Machine Learning-Based Predictors for ICU Admission of COVID-19 Patients

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Abstract. The burden on the health sector has increased when covid-19 was declared as a critical pandemic, making the decision-taking more crucial. This study aimed mainly to build predictors to aid in making decisions for severe patients to predict whether a patient has to be admitted to the intensive care unit (ICU) based only on the vital records. Statistical techniques were used on the electrical health records (EHR) that were accessible for the covid-19 patients. Samples were processed and then extracted based on criteria that support data imputation. Then, several feature selection techniques were utilized based on the field knowledge, Pearson correlation coefficient, and finally by taking the permutation importance of a hypothetical model to retain features that have the highest relationship with the target variable. Then two versions of data were obtained as stateless and grouped data with and without feature selection which were used to build models with various machine learning algorithms; logistic regression, linear support vector machine SVM, SVM with radial basis function RBF, and artificial neural network ANN. In this respect, the models reached an accuracy of more than 95% in most of the used classifiers and the best one scored is RBF-SVM with accuracy