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DATABASE ANALYSIS

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Machine Learning and Clinical Predictors of Mortality in Cardiac Arrest Patients: A Comprehensive Analysis

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Background: Cardiac arrest (CA) is a global public health challenge. This study explored the predictors of mortality and their interactions utilizing machine learning algorithms and their related mortality odds among patients following CA.

Material/Methods: The study retrospectively investigated 161 medical records of CA patients admitted to the Intensive Care Unit (ICU). The random forest classifier algorithm was used to assess the parameters of mortality. The best classification trees were chosen from a set of 100 trees proposed by the algorithm. Conditional mortality odds were investigated with the use of logistic regression models featuring interactions between variables.

Results: In the logistic regression model, male sex was associated with 5.68-fold higher mortality odds. The mortality odds among the asystole/pulseless electrical activity (PEA) patients were modulated by body mass index (BMI) and among ventricular fibrillation/pulseless ventricular tachycardia (VF/pVT) patients were by serum albumin concentration (decrease by 2.85-fold with 1 g/dl increase). Procalcitonin (PCT) concentration, age, high-sensitivity C-reactive protein (hsCRP), albumin, and potassium were the most influential parameters for mortality prediction with the use of the random forest classifier. Nutritional status-associated parameters (serum albumin concentration, BMI, and Nutritional Risk Score 2002 [NRS-2002]) may be useful in predicting mortality in patients with CA, especially in patients with PCT >0.17 ng/ml, as showed by the decision tree chosen from the random forest classifier based on goodness of fit (AUC score).

Conclusions: Mortality in patients following CA is modulated by many co-existing factors. The conclusions refer to sets of conditions rather than universal truths. For individual factors, the 5 most important classifiers of mortality (in descending order of importance) were PCT, age, hsCRP, albumin, and potassium.

Keywords: **Death, Sudden, Cardiac • Machine Learning • Malnutrition • Mortality • Return of Spontaneous Circulation**

Abbreviations: **AIC** – Akaike Information Criterion; **ALS** – advanced life support; **BLS** – basic life support; **BMI** – body mass index; **CA** – cardiac arrest; **hsCRP** – high-sensitivity C-reactive protein; **ICU** – Intensive Care Unit; **IHCA** – in-hospital cardiac arrest; **K** – potassium; **LYM** – lymphocyte; **ML** – machine learning; **NA** – sodium; **NRS-2002** – Nutrition Risk Screening 2002; **OHCA** – out-of-hospital cardiac arrest; **OR** – odds risk; **PCT** – procalcitonin; **PEA** – pulseless electrical activity; **pVT** – pulseless ventricular tachycardia; **ROSC** – return of spontaneous circulation; **TChol** – total cholesterol; **TG** – triglycerides; **TSH** – thyroid-stimulating hormone; **VF** – ventricular fibrillation

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Introduction

Cardiac arrest (CA), a critical public health issue, manifests differently when occurring inside versus outside hospital settings. Out-of-hospital cardiac arrest (OHCA) presents significant challenges globally, with an incidence among adults ranging from 40 to 52 per 100 000 person-years [1,2]. Despite emergency interventions, only about 22% of OHCA patients survive to be admitted to the hospital, and the survival rate to hospital discharge is as low as 9% for this group [3].

In contrast, in-hospital cardiac arrest (IHCA) shows comparatively higher recovery rates. Approximately one-third to two-thirds of IHCA patients achieve return of spontaneous circulation (ROSC) after cardiopulmonary resuscitation [4,5]. Furthermore, survival rates to hospital discharge have been improving, currently standing around 25% in the United States and up to 35% in European countries [6,7]. Survival variations after CA are influenced by numerous factors, including the structure of the emergency medical system, the promptness of basic life support (BLS) initiation by witnesses, the quality of advanced life support (ALS), and post-resuscitation care in intensive care units (ICU) [8]. To manage these critical situations, mortality prediction tools are frequently utilized in clinical practice for patients admitted to the ICU with life-threatening conditions [9].

In recent years, there has been rising interest in use of machine learning (ML) for medical purposes to develop a more personalized treatment approach based on more precise assessment of survival rates. The high applicability of ML algorithms stems from the fact that, as opposed to classic statistical methods, they simulate the process of learning and adapting (in some cases even through forgetting information) to the variability in the analyzed data. This important feature of ML divulges into a more optimal fit of such models to the empiric data. Contemporary medicine utilizes ML algorithms to assess the relationship between in-hospital survival and the various factors associated with the features of cardiac arrest and its comorbidities [10-15], treatment [16-19], demography, or even time- and date-related parameters [20]. Such multivariate analyses are performed to enable assessment of the odds of death in each patient; therefore, allowing ICUs to focus on the most endangered individuals [21,22]. The potential of ML in improving ICU outcomes extends beyond mere prediction – it enhances the decision-making process, tailoring interventions that are specific to the physiological profile of each patient. Recent studies illustrate how ML algorithms can optimize the treatment protocols by analyzing real-time data, thus potentially increasing survival rates in critical care settings. For instance, ML-based tools have shown promise in predicting severe complications and optimizing resource allocation in ICUs, which are crucial for improving outcomes in cardiac arrest cases [23,24]. Furthermore, ongoing advancements in ML are paving the way for more sophisticated models that integrate continuous data streams from ICU monitoring devices, offering deeper insights into patient status and likely trajectories [25].

Taking into account the potential of machine learning to significantly enhance outcomes in ICU settings, this study was designed to deepen our understanding of cardiac arrest mechanisms and their outcomes. Our research focused on investigating the differences in clinical parameters across asystole/pulseless electrical activity (PEA) and ventricular fibrillation/pulseless ventricular tachycardia (VF/pVT). We aimed to delineate how these parameters influence patient survival, define the critical conditions that contribute to mortality, and assess the odds of death, with a particular emphasis on identifying significant interactions between these conditions. Additionally, we explore the application of inherently explainable machine learning algorithms to predict survival status in patients after cardiac arrest, assessing the effectiveness of these tools in predicting outcomes based on the complex data available in ICU settings.

Material and Methods

Study Design and Setting

We performed a retrospective analysis of 161 medical records of patients admitted due to CA to the adult ICU at the University Hospital (Wrocław, Poland) between January 2017 and February 2022 (ICD10: I46). The study followed the STROBE guidelines (Strengthening the Reporting of Observational Studies in Epidemiology).

Study Population and Data

We analyzed all the patients who met the inclusion criteria (admitted to the ICU after CA, age ≥18 years old, and CA not caused by trauma or suicide attempt). The analysis included data such as age, sex, body mass index (BMI), Nutrition Risk Screening (NRS-2002), comorbidities, in-hospital mortality, and laboratory results including lymphocyte (LYM); procalcitonin (PCT); total cholesterol (TChol), triglycerides (TG), thyroid-stimulating hormone (TSH), high-sensitivity C-reactive protein (hsCRP), potassium (K), sodium (NA), and albumin. In-hospital mortality was defined as death from any cause occurring within the confines of the hospital, up until the time of discharge from the ICU.

We used as an auxiliary assessment of differences in the continuous variables. BMI was assessed as non-obese (BMI <30) and obese (BMI ≥30). Blood for laboratory tests was drawn

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by a nurse at the time of admission to the ICU. The physician admitting the patient to the ICU decided which tests the patient needed.

Statistical Analysis

The analysis was performed based on our previous study in the same population sample, in which the association between categorical parameters (such as comorbidities) was studied [26].

Data pre-processing and visualization was performed with the use of Python 3.9.13. Statistical analyses were performed with use of Python 3.9.13 or STATISTICA 13.3 (package on license of Wrocław Medical University). The following Python packages were utilized: numpy 1.23.0, pandas 1.4.3, scipy 1.9.3, statsmodels 0.13.2, zepid 0.9.1, matplotlib 3.6.0, and dtreeviz 1.4.1. Logistic regression models were derived in the STATISTICA 13.3 package, while the machine learning model (Random Forest Classifier) was trained and tested with use of Python 3.9.13. (scikit-learn 1.1.3 package). Statistical inference was based on α=0.05.

Analysis of the distribution of values of variables, their scale of measurement, and the incidence of outliers or extreme values in the dataset was taken into account in the process of selecting the most suitable methods for statistical inference. Differences between values after grouping by different categories were checked with use of the Mann-Whitney U test.

The first algorithm used in survival status-related classification was logistic regression with effect coding. The initial set of variables was chosen based on the amount of missing data to minimalize loss of information. Information on this set of variables and the derivation of the base model (on which this study is based) is shown in **Supplementary Materials** (**Supplementary Table 1**) of our previous study on the same population sample [26]. The univariate analysis and interaction assessment formed the basis for implementing multivariate models. For the purpose of easier interpretability of the models, featured continuous variables, taking part in interactions within a model, were centered (value – mean value). The assumption of linearity between the predictors and the logit was checked using the Box-Tidwell test. Goodness of fit was assessed with: Hosmer-Lemeshow test, Akaike Information Criterion (AIC), Bayesian Information Criterion, and Nagelkerke's pseudo-R^2. Hypothesis that β=0 was tested with the Lagrange multiplier (score) test. Prediction power was analyzed based on the assessment of testing: AUC computed with 10-fold cross-validation. The best model was then described by metrics: including precision, recall, specificity, and accuracy, with use of the optimal cut-off value based on Youden's J index.

Random Forest Classifier was the second algorithm used in the aforementioned classification. The method is based on creating a random set of decision trees (forming a forest). While originally the classifier is used to predict patient states (such as mortality) based on the whole ensemble of these decision trees, this study utilized the algorithm to choose a decision tree of the best fit from all the random trees in the ensemble. The algorithm was fit to the same dataset, and the same set of initial variables was used to assess which variables were featured the most (eg, 'feature importance') in all of the trees in the forest. Before fitting the algorithm to the data, the dataset was randomly shuffled and divided into training (65%) and testing (35%) subsets. Bootstrap samples were used when building trees. The classification was performed with use of 100 estimators (trees), among which the 2 best were selected for visualization (based on testing: accuracy or AUC, **Supplementary Table 2**). These 2 models were subsequently validated with use of 10-fold cross-validation performed on the whole dataset. The maximum tree depth was 5. The square root of the total number of used features was set as the maximum number of features to perform splits. Splits were performed if n ≥2. Leaves of the trees consisted of at least 1 record. The quality of splits was assessed with Gini impurity:

$$\textit{Gini Impurity Index}\ (\mathrm{GI}) = 1 - \sum_{t=1}^{n} p_i^2$$

in which n is the count of predicted class categories and p_i is the proportion of the i^{th} class category. Feature importance was assessed based on the accumulation of impurity decrease within the trees.

Results

Characteristics of analyzed population sample

The patients were aged 26-88 years old (mean value 64.07, SD 14.74, median value 67, 1st to 3rd interquartile range 56-74). The count of male patients was approximately 2.04-fold higher than the count of female patients.

