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Comparison of Machine Learning Tools for the Prediction of ICU Admission in COVID-19 Hospitalized Patients

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Abstract

Background: The rapid coronavirus disease 2019 (COVID-19) outbreak has overwhelmed many healthcare systems worldwide and put them at the edge of collapsing. As the capacity of intensive care units (ICUs) is limited, deciding on the proper allocation of required resources is crucial.

Objectives: This study aimed to create a machine learning (ML)-based predictive model of ICU admission among COVID-19 inhospital patients at the initial presentation.

Methods: This retrospective study was conducted on 1225 laboratory-confirmed COVID-19 hospitalized patients during January 9, 2020 - January 20, 2021. The top clinical parameters contributing to COVID-19 ICU admission were identified based on a correlation coefficient at P-value < 0.05. Next, the predictive models were constructed using five ML algorithms. Finally, to evaluate the performances of models, the metrics derived from the confusion matrix, classification error, and receiver operating characteristic were calculated.

Results: Following feature selection, a total of 11 parameters were selected as the top predictors to build the prediction models. The results showed that the best performance belonged to the random forest (RF) algorithm with the mean accuracy of 99.5%, mean specificity of 99.7%, mean sensitivity of 99.4%, Kappa metric of 95.7%, and root mean squared error of 0.015.

Conclusions: The ML algorithms, particularly RF, enable a reasonable level of accuracy and certainty in predicting disease progression and ICU admission for COVID-19 patients. The proposed models have the potential to inform frontline clinicians and health authorities with quantitative tools to assess illness severity and optimize resource allocation under time-sensitive and resource-constrained situations.

Keywords: Coronavirus, COVID-19, Decision Support Systems, Intensive Care Unit, Machine Learning

1. Background

Since December 2019, the coronavirus disease 2019 (COVID-19) has been spreading aggressively worldwide, and the health systems have encountered an increasing shortage of critical care resources, such as personal protective equipment, intensive care unit (ICU) beds, and ventilators (1). So far, this virus has affected almost all countries, with more than two million deaths worldwide (2). Approximately 20% of COVID-19 patients need hospitalization, and 20%-30% of COVID-19 in-hospital patients are admitted to ICU (3). In Iran, the ICU admission rate is esti-

mated to be 32% of hospitalized patients, and the ICU death rate is about 39% (4). The ICU resources are currently restricted, and more than 50% of ICU beds are occupied under normal conditions (5).

The unexpected outbreak, rapid transmission, ambiguous disease course, and prognosis, as well as emerging new mutations of COVID-19, along with health systems being not prepared for large-scale epidemic responses, created a situation in which the management of intensive care resources is crucial (6). Under this condition, it is urgent to construct and test effective clinical risk prediction tools for appropriately triaging critical patients (7, 8). Ac-

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cordingly, predicting the individual disease courses and outcomes is essential for triaging patients, customized care service provision, utilizing life-saving resources in the best possible way, and directing them toward vulnerable and at-risk sub-groups deteriorating to critical COVID-19. Furthermore, many problems resulting from the shortage of hospital resources can be overcome by predicting the risk of patient deterioration, determining the length of stay, using hospital resources efficiently, and managing bed turnover (9, 10).

Innovative approaches for the early identification and triaging of patients at the time of admission will be greatly beneficial and effective in estimating which patients are at the high risk of clinical deterioration and have poor outcomes requiring ICU admission (8, 9). In such conditions, the design and implementation of clinical decision support systems equipped with machine learning (ML)-based prediction models will be critical for the optimal use of limited hospital resources and supporting clinical decisions. The ML, as a sub-form of artificial intelligence technologies, provides new insight or knowledge through extracting functional patterns and applicable rules from the large raw datasets (7, 10).

In the previous researches, a large number of ML algorithms were trained for the prediction of COVID-19 disease progression, patient condition deterioration (9, 10), ICU hospitalization (8, 9, 11-13), and death (8, 11, 14-19).

2. Objectives

The present study aimed to develop and validate a data-driven framework using five ML techniques to predict the patients who need transfer to ICU and find out the contributing clinical predictors by analyzing the available data at the time of admission.

