risk factors, and present with more complex coronary artery disease [4,5]. The increasing clinical burden associated with NSTEMI highlights the importance of identifying patients at high risk for adverse outcomes. Early identification could enhance patient outcomes and optimize healthcare resource utilization by prioritizing care for those at higher risk.

Risk scores such as the thrombolysis in myocardial infarction (TIMI) [6] and the global registry of acute coronary events (GRACE) [7] were developed for predicting cardiovascular outcomes in patients with AMI [8,9]. Although these traditional risk scores are validated, their predictive accuracy at an individual patient level is limited, and they are generally not used in routine clinical practice. They assume a linear relationship between outcomes and risk factors, oversimplifying the complexity of cardiovascular disease. Additionally, these models primarily focus on conventional prognostic factors, ignoring many newer information sources and variables now identified as independent predictors of mortality. To overcome the limitations of traditional risk scores and enhance predictive capabilities, machine learning (ML) models have been widely used to predict adverse outcomes in patients with AMI, such as mortality (in-hospital, 30-day and 1-year) [10–12], readmission [13], and prolonged length of in-hospital stay [14].

Most ML methods for mortality prediction use binary classification (death/alive) or regression and ignore time-to-event information. In contrast, survival analysis incorporates time-to-event data and accounts for individuals who have not experienced the event during follow-up, known as censored cases. By considering the timing of events (deaths in case of mortality prediction), survival models can distinguish between events occurring within two weeks versus after 1 year, offering valuable clinical insights and improving patient prognosis. Earlier studies have shown promising performance in predicting mortality across various patient cohorts using survival models [15,16]. However, these studies primarily relied on continuous and categorical data from patients' admission records for survival analysis. With the rapid advancement of artificial intelligence, it is crucial to explore and evaluate new sources of information for identifying high-risk patients. The aortic pressure (AP) wave is a physiological marker describing cardiovascular health [17,18] and can provide valuable information about changing physiological status among patients undergoing coronary revascularization.

Our prior research, which examined the role of AP signals in predicting mortality and mobility among STEMI patients, was the first of its kind [12]. Here, we investigated the role of AP signals, recorded during cardiac catheterization, for predicting mortality in patients with NSTEMI. In addition, using the Shapley additive explanations (SHAP) method, we identified the role and predictive value of AP-derived features for this prediction. This provides a deeper understanding of the risk factors for high-risk patients and can be applied independently or in combination with other variables to enhance future ML-based risk prediction algorithms, thereby offering a promising avenue for improving risk stratification and clinical decision-making.

2. Materials and Methods

2.1. Study Design and Study Population

This retrospective study included data from patients with NSTEMI who were referred to St. Boniface General Hospital in Winnipeg, MB, Canada, for potential PCI between

January 2020 to October 2021. Their NSTEMI diagnoses were confirmed through a review of the electronic patient record (EPR). After reviewing patients' cardiac catheterization details, the AP signals recorded during PCI were captured by MacLab recording system (GE Healthcare, Milwaukee, WI, USA). MacLab is a device designed to record, display, and analyze cardiovascular data and is part of the comprehensive cardiac catheterization laboratory workflow infrastructure. Catheterization data included the ejection systolic time (EST, s/beat) and ejection systolic period (ESP, s/min), captured during the pullback of the catheter from the left ventricle to the aorta. ESP is a surrogate marker of cardiac output, and EST, a surrogate marker of stroke volume (blood flow per heartbeat), can be calculated by dividing ESP by heart rate. Patient demographics and risk factors were obtained from the EPR. The study was approved by the local research and ethics board at the University of Manitoba. An overview of the study is shown in Figure 1.

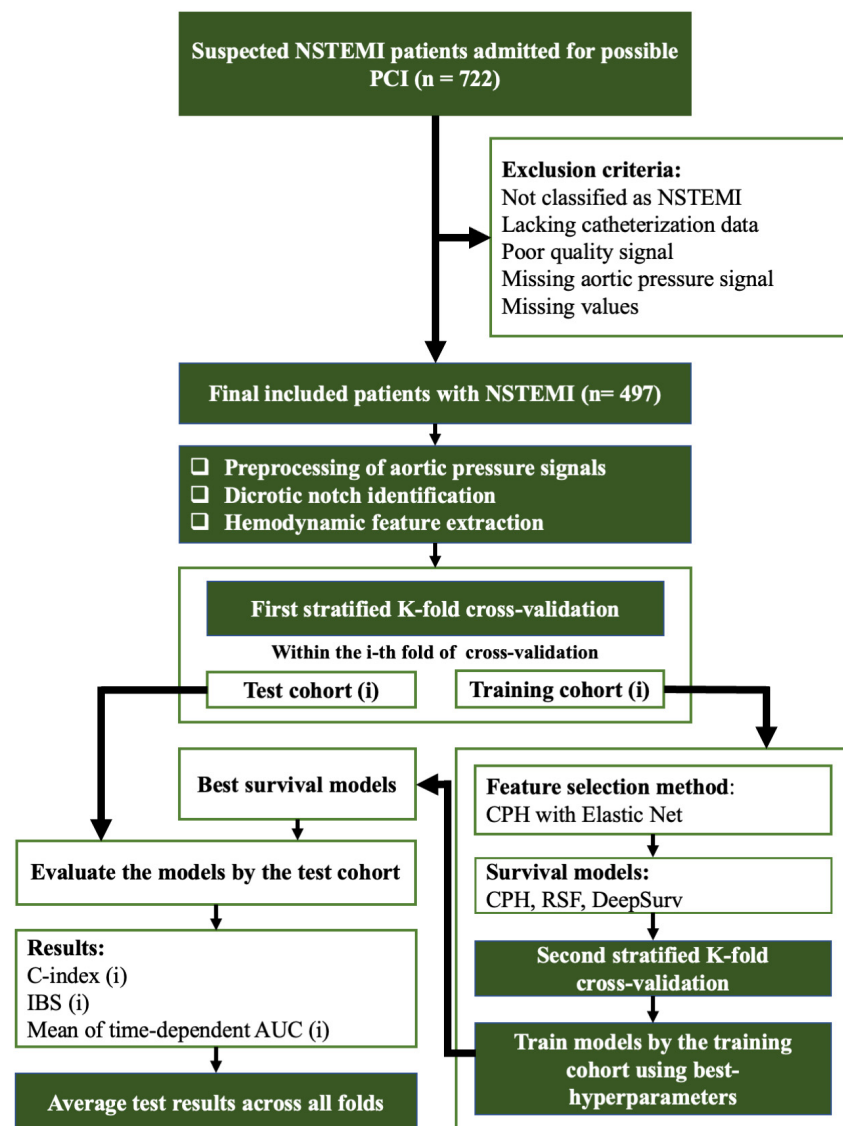


Figure 1. Block diagram of the proposed methodology. CPH = Cox proportional hazards, RSF = random survival forest, C-index= concordance index, and IBS = integrated brier score. The green squares highlight the key stages of the study, including signal preprocessing, feature selection, and the implementation of two stratified K-fold cross-validation steps for model development and evaluation.

2.2. Statistical Analysis

Categorical variables were analyzed using either the chi-square (χ^2) test or Fisher's exact test, depending on whether the sample sizes were large enough. Continuous variables were analyzed using either Student's *t*-test or the Mann–Whitney U-test based on the results of the Kolmogorov–Smirnov test for normality. A two-tailed test was employed to determine statistical significance, with a *p*-value threshold of 0.05. To standardize the data, z-score transformation was used. The effect size was assessed using the phi coefficient (ϕ) for categorical variables and Cohen's *d* for continuous variables.

2.3. Pre-Processing and Detecting Dicrotic Notch

Denoising the AP signal is an important step before extracting features. In this study, we used the denoising method described in our previous work investigating STEMI patients [19] because of its effective performance and to be comparable with the previous studies. The process starts by splitting the AP signal into smaller windows and discarding the noisy windows based on three characteristics: mean, standard deviation (SD), and Katz fractal dimension. Next, we detected the dicrotic notch (DN) using a rule-based method described in [12]. Figure A1 in Appendix A shows an example of an extracted AP waveform with the detected DN. As shown in Figure A1, DN appears as a local minimum after the systolic peak of the AP waveform, but it is not always clear and may sometimes be absent. To detect the DN, we applied a 15 Hz Butterworth low-pass filter to the signal and then calculated the first and second derivatives of the AP waveform. When DN was visible, we used the first-order derivative together with the systolic peak location [20]. A window was defined from the systolic peak to the midpoint between the peak and the end of the current AP waveform. Within this window, the major maximum in the first-order derivative was detected. The DN was then defined as the nearest minimum in the AP waveform moving toward the systolic peak from this maximum. If no DN was observed after the systolic peak, we identified the major minimum of the first derivative within the previously defined window of the AP waveform. From that point to the end of the window, we determined the location where the second derivative was zero [21].

2.4. Feature Extraction

After identifying the DN, we proceeded to extract a set of features from each AP waveform, as detailed in Table 1. The AP waveform is the cyclic change in pressure within the aorta as the heart pumps blood into it. While blood pressure is commonly expressed as two values (systolic and diastolic pressures), it contains far greater complexity and valuable information. This becomes evident when blood pressure is measured continuously, as demonstrated in Figure A1 in Appendix A. Many factors influence the AP waveform, and it can provide more comprehensive hemodynamic information about a patient than just systolic and diastolic pressures. In this study, we extracted various features, including absolute and relative pressures, durations, slopes, and areas, from different parts of the waveform, which contain valuable information about different parts of the cardiac cycle and may be helpful for predicting 1-year mortality in patients with NSTEMI. More information on the definition and the purpose of the extracted features is provided in Table A1 in Appendix A.

Except for the overall time, which represents the total duration of the cardiac catheterization procedure for each subject, all other features listed in Table 1 have multiple values. This is because a different number of AP waveforms were extracted for each subject, depending on the duration of their cardiac catheterization procedure. For each multi-value feature, four summary values were calculated: their mean, standard deviation (SD), and

the slope and intercept of a fitted line. Thus, regardless of the AP signal's duration, only four values were obtained per subject for each multi-value feature listed in Table 1.

Table 1. The extracted features. These extracted features are similar to the features we extracted from STEMI patients in our previous study [12].