Differences in Values of Selected Parameters Between The 2 Cardiac Arrest Mechanisms

The 2 mechanisms of cardiac arrest differed significantly in age (p≈0.005) and concentrations of albumin (p≈0.042), PCT (p≈0.021), and hsCRP (p<0.001). Patients with the asystole/PEA mechanism were older and exhibited an 4.91% lower median value of albumin compared to the VF/pVT patients. The values of PCT and hsCRP in the asystole/PEA group were markedly higher (3.30-fold or 3.98-fold higher, respectively). The descriptive statistics of qualitative parameters are shown in **Table 1**.

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Table 1. Values of selected quantitative parameters in context of different cardiac arrest mechanisms.

Variable	Asystole/PEA		VF/pVT		p
	n	[1st Q, Me, 3rd Q]	n	[1st Q, Me, 3rd Q]	
Age [years]	90	[59.50, 69.00, 77.00]	70	[52.00, 62.00, 73.00]	**0.005**
Albumin [g/dl]	78	[2.42, 2.90, 3.30]	58	[2.62, 3.05, 3.70]	**0.042**
BMI [kg/m^2]	71	[22.67, 25.95, 30.00]	58	[24.34, 26.30, 30.50]	0.197
K [mmol/l]	90	[3.79, 4.30, 5.08]	68	[3.77, 4.50, 5.02]	0.815
LYM [%]	45	[5.10, 9.20, 16.10]	28	[5.98, 10.60, 16.75]	0.687
Na [mmol/l]	90	[134.00, 138.50, 142.00]	68	[136.00, 138.00, 140.25]	0.894
NRS2002	90	[3.00; 3.00; 4.00]	71	[3.00; 3.00; 4.00]	0.371
PCT [ng/ml]	89	[0.13, 0.99, 4.63]	68	[0.13, 0.30, 1.53]	0.021
TChol [mg/dl]	58	[106.25, 129.50, 168.75]	47	[126.00, 154.00, 174.00]	0.102
TG [mg/dl]	52	[82.75, 122.00, 188.25]	47	[101.50, 155.00, 210.00]	0.160
TSH [uIU/ml]	57	[0.66, 1.66, 3.39]	42	[1.16, 1.82, 2.98]	0.871
hsCRP [mg/l]	89	[5.12, 26.06, 88.97]	68	[1.70, 6.54, 24.44]	**<0.001**

Values are given as [1st quartile; median value; 3rd quartile]. Statistically-significant (p<0.05) differences are **marked in bold**. BMI – body mass index; LYM – lymphocyte count; NRS2002 – Nutrition Risk Screening 2002; PCT – procalcitonin; TChol – total cholesterol concentration; TG – triglycerides; TSH – thyroid-stimulating hormone; hsCRP – high sensitivity C-reactive protein concentration; PEA – pulseless electrical activity; Pvt – pulseless ventricular tachycardia; VF – ventricular fibrillation.

Table 2. Values of selected qualitative parameters in context of different cardiac arrest mechanisms.

Variable	Category	Asystole/PEA	VF/pVT	χ^2	p
Sex	Female	39 [0.74]	14 [0.26]	10.023	**0.002**
	Male	51 [0.47]	57 [0.53]		
Obesity	Obese	20 [0.54]	17 [0.46]	0.066	0.797
Cardiac arrest location	OHCA	32 [0.43]	43 [0.57]	9.975	**0.002**
	IHCA	58 [0.67]	28 [0.33]	9.975	**0.002**
ACS	Yes	15 [0.56]	12 [0.44]	0.002	0.968
CS	Yes	8 [0.57]	6 [0.43]	0.010	0.922
CKD	Yes	8 [0.5]	8 [0.5]	0.251	0.616
HF	Yes	11 [0.52]	10 [0.48]	0.121	0.728
DM	Yes	21 [0.54]	18 [0.46]	0.088	0.767
HT	Yes	30 [0.51]	29 [0.49]	0.965	0.326

Values are given as: count [frequency in categories (rows)]. The 'All' margins indicate sums of counts. Expected counts are given in columns labeled with the 'expected n' term. Statistically-significant (p<0.05) differences are **marked in bold**. ACS – acute coronary syndrome; CS – cerebral stroke; CKD – chronic kidney disease; HF – heart failure; DM – diabetes mellitus; HT – hypertension; PEA – pulseless electrical activity; Pvt – pulseless ventricular tachycardia; VF – ventricular fibrillation.

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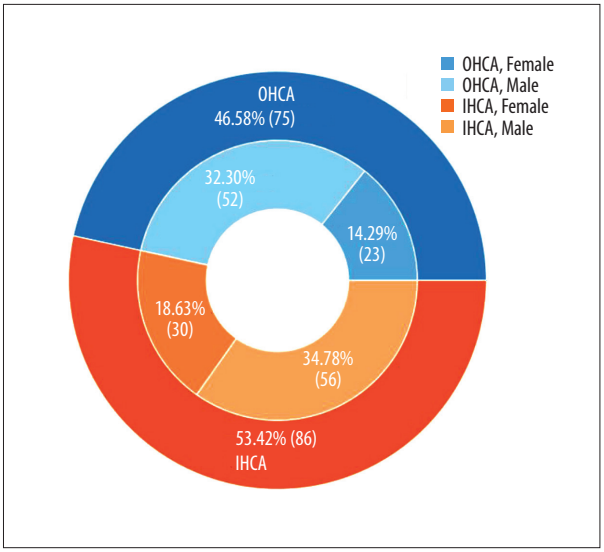

Figure 1. Sex-related frequencies among the 2 cardiac arrest locations.

Male patients were more likely to suffer from the VF/pVT mechanism (p≈0.002, **Table 2**), showing over 3-fold higher odds compared to their female counterparts. Over 2/3 of the total inter-hospital cases of cardiac arrest were of asystole/PEA mechanism, which is significantly more frequent compared to the OHCA individuals (p≈0.002, **Table 2**). Interestingly, these findings are not associated with each other since the male-to-female ratio did not differ in context of cardiac arrest location (p≈0.570, **Figure 1**). Moreover, the 2 mechanisms were associated with comparable comorbidity status (**Table 2**).

Differences in Values of Selected Quantitative Parameters in Context of Survival and Cardiac Arrest Mechanism

Among the non-survivors (**Figure 2A**), asystole/PEA patients showed higher PCT concentration (p≈0.022) but lower TG concentration compared to the VF/pVT patients (p≈0.028). Interestingly, among the survivors (**Figure 2B**), VF/pVT patients showed higher BMI (p≈0.012) and albumin concentration

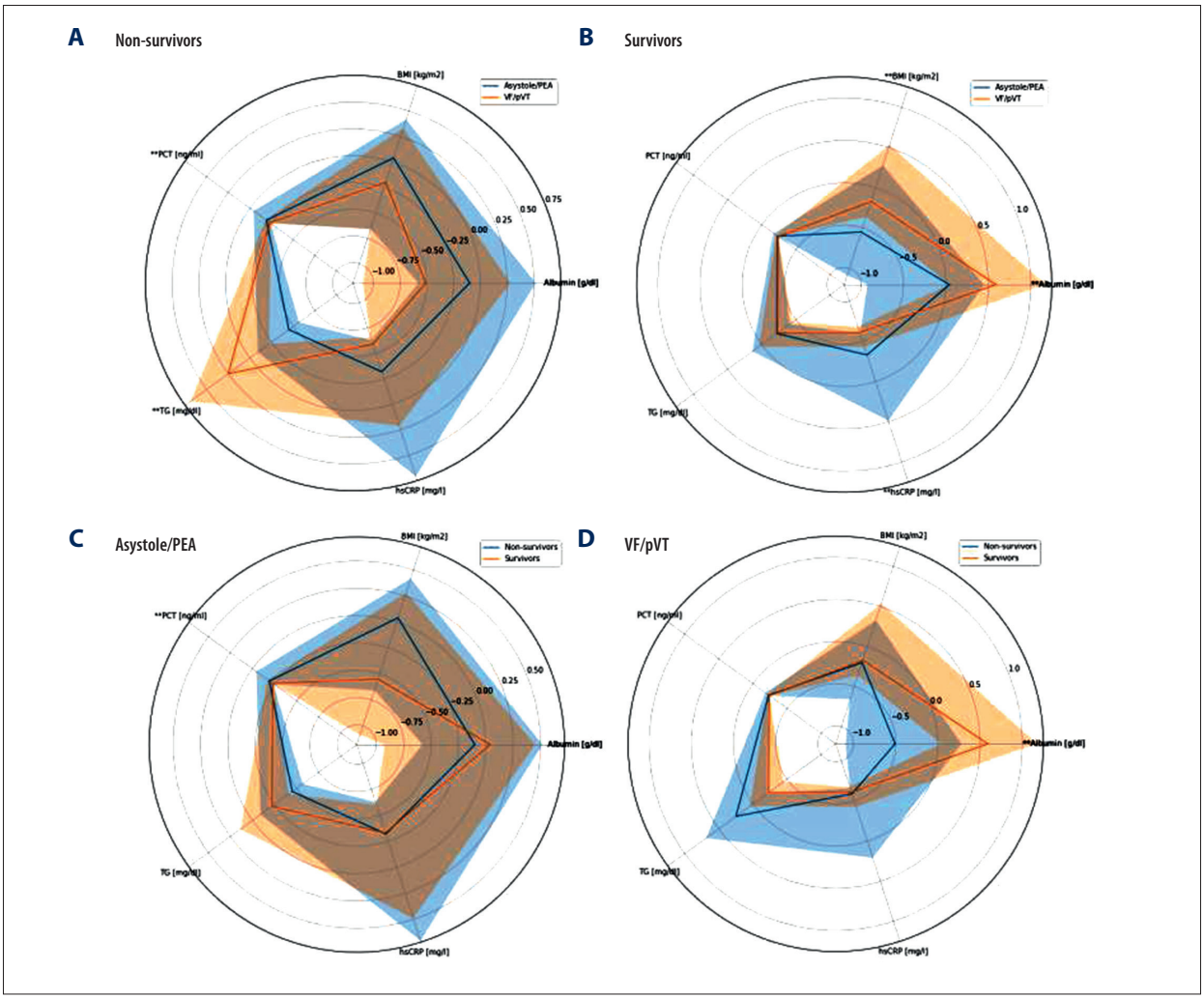

Figure 2. Key differences in values of quantitative parameters in context of CA mechanism and survival status.

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(p≈0.003) but significantly lower hsCRP concentration (p≈0.003) compared to the asystole/PEA patients.

Although there were no survival status-associated differences in PCT concentration among the VF/pVT patients (p≈0.566), the asystole/PEA mechanism was associated with markedly higher PCT concentration observed in non-survivors when compared to the survivors (p≈0.018, **Figure 2C**). Among the VF/pVT patients, survivors showed higher albumin concentration (p<0.001, **Figure 2D**). This difference did not occur among the asystole/PEA patients (p≈0.524). Descriptive statistics are shown in **Table 3** (total sample size in each group: Asystole/PEA: 29 survivors, 61 non-survivors; VF/pVT: 40 survivors, 31 non-survivors).