3. Methods

This retrospective single-center cross-sectional study was conducted in 2021 to predict admission to ICU based on selected data-driven ML techniques.

3.1. Dataset and Participants

In this study, a COVID-19 hospital-based registry database from Taleghani Hospital, Abadan, Iran, was reviewed retrospectively. Only hospitalized confirmed COVID-19 patients aged \geq 18 years and admitted during January 9, 2020 - January 20, 2021, met our inclusion criteria. During this period, a total of 13885 suspected cases with COVID-19 were referred to Taleghani Hospital, 3350 of which were confirmed as COVID-19 by RT-PCR

test. The exclusion criteria entailed non-COVID-19 cases, non-hospitalized COVID-19 patients, cases with unknown disposition, patients under 18 years old, incomplete case records (missing more than 70%), and admission time before January 9, 2020, or after January 20, 2021. Following applying the exclusion criteria, finally, 1225 records were entered in the study (Figure 1).

3.2. Feature Selection

Feature selection is an effective technique for determining the most significant variables, reducing the dimensions of the dataset, and improving the efficiency of ML algorithms (20). The included cases are defined based on 53 primary risk factors. In the current study, the variables with a correlation coefficient value less than 0.05 (Pvalue < 0.05) were identified as influential risk factors in predicting ICU admission.

3.3. Model Development

To predict ICU admission for COVID-19 patients, several ML classification algorithms, including Artificial Neural Network (ANN), K-Nearest Neighbor (KNN), Support Vector Machine (SVM), Decision Tree (DT), and Random Forest (RF), were used. We applied a set of parameters as shown in Table 1.

Table 1. Parameters for ML Algorithms		
Model	Parameters	
KNN	K = 1, 3, 5	
SVM	Kernel function = Gaussian	
RF	-	
DT	-	
ANN	57-10-5-2	

3.4. Study Roadmap and Experiment Environment

All experiments on the classification algorithms described in this study were implemented using Python version 3.7.7. The Python experiment environment offers a well-defined framework for researchers and developers to run and assess their ML models. The roadmap of the proposed prediction model in this work is depicted in Figure 2.

3.5. Preprocessing

In the preprocessing stage, in order to use the data effectively in classifiers, raw data input was performed utilizing several preprocessing techniques, such as deleting missing values (missing more than 70%), minimum and maximum scalar values, and standard scalar.



Figure 1. Flowchart describing patient selection

3.6. Experiment Evaluation

In this study, the performance of ML algorithms was calculated based on the 10-fold cross-validation method. To better compare the performance of algorithms, we assessed the effectiveness of five ML algorithms in terms of accuracy, specificity, sensitivity, error rate (Equations 1-4), receiver operating characteristic (ROC) curve, time to build the model, correctly classified instances, incorrectly classified instances, Kappa statistic, mean absolute error (MAE), root mean squared error (RMSE), relative absolute error, and root relative squared error (RRSE).

$$Classification \ accuracy = \frac{TP + TN}{TP + TN + FP + FN} \ \times 100$$
 (1)

$$Classification \ sensitivity = \frac{TP}{TP + FN} \ \times \ 100 \tag{2}$$

$$Classification specificity = \frac{TN}{TN + FP} \times 100$$
(3)

$$Classification\ error = \frac{FP + FN}{TP + TN + FP + FN} \times 100 \tag{4}$$

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Figure 2. Block diagram of the proposed system for predicting ICU admission in patients with COVID-19

3.7. Ethical Considerations

The present study was approved by the Ethics Committee of Abadan University of Medical Sciences (Ethics code: IR.ABADANUMS.REC.1400.054). In order to protect the privacy and confidentiality of patients, we concealed the unique identification information of all patients in the process of data collection and presentation.

4. Results

4.1. Demographic and Clinical Characteristics

After applying the exclusion criteria, a total of 1225 patients were eligible (Figure 1). Of 1225 hospitalized COVID-19 cases, 664 (54.2%) were male, and 561 (45.8%) were women. Moreover, the median age of participants was 57.25 years (interquartile 18 - 100 years). We observed that 170 (13.87%) individuals were hospitalized in the ICU, and 1055 (86.13%) cases were hospitalized in general wards. Among the eligible patients, 1136 (92.75%) recovered, and 89 (7.25%) were deceased. Descriptive statistics for the 1225 records in this dataset are summarized in Table 2.