Feature	Abbreviation	Definition
Absolute pressures		
Diastolic blood pressure	DBP	Min (p)
Systolic blood pressure	SBP	Max (p)
Mean aortic pressure	MAP	$(2 \times \text{DBP} + \text{SBP})/3$
Dicrotic notch pressure	DNP	p @ dicrotic notch
Relative pressures		
Pulse pressure	PP	$\text{SBP} - \text{DBP}$
Relative dicrotic notch pressure	rDNP	$\text{DNP} - \text{DBP}$
Dicrotic notch index	DNIx	$(\text{rDNP}/\text{PP}) * 100$
Descending pressure	DesP	$\text{SBP} - \text{DNP}$
Descending index	DesIx	$(\text{DesP}/\text{PP}) * 100$
Durations		
Duration heartbeat	DHB	(t @ end)
Heartrate	HR	$60/(\text{t @ end})$
Duration systole	DS	t @ dicrotic notch
Duration upstroke systole	DUS	t @ systolic peak
Duration downstroke systole	DDS	$\text{DS} - \text{DUS}$
Duration diastole	DD	$\text{DHB} - \text{DS}$
Descending time	DesT	$\text{DHB} - \text{DUS}$
Overall time	OT	whole time of the cardiac catheterization procedure
Slopes		
Systolic upstroke slope	SUS	$(\text{SBP} - \text{DBP})/\text{DUS}$
Systolic downstroke slope	SDS	$(\text{DNP} - \text{SBP})/\text{DDS}$
Maximum slope	MS	Max (p')
Areas		
Area under the pressure curve	AUCp	$\int p$
Systolic area	SysA	$\int p$ (systole)
Diastolic area	DiaA	$\int p$ (diastole)
Myocardial oxygen supply/demand ratio	O ₂ ratio	DiaA/SysA
Ascending area	AscA	$\int p$ (ascending portion of p)
Descending area	DesA	$\text{AUCp} - \text{AscA}$
Area ratio	AR	AscA/DesA
Other		
Fractal dimension of p	FDp	Kats FD of p
Skewness of p	SK	$E(p - \mu)^3/\sigma^3$
Kurtosis of p	KU	$E(p - \mu)^4/\sigma^4$
Spectral entropy of p	SE	- Sum (norm (PSD) $\times \log_2$ (norm (PSD)))
Average spectral power of p	Pave	Sum (PSD)/N
Maximum spectral power	MSP	Maximum amplitude of PSD
Maximum spectral power frequency	MSPF	Frequency of the maximum amplitude of PSD
Shock index	SI	HR/SBP
Age shock index	SI _{age}	$\text{Age} \times \text{SI}$
Modified shock index	mSI	HR/MAP
Age-modified shock index	mSI _{age}	$\text{Age} \times \text{mSI}$

p is a single AP waveform and p' is the first derivation of the waveform. t is time, N is the number of frequency bins, μ is the mean of samples of the waveform, σ is the standard deviation, $E()$ represents the expected value, FD is fractal dimension, and PSD is power spectral density.

To calculate the mean and SD, we first sorted all the values. We then removed the top and bottom 20% and calculated the mean and SD from the remaining values. The trimmed 20% mean is recommended in other studies [22]. It offers a balanced alternative to both the median and the mean. It also maintains high power in both sampling from normal

distribution and when there are outliers. The concept of using the slope and intercept of a fitted line as features was developed in our previous study, which focused on predicting prolonged length of in-hospital stay after cardiac catheterization and demonstrated its effectiveness [14]. To determine the slope and intercept for each multi-value feature, we fitted a first-order line to all values of that feature extracted from each AP waveform throughout the cardiac catheterization procedure for each subject. The slope and intercept of the fitted line were then used as summary values.

2.5. Feature Selection and Survival Models

To identify the most relevant features for survival modeling, we employed a Cox proportional hazards (CPH) model with elastic net regularization [23]. It combines L1 (Lasso) and L2 (Ridge) penalties, promoting both sparsity and stability in feature selection. As described in Figure 1, we used a stratified 5-fold cross-validation strategy to divide the dataset into training and test sets, and we performed feature selection on the training set of each fold to avoid data leakage. We identified the optimal values of the regularization parameter and the mixing parameter (balances between different penalty terms) in a grid search manner (using all possible hyperparameters settings combinations) with cross-validation.

Subsequently, we developed three survival models to predict 1-year all-cause mortality in patients with NSTEMI, using the multivariate CPH [24], DeepSurv [25] and random survival forest (RSF) [26]. The multivariate CPH is a semi-parametric model used in survival analysis. It is the most important model in survival analysis [27] and is widely used by researchers for survival analysis. A systematic review included 33 studies on predicting survival outcomes in patients with cardiovascular disease [28]. The review concluded that RSF and DeepSurv are currently the optimal models for predicting cardiovascular disease outcomes. It also noted that these two models are among the most widely used and best-performing approaches, showing strong results across different variable types and populations. Our focus in this study is to demonstrate the application and efficiency of features extracted from the AP signal as a new tool for predicting mortality in NSTEMI cohort. Therefore, instead of using newer survival models that might offer slightly better performance, we chose to apply the most commonly used models to ensure comparability with current and future survival analyses in patients with NSTEMI.

The models were trained on the features identified through the feature selection process, along with additional features from demographics, risk factors, and catheterization data. These additional features were selected based on their *p*-values and effect size. All the models and analyses were implemented using Python 3.12.7. The CPH and RSF models were developed using scikit-survival (version 0.23.1) [29], and the DeepSurv model was implemented using Pycox (version 0.3.0). More details on the developed survival models are provided in Appendix A.

2.6. Experimental Analysis

We used a two-layer stratified 5-fold cross-validation strategy (Figure 1). In the first layer, the dataset was divided into training and test sets while preserving the class distribution (survived and non-survived). The model's performance was assessed on the test set for each fold, and the results were averaged between the folds for final reporting. For the DeepSurv model, a slightly modified data splitting strategy was used. In each training fold of the 5-fold cross-validation, 15% of the training data was allocated as a validation set to identify the optimal epoch using early stopping. For clarification of the first layer of stratified 5-fold cross-validation, the dataset consisted of 497 patients, of whom 31 died within 1 year. For the CPH and RSF models, each fold included approximately

373 survived and 25 non-survived patients in the training set, and 93 survived and 6 non-survived patients in the test set. For DeepSurv, 15% of the training set (approximately 56 survived and 4 non-survived patients) was further used as a validation set for early stopping with a maximum of 1024 epochs. Within each outer fold, an inner stratified 5-fold cross-validation was used on the training set to fine-tune hyperparameters through a grid search, aiming to minimize overfitting. The full set of hyperparameter combinations evaluated for RSF and DeepSurv is presented in Table A2 in Appendix A.

The model's performance was evaluated using multiple metrics, including Uno's concordance index (C-index) [30], integrated brier score (IBS) [31], and time-dependent receiver operating characteristic (ROC) curve's area under the curve (AUC) [32]. Additionally, further evaluation of the optimal model was performed using decision curve analysis (DCA) [33]. We also plotted the 1-year ROC curve, which illustrates the sensitivity (true positive rate) against 1-specificity (false positive rate) across all possible thresholds, highlighting the model's discriminatory ability.

The C-index measures how accurately a model predicts the ordering of patients' survival times, with 0.5 indicating random prediction and 1.0 a perfect death-time prediction. The brier score (BS) assesses prediction accuracy in survival analysis. It is like the mean squared error in regression, with lower values indicating better performance. To improve interpretability over time, the IBS averages the BS across all prediction time points. The ROC curve in classification illustrates a model's performance across all possible thresholds. It plots the true positive rate (sensitivity) against the false positive rate (equal to one minus specificity). The AUC summarizes this trade-off and reflects the model's overall discriminative ability. In survival data, however, a patient's status changes over time, making sensitivity and specificity time dependent. To address this, the time-dependent AUC was introduced, which evaluates model discrimination at different time points even in the presence of censored data. The mean time-dependent AUC represents the weighted average of all time-dependent AUCs.

DCA evaluates net benefit by balancing true and false positives across threshold probabilities. The unit of net benefit is true positives. It is equal to the true positive rate minus the false positive rate weighted by the odds of the chosen threshold probability ($Pt/(1 - Pt)$, where Pt is the threshold probability). Thus, net benefit represents the net increase in true positive findings per patient population after accounting for false positives at the specified threshold probability. A model with a higher net benefit is considered to have greater clinical value [34].

2.7. Model Explanation and Feature Importance

To further enhance interpretability of the model's decision-making process, we used the SHAP [35] method. The SHAP method provides a solid theoretical foundation for explaining black-box models and has been shown to effectively enhance model interpretability [36]. Beyond improving interpretability, it also helps us compare features and identify the most characteristic ones.

3. Results

3.1. Patients' Characteristics

From a cohort of 722 patients, a total of 497 patients with a confirmed diagnosis of NSTEMI were included in the analysis. Patient selection has been described in Figure 1. The average age was 66.3 ± 12.9 years, with 37.6% (187 patients) being female. Within 1-year of hospital presentation, 31 patients (6.24%; 38.7% females) had died. For the remaining 466 patients (93.76%), no further information on survival status beyond the 1-year follow-up was available. These patients are considered censored, which can cause imbalance problems

when using standard binary classification methods. However, survival models can account for censored cases and more effectively estimate survival probabilities for patients at risk of death. Table 2 summarizes the demographics, risk factors, and catheterization data, comparing survived and non-survived patients. *p*-values indicate the statistical significance of the differences observed, while effect sizes describe their magnitude.

Table 2. Demographics, risk factors, and catheterization data for patients with NSTEMI and for 1-year mortality.

Characteristics	Total	No Death	Death < 1 Year	No Death vs. Death < 1 Year	
# of patients	497	466 (93.76%)	31 (6.24%)	<i>p</i> -value	Effect Size
Demographics					
Age, years	66.3 ± 12.9	65.5 ± 12.7	78.4 ± 10.2	****	1.02
Sex (female/male)	187 (37.6%)/ 310 (62.4%)	175 (37.6%)/ 291 (62.4%)	12 (38.7%)/ 31 (61.3%)	NS	0.01
Height, cm	168.86 ± 10.07	168.97 ± 10.08	167.29 ± 10.05	NS	0.17
Weight, kg	85.43 ± 21.04	85.74 ± 20.82	80.78 ± 23.97	NS	0.24
BMI, kg/m ²	29.83 ± 6.31	29.91 ± 6.28	28.53 ± 6.73	NS	0.22
Risk Factors					
Hypertension	359 (72.23%)	329 (70.60%)	30 (96.77%)	**	0.14
DM	187 (37.63%)	166 (35.62%)	21 (67.74%)	***	0.16
Dyslipidemia	279 (56.14%)	256 (54.94%)	23 (74.19%)	*	0.09
Stroke or TIA	34 (6.84%)	32 (6.87%)	2 (6.45%)	NS	0.00
PVD	30 (6.04%)	16 (3.43%)	14 (45.16%)	****	0.42
CKD	80 (16.10%)	66 (14.16%)	14 (45.16%)	****	0.22
Dialysis	9 (1.81%)	6 (1.29%)	3 (9.68%)	*	0.15
History of IHD	170 (34.21%)	153 (32.83%)	17 (54.84%)	*	0.11
PCI or CABG	140 (28.17%)	125 (26.82%)	15 (48.39%)	**	0.12
Catheterization Data					
ESP, s/min	18.68 ± 3.17	18.80 ± 3.17	16.80 ± 2.44	****	0.64
EST, s/beat	0.25 ± 0.04	0.25 ± 0.04	0.21 ± 0.04	****	1.07

Continuous and categorical variables are expressed as mean ± SD and number (percentage), respectively. *, **, *** and **** represent *p*-values less than 0.05, 0.01, 0.001 and 0.0001, respectively. NS = not significant, BMI = body mass index, DM = diabetes mellitus, TIA = transient ischemic attack, PVD = peripheral vascular disease, CKD = chronic kidney disease, IHD = ischemic heart disease, PCI = percutaneous coronary intervention, CABG = coronary artery bypass graft, ESP = ejection systolic period, and EST = ejection systolic time.