Prediction of Mortality Status

Logistic Regression Analysis Exploring the odds of Death Among Different Cardiac Arrest Mechanism Types

The base model utilized 2 significant effects selected by an iterative procedure: cardiac arrest mechanism (p≈0.038) and hsCRP (p≈0.038) (**Supplementary Table 3**: model 1). The iterative derivation of this model could be seen in our previous study, although the cut-off for leaving the variables in the model in that study was higher. As the prediction value of the model was questionable (testing AUC 0.645±0.0650), this model was expanded with additional effects and interactions. Adding the information on BMI and serum albumin concentration values, sex, and several interactions to the base model increased the prediction accuracy. The final model was created based on 2 intermedial models (**Supplementary Table 1** (models 2 and 3) and **Supplementary Table 3**).

The best model (**Table 4**) utilized sex, cardiac arrest mechanism, BMI, albumin and hsCRP concentrations, and the 2nd-degree interactions of cardiac arrest mechanism with BMI, albumin, and hsCRP. This model proved to correctly classify approximately 76.2% of patients (testing AUC 0.762±0.0466). Its metrics at the optimal cut-off point (**Supplementary Table 4**) were 0.830 precision, 0.650 recall, 0.843 specificity, and 0.739 accuracy.

Men who suffered from asystole/PEA cardiac arrest showed approximately 5.68-fold higher (p≈0.007) odds of death compared to women with the same cardiac arrest mechanism. Interestingly, no sex-related differences in these odds were observed among patients with asystole/PEA cardiac arrest mechanism (p≈0.356).

The odds of death among men of 27.42 BMI and 2.97 g/dl serum albumin concentration (mean values from the population sample) were 8-fold lower (p≈0.001) among the VF/pVT stratum when compared to asystole/PEA. The differences in odds of death in the context of the cardiac arrest mechanism were insignificant among women (p≈0.620).

The association between serum albumin concentration and BMI values and the odds of death differed depending on cardiac arrest mechanism. Upon a 1-unit increase of BMI, the VF/pVT-to-asystole/PEA ratio of odds of death decreased approximately 1.26-fold (p≈0.016). This observation was associated with 1.18-fold increase (p≈0.032) in these odds with every 1-unit increase in BMI among patients with asystole/PEA mechanism. Interestingly, upon increase in serum albumin concentration by 1 g/dl, the odds of death decreased by 2.85-fold (p≈0.038) among patients suffering from the VF/pVT cardiac arrest type. Odds ratios, depending on the strata, are shown in **Supplementary Table 1 and Figure 3**.

Random Forest Classifier – Which Features Are the Most Important in Survival Status Classification Performed in Patients with Cardiac Arrest?

As previously shown, none of the categorical variables on their own could perfectly distinguish non-survivors from the whole population sample. Continuous variables also did not allow such classification (**Figure 4**). The ensemble of 100 random trees failed to achieve an AUC score comparable to the score of the aforementioned logistic regression model (AUC: 0.674 for random forest vs 0.762 for logistic regression). The ensemble suffered from poor precision in detecting the non-survivors (0.52), while the recall was relatively good (0.75). The confusion matrix of the ensemble is given in **Supplementary Figure 1**. Upon testing the classifier with 10-fold cross-validation, the ensemble yielded the following metrics: 0.656±0.210 precision, 0.700±0.222 recall, 0.606±0.156 specificity, 0.651±0.127 accuracy, and 0.715±0.132 AUC. The 3 features (variables) of most importance were PCT (0.183), age (0.133), and hsCRP (0.128). Interestingly, albumin was ranked 4th with feature importance of 0.108. BMI, sex, and cardiac arrest mechanism proved to be of less importance (**Figure 5**).

Precision, recall, accuracy, and AUC scores of each estimator (tree) are shown in **Supplementary Table 2**. Despite the fact that the whole ensemble of trees failed to classify survival status satisfyingly, 2 individual trees achieved good accuracy (tree ID 28, testing subset accuracy: 0.7179) or AUC score comparable to the value estimated for the featured logistic regression model (tree ID 25, testing subset AUC: 0.7582).

The tree with the best accuracy (tree ID 28, **Figure 6**) achieved an exceptional precision score (0.8333) at the cost of rather mediocre recall (0.6521). Based on this, hsCRP and age were the most useful features for performing splits. Underweight patients with a BMI ≤17.51 and a hsCRP >151.07 mg/l, would be considered as survivors. The error in classification performed

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Table 3. Values of selected quantitative parameters in context of cardiac arrest mechanism and survival status.

Variable	A: Asystole/PEA, Non-survivors		B: Asystole/PEA, Survivors		C: VF/pVT, Non-survivors		D: VF/pVT, Survivors	
	N	[1st Q, Me, 3rd Q]	N	[1st Q, Me, 3rd Q]	N	[1st Q, Me, 3rd Q]	N	[1st Q, Me, 3rd Q]
Albumin [g/dl]	51	[2.55, 2.90, 3.35]	27	[2.30, 3.00, 3.30]	22	[2.17, 2.60, 3.18]	36	[3.00, 3.40, 3.82]
BMI [kg/m^2]	48	[23.15, 27.68, 30.21]	23	[20.06, 23.88, 29.38]	24	[23.14, 26.12, 29.69]	34	[24.84, 26.30, 31.02]
hsCRP [mg/l]	60	[4.66, 26.60, 99.22]	29	[6.62, 26.06, 83.97]	28	[2.71, 7.64, 63.81]	40	[1.48, 6.04, 19.17]
K [mmol/l]	61	[3.79, 4.34, 5.04]	29	[3.80, 4.20, 6.03]	28	[4.16, 4.80, 5.88]	40	[3.76, 4.22, 4.81]
LYM [%]	24	[5.07, 8.55, 16.62]	21	[5.40, 10.40, 14.50]	6	[3.18, 4.70, 10.12]	22	[6.90, 13.00, 16.85]
Na [mmol/]	61	[134.00, 139.00, 143.00]	29	[134.00, 138.00, 141.00]	28	[136.00, 138.50, 142.00]	40	[136.00, 138.00, 140.00]
NRS2002	61	[3.00, 3.00, 4.00]	29	[3.00, 3.00, 4.00]	31	[3.00, 3.00, 4.00]	40	[3.00, 3.00, 4.00]
PCT [ng/ml]	60	[0.25, 1.77, 6.33]	29	[0.09, 0.37, 2.24]	28	[0.16, 0.36, 2.13]	40	[0.13, 0.24, 1.12]
TChol [mg/dl]	35	[100.50, 125.00, 158.00]	23	[115.00, 139.00, 173.50]	12	[91.75, 127.00, 186.75]	35	[130.00, 156.00, 169.50]
TG [mg/dl]	30	[81.00, 101.50, 160.00]	22	[107.25, 139.50, 197.00]	11	[139.00, 215.00, 288.00]	36	[100.75, 137.00, 181.75]
TSH [uIU/ml]	36	[1.08, 2.00, 3.37]	21	[0.62, 1.19, 3.39]	9	[1.67, 2.12, 3.35]	33	[1.12, 1.65, 2.73]

Variable	A vs B p	C vs D p	A vs C p	B vs D p
Albumin [g/dl]	0.524	**<0.001**	0.200	**0.003**
BMI [kg/m^2]	0.082	0.438	0.910	**0.012**
hsCRP [mg/l]	0.885	0.328	0.127	**0.003**
K [mmol/l]	0.969	0.080	0.182	0.720
LYM [%]	0.927	0.078	0.195	0.258
Na [mmol/]	0.447	0.420	0.993	0.966
NRS2002	0.949	0.641	0.319	0.750
PCT [ng/ml]	**0.018**	0.566	**0.022**	0.927
TChol [mg/dl]	0.162	0.218	0.961	0.479
TG [mg/dl]	0.124	0.111	**0.028**	0.569
TSH [uIU/ml]	0.462	0.500	0.787	0.445

Values are given as [1st quartile; median value; 3rd quartile]. Statistically-significant ($p<0.05$) differences are **marked in bold**.
BMI – body mass index; LYM – lymphocyte count; NRS2002 – Nutrition Risk Screening 2002; PCT – procalcitonin; TChol – total cholesterol concentration; TG – triglycerides; TSH – thyroid-stimulating hormone; hsCRP – high sensitivity C-reactive protein concentration; PEA ,– pulseless electrical activity; pVT – pulseless ventricular tachycardia; VF – ventricular fibrillation.

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Table 4. The association between selected parameters and the odds of death – multivariate logistic regression.

MODEL4										
Hosmer-Lemeshow p		**β=0 hypothesis p**			**AIC**	**BIC**	**Pseudo-R²**		**AUC (learning)**	**AUC (testing)**
0.055		<0.001			132.08	156.47	0.3964		0.835± 0.0403	0.762± 0.0466
Effect/interaction	**Analyzed cat.**	**β_i**	**β_i SE**	**Wald χ^2**	**χ^2 -95% CI**	**χ^2 95% CI**	**p**	**OR**	**OR -95% CI**	**OR 95% CI**
β_0 intercept	–	0.004	0.451	0.00	-0.88	0.89	0.993	1.00	0.42	2.43
Sex	Male	1.737	0.645	7.26	0.47	3.00	**0.007**	**5.68**	1.61	20.09
Cardiac arrest mechanism	VF/pVT	0.430	0.867	0.25	-1.27	2.13	0.620	1.54	0.28	8.40
BMI	–	0.164	0.076	4.62	0.01	0.31	**0.032**	**1.18**	1.01	1.37
Albumin [g/dl]	–	0.042	0.477	0.01	-0.89	0.98	0.929	1.04	0.41	2.66
hsCRP [mg/l]	–	0.008	0.004	3.84	0.00	0.02	**0.050**	**1.01**	1.00	1.02
Cardiac arrest mechanism*Albumin	–	-1.081	0.679	2.53	-2.41	0.25	0.112	0.34	0.09	1.28
Cardiac arrest mechanism*BMI	–	-0.233	0.096	5.84	-0.42	-0.04	**0.016**	**0.79**	0.66	0.96
Cardiac arrest mechanism*Sex	–	-2.510	1.048	5.74	-4.56	-0.46	**0.017**	**0.08**	0.01	0.63

The 'Analyzed cat.' column refers to categories which are compared to reference categories in terms of odds of death. AIC – Akaike Information Criterion; BIC – Bayesian Information Criterion; β_i – regression coefficient; SE – standard error; OR – odds ratio; CI – confidence interval; BMI – body mass index; PEA – pulseless electrical activity; pVT – pulseless ventricular tachycardia; VF – Ventricular fibrillation; hsCRP – high sensitivity C-reactive protein concentration. The 'AUC (learning)' and 'AUC (testing)' columns show AUC values from 10-fold cross validation. Information on other models is shown in Supplementary Table 3.

on the learning subset occurred solely among patients of with K ≤7.44 mmol/l and hsCRP ≤55.25 mg/l. Of patients aged ≤62.50, the VF/pVT cardiac arrest mechanism occurred mostly among the survivors.