4.2. Top Predictors of ICU Admission

The most important predictors affecting ICU admission and disease progression were determined using the correlation coefficient at P-value < 0.05. As shown in Table 3, the top 11 ICU admission predictors were age, white cell count, neutrophil count, and lymphocyte count, blood urea nitrogen (BUN), aspartate transaminase (AST)/alanine transaminase (ALT), lactate dehydrogenase (LDH), cough, dyspnea, and oxygen therapy.

4.3. Model Development

In this study, to construct the ICU admission prediction model, we used five classification algorithms, namely ANN, KNN, SVM, DT, and RF, with k-fold (k = 10) cross-validation methods. The mean metrics of 10-fold cross-validation methods were measured. Table 4 shows the 10-fold crossvalidation results of five classifiers.

4.4. ANN Configuration

In this structure, according to Table 5, the input data consisted of 57 variables, two hidden layers with ten and five neurons, and two outputs (configuration: 57-10-5-2).

Variables	Pearson's Correlation	P-Value	Variables	Pearson's Correlation	P-Value
Age	-0.045	*0.019	Blood type	-0.025128	0.274
Height	-0.24	0.409	Gender	-0.107	0.38
Weight	-0.25	0.388	Cough	0.299	*0.041417
Temperature	-0.32	0.268	Contusion	-0.122	0.342
Creatinine	-0.066	0.119	Hypertension	-0.1744378	0.0541
Red cell count	0.029	0.315	Cardiovascular	0.2746594	0.125
White cell count	-0.054	*0.047	Alcohol consumption	0.7923469	0.218
Hematocrit	-0.017	0.562	Smoking	0.3123146	0.354
Hemoglobin	-0.1	0.724	Diabetes	0.0980716	0.104
Platelet count	0.018	0.532	Other underline disorders	0.0904762	0.465
Absolute lymphocyte count	-0.057	*0.044	Sore throat	0.0591151	0.64
Absolute neutrophil count	0.061	*0.033	Runny noise	-0.1446846	0.253
Calcium	-0.055	0.055	Loss of smell	0.0335175	0.811
Phosphorus	-0.02	0.476	Loss of taste	-0.1192558	0.414
Magnesium	-0.033	0.243	Dyspnea	0.4443414	*0.017
Sodium	-0.015	0.59	Oxygen therapy	0.460136	*0.008
Potassium	0.015	0.607	Pneumonia	0.2690936	0.115
Bun	-0.059	*0.038	Fever	0.0241734	0.842
Total bilirubin	-0.003	0.915	Chill	0.0269847	0.824
Asp	0.054	*0.033	Muscular pain	0.0885438	0.466
Alt	0.047	*0.027	GI complications	-0.20181	0.179
Albumin	0.024	0.394	Headache	-0.0297449	0.831
Glucose	0.017	0.552	Vomit	0.0525788	0.696
Ldh	0.056	*0.049	Nausea	0.0083105	0.949
Activated partial thromboplastin time	-0.036	0.213	ESR	0.04	0.157
Prothrombin time	0.01	0.714	Hyper sensitive troponin	-0.2146846	0.439
Alkaline phosphatase	-0.003	0.929	C-reactive protein	0.0258788	0.196

Table 4. Average Performance of Ten Independent Runs of Classifiers Based on 10-Fold Cross-validation					
Evaluation Criteria		Classifier			
Evaluation Chiteria	ANN	DT	KNN	SVM	RF
Best time to build a model (s)	38	22	27	14	31
Correctly classified instances	1,747	1,654	1,783	1,637	1,885
Incorrectly classified instances	148	241	112	258	10
Mean accuracy (%)	92.2	87.3	94.1	86.4	99.5
Mean specificity(%)	96.8	85.4	88.7	87.5	99.7
Mean sensitivity (%)	87.6	89.3	99.5	85.3	99.4