Figure 2 shows the Kaplan–Meier curves for the training and testing datasets in fold 3. A Kaplan–Meier curve shows how survival changes over time. There was no statistically significant difference in 1-year survival between the training and testing datasets (log-rank *p*-value = 0.93, Figure 2). The overlap between the two curves suggests that the distribution of deaths is similar across both groups. Another notable feature of the figure is the step-like shape of the Kaplan–Meier curves, which reflects the timing of observed deaths. Each downward step corresponds to a death occurring in either the training or testing dataset. Although censored patients are not directly shown, Kaplan–Meier curves inherently account for censoring, which is why the survival probability never truly reaches zero. The Kaplan–Meier curves for folds 1, 2, 4, and 5 are presented in Figures A2–A5 in Appendix A, respectively. Note that in Section 3, we only present the plots related to fold 3 as an example.

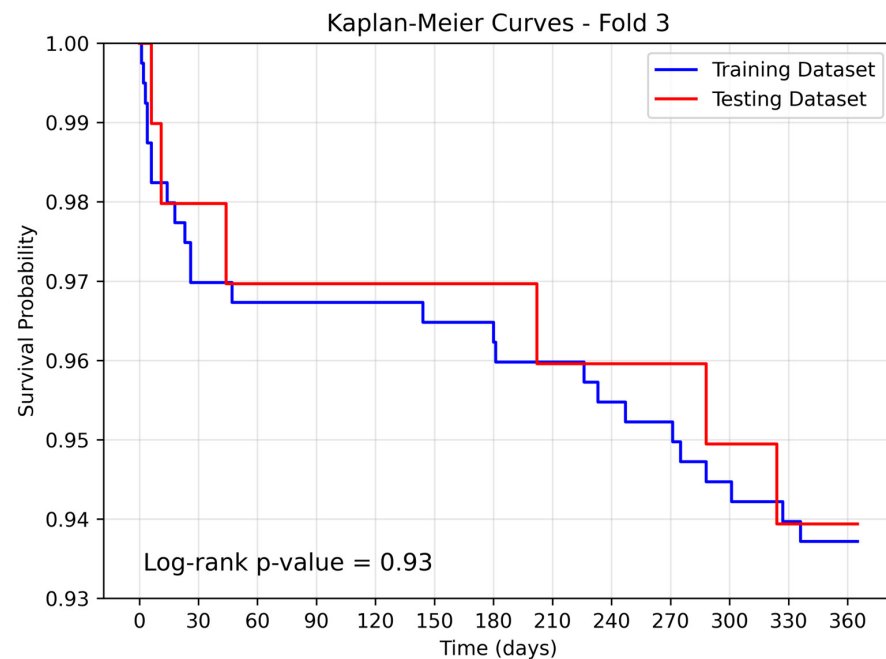


Figure 2. Kaplan–Meier curves of training and testing datasets of fold 3.

3.2. Results of Survival Analysis

As shown in the block diagram in Figure 1, we applied stratified 5-fold cross-validation to divide the data into training and test sets. For each fold, feature selection was performed only on the training set to prevent data leakage (or double-dipping). As a result, our developed feature selection method selected a different set of features for each fold, resulting in 12, 9, 9, 9, and 11 features being chosen for folds 1 to 5, respectively.

In addition to the features selected by our feature selection method (described in Section 2.5), we included additional information such as demographics, risk factors, and catheterization data (listed in Table 2). These additional features were chosen based on having a p -value < 0.01 and an effect size > 0.2 . The additional features selected for survival analysis were age, PVD (peripheral vascular disease), CKD (chronic kidney disease), ESP, and EST.

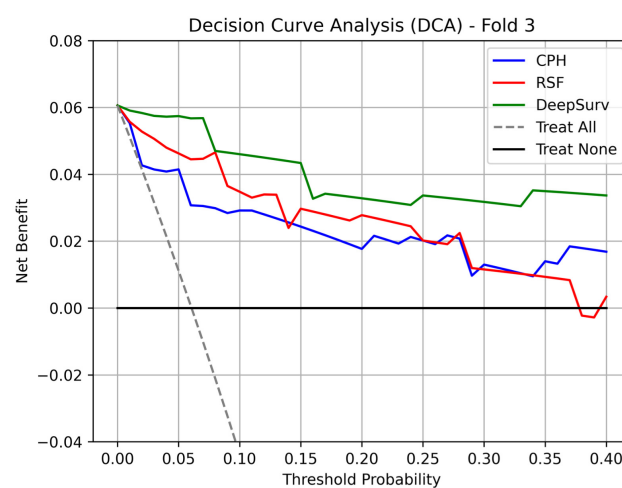
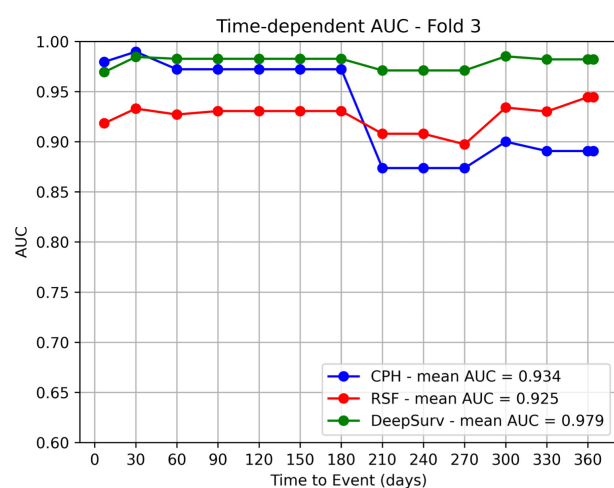
Table 3 presents the performance results of the survival models. We compared the C-index, IBS, and mean time-dependent AUC across all folds for all three developed survival models. DeepSurv performed better significantly with C-index and mean time-dependent AUC of over 0.9 for all folds, average IBS of 0.028 which outperformed CPH model and RSF. Figure 3 shows the time-dependent AUC, DCA, and ROC curves, for all models trained on fold 3 as an example. The time-dependent AUC, DCA, and ROC curves for the other folds are provided in Appendix A (Figures A6–A9).

Table 3. The performance of the models.

Model	Folds	Results		
		C-Index	IBS	Mean Time-Dependent AUC
CPH	Fold 1	0.869	0.030	0.868
	Fold 2	0.902	0.045	0.911
	Fold 3	0.887	0.034	0.934
	Fold 4	0.846	0.033	0.832
	Fold 5	0.894	0.040	0.897
	Average	0.880	0.036	0.888

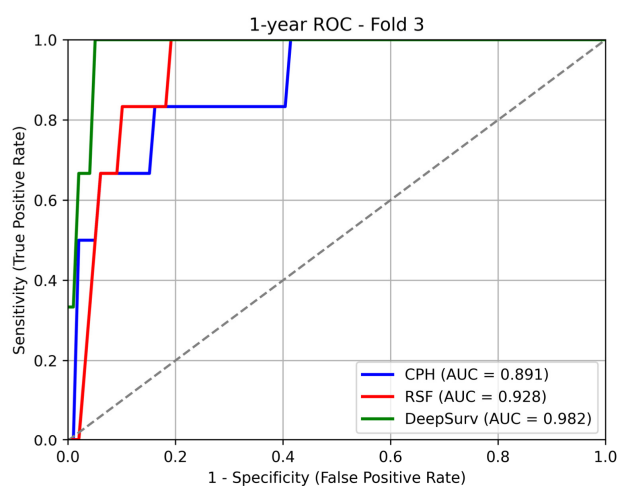
Table 3. *Cont.*

Model	Folds	Results		
		C-Index	IBS	Mean Time-Dependent AUC
RSF	Fold 1	0.902	0.033	0.900
	Fold 2	0.872	0.031	0.883
	Fold 3	0.921	0.030	0.925
	Fold 4	0.873	0.035	0.888
	Fold 5	0.904	0.035	0.908
	Average	0.894	0.033	0.901
DeepSurv	Fold 1	0.922	0.024	0.916
	Fold 2	0.906	0.031	0.918
	Fold 3	0.972	0.022	0.979
	Fold 4	0.944	0.029	0.954
	Fold 5	0.932	0.033	0.938
	Average	0.935	0.028	0.939



A

B



C

Figure 3. Performance of Cox proportional hazards (CPH), Random Survival Forest (RSF), and DeepSurv models on fold 3. **(A)** Time-dependent AUCs. **(B)** 1-year DCA. **(C)** ROC curves evaluated at 1-year. The diagonal dashed gray line depicts the line of no discrimination (AUC = 0.5).

3.3. Feature Importance Results Based on SHAP Method

To interpret the influence of the selected features on the model's predictions, we applied the SHAP method. The top 10 most impactful features were identified based on their mean absolute SHAP values, illustrated in Figure 4A for fold 3 of our 5-fold stratified cross-validation. Figure 4B presents the SHAP summary plot for fold 3, highlighting feature contributions and their direction of effect. SHAP results for folds 1, 2, 4, and 5 are shown in Figures A10–A13 in Appendix A, respectively.

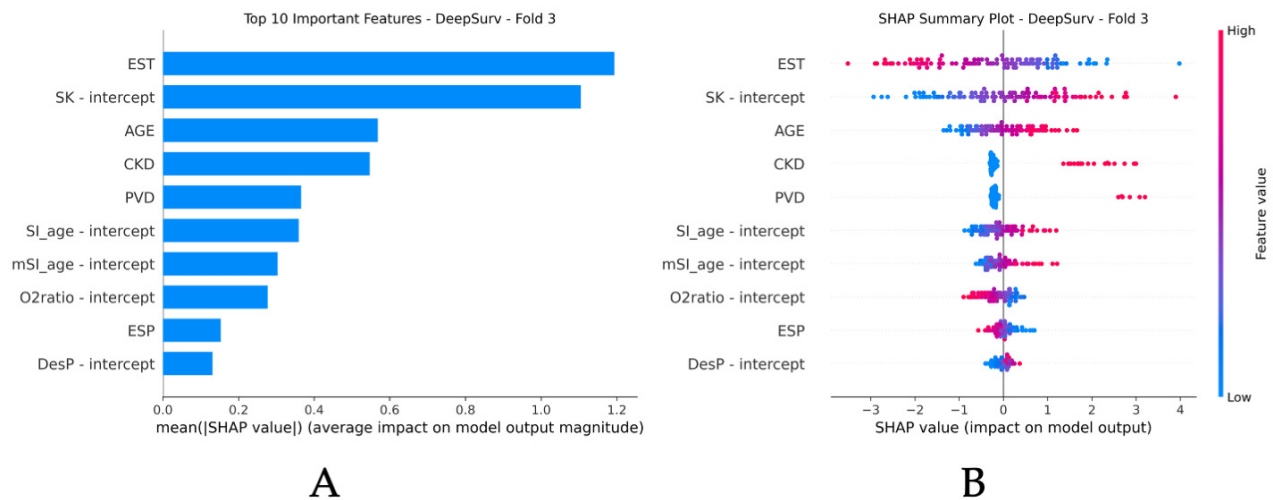


Figure 4. Model interpretation of DeepSurv on fold 3. (A) Importance ranking of the top 10 features based on the mean ($|SHAP\ value|$). (B) SHAP summary plot.