The tree with the best AUC score (tree ID 25) was more complex (**Figure 7**). Its precision and recall scores were 0.8235 and 0.6086, respectively. It utilized PCT instead of hsCRP and, interestingly, used nutrition-associated parameters (albumin, NRS2002, and BMI) for performing splits. Patients with PCT >0.17 ng/ml, albumin ≤2.85 g/dl, NRS ≤3.50, and IHCA cardiac arrest location were classified as non-survivors.

The classification capability of both trees was then assessed with 10-fold cross-validation. The tree which utilized nutritional status-associated parameters (**Figure 7**) proved to be markedly superior, scoring 0.745±0.178 precision, 0.754±0.091 recall, 0.708±0.148 specificity, 0.739±0.101 accuracy, and 0.754±0.137 AUC. The other tree (**Figure 6**) scored: 0.689±0.196 precision, 0.690±0.149 recall, 0.648±0.204 specificity, 0.677±0.129 accuracy, and 0.674±0.129 AUC.

Discussion

Our study shows how ML can be used to predict the odds of in-hospital mortality in patients admitted to the ICU after CA. The most important single factors for predicting mortality are PCT age and hsCRP. However, predictive models taking into account multiple variables, including those related to nutritional status (BMI, NRS-2002, and albumin), had higher accuracy.

In the context of cardiac arrest (CA), understanding the interplay between nutritional status and systemic inflammation is crucial for predicting patient outcomes. Nutritional status-related parameters, such as serum albumin concentration, BMI, and Nutritional Risk Score 2002 (NRS 2002), are closely linked to patient survival due to their ability to reflect both the nutritional intake and systemic response [27,28]. Albumin and C-reactive protein (CRP) serve as pivotal biomarkers in these scenarios, where their levels not only reflect nutritional and inflammatory status but also the severity of systemic response, influencing outcomes and recovery processes [29]. Poor nutritional status can lead to weakened immunity, impaired muscle

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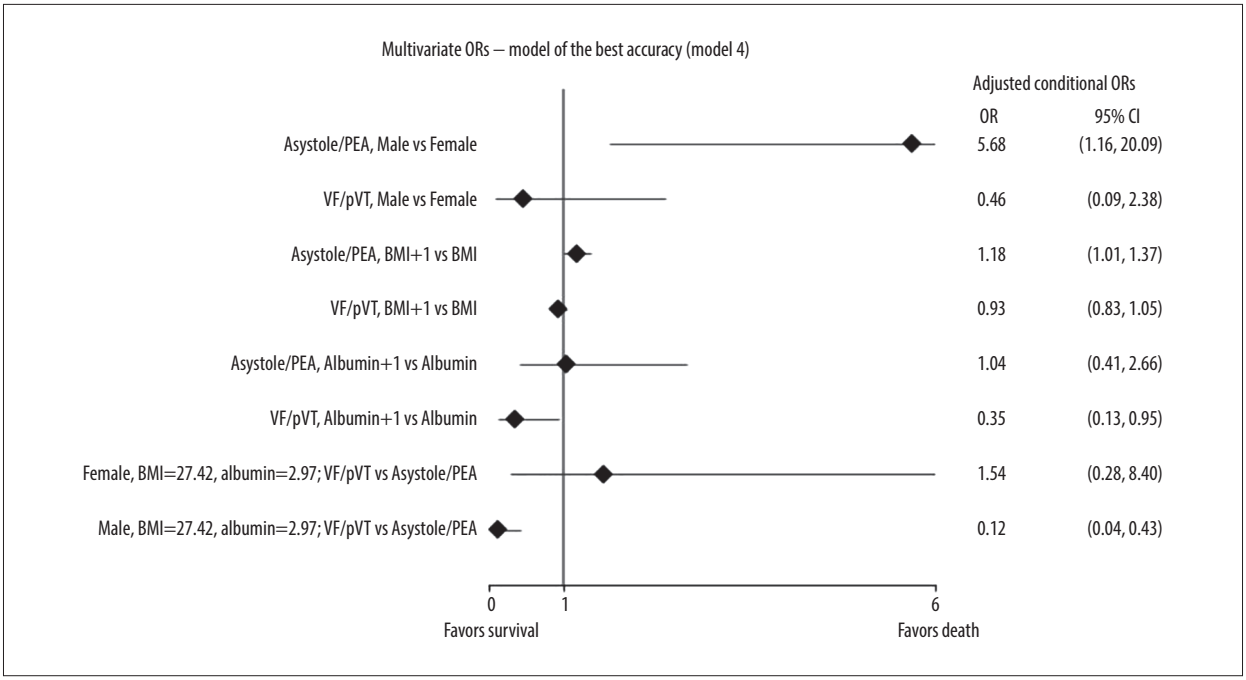

Figure 3. Forest plot of multivariate conditional odds ratios (ORs) associated with the selected model.

function, and overall reduced physiological resilience, which are detrimental in the acute recovery phase [30,31]. Malnutrition may therefore increase the risk of adverse outcomes by exacerbating the severity of existing conditions and hindering recovery processes[32-34]. Elevated PCT levels are notably important in the post-cardiac arrest setting, where they not only indicate systemic inflammation associated with post-resuscitation syndrome but also correlate with nutritional deficiencies [35]. Studies have shown that procalcitonin is elevated in patients who undergo resuscitation, reflecting its role as a critical marker in assessing the severity of underlying conditions and potential outcomes [35]. This association underscores the inclusion of these parameters in our predictive models, aiming to provide a comprehensive assessment of factors that influence survival odds after CA.

Many studies have tried to predict the odds of mortality in critically ill patients after IHCAs and OHCAs using ML [36]. It should be noted that this study, unlike many studies found in the literature, utilized interactions in logistic regression models. This strategy allowed us to better adjust the model for its applicability in real-life situations since the presented odds are conditional (the impact of some factors depends on the status/values of others). Interestingly, the introduction of interactions rendered logistic regression better than random forest classifier in terms predicting death status among the patients (AUC: 0.762 vs 0.674). In interpreting our results, we acknowledge the potential for confounding bias, particularly regarding the correlation between specific laboratory values and cardiac arrest outcomes. While laboratory markers provide critical insights, the underlying etiologies of cardiac arrest may be equally important predictors of patient prognosis. Recent advances in machine learning (ML) offer a promising avenue for refining mortality predictions beyond traditional scoring systems such as SOFA and APACHE II, which have historically guided prognostic assessments in the ICU. Studies have highlighted the ability of ML algorithms to integrate complex datasets and reveal subtle patterns that may escape conventional analysis. For example, ML approaches have demonstrated superior performance in predicting mortality by effectively synthesizing disparate predictors, including those related to nutritional and metabolic disturbances that often accompany cardiac arrest scenarios [37-39].

Based on the logistic regression model, it could be seen that sex, BMI, albumin concentration, and cardiac arrest mechanism type, together, modulate the odds of death. Previous studies show that each of these factors individually can be an independent predictor of odds of in-hospital mortality in patients with life-threatening emergencies [2,26,40,41]. In this study, these nutritional status parameters were modulating the effect of variable cardiac arrest mechanism on the odds of death. The said modulation was investigated based on the analysis of 2nd-degree interactions between each one of these variables and cardiac arrest mechanism. This approach revealed that, although the nutritional status modulated the mortality rate in both CA mechanisms (asystole/PEA, VF/pVT), this modulation was manifested with the effect of BMI.

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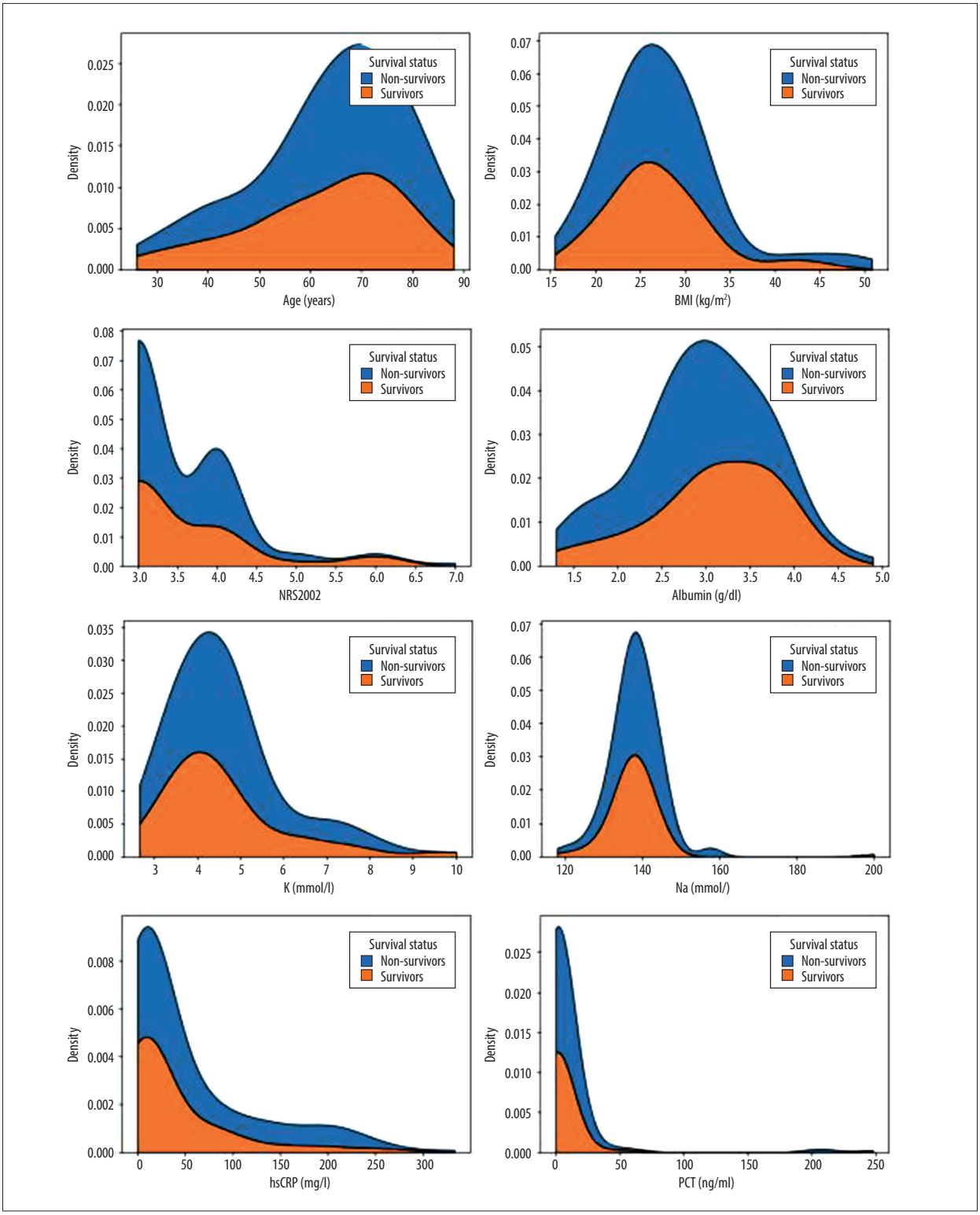

Figure 4. Kernel density (KDE) plots showing the observed distributions of the continuous variables used in survival status prediction.