<i>iable 5.</i> ANN Configuration				
Model	Parameters	Values		
	Grid weights	Random (between 1 and -1)		
	Network error	According to MSE		
	Training ratio	0.7		
	Validation ratio	0.15		
	Test ratio	0.15		
ANN	Optimization	Using Trainlm, which is a network training function that updates weight and bias values according to Levenberg-Marquardt optimization		
	Maximum epochs	1000		
	Maximum training time	Inf		
	Performance goal	0		
	Minimum gradient	min_grad: 1e-07		
	Maximum validation checks	max_fail: 6		
	Ми	0.001		
	Mu decrease ratio	mu_dec: 0.1		
	Mu increase ratio	mu_inc: 10		
	Maximum mu	mu_max: 1000000000		

According to the experimental results of evaluating selected ML models in 10-iterations, the KNN algorithm (with K = 5) had 94.1% accuracy, 88.7% specificity, and 99.5% sensitivity. After running ANN, the algorithm achieved an accuracy of 92.2%, a specificity of 96.8%, and a sensitivity of 87.6%. The RF algorithm showed high performance with 99.5% accuracy, 99.7% specificity, and 99.4% sensitivity. The SVM algorithm had 87.5%, 85.3%, and 86.4% specificity, sensitivity, and accuracy, respectively. Furthermore, the DT algorithm demonstrated 87.3% accuracy, 85.4% specificity, and 89.3% sensitivity. Based on the analysis of variance, the five selected algorithms were significantly different (P < 0.05). The error rate of classifiers and computation time of implemented models on the given dataset are shown in Figure 3.

The results obtained for the error rate of selected classifiers revealed that the RF algorithm had the highest Kappa metric of 95.7%. In addition, it has the lowest MAE (0.02), RMSE (0.015), and RRSE (22%). The results of comparing confusion matrix metrics and area under the curve (AUC)-ROC of different classifiers are shown in Figures 4 and 5.

According to Figures 4 and 5, the RF algorithm was the best classifier for predicting ICU admission based on evaluation criteria. The SVM algorithm has the best computation time of processing with 14 s. The results for ten independent runs of RF are summarized in Table 6.

Table 6. Performance of RF in Ten Independent Runs Run Specificity Sensitivity Accuracy 1 99.1425 99.5817 99.77514 99.2141 99.458 99.8541 2 99.3236 99.6745 99.75114 3 4 99.2451 99.8542 99.347 5 99.6173 99.5841 99.471 6 99.657 99.37414 99.3445 7 99.4235 99.335 99.5457 8 99.741 99.421 99.247 99.2351 99.9524 9 99.741 10 99.541 99.3541 99.8242 Std 99.41402 99.55891 99.59008 Min 0.212369 0.21395 0.226258 Max 99.1425 99.335 99.247 Mean 99.741 99.9524 99.8541

5. Discussion

Given the heterogeneity of the clinical manifestations of COVID-19, it is critical to develop models for predicting the likelihood of ICU admission by ML techniques. This study created five ML-based models using the most relevant variables in determining the risk of ICU admission derived from a correlation coefficient analysis. The tech-



Figure 3. Error rate of the classifiers on the given dataset



niques used herein included ANN, DT, KNN, SVM, and RF, which were trained through the most significant predictors from 1225 laboratory-confirmed COVID-19 patients at the time of admission. Finally, based on our analysis of selected algorithms, we found that RF with a mean accuracy of 99.5%, a mean specificity of 99.7%, and a mean sensitivity of 99.4% have better performance than other ML algorithms in predicting the probability of ICU transfer after hospital admission.