4. Discussion

This study is the first to investigate the application of features extracted from the AP signal recorded during cardiac catheterization to predict 1-year all-cause mortality in patients with NSTEMI. By combining the AP signal features with survival models, we achieved strong predictive performance in identifying patients at higher risk of mortality. Furthermore, through the application of the SHAP method, we identified the most characteristic features contributing to mortality prediction.

4.1. Comparison with Previous Studies on Predicting Mortality

Various studies have previously explored the possibility of using survival models for predicting mortality using different methodologies and patient cohorts. Similarly to this study, a study examining 9270 patients with acute coronary syndrome [15] compared CPH, RSF, and DeepSurv models and assessed their effectiveness in predicting 1-year mortality. In contrast to this study, in which DeepSurv performed better, their study found that RSF achieved the highest performance, with a Harrell's C-index of 0.924 on the test set. They also evaluated their models using external validation on 206,915 patients, where RSF demonstrated superior performance with a Harrell's C-index of 0.811.

There are other studies that focused on using RSF and CPH to predict mortality. In one of them [16], researchers evaluated the performance of RSF and CPH models in predicting mortality in 2990 patients with hemorrhagic stroke admitted to the intensive care unit. RSF consistently outperformed Cox regression, achieving higher mean AUCs for both 7-day (0.875 vs. 0.761) and 28-day (0.794 vs. 0.649) mortality predictions. Another study [37] included 893 patients with STEMI. Among them, 82 died (median overall survival 8.5 months) and 811 survived (median 37 months). Using LASSO regression, researchers selected 11 predictors to build CPH and RSF models. RSF consistently outperformed CPH, achieving a higher C-index (0.941 vs. 0.771), better cumulative/dynamic AUC

(0.698 vs. 0.613), and a lower BS (0.047 vs. 0.063). These two studies emphasized the predictive power of RSF and its strong performance in mortality prediction. Similarly, in our study, we also achieved better performance with RSF compared to CPH.

Although these studies share the goal of predicting mortality using survival models, they vary considerably in methodology, particularly in the selection of the patient's data and feature sets. These differences make direct comparison with our work challenging. However, our promising performance is comparable to findings from previous studies and highlights the strong predictive value of the features extracted from AP signals recorded during revascularization. In our previous study on patients with STEMI [12], we applied four different tree-based classifiers and used features extracted from the AP waveform to predict 1-year all-cause mortality. In that study, using binary classification, we achieved an average AUC of 0.82 for predicting 1-year mortality. This study expands on that work by using additional features extracted from the AP signal and applying a survival analysis framework. As a result, we improved performance, increasing the average AUC, and more importantly, we demonstrated the potential of AP-derived features for predicting mortality in patients with NSTEMI.

4.2. Prediction Results

DeepSurv outperformed both CPH and RSF models—not only on average but also across all folds. Although CPH and RSF produced lower performance compared to DeepSurv, they still achieved relatively high results. As a non-parametric model, RSF avoids the assumptions and limitations of CPH and DeepSurv, making it a strong alternative. These findings highlight the strong predictive power of our AP signal-derived features and survival models for mortality prediction in the NSTEMI cohort. We used grid search with cross-validation to tune model parameters and monitored for overfitting at every stage of model development. We ensured that the models generalize well and do not have overfitting.

DCA shows the clinical benefit of the models. The “Treat All” strategy assumes all patients are at risk, while the “Treat None” strategy assumes no patients are at risk. Compared to both strategies, our models show a higher net benefit over a range of threshold probabilities. Although we compared the net benefits of different models, further studies are required to validate our findings before implementing them in routine clinical practice. Specifically, identifying an appropriate range of threshold probabilities is essential to ensure that the models provide meaningful benefit. This decision should be informed by the relative harms of missing high-risk patients versus overtreating low-risk ones, as well as the availability of resources for delivering personalized treatment for high-risk patients.

The time-dependent AUC (Figures 3 and A6–A9 in Appendix A) illustrates how well each model discriminates between subjects who experience death by time t . Clinically, a higher time-dependent AUC indicates better risk stratification, meaning that at any given time point, the model more accurately ranks patients according to their risk. By comparing the figures, we observe that DeepSurv achieved a higher mean time-dependent AUC than all other models across all folds. For most time points, it also demonstrated superior discrimination and maintained consistently high AUC values, suggesting stable performance over time. When the curves cross, it implies that different models provide relatively better discrimination at different time points. For instance, in Figure 3A, the CPH model shows stronger performance before 180 days, while RSF demonstrates better discrimination after that point and through the remainder of the 1-year follow-up.

4.3. Characteristic Features

Using the SHAP method, we gained a deeper understanding of the characteristic features associated with 1-year mortality in the NSTEMI cohort. Identifying these features helps highlight clinical predictors that are correlated with mortality after cardiac catheterization. In addition, several more complex features identified by SHAP may be combined with other admission-derived variables to support the future development of ML models aimed at further improving prediction in this patient population. We considered two levels of characteristic features: first, features consistently selected among the top 10 most important across all folds; and second, features selected in at least four out of five folds in our developed DeepSurv model. Based on average SHAP values, EST, the difference between systolic blood pressure and DN pressure (DesP—intercept), skewness (SK—intercept), age, and CKD were consistently ranked among the top features across all folds. Additionally, ESP, the age-modified shock index (mSI_age—intercept), the myocardial oxygen supply/demand ratio (O2ratio—intercept), and PVD were selected in four out of five folds. The selected features highlight important aspects of the AP waveform associated with mortality.

In patients with myocardial infarction, age is a well-established independent risk factor for adverse outcomes, including mortality [38]. Advancing age is typically associated with a higher burden of comorbidities. CKD is associated with excess risk of developing cardiovascular disease [39], as well as cardiovascular and all-cause mortality [40]. Similarly, PVD is an independent cardiovascular risk factor that is also associated with adverse outcomes even in patients undergoing coronary revascularization [41].

In our analysis, EST and ESP were identified as the characteristic features based on the SHAP method. EST, or the duration of the ventricular contraction, is a surrogate marker of blood flow per heartbeat (also known as stroke volume). Our previous work demonstrated that EST has been independently associated with an increased risk of morbidity and mortality [42]. In the current study, using survival analysis, we demonstrated an association of both EST and ESP with a higher predicted probability of mortality in patients with NSTEMI. In addition, DesP was also identified by the SHAP method. It is defined as the difference between systolic blood pressure and DN pressure at the aortic level and serves as a marker of ventricular-arterial coupling. A lower DesP value indicates more efficient coupling and reduced systemic vascular resistance [43]. Skewness was selected in all folds and reflects the lack of symmetry in an AP waveform. As shown in the SHAP results, non-surviving patients seem to have higher skewness values. In a previous study [44], skewness and kurtosis were extracted from ECG leads and used as inputs to a deep neural network for the detection of myocardial infarction.

The age-modified shock index was selected in four out of five folds based on the SHAP method. In our previous work, we demonstrated its role in predicting prolonged length of in-hospital stay in patients with NSTEMI [14]. Similarly, another study [45] highlighted the predictive value of both SI_age and mSI_age for in-hospital cardiovascular events, as well as for 6-month and long-term all-cause mortality in patients with STEMI. The myocardial oxygen supply/demand ratio reflects the myocardial oxygenation, especially subendocardial myocardial ischemia due to imbalance between myocardial oxygen supply and demand [46]. Originally, the diastolic pressure-time index (DPTI), an indicator of oxygen supply to the myocardium, was calculated as the area between the diastolic aortic and left ventricular pressures, while the systolic pressure-time index (SPTI), an indicator of oxygen demand by the myocardium, was defined as the area under the left ventricular pressure curve during systole [46,47]. In our study, we estimated this ratio (DPTI/SPTI) by using the area under the diastolic portion of the AP waveform as a surrogate for DPTI (albeit we did not have left ventricular diastolic pressure) and the area under the systolic

portion as a surrogate for SPTI. The resulting supply/demand ratio (O2ratio) was identified as a characteristic feature in our analysis, highlighting its potential value in predicting adverse outcomes.

4.4. Limitations of the Study Features

Our study has several limitations. Firstly, the patient data was gathered from a single institution, which could potentially limit the generalizability of the findings. However, our hospital is the only center offering tertiary cardiac care within the province of Manitoba, Canada. Second, although we used stratified 5-fold cross-validation and the models performed well, the lack of external validation is an important limitation. This could affect how well our findings generalize to other patient groups, and future studies using independent datasets will be needed to confirm our findings. Third, we did not have access to all potential risk factors known to influence mortality prediction in NSTEMI patients, such as Killip class. Fourth, as described in the feature selection and survival models section, we chose to use the most commonly applied survival models in this study to ensure comparability with existing work and to demonstrate the effectiveness of AP-derived features. Although we achieved relatively high performance with DeepSurv, newer models and those with fewer assumptions may offer further improvements. For example, DeepHit could be advantageous because it does not rely on the proportional hazard assumption [48], and we plan to explore this model in future work. Fifth, we used stratified 5-fold cross-validation to maintain a balanced distribution of events across folds. However, given the small number of observed events and the use of all-cause mortality, some variability in SHAP feature ordering is expected. Expanding the dataset would likely further improve the stability and robustness of SHAP-based feature ranking. Finally, we were unable to compare our results with traditional risk scoring methods (such as the TIMI and GRACE scores) due to the unavailability of Killip class data, which is essential for calculating these scores [49]. Nevertheless, previous studies have demonstrated that ML approaches can outperform traditional methods in mortality prediction [10,11]. Moreover, our survival models also incorporate additional time-to-event information, making direct comparison with traditional methods challenging.

5. Conclusions

In conclusion, our study demonstrates that features extracted from AP signals can effectively identify high-risk NSTEMI patients. This novel framework, which relies on survival analysis, provides a predictive tool with the potential to enhance outcomes in high-risk NSTEMI patients by guiding more targeted management strategies. Further studies are necessary to validate these findings and to assess their broader applicability.

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Institutional Review Board Statement: This study was approved by the local Research and Ethics Board, University of Manitoba [REB: HS25542 (H2022:196)—approval date: 15 September 2023].