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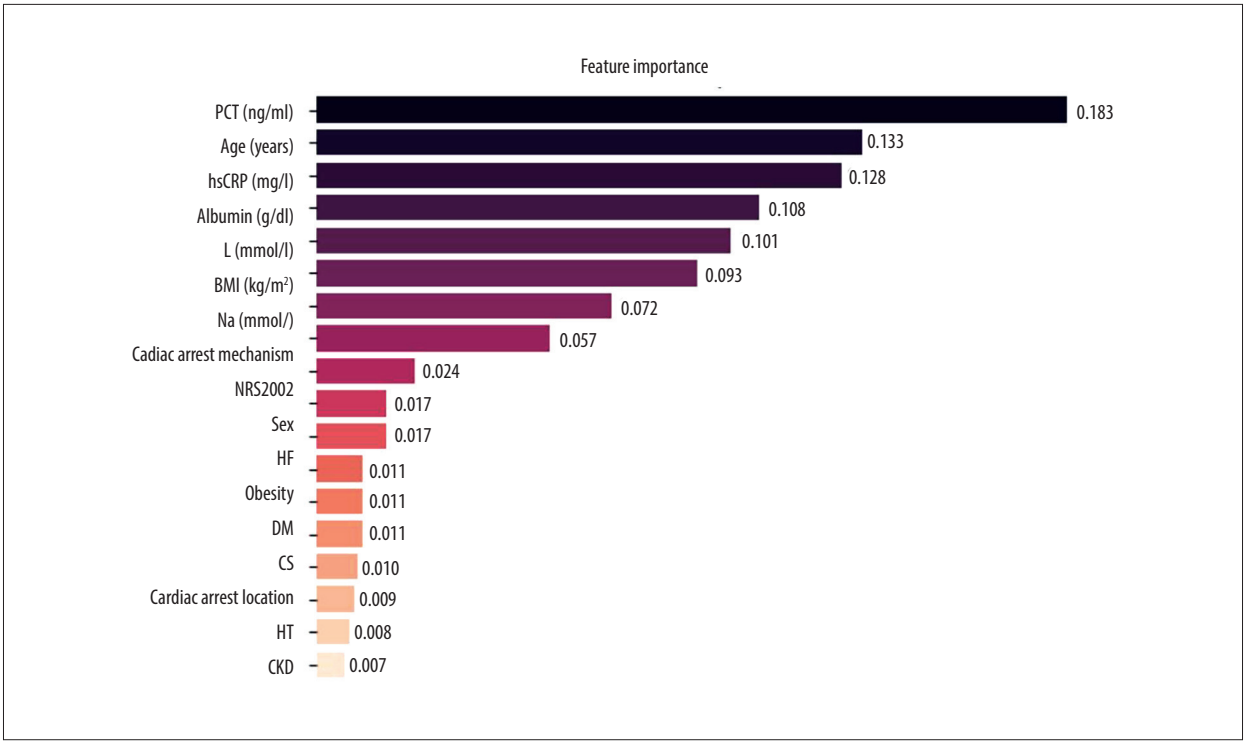

Figure 5. Feature (variable) importance according to the implemented Random Forest Classifier.

To unveil these more complex models, specific clinical scenarios have to be assumed. In the case of comparing a male and female patient of the same initial rhythm cardiac arrest type, being a male would be a more relevant in patients with non-shockable initial rhythm (OR 5.68, men vs women) compared to those with shockable initial rhythm (no significant difference between men and women).

When comparing patients with both initial rhythm CA across the 2 sexes separately, men would be the only stratum which would show any difference in mortality (OR 0.12 VF/pVT vs asystole/PEA). Numerous studies show that a shockable initial rhythm is a predictor of survival [42-44]. In addition, Akahane et al also showed that patients with a shockable initial rhythm had similar overall survival rates independent of sex [45].

As mentioned before, the odds of death among patients with asystole/PEA and VF/pVT were also modulated by different nutritional status-associated parameters. BMI increased the odds of death in cases of asystole/PEA and albumin decreased these odds in VF/pVT patients. These associations may show that malnutrition increases the odds of death, although the tools of its assessment ought to be different among different CA mechanism types if one wanted to predict mortality status. However, it should be emphasized that the introduction of both albumin and BMI to the mortality prediction in real-life settings would require more complex models to be created due to the non-specificity in the association between both albumin and BMI and the nutritional status. As an example, utilizing information about albumin concentration could prove to be troublesome in mortality prediction in case of patients with liver and/or kidney diseases, while the use of BMI would be limited to patients of normal musculature. The results of this study show the possible auxiliary role of nutritional status assessment of the post-CA patients. A number of studies confirm that malnutrition diagnosed on hospital admission can be a predictor of mortality in patients with life-threatening conditions [33,34,46-48].

The aforementioned hypothesis is consistent with the results from decision tree analysis. To avoid unnecessary human-associated bias, the 2 trees shown in the study were chosen from a set of 100 random decision trees (random forest classifier). The tree which utilized nutritional status-associated parameters (BMI, albumin concentration, NRS2002) performed markedly better (accuracy: 0.739±0.101 vs 0.677±0.129) in 10-fold cross-validation compared to the other tree, which did not feature such parameters. Interestingly, these 3 parameters were especially useful in mortality prediction among patients whose PCT levels were above the reference range, indicating inflammatory status (PCT >0.17; ref. range in adults <0.15 ng/ml). The fact that, according to the decision tree (**Figure 7**), the patients who had >0.17 ng/ml PCT, ≤2.85 g/dl albumin, and NRS2002 >3.5 further elucidates the linkage between malnutrition and CA-associated death. Moreover, it is important to note that, according to the random forest classifier algorithm,

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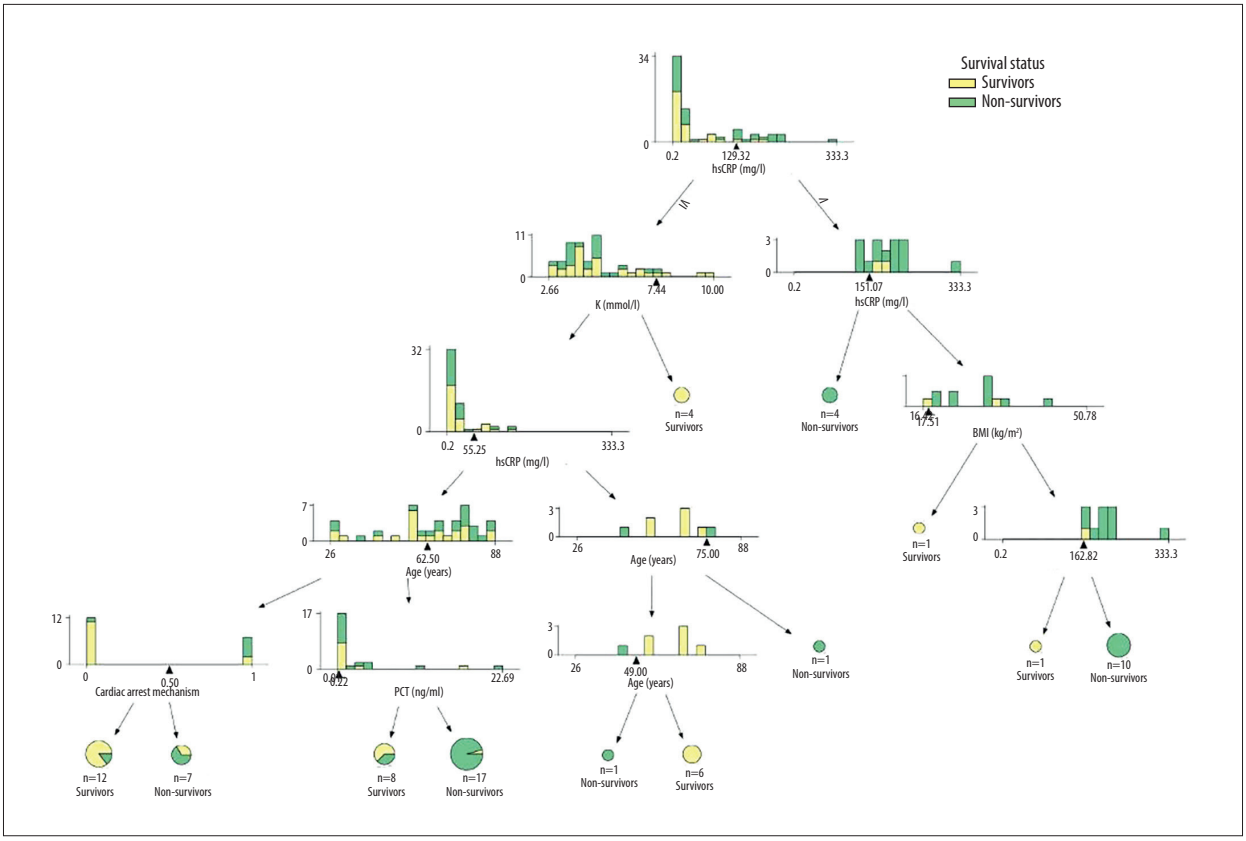

Figure 6. Decision tree of the best accuracy in predicting survival status in the testing subset.