In the ICU, the need for informed decision-making is critical, especially in crisis circumstances, such as the current COVID-19 pandemic, where the healthcare systems encountered an increasing surge of patients and severe shortage in hospital resources (21, 22). The models developed in this study could be simply computerized as an alternative to manual and subjective clinical assessment methods. To



correctly extract clinical predictors for estimating the potential need for ICU services, we evaluated clinical features at the time of admission and not at the progressive/severe course of the disease. In addition, the critical patients at admission time were discarded from the analysis. Thus, if validated, these features could be applied for predicting the likelihood to enter in ICU at the first hospitalization. For this purpose, Feature selection is a significant step to prepare the data before entering into the model (23). Hence, we identified the most important variables (n = 11) through correlation coefficient at P-value < 0.05. The most significant predictors of ICU admission were older age, high creatinine, leukocytosis, increased BUN, elevated ASP/ALT, augmented LDH, dry cough, hypertension, cardiovascular disorders, diabetes, dyspnea, decreased SPO₂, pneumonia, and high C-reactive protein.

Many studies have focused on determining the key risk factors for ICU admission (8, 9, 11, 13, 24, 25). The ten top clinical variables predicting ICU risk in reviewed studies encompassed age (older age), body temperature (high), oxygen saturation (decreased), neutrophil count and lymphocyte count (raised), C-reactive protein (elevated), D-dimer (increased), ALT and/or AST (augmented), LDH (elevated), loss of consciousness, and hypertension/cardiovascular diseases. In general, high compliance was observed between the results of reviewed studies and the most common variables in the current study.

In general, the developed ML algorithms in this study, similar to those reported in the previous studies (26), have achieved optimum results with an accuracy range of 86.4% - 90.37%. In particular, the experimental findings showed that RF had the best performance compared to the other four ML techniques with the mean accuracy of 99.5%, mean specificity of 99.7%, mean sensitivity of 99.4%, Kappa metric of 95.7%, and RMSE of 0.015. According to the results of the previous studies, the ANN and RF techniques have the most remarkable performance in predicting COVID-19 outcomes, which is consistent with the present study.

As a screening instrument for the development of severe disease, model developed in our study has several opportunities for clinical use. These models decrease the existing uncertainty and ambiguity in COVID-19 clinical practice by presenting measurable, non-subjective, and evidence-based approaches (12, 18). Accurate ICU admission prediction can support the sharing of limited hospital resources and improve the quality of care along with patient survival chance (12). The timely identification of at-risk patients could diminish the need for imminent ICU beds and invasive mechanical ventilators. Moreover, using proposed model in present study can surge the tolls of timely ICU transfers, resulting in reduced mortality and shorter lengths of ICU stay. Designing a scientific and valid ML-based prediction model would assist in early detection and effective supportive intervention to improve patient outcomes, the quality of care, and ultimately a reduction in the mortality rate of COVID-19 patients. Ambiguity declines due to offering quantitative, objective, and evidencebased models for risk stratification, prediction, and care planning(9, 10).

This study had several limitations. First, we retrospectively analyzed a dataset without control over data fields or incomplete data. Second, the dataset was extracted from a single hospital with a low sample size of 1225, making the results ungeneralizable. Third, this study only included 11 clinical features at admission to the hospital. It does not mean that these should be the only criteria for determining ICU admission. Longitudinal changes in these clinical features need to be investigated. Moreover, we only used five ML algorithms for prediction analyses. Finally, the selected dataset lacked some critical clinical variables, such as radiological indicators. In the future, the performance accuracy of our model and its generalizability will be enhanced if we test more ML techniques for larger, multicenter, and prospective datasets equipped with more qualitative and validated data.

5.1. Conclusions

We trained and validated different ML algorithms to predict the need for ICU transfer in COVID-19 hospitalized patients based on the data collected easily and routinely at the time of hospital admission. This study first identified the highly ranked clinical predictors that can predict the likelihood of ICU admission more precisely. Second, we developed and compared five ML-driven prediction models based on these selected predictors. It was observed that the RF model performed best on classification accuracy compared to the other ML algorithms. This method has the potential to provide frontline clinicians with an objective instrument to manage COVID-19 patients more efficiently in such time-sensitive, resource-demanding, stressful, and potentially resource-constrained situations. Finally, the results of comparing the performance of prediction models in this study were satisfactory to some extent, and we believe that further investigations are needed to validate our model for a larger, multi-central, and more qualitative dataset.

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Footnotes

Authors' Contribution: M.Sh. and H.K.A. designed the study. M.R.A. and H.H. performed data mining. M.A. performed the statistical analysis. LE and M.SH. reported the results.