Informed Consent Statement: The authors confirm that patient consent is not applicable to this article. This retrospective study utilized deidentified data; therefore, individual patient consent was not required. The local REB approved consent waiver for this study.

Data Availability Statement: The datasets presented in this article are not readily available as the data are part of an ongoing study. Requests for accessing the dataset should be directed to Ashish H. Shah.

Conflicts of Interest: The authors declare no conflicts of interest.

Appendix A

Survival analysis aims to estimate the survival function $S(t)$, which represents the probability that a patient survives beyond a given time t . The survival function is defined in Equation (A1). Its values range between 0 and 1, and it is a non-increasing function of t .

$$S(t) = \Pr(T > t) \quad (\text{A1})$$

The Hazard function $h(x)$, shown in Equation (A2), is the probability of the death event occurring at time t , given that the subject has survived up to that time.

$$h(t) = \lim_{\delta t \rightarrow 0} \frac{\Pr(t \leq T \leq t + \delta t | T > t)}{\delta t} \quad (\text{A2})$$

In contrast to survival function, the hazard function does not start at 1 and decrease to 0. It changes over time, and a larger hazard value corresponds to a greater risk of death at that moment. The survival function is related to the hazard function, and they can be computed from one another, as shown in Equation (A3).

$$S(t) = \exp(-H(t)) \quad (\text{A3})$$

where $H(t)$ being the cumulative hazard function, defined as the integral of the hazard function $h(t)$:

$$H(t) = \int_0^t h(x) dx \quad (\text{A4})$$

Cox proportional hazards (CPH) is a semi-parametric model widely used in survival analysis. It assumes that all subjects share a common baseline hazard function, $\lambda_0(t)$, which is scaled by a factor determined by the subject's features. The hazard function for subject i is defined as:

$$h(t|X_i) = \lambda_0(t) \exp(X_i \cdot \beta_i) \quad (\text{A5})$$

where $X_i = (X_{i1}, \dots, X_{in})$ shows the feature vector for the patient i with n features, and $\beta_i = (\beta_{i1}, \dots, \beta_{in})$ represents the corresponding coefficients. The coefficients β are estimated by maximizing the partial likelihood. A key assumption, as we mentioned earlier, is the proportionality of hazards. This assumption was evaluated using the Schoenfeld residuals in this study. Additionally, CPH model assumes that outcome (in this study, mortality) is a linear function of input features.

DeepSurv extends the CPH model by replacing the linear risk function with a multi-layer feed forward neural network that captures nonlinear relationships among features. It allows non-linear relationships that the traditional CPH model cannot.

$$h(t|X_i) = \lambda_0(t) \exp(\psi(X_i)) \quad (\text{A6})$$

Here, $\psi(X_i)$ represents a nonlinear transformation of the input features, parameterized by the weights of the neural network.

Random survival forest (RSF) is a non-parametric model and an extension of the traditional random forest algorithm, designed to handle right-censored survival data. Instead of building trees for classification or regression, RSF grows survival trees that can directly handle censored patients by using modified splitting rules and stopping conditions.

At each node of a tree, beginning from the root, patients are divided into two groups based on a chosen feature and threshold. The algorithm chooses the split that maximizes the difference between the survival curves of the resulting groups. Whereas regression and classification trees typically use variance or Gini impurity to decide where to split, survival forests usually rely on the log-rank splitting rule. This recursive splitting continues until a stopping condition is reached, such as maximum depth, or when no further meaningful division is possible.

Each survival tree provides an estimate of the cumulative hazard function for individuals in its terminal nodes, typically via the Nelson-Aalen estimator. The ensemble cumulative hazard function is then obtained by averaging the cumulative hazard functions across all trees in the forest. From this, the survival function can be derived using Equation (A3). This approach allows RSF to model complex, nonlinear relationships without relying on proportional hazards or linearity assumptions.

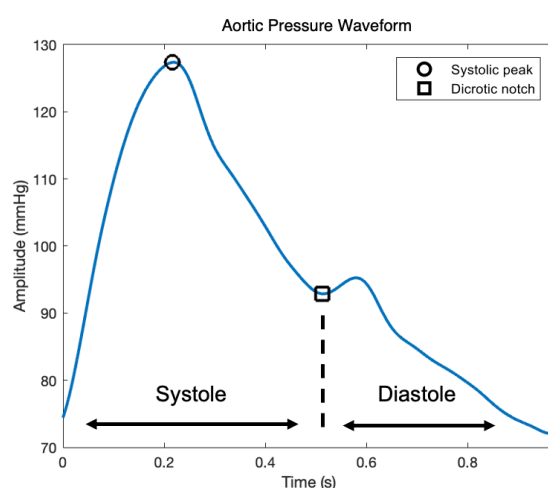


Figure A1. A typical extracted AP waveform showing the systolic peak and dicotic notch. The dashed vertical line at the dicotic notch separates the AP waveform into systolic and diastolic phases.

Table A1. Detailed definitions and purposes of the extracted features from each AP waveform.

Feature	Definition and Purpose
Absolute pressures	SBP, DBP, MAP, and DNP were extracted to capture important components of the AP waveform. SBP represents the maximum of the AP waveform, while DBP represents the minimum pressure just before the next contraction. Both SBP and DBP have been shown to independently influence the risk of adverse cardiovascular events [50].
Diastolic blood pressure (DBP)	MAP represents the average pressure in a person's arteries during one cardiac cycle. We used the commonly used definition of MAP as $(2 \times \text{DBP} + \text{SBP})/3$. It has been shown that in patients with cardiogenic shock treated with inotropic therapy, lower MAP is associated with worse clinical outcomes [51].
Systolic blood pressure (SBP)	
Mean aortic pressure (MAP)	
Dicotic notch pressure (DNP)	
	DNP is the pressure at dicotic notch (see Figure A1). A higher DNP indicates effective closure of the aortic valve [52]. In addition, we calculated this value to extract other features, such as DesP (described below).

Table A1. *Cont.*

Feature	Definition and Purpose
Relative pressures	PP, defined as the difference between SBP and DBP, reflects the strength of each cardiac contraction. It is shown that PP measured at admission is an independent marker to predict mortality and recurrence of myocardial infarction in patients with acute coronary syndrome [53].
Pulse pressure (PP)	rDNP is the difference between dicrotic notch pressure and diastolic blood pressure. We extracted this feature and its index (DNIX, defined as the ratio of rDNP to PP) to examine their predictive power for predicting mortality in the NSTEMI cohort.
Relative dicrotic notch pressure (rDNP)	
Dicrotic notch index (DNIX)	
Descending pressure (DesP)	
Descending index (DesIX)	
	DesP, the difference between systolic blood pressure and dicrotic notch pressure at the aortic level, serves as a marker of ventricular-arterial coupling. DesIX which is the divide of DesP over PP has been shown that can be used to detect aortic regurgitation [54].
Durations	HR is the heart rate measured in beats per minute (bpm), and it has previously been shown to be an independent predictor of adverse outcomes in patients with coronary artery disease [55].
Duration heartbeat (DBP)	It has been reported that the duration from the start of the arterial pressure waveform to the dicrotic notch reflects systolic function [52]. Moreover, in patients with impaired cardiac contractility, an increased heart rate often acts as a compensatory mechanism to maintain cardiac output. This can affect the timing of different parts of the cardiac cycle. Therefore, we extracted several timing-related features from the AP waveform, even though some of them have not previously been linked to outcomes in patients with myocardial infarction. Specifically, we measured the upstroke and downstroke portions of systole, as well as overall systolic and diastolic intervals, to capture changes in cardiac function.
Heartrate (HR)	
Duration systole (DS)	
Duration upstroke systole (DUS)	
Duration downstroke systole (DDS)	
Duration diastole (DD)	
Descending time (DesT)	
Overall time (OT)	
	Moreover, we extracted the overall time of the cardiac catheterization (OT), as a longer duration may suggest that the procedure was more complex or challenging. The exact definition of each duration is listed in Table 1.
Slopes	Abrupt myocardial damage compromises the myocardial ability to maintain adequate amount of blood ejected per heartbeat (also known as stroke volume). Patients with low stroke volume have slow uprise of the AP tracing, or smaller AUCp [56,57]. A slow uprise can be captured using SUS, which is the slope of the line from the start of the AP waveform to the systolic peak. In addition to SUS, we calculated other slopes that might be important in patients with NSTEMI.
Systolic upstroke slope (SUS)	
Systolic downstroke slope (SDS)	
Maximum slope (MS)	
Areas	As mentioned in the slopes section, patients who eject a smaller amount of blood per heartbeat may have a smaller area under the AP curve, represented as AUCp in this study.
Area under the pressure curve (AUCp)	Aside from AUCp, myocardial infarction can impair the heart's ability to pump blood during systole. For example, MI can reduce cardiac contractility [58], which in turn may affect the area under the systolic curve (SysA).
Systolic area (SysA)	
Diastolic area (DiaA)	The myocardial oxygen supply/demand ratio reflects the myocardial oxygenation, specially subendocardial myocardial ischemia due to imbalance between myocardial oxygen supply and demand [46].
Myocardial oxygen supply/demand ratio (O2ratio)	
Ascending area (AscA)	In addition, we extracted areas from other parts of the AP waveform to determine whether any of them could help identify patients at risk of mortality in the NSTEMI cohort. The definitions of these features, along with the parts of the waveform from which they were extracted, are listed in Table 1.
Descending area (DesA)	
Area ratio (AR)	

Table A1. *Cont.*

Feature	Definition and Purpose
Other	Other than pressures, slopes, durations, and areas, we extracted additional features that we suspected might be important for identifying NSTEMI patients at risk of mortality.
Fractal dimension of <i>p</i> (FDp)	The FDp is the fractal dimension of each AP waveform. In time-series analysis, fractal dimension provides a measure of how complex or irregular a waveform is [59]. Skewness (SK) quantifies the asymmetry of the waveform, while kurtosis (KU) assesses whether the waveform has heavier or lighter tails compared to a normal distribution. We used these features to identify potential patterns that may help in detecting high-risk NSTEMI patients
Skewness of <i>p</i> (SK)	
Kurtosis of <i>p</i> (KU)	
Spectral entropy of <i>p</i> (SE)	
Average spectral power of <i>p</i> (Pave)	
Maximum spectral power (MSP)	SE, Pave, MSP, and MSPF were the only features extracted from the frequency domain to assess whether they carried information relevant to mortality prediction. For example, SE measures the irregularity or complexity of a signal in the frequency domain, while Pave indicates the mean energy of the signal. MSP and MSPF represent the dominant spectral peak and its corresponding frequency, respectively.
Maximum spectral power frequency (MSPF)	
Shock index (SI)	SI is defined as heart rate divided by systolic blood pressure. It was first introduced as an additional tool for evaluating hemodynamic stability of patients [60]. Since then, it has been widely used for risk stratification; for example, it has been applied to predict short-term adverse outcomes in STEMI patients [61] and to predict in-hospital mortality in NSTEMI patients [62]. The modified shock index (mSI) is defined as the ratio of heart rate to mean arterial pressure.
Age shock index (SI_age)	
Modified shock index (mSI)	
Age-modified shock index (mSI_age)	SI_age and mSI_age are like SI and mSI but are calculated by multiplying SI and mSI by age. A study demonstrated that SI_age and mSI_age are even better predictors than SI and mSI for in-hospital cardiovascular events, as well as 6-month and long-term all-cause mortality, in a STEMI cohort [45].

p is a single AP waveform.