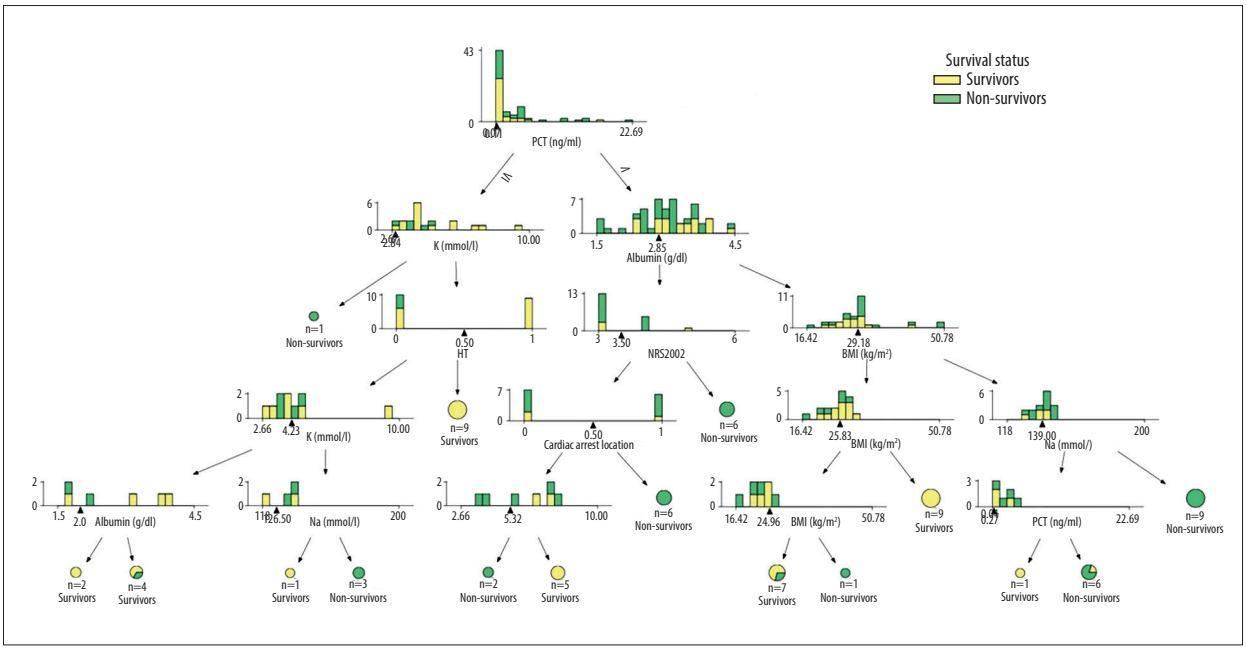

Figure 7. Decision tree of the best AUC score in predicting survival status in the testing subset.

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albumin, BMI, and NRS2002 were among the 9 most important variables used in classification, ranking 4th, 6th, and 9th, respectively among variables such as concentration of electrolytes (Na/K), inflammatory parameters (eg, PCT and hsCRP), and age.

Interestingly, the best decision tree performed comparably to the before-mentioned logistic regression. This fact may demonstrate that regardless of the employed classification (prediction) strategy, the use of nutritional status as a source of information could provide a benefit in mortality assessment among patients after ROSC. However, the choice of the variables taken into consideration would vary between these 2 methods. While it was not examined, it may be possible to combined both of these models to further increase the accuracy of prediction. This study aimed to provide a preliminary body of work for future mortality assessment among CA patients, which is why highly-interpretable models were utilized. Further studies are needed to validate and expand these models with new variables, and also focus on model performance, employing less interpretable algorithms (eg, k-Nearest Neighbor Classification, Support Vector Classification, and Long Short-Term Memory network).

Study Limitations

The study had some limitations. Firstly, in some cases the patient data were incomplete, as it was not always possible to obtain an outcome due to the critical situation and severe condition of the patients. This limitation could have affected the accuracy of our predictive models, as missing data points might lead to less reliable or biased predictions. Secondly, the number of patients was small, although it should be noted that the study included patients who were admitted to the ICU after OHCA/IHCA and only a small number of patients achieved ROSC. This small sample size might limit the generalizability of our results and affect the statistical power of our analyses, possibly obscuring smaller yet clinically significant effects. A larger sample size would have allowed us to analyze more complex (higher-degree) interactions between variables, as well as to investigate whether the interactions shown in this study are biased due to being modulated by other variables. Moreover, as the model studied only the categorical mortality status (survival or its lack), its use (after validation and further model development) would be limited in case the hospital would want to strategize the treatment based on the admission-to-death time. Although the mentioned time was investigated in our previous study, interactions were not included in that (multivariate) model [26]. The data in this study were analyzed retrospectively. Due to the anonymized data, information on long-term survival could not be obtained. Furthermore, specific details such as the exact cause and duration of the cardiac arrests were often not recorded, particularly for patients transferred from other institutions, which might have affected interpretation of associated risk factors and outcomes described in our findings. Also, variations in clinical practice over time and between different providers at the same institution could introduce additional variability into our findings.

Moreover, it should be emphasized that machine learning is only a tool which should be maintained by professionals, in accordance with the a priori clinical aims. In this study, random forest classifier, due to its subpar classification performance, was used to extract the optimal decision trees, based on accuracy and the AUC score. Both these metrics presume that sensitivity (% of true classifications among the non-survivors) and specificity (% of true classifications among the survivors) are equally important to the medical professionals who would be using these algorithms. In extreme cases in which sensitivity or specificity would have to be set close to 100% threshold (100% sensitivity if the algorithm would be used as a screening test, or 100% specificity if the algorithm was used as an auxiliary, after employing more sensitive assessment tools), the classification trees would not only be affected by different cut-off values, but would also probably utilize different variables. Therefore, assumptions need to be discussed among professionals who would want to further validate these, or similar, machine learning algorithms in real-life situations.

Practical Implications

The preliminary findings from our study indicate significant potential for the use of machine learning algorithms in improving treatment outcomes for cardiac arrest cases. Despite the promising results, it is crucial to conduct further, expanded research on larger and more diverse patient groups. Such studies will allow for a more detailed analysis and validation of predictive models and their efficacy in real clinical settings. The development and refinement of these technologies, in close collaboration with medical professionals and data scientists, should focus on integration with existing healthcare systems and adaptation to specific needs and treatment protocols. This could significantly enhance the quality of healthcare and patient outcomes.

Conclusions

- Procalcitonin concentration, age, hsCRP, albumin, and potassium were the most utilized (important) variables according to the Random Forest Classifier (100 random decision trees). Less important classifiers were BMI, sex, and CA initiating rhythm. The remaining factors were of minor importance.

- According to the classification tree of the best fit generated with Random Forest Classifier (100 trees), gathering the

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information on BMI and NRS2002 was especially helpful in mortality classification in cases when the PCT >0.17 ng/ml.

- With each 1-unit increase of BMI, the odds of death ratio increased by 1.18-fold exclusively among the patients with asystole/PEA CA mechanism. Conversely, patients with the VF/pVT CA mechanism showed a 2.85-fold decrease of the odds of death with every 1 g/dl increase in serum albumin concentration. Male patients with BMI equal to 27.4, serum albumin concentration equal to 2.97 g/dl showed markedly lower (OR 0.12) odds of death in case they suffered from the VF/pVT CA mechanism, compared to their male counterparts with the asystole/PEA CA mechanism. This difference in odds was not significant in women. Moreover, sex appeared to affect the odds of death exclusively among the asystole/PEA patients (OR=5.68, male vs female).

- Development of the use of machine learning algorithms may help classify patients with CA to ensure proper medical care and treatment strategies based on the predicted odds of death.

Statement

The study was conducted following the principles of the Declaration of Helsinki and was approved by the independent Bioethics Committee of Wrocław Medical University, protocol no. KB-776/2022. The study followed the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE). This study used only de-identified retrospective patient data, and individual participant informed consent was waived by the Bioethics Committee of Wrocław Medical University.

Declaration of Figures' Authenticity

All figures submitted have been created by the authors, who confirm that the images are original with no duplication and have not been previously published in whole or in part.

Supplementary Materials

Supplementary Table 1. Conditional odds ratios associated with all analyzed multivariate logistic regression models.

Model	Conditions	Analyzed var.	Analyzed cat.	Reference cat.	p	OR	OR -95% CI	OR 95% CI
2	Asystole/PEA	Sex	Male	Female	**0.005**	**5.23**	1.64	16.61
2	VF/pVT	Sex	Male	Female	0.297	0.45	0.10	2.01
2	Female, BMI=27.42	Cardiac arrest mechanism	VF/pVT	Asystole/PEA	0.625	1.48	0.31	7.12
2	Male, BMI=27.42	Cardiac arrest mechanism	VF/pVT	Asystole/PEA	**<0.001**	**0.13**	0.04	0.37
3	Asystole/PEA	BMI	–	–	**0.028**	**1.17**	1.02	1.34
3	VF/pVT	BMI	–	–	0.266	0.94	0.84	1.05
3	Asystole/PEA	Albumin	–	–	0.058	1.01	1.00	1.02
3	VF/pVT	Albumin	–	–	**0.028**	**0.33**	0.12	0.89
4	Asystole/PEA	Sex	Male	Female	**0.007**	**5.68**	1.61	20.09
4	VF/pVT	Sex	Male	Female	0.356	0.46	0.09	2.38
4	Asystole/PEA	BMI	–	–	**0.032**	**1.18**	1.01	1.37
4	VF/pVT	BMI	–	–	0.241	0.93	0.83	1.05
4	Asystole/PEA	Albumin	–	–	0.929	1.04	0.41	2.66
4	VF/pVT	Albumin	–	–	**0.038**	**0.35**	0.13	0.95
4	Female, BMI=27.42, albumin=2.97	Cardiac arrest mechanism	VF/pVT	Asystole/PEA	0.620	1.54	0.28	8.40
4	Male, BMI=27.42, albumin=2.97	Cardiac arrest mechanism	VF/pVT	Asystole/PEA	**0.001**	**0.12**	0.04	0.43

This table features conditional odds ratios (ORs) of death between the 'Analyzed cat.' and 'Reference cat.' categories on condition of assumptions shown in the 'Conditions' column. These ORs are associated with multivariate logistic regression models shown in Supplementary Table 3.

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Supplementary Table 2. Selected performance metrics (precision, recall, accuracy, AUC score) of the Random Forest Classifier estimators (trees) implemented on the testing subset (n=39).