Conflict of Interests: The authors declare that they have no conflicts of interest.

Ethical Approval: The current study was approved by the Ethics Committee of Abadan University of Medical Sciences (Ethics code: IR.ABADANUMS.REC.1400.054). In order to protect the privacy and confidentiality of patients, we concealed the unique identification information of all patients in the process of data collection and presentation.

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Table 2. Descriptive Statistics of the Study Variables After Preprocessing^a

Variables Values	
Qualitative	
Blood type	
A-, A+ 17, 552	
B-, B+ 13, 126	
0-, 0+ 29, 421	
AB-, AB+ 6, 61	
Gender	
Male 664	
Female 561	
Cough	
Yes 958	
No 267	
Contusion	
Yes 409	
No 816	
Nausea	
Yes 401	
No 824	
Vomit	
Yes 346	
No 879	
Headache	
Yes 312	
No 913	
Gastrointestinal symptoms	
Yes 252	
No 973	
Muscular pain	
Yes 623	
No 602	
Chill	
Yes 591	
No 634	
Fever	
Yes 628	
No 597	
Pneumonia	
Yes 1044	
No 181	

Oxygen therapy	
Yes	1053
No	172
Dyspnea	
Yes	1078
No	147
Loss of taste	
Yes	272
No	953
Loss of smell	
Yes	305
No	920
Runny noise	
Yes	437
No	788
Sore throat	
Yes	444
No	781
Other underlying diseases	
Yes	735
No	490
Cardiac disease	
Yes	306
No	919
Hypertension	
Yes	395
No	830
Diabetes	
Yes	268
No	957
Smoking	
Yes	41
No	1184
Alcohol addiction	
Yes	11
No	1214
C-Reactive protein	
Positive	1063
Negative	162
Hypersensitive troponin	
Positive	58
Negative	1167
ICI admission (outcome)	107
ICU admission (outcome)	

Yes	1055		
No	170		
Quant	itative		
Age (y)	57.25 ± 17.8 (18 - 100)		
Height	168.53 ± 8.5 (92 - 195)		
Weight	75.20 ± 13 (6.5 - 163)		
Creatinine	1.39 ± 1.4 (0.1-17.9)		
Red cell count	$4.56\pm 0.9(1.38\text{-}13.1)$		
White cell count	8182.34 ± 4897.4 (1300 - 63000)		
Hematocrit	39.20 ± 6.7 (3.6 - 73.9)		
Hemoglobin	13.21 ± 2.4 (3.7-46)		
Platelet count	215493.66 ± 88380.1 (108000 - 691000)		
Absolute lymphocyte count	23.74 ± 11.8 (2 - 95)		
Absolute neutrophil count	74.52 ± 12.3 (8 - 98)		
Calcium	$9.68 \pm 0.8 (0.9$ - 14.1)		
Phosphorus	3.5±0.5(2-12.4)		
Magnesium	2.16 ± 0.6 (1.14 - 19.1)		
Sodium	137.94 ± 5.3 (37 - 157)		
Potassium	3.98 ± 0.7(2.5-14.2)		
Blood urea nitrogen	$42.52\pm 31.7(0.5\text{-}251)$		
Total bilirubin	$0.72 \pm 0.7 (0.01 - 10)$		
Aspartate aminotransferase	44.45 ± 53.5 (3.8 - 924)		
Alanine aminotransferase	38.29 ± 41.6 (2 - 672)		
Albumin	$4.02 \pm 0.5 (0.2 - 8.9)$		
Glucose	136.09 ± 74.2 (18 - 994)		
Lactate dehydrogenase	555.68 ± 339 (4.6 - 6973)		
Activated partial thromboplastin time	28.56 ± 11.4 (1-120)		
Prothrombin time	12.82 ± 1.9 (0.9 - 46.8)		
Alkaline phosphatase	213.12 ± 139.2 (9.6 - 2846)		
Erythrocyte sedimentation rate	40.65 ± 28.8 (2 - 258)		

^a Values are expressed as No. (%) or mean \pm SD (range).