Table A2. Hyperparameter combinations evaluated for the RSF and DeepSurv models during grid search.

Model	Hyperparameter	Values
RSF	n_estimators	50–1000
	max_depth	None (no limit), 1–20
	min_samples_split	1–20
	min_samples_leaf	1–20
	max_features	Sqrt, none (all features)
DeepSurv	optimizer	AdamW
	activation	SELU, ReLU
	number of layers	2–5
	number of nodes	16, 32, 64, 128, 256, 512
	dropout rate	0.001, 0.01, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8
	learning rate	0.0001–0.1
	weight decay	0, 0.0001–0.01

n_estimators refers to the number of trees in the forest, max_depth is the maximum tree depth, min_samples_split is the minimum number of samples required to split an internal node, min_samples_leaf is the minimum number of samples required to be at a leaf node, and max_features represents the number of features considered when searching for the best split.

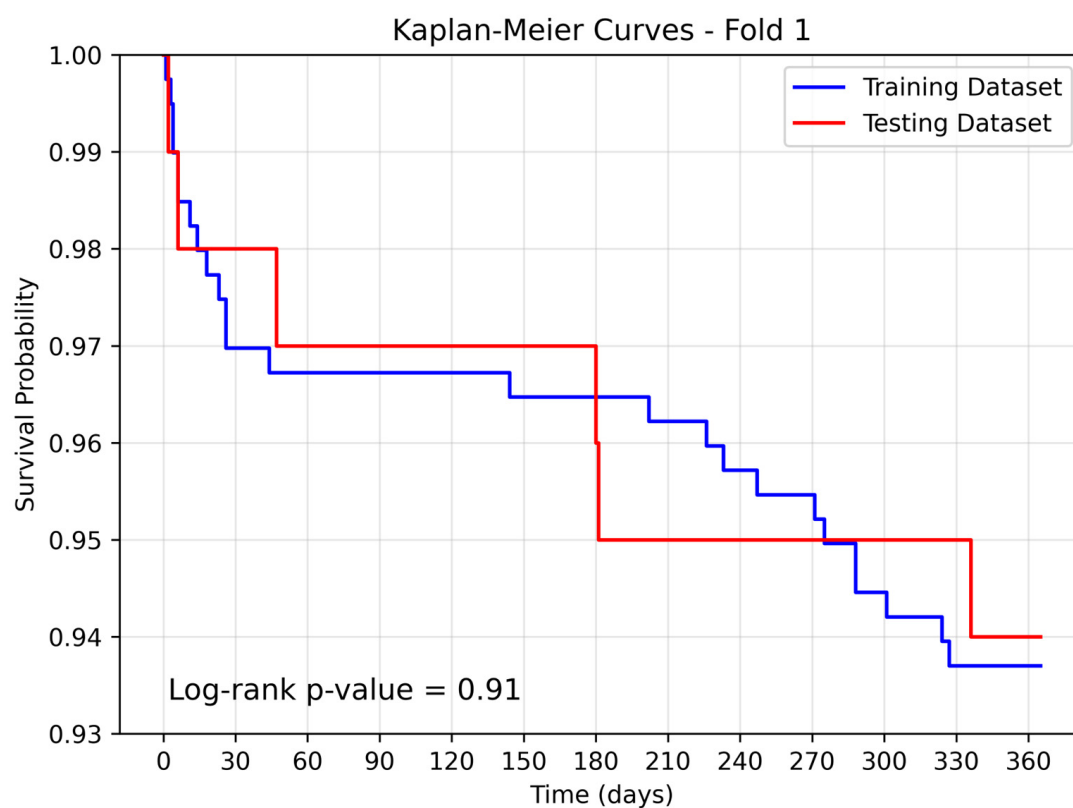


Figure A2. Kaplan–Meier curves of training and testing datasets of fold 1.

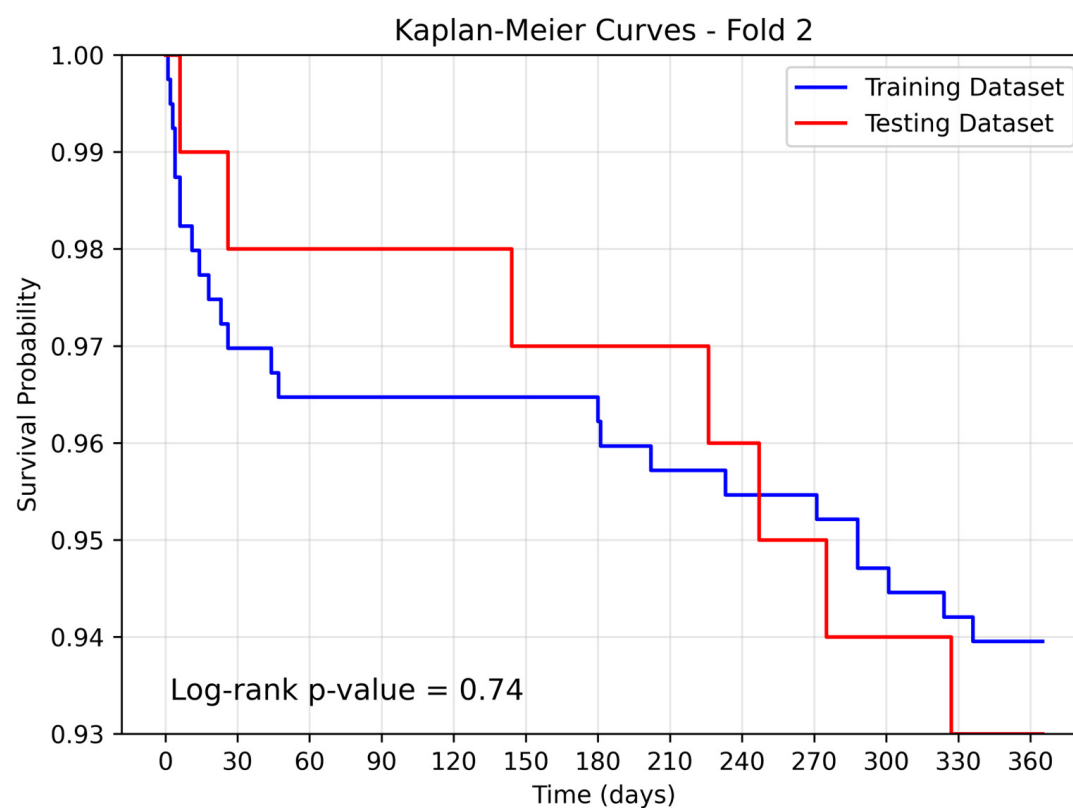


Figure A3. Kaplan–Meier curves of training and testing datasets of fold 2.

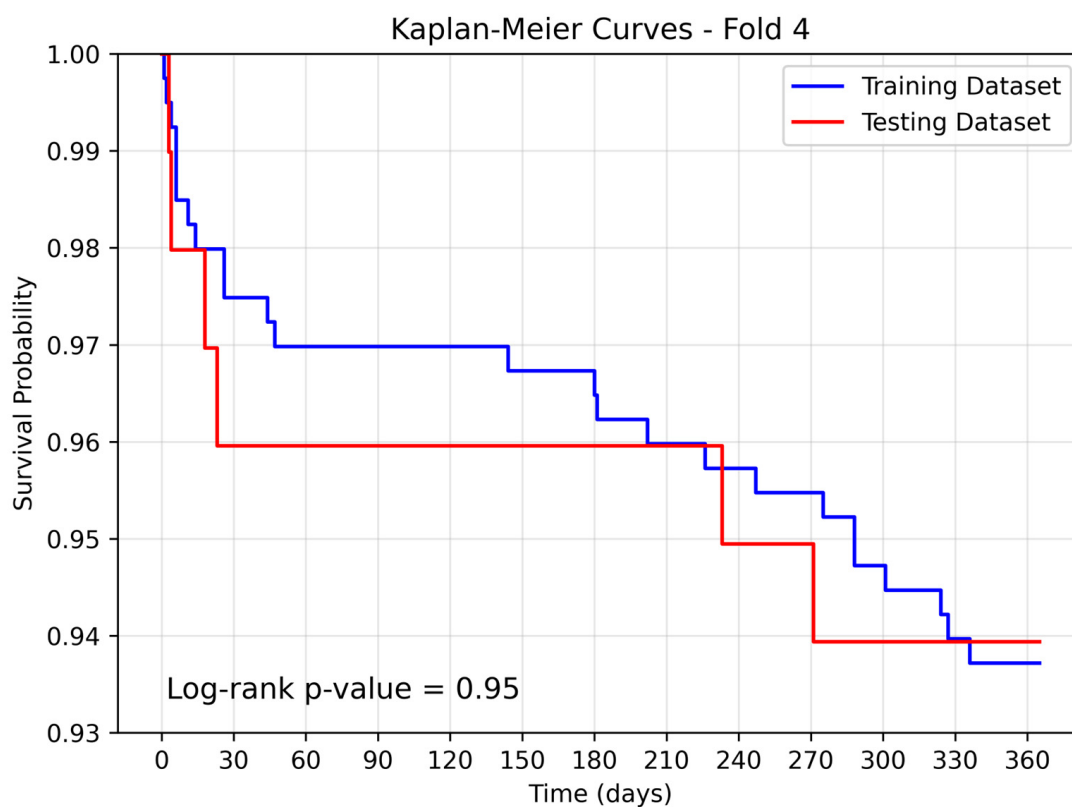


Figure A4. Kaplan–Meier curves of training and testing datasets of fold 4.