tree ID	Precision	Recall	Accuracy	AUC
0	0.6111	0.4783	0.5128	0.6155
1	0.6000	0.5217	0.5128	0.5367
2	0.7222	0.5652	0.6154	0.6196
3	0.5714	0.3478	0.4615	0.4959
4	0.7368	0.6087	0.6410	0.6413
5	0.6667	0.2609	0.4872	0.5584
6	0.6316	0.5217	0.5385	0.5883
7	0.7143	0.4348	0.5641	0.6073
8	0.6667	0.6957	0.6154	0.6658
9	0.6471	0.4783	0.5385	0.5503
10	0.7143	0.6522	0.6410	0.6413
11	0.7391	0.7391	0.6923	0.7188
12	0.7059	0.5217	0.5897	0.6046
13	0.7000	0.3043	0.5128	0.5000
14	0.7778	0.3043	0.5385	0.5774
15	0.5000	0.3043	0.4103	0.4375
16	0.7692	0.4348	0.5897	0.6168
17	0.7778	0.3043	0.5385	0.5829
18	0.6538	0.7391	0.6154	0.5870
19	0.7059	0.5217	0.5897	0.5734
20	0.6154	0.6957	0.5641	0.5571
21	0.6842	0.5652	0.5897	0.6848
22	0.9167	0.4783	0.6667	0.7527
23	0.6500	0.5652	0.5641	0.5788
24	0.5556	0.2174	0.4359	0.5489
25	0.8235	0.6087	0.6923	**0.7582**
26	0.5556	0.4348	0.4615	0.4511
27	0.6111	0.4783	0.5128	0.4715
28	0.8333	0.6522	**0.7179**	0.6916
29	0.6250	0.4348	0.5128	0.5842
30	0.8000	0.5217	0.6410	0.6549
31	0.5882	0.4348	0.4872	0.4470
32	0.6500	0.5652	0.5641	0.5774
33	0.8235	0.6087	0.6923	0.7296
34	0.8571	0.5217	0.6667	0.6766
35	0.7368	0.6087	0.6410	0.6277
36	0.5263	0.4348	0.4359	0.4606
37	0.6875	0.4783	0.5641	0.5774
38	0.7059	0.5217	0.5897	0.6005
39	0.4444	0.1739	0.3846	0.3587
40	0.5500	0.4783	0.4615	0.4266
41	0.5714	0.5217	0.4872	0.4837
42	0.6875	0.4783	0.5641	0.6005
43	0.7037	0.8261	0.6923	0.6630
44	0.2941	0.2174	0.2308	0.2459
45	0.8182	0.3913	0.5897	0.5761
46	0.6667	0.3478	0.5128	0.5978
47	0.7273	0.3478	0.5385	0.6128
48	0.6316	0.5217	0.5385	0.5190
49	0.6667	0.2609	0.4872	0.6848
50	0.4615	0.2609	0.3846	0.5231
51	0.7619	0.6957	0.6923	0.7283
52	0.6429	0.3913	0.5128	0.4783
53	0.6923	0.3913	0.5385	0.5082
54	0.6667	0.4348	0.5385	0.6889
55	0.5385	0.3043	0.4359	0.4348
56	0.6087	0.6087	0.5385	0.5394
57	0.8000	0.5217	0.6410	0.7554
58	0.6087	0.6087	0.5385	0.5299
59	0.8235	0.6087	0.6923	0.6821
60	0.5217	0.5217	0.4359	0.4022
61	0.6400	0.6957	0.5897	0.5856
62	0.7500	0.2609	0.5128	0.7391
63	0.6333	0.8261	0.6154	0.5897
64	0.6087	0.6087	0.5385	0.5285
65	0.6800	0.7391	0.6410	0.6793
66	0.5000	0.5652	0.4103	0.3478
67	0.7143	0.4348	0.5641	0.5707
68	0.5714	0.6957	0.5128	0.4565
69	0.6471	0.4783	0.5385	0.5435
70	0.6190	0.5652	0.5385	0.5258
71	0.7059	0.5217	0.5897	0.6264
72	0.6400	0.6957	0.5897	0.5666
73	0.6000	0.3913	0.4872	0.5231
74	0.5833	0.6087	0.5128	0.4375
75	0.5714	0.3478	0.4615	0.5679
76	0.5882	0.4348	0.4872	0.5054
77	0.5556	0.2174	0.4359	0.4837

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Supplementary Table 2 continued. Selected performance metrics (precision, recall, accuracy, AUC score) of the Random Forest Classifier estimators (trees) implemented on the testing subset (n=39).

tree ID	Precision	Recall	Accuracy	AUC
78	0.6154	0.3478	0.4872	0.4837
79	0.6667	0.4348	0.5385	0.5707
80	0.6500	0.5652	0.5641	0.5313
81	0.6667	0.6087	0.5897	0.6590
82	0.8182	0.3913	0.5897	0.5992
83	0.8000	0.3478	0.5641	0.6087
84	0.5455	0.2609	0.4359	0.4579
85	0.8889	0.3478	0.5897	0.6413
86	0.7368	0.6087	0.6410	0.7228
87	0.6111	0.4783	0.5128	0.5666
88	0.7692	0.4348	0.5897	0.6766
89	0.7000	0.6087	0.6154	0.6073
90	0.6923	0.3913	0.5385	0.5774
91	0.5714	0.1739	0.4359	0.5285
92	0.6923	0.7826	0.6667	0.6196
93	0.7143	0.2174	0.4872	0.6603
94	0.6522	0.6522	0.5897	0.5448
95	1.0000	0.1304	0.4872	0.6685
96	0.8125	0.5652	0.6667	0.7120
97	0.5789	0.4783	0.4872	0.4891
98	0.6250	0.4348	0.5128	0.5231
99	0.5000	0.3043	0.4103	0.3981

Rows describing the two trees of best accuracy or AUC score are white.

Supplementary Table 3. The association between selected parameters and the odds of death (multivariate logistic regression – all analyzed models).

MODEL1 (stepwise propagation, p threshold=0.05)										
Hosmer-Lemeshow p		β=0 hypothesis p			AIC	BIC	Pseudo-R^2		AUC (learning)	AUC (testing)
0.450		0.003			101.67	108.78	0.1936		0.712± 0.0601	0.645± 0.0650
Effect/interaction	**Analysed cat.**	**β_i**	**β_i SE**	**Wald χ^2**	**χ^2 -95% CI**	**χ^2 95% CI**	**p**	**OR**	**OR -95% CI**	**OR 95% CI**
β_0 intercept	–	-0.220	0.390	0.32	-0.98	0.54	0.572	0.80	0.37	1.72
hsCRP [mg/l]	–	0.010	0.005	4.32	0.00	0.02	**0.038**	1.01	1.00	1.02
Cardiac arrest mechanism	VF/pVT	-1.048	0.505	4.31	-2.04	-0.06	**0.038**	0.35	0.13	0.94
MODEL2										
Hosmer-Lemeshow p		β=0 hypothesis p			AIC	BIC	Pseudo-R^2		AUC (learning)	AUC (testing)
0.414		<0.001			158.02	177.93	0.2873		0.768± 0.0433	0.682± 0.0491
Effect/interaction	**Analyzed cat.**	**β_i**	**β_i SE**	**Wald χ^2**	**χ^2 -95% CI**	**χ^2 95% CI**	**p**	**OR**	**OR -95% CI**	**OR 95% CI**
β_0 intercept	–	0.025	0.410	0.00	-0.78	0.83	0.951	1.03	0.46	2.29
Sex	M	1.654	0.590	7.86	0.50	2.81	**0.005**	**5.23**	1.64	16.61
Cardiac arrest mechanism	VF/pVT	0.392	0.801	0.24	-1.18	1.96	0.625	1.48	0.31	7.12
BMI	–	0.126	0.060	4.47	0.01	0.24	**0.035**	**1.13**	1.01	1.27
hsCRP [mg/l]	–	0.008	0.004	5.05	0.00	0.02	**0.025**	**1.01**	1.00	1.02
Cardiac arrest mechanism*BMI	–	-0.163	0.077	4.43	-0.31	-0.01	**0.035**	**0.85**	0.73	0.99
Cardiac arrest mechanism*Sex	–	-2.445	0.953	6.58	-4.31	-0.58	**0.010**	**0.09**	0.01	0.56

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Supplementary Table 3 continued. The association between selected parameters and the odds of death (multivariate logistic regression – all analyzed models).

MODEL3										
Hosmer-Lemeshow p		**β=0 hypothesis p**			**AIC**	**BIC**	**Pseudo-R²**		**AUC (learning)**	**AUC (testing)**
0.775		<0.001			137.08	156.04	0.3171		0.788± 0.0434	0.712± 0.0492
Effect/interaction	**Analyzed cat.**	**β_i**	**β_i SE**	**Wald χ^2**	**χ^2 -95% CI**	**χ^2 95% CI**	**p**	**OR**	**OR -95% CI**	**OR 95% CI**
β_0 intercept	–	0.871	0.333	6.84	0.22	1.52	**0.009**	**2.39**	1.24	4.59
Cardiac arrest mechanism	VF/pVT	-1.056	0.470	5.04	-1.98	-0.13	**0.025**	**0.35**	0.14	0.87
BMI	–	0.153	0.070	4.80	0.02	0.29	**0.028**	**1.17**	1.02	1.34
Albumin [g/dl]	–	0.034	0.436	0.01	-0.82	0.89	0.939	1.03	0.44	2.43
hsCRP [mg/l]	–	0.007	0.004	3.60	0.00	0.01	0.058	1.01	1.00	1.02
Cardiac arrest mechanism*Albumin	–	-1.142	0.652	3.07	-2.42	0.14	0.080	0.32	0.09	1.14
Cardiac arrest mechanism*BMI	–	-0.218	0.091	5.72	-0.40	-0.04	**0.017**	**0.80**	0.67	0.96
MODEL4										
Hosmer-Lemeshow p		**β=0 hypothesis p**			**AIC**	**BIC**	**Pseudo-R2**		**AUC (learning)**	**AUC (testing)**
0.055		<0.001			132.08	156.47	0.3964		0.835± 0.0403	0.762± 0.0466
Effect/interaction	**Analyzed cat.**	**β_i**	**β_i SE**	**Wald χ^2**	**χ^2 -95% CI**	**χ^2 95% CI**	**p**	**OR**	**OR -95% CI**	**OR 95% CI**
β_0 intercept	–	0.004	0.451	0.00	-0.88	0.89	0.993	1.00	0.42	2.43
Sex	M	1.737	0.645	7.26	0.47	3.00	**0.007**	**5.68**	1.61	20.09
Cardiac arrest mechanism	VF/pVT	0.430	0.867	0.25	-1.27	2.13	0.620	1.54	0.28	8.40
BMI	–	0.164	0.076	4.62	0.01	0.31	**0.032**	**1.18**	1.01	1.37
Albumin [g/dl]	–	0.042	0.477	0.01	-0.89	0.98	0.929	1.04	0.41	2.66
hsCRP [mg/l]	–	0.008	0.004	3.84	0.00	0.02	**0.050**	**1.01**	1.00	1.02
Cardiac arrest mechanism*Albumin	–	-1.081	0.679	2.53	-2.41	0.25	0.112	0.34	0.09	1.28
Cardiac arrest mechanism*BMI	–	-0.233	0.096	5.84	-0.42	-0.04	**0.016**	**0.79**	0.66	0.96
Cardiac arrest mechanism *Sex	–	-2.510	1.048	5.74	-4.56	-0.46	**0.017**	**0.08**	0.01	0.63

The 'Analyzed cat.' column refers to categories which are compared to reference categories in terms of odds of death. AIC – Akaike Information Criterion; BIC – Bayesian Information Criterion; β_i – regression coefficient; SE – standard error; OR – odds ratio; CI – confidence interval. The 'AUC (learning)' and 'AUC (testing)' columns show AUC values from 10-fold cross validation.

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Supplementary Table 4. Selected metrics of the best logistic regression model (Supplementary Table 3: model 4).

Cut-off point	Recall	Specificity	Accuracy	Precision	NPV	FPR	FNR	Youden's J statistic
0.998	0.033	1.000	0.477	1.000	0.468	0.000	0.967	0.033
0.995	0.050	1.000	0.486	1.000	0.472	0.000	0.950	0.050
0.993	0.067	1.000	0.495	1.000	0.477	0.000	0.933	0.067
0.984	0.083	0.980	0.495	0.833	0.476	0.020	0.917	0.064
0.976	0.100	0.980	0.505	0.857	0.481	0.020	0.900	0.080
0.975	0.117	0.980	0.514	0.875	0.485	0.020	0.883	0.097
0.972	0.133	0.980	0.523	0.889	0.490	0.020	0.867	0.114
0.953	0.133	0.961	0.514	0.800	0.485	0.039	0.867	0.094
0.937	0.150	0.961	0.523	0.818	0.490	0.039	0.850	0.111
0.922	0.183	0.961	0.541	0.846	0.500	0.039	0.817	0.144
0.913	0.200	0.961	0.550	0.857	0.505	0.039	0.800	0.161
0.903	0.217	0.961	0.559	0.867	0.510	0.039	0.783	0.177
0.901	0.233	0.961	0.568	0.875	0.516	0.039	0.767	0.194
0.871	0.250	0.961	0.577	0.882	0.521	0.039	0.750	0.211
0.864	0.267	0.961	0.586	0.889	0.527	0.039	0.733	0.227
0.861	0.283	0.961	0.595	0.895	0.533	0.039	0.717	0.244
0.852	0.300	0.961	0.604	0.900	0.538	0.039	0.700	0.261
0.837	0.317	0.961	0.613	0.905	0.544	0.039	0.683	0.277
0.833	0.333	0.961	0.622	0.909	0.551	0.039	0.667	0.294
0.827	0.350	0.961	0.631	0.913	0.557	0.039	0.650	0.311
0.819	0.367	0.961	0.640	0.917	0.563	0.039	0.633	0.327
0.817	0.400	0.961	0.658	0.923	0.576	0.039	0.600	0.361
0.801	0.417	0.961	0.667	0.926	0.583	0.039	0.583	0.377
0.792	0.417	0.941	0.658	0.893	0.578	0.059	0.583	0.358
0.79	0.417	0.922	0.649	0.862	0.573	0.078	0.583	0.338
0.778	0.433	0.922	0.658	0.867	0.580	0.078	0.567	0.355
0.768	0.450	0.922	0.667	0.871	0.588	0.078	0.550	0.372
0.759	0.467	0.922	0.676	0.875	0.595	0.078	0.533	0.388
0.742	0.483	0.922	0.685	0.879	0.603	0.078	0.517	0.405
0.734	0.500	0.902	0.685	0.857	0.605	0.098	0.500	0.402
0.718	0.517	0.902	0.694	0.861	0.613	0.098	0.483	0.419
0.714	0.533	0.902	0.703	0.865	0.622	0.098	0.467	0.435
0.710	0.550	0.902	0.712	0.868	0.630	0.098	0.450	0.452
0.707	0.567	0.902	0.721	0.872	0.639	0.098	0.433	0.469

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Supplementary Table 4 continued. Selected metrics of the best logistic regression model (Supplementary Table 3: model 4).

Cut-off point	Recall	Specificity	Accuracy	Precision	NPV	FPR	FNR	Youden's J statistic
0.702	0.583	0.902	0.730	0.875	0.648	0.098	0.417	0.485
0.669	0.583	0.882	0.721	0.854	0.643	0.118	0.417	0.466
0.662	0.583	0.863	0.712	0.833	0.638	0.137	0.417	0.446
0.65	0.583	0.843	0.703	0.814	0.632	0.157	0.417	0.426
0.645	0.600	0.843	0.712	0.818	0.642	0.157	0.400	0.443
0.636	0.617	0.843	0.721	0.822	0.652	0.157	0.383	0.460
0.634	0.633	0.843	0.730	0.826	0.662	0.157	0.367	0.476
0.632	0.650	0.843	0.739	0.830	0.672	0.157	0.350	0.493
0.629	0.650	0.824	0.730	0.813	0.667	0.176	0.350	0.474
0.624	0.650	0.804	0.721	0.796	0.661	0.196	0.350	0.454
0.604	0.650	0.784	0.712	0.780	0.656	0.216	0.350	0.434
0.593	0.650	0.765	0.703	0.765	0.650	0.235	0.350	0.415
0.585	0.650	0.745	0.694	0.750	0.644	0.255	0.350	0.395
0.564	0.667	0.745	0.703	0.755	0.655	0.255	0.333	0.412
0.551	0.683	0.745	0.712	0.759	0.667	0.255	0.317	0.428
0.538	0.700	0.745	0.721	0.764	0.679	0.255	0.300	0.445
0.531	0.700	0.725	0.712	0.750	0.673	0.275	0.300	0.425
0.521	0.700	0.706	0.703	0.737	0.667	0.294	0.300	0.406
0.513	0.717	0.706	0.712	0.741	0.679	0.294	0.283	0.423
0.512	0.717	0.667	0.694	0.717	0.667	0.333	0.283	0.383
0.508	0.733	0.667	0.703	0.721	0.680	0.333	0.267	0.400
0.501	0.733	0.647	0.694	0.710	0.673	0.353	0.267	0.380
0.498	0.750	0.647	0.703	0.714	0.688	0.353	0.250	0.397
0.487	0.767	0.647	0.712	0.719	0.702	0.353	0.233	0.414
0.480	0.767	0.627	0.703	0.708	0.696	0.373	0.233	0.394
0.477	0.767	0.608	0.694	0.697	0.689	0.392	0.233	0.375
0.466	0.767	0.588	0.685	0.687	0.682	0.412	0.233	0.355
0.45	0.783	0.588	0.694	0.691	0.698	0.412	0.217	0.372
0.426	0.783	0.569	0.685	0.681	0.690	0.431	0.217	0.352
0.418	0.800	0.569	0.694	0.686	0.707	0.431	0.200	0.369
0.417	0.800	0.549	0.685	0.676	0.700	0.451	0.200	0.349
0.405	0.817	0.549	0.694	0.681	0.718	0.451	0.183	0.366
0.402	0.833	0.549	0.703	0.685	0.737	0.451	0.167	0.382
0.394	0.833	0.529	0.694	0.676	0.730	0.471	0.167	0.363

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Supplementary Table 4 continued. Selected metrics of the best logistic regression model (Supplementary Table 3: model 4).

Cut-off point	Recall	Specificity	Accuracy	Precision	NPV	FPR	FNR	Youden's J statistic
0.363	0.833	0.510	0.685	0.667	0.722	0.490	0.167	0.343
0.361	0.833	0.490	0.676	0.658	0.714	0.510	0.167	0.324
0.347	0.833	0.471	0.667	0.649	0.706	0.529	0.167	0.304
0.342	0.850	0.471	0.676	0.654	0.727	0.529	0.150	0.321
0.34	0.850	0.451	0.667	0.646	0.719	0.549	0.150	0.301
0.332	0.867	0.451	0.676	0.650	0.742	0.549	0.133	0.318
0.320	0.867	0.431	0.667	0.642	0.733	0.569	0.133	0.298
0.311	0.883	0.431	0.676	0.646	0.759	0.569	0.117	0.315
0.309	0.883	0.412	0.667	0.639	0.750	0.588	0.117	0.295
0.296	0.883	0.392	0.658	0.631	0.741	0.608	0.117	0.275
0.286	0.883	0.373	0.649	0.624	0.731	0.627	0.117	0.256
0.281	0.883	0.353	0.640	0.616	0.720	0.647	0.117	0.236
0.279	0.883	0.333	0.631	0.609	0.708	0.667	0.117	0.217
0.276	0.883	0.314	0.622	0.602	0.696	0.686	0.117	0.197
0.272	0.883	0.294	0.613	0.596	0.682	0.706	0.117	0.177
0.262	0.883	0.275	0.604	0.589	0.667	0.725	0.117	0.158
0.244	0.883	0.255	0.595	0.582	0.650	0.745	0.117	0.138
0.237	0.883	0.235	0.586	0.576	0.632	0.765	0.117	0.119
0.229	0.883	0.216	0.577	0.570	0.611	0.784	0.117	0.099
0.228	0.883	0.196	0.568	0.564	0.588	0.804	0.117	0.079
0.22	0.900	0.196	0.577	0.568	0.625	0.804	0.100	0.096
0.216	0.917	0.196	0.586	0.573	0.667	0.804	0.083	0.113
0.213	0.917	0.176	0.577	0.567	0.643	0.824	0.083	0.093
0.206	0.917	0.157	0.568	0.561	0.615	0.843	0.083	0.074
0.199	0.917	0.137	0.559	0.556	0.583	0.863	0.083	0.054
0.181	0.933	0.137	0.568	0.560	0.636	0.863	0.067	0.071
0.18	0.933	0.118	0.559	0.554	0.600	0.882	0.067	0.051
0.173	0.950	0.118	0.568	0.559	0.667	0.882	0.050	0.068
0.157	0.950	0.098	0.559	0.553	0.625	0.902	0.050	0.048
0.154	0.967	0.098	0.568	0.558	0.714	0.902	0.033	0.065
0.112	0.967	0.078	0.559	0.552	0.667	0.922	0.033	0.045
0.110	0.967	0.059	0.550	0.547	0.600	0.941	0.033	0.025
0.076	0.967	0.039	0.541	0.542	0.500	0.961	0.033	0.006
0.07	0.967	0.020	0.532	0.537	0.333	0.980	0.033	-0.014

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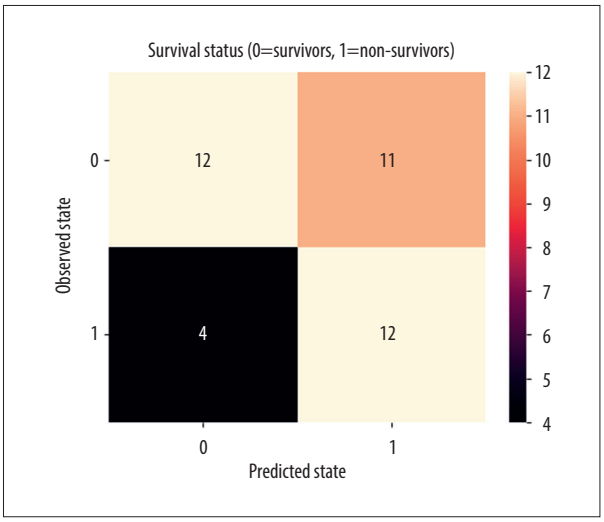
Supplementary Table 4 continued. Selected metrics of the best logistic regression model (Supplementary Table 3: model 4).

Cut-off point	Recall	Specificity	Accuracy	Precision	NPV	FPR	FNR	Youden's J statistic
0.065	0.967	0.000	0.523	0.532	0.000	1.000	0.033	-0.033
0.043	0.983	0.000	0.532	0.536	0.000	1.000	0.017	-0.017
0.016	1.000	0.000	0.541	0.541		1.000	0.000	0.000

The best cut-off value and its associated metrics are colored. NPV – negative predictive value; FPR – false positive ratio, FNR – false negative ratio.



Supplementary Figure 1. Confusion matrix for the Random Forest Classifier algorithm ensemble implemented on the testing subset (n=39).

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