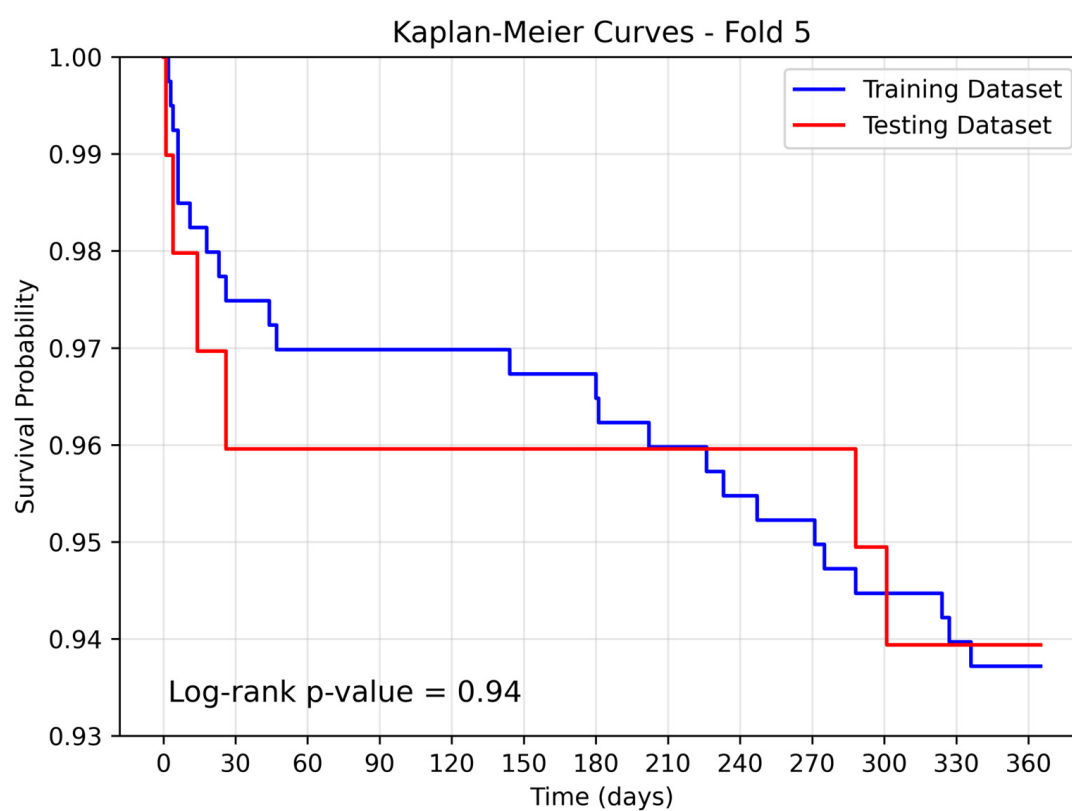


Figure A5. Kaplan–Meier curves of training and testing datasets of fold 5.

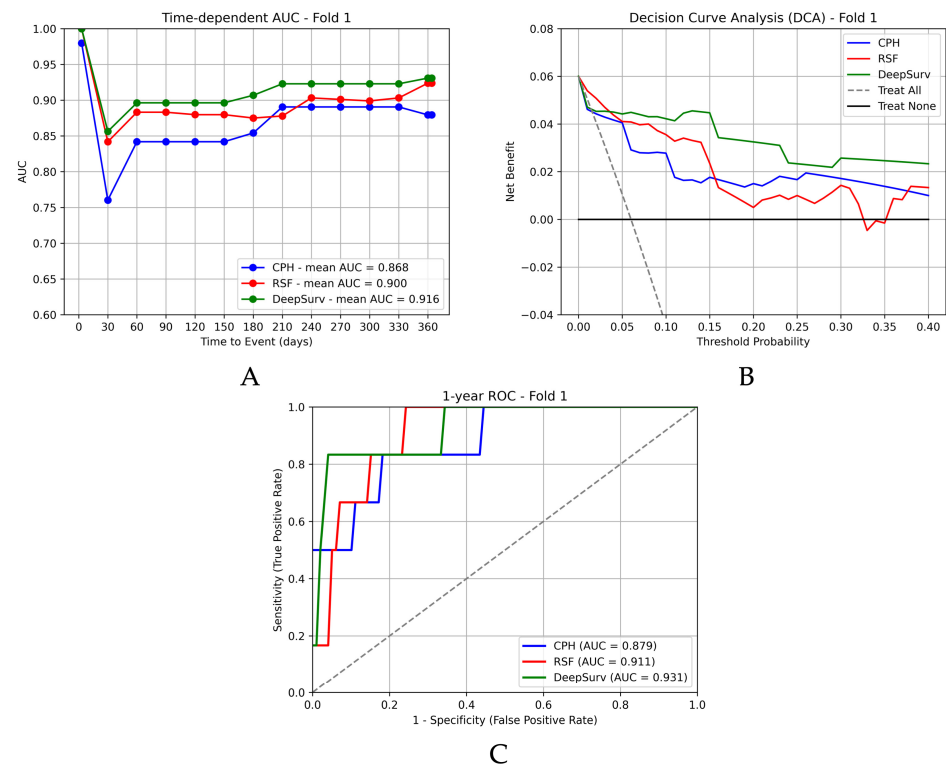


Figure A6. Performance of Cox proportional hazards (CPH), Random Survival Forest (RSF), and DeepSurv models on fold 1. (A) Time-dependent AUCs. (B) 1-year DCA. (C) ROC curves evaluated at 1-year. The diagonal dashed gray line depicts the line of no discrimination (AUC = 0.5).

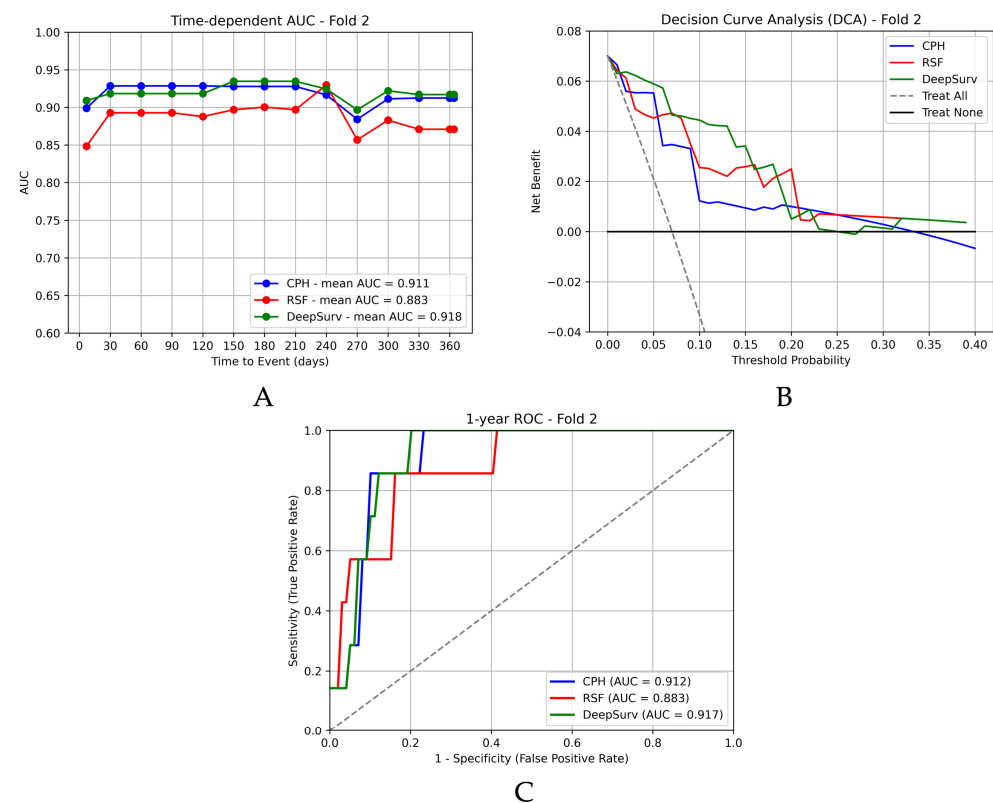


Figure A7. Performance of Cox proportional hazards (CPH), Random Survival Forest (RSF), and DeepSurv models on fold 2. (A) Time-dependent AUCs. (B) 1-year DCA. (C) ROC curves evaluated at 1-year. The diagonal dashed gray line depicts the line of no discrimination (AUC = 0.5).

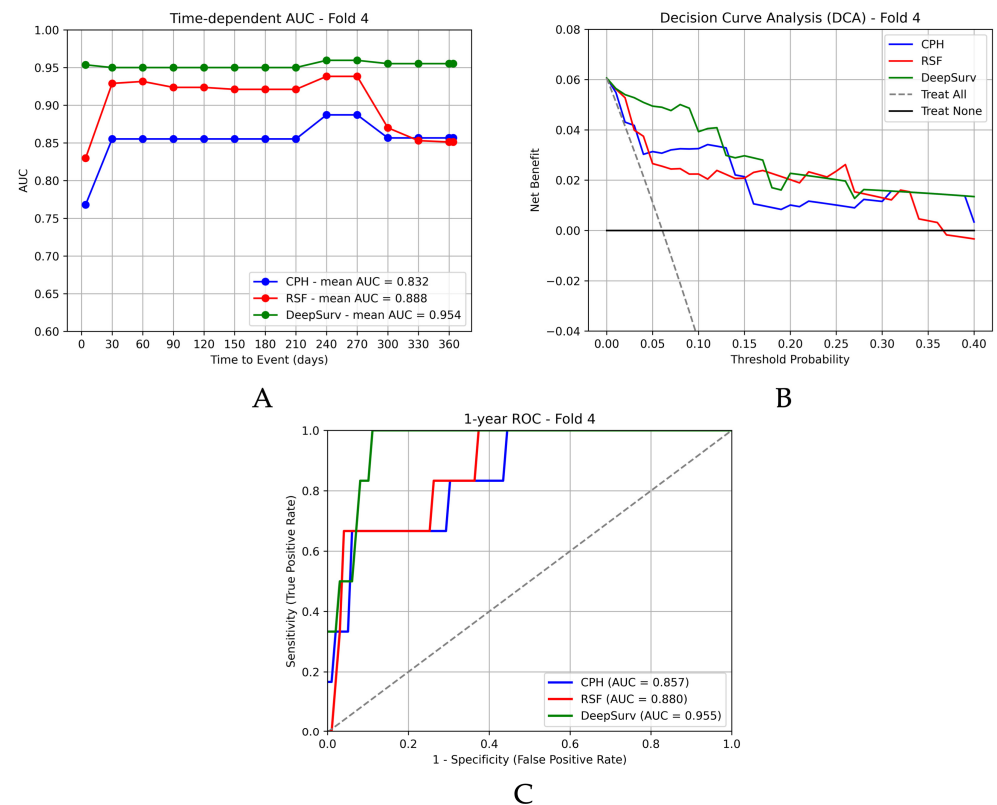


Figure A8. Performance of Cox proportional hazards (CPH), Random Survival Forest (RSF), and DeepSurv models on fold 4. **(A)** Time-dependent AUCs. **(B)** 1-year DCA. **(C)** ROC curves evaluated at 1-year. The diagonal dashed gray line depicts the line of no discrimination (AUC = 0.5).

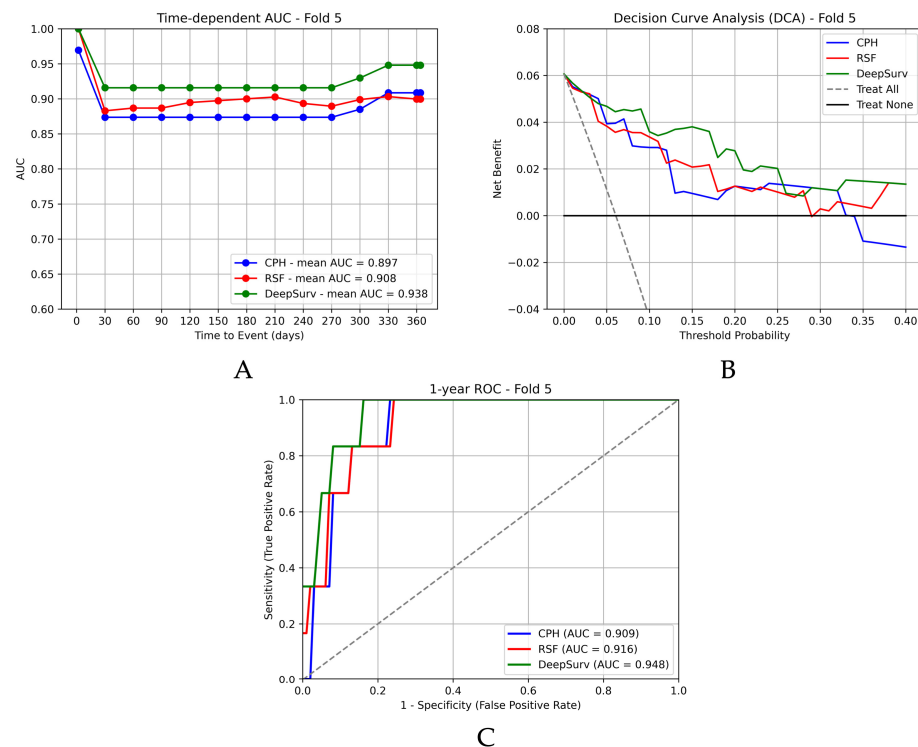


Figure A9. Performance of Cox proportional hazards (CPH), Random Survival Forest (RSF), and DeepSurv models on fold 5. **(A)** Time-dependent AUCs. **(B)** 1-year DCA. **(C)** ROC curves evaluated at 1-year. The diagonal dashed gray line depicts the line of no discrimination (AUC = 0.5).

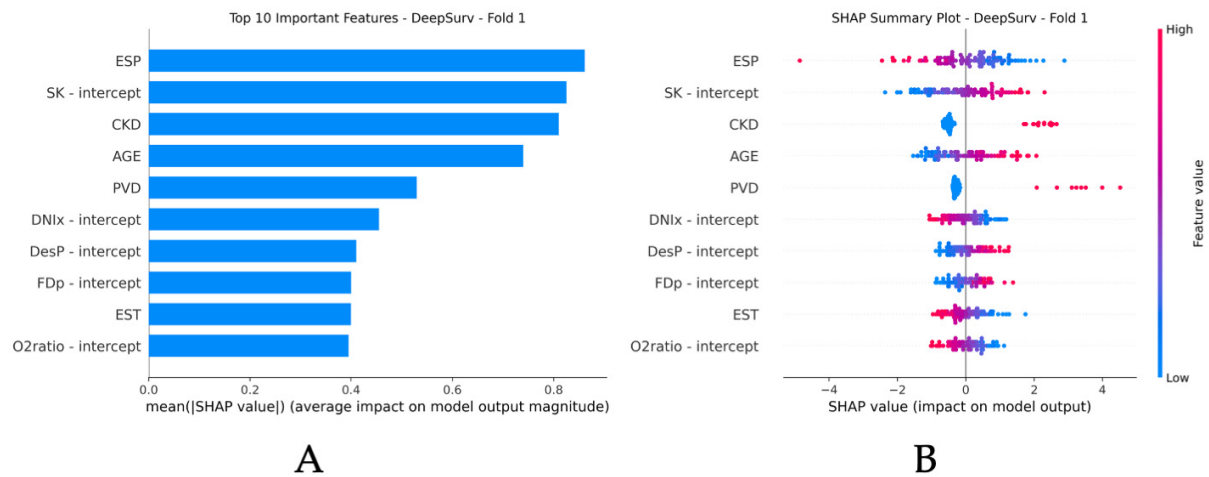


Figure A10. A Model interpretation of DeepSurv on fold 1. (A) Importance ranking of the top 10 features based on the mean ($|SHAP\ value|$). (B) SHAP summary plot.

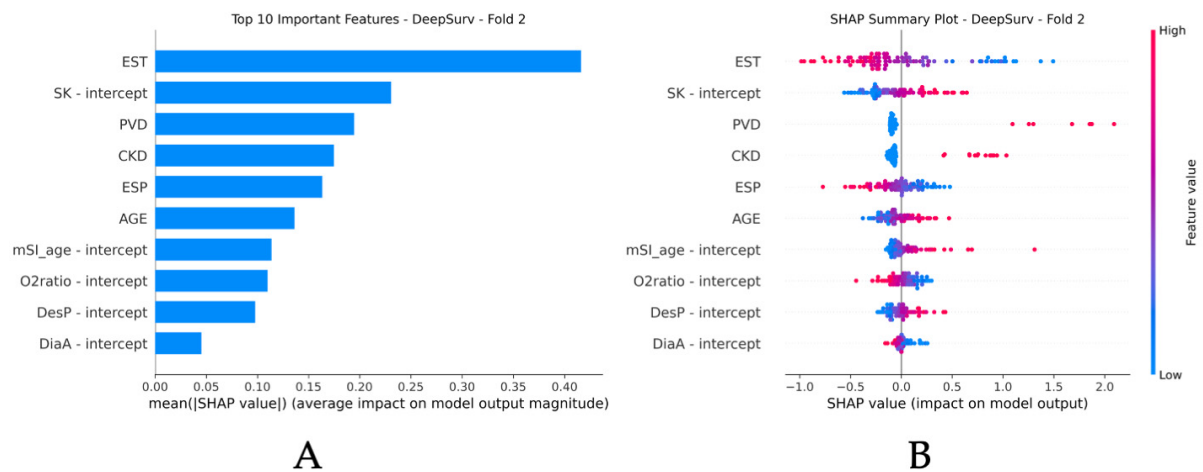


Figure A11. Model interpretation of DeepSurv on fold 2. (A) Importance ranking of the top 10 features based on the mean ($|SHAP\ value|$). (B) SHAP summary plot.

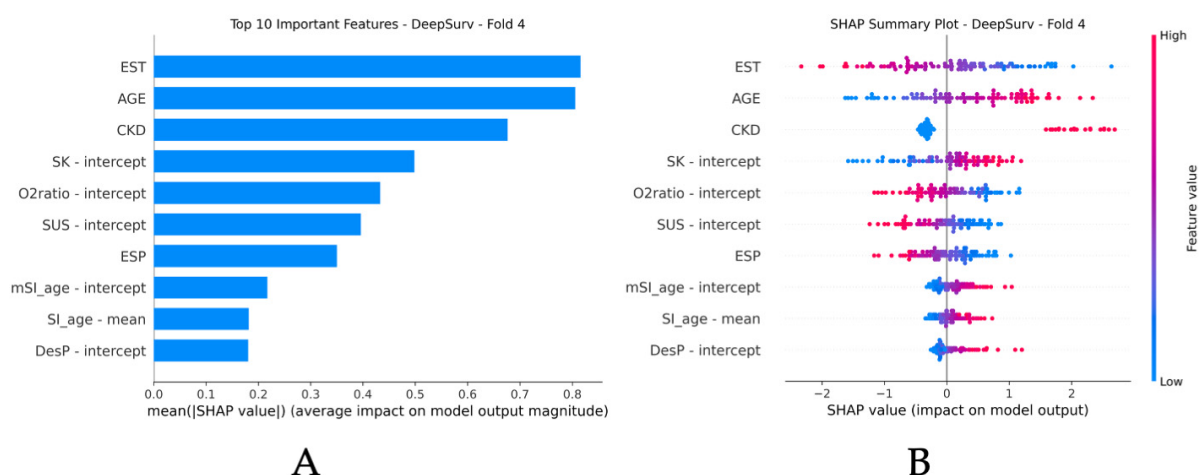


Figure A12. Model interpretation of DeepSurv on fold 4. (A) Importance ranking of the top 10 features based on the mean ($|SHAP\ value|$). (B) SHAP summary plot.

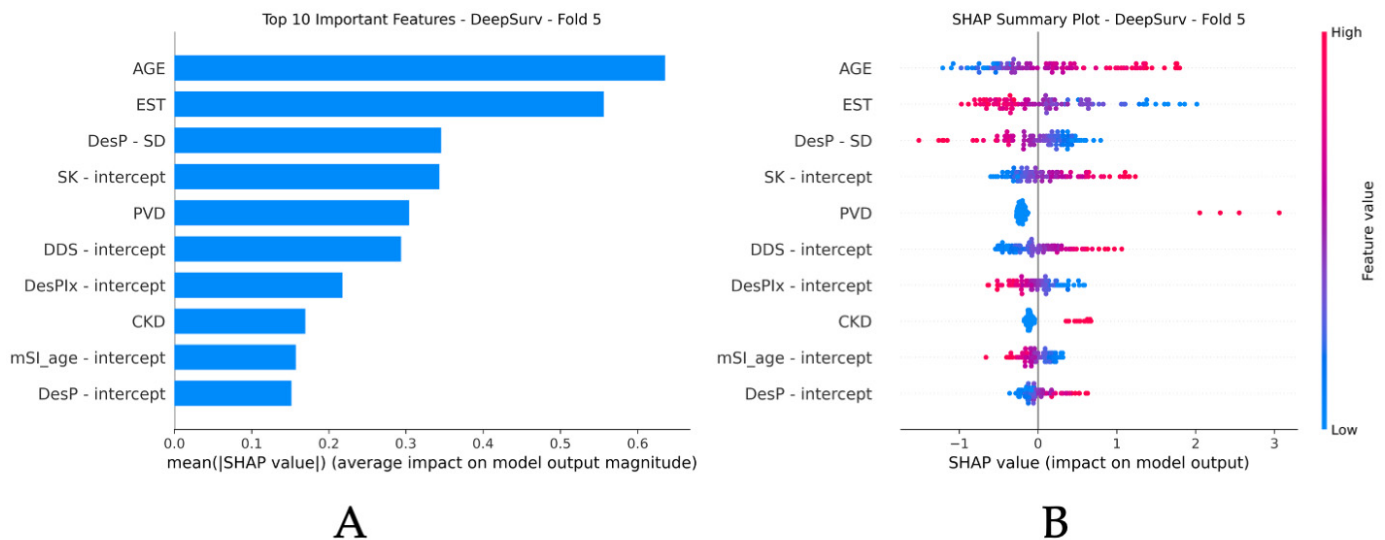


Figure A13. Model interpretation of DeepSurv on fold 5. (A) Importance ranking of the top 10 features based on the mean (|SHAP value|). (B) SHAP summary plot.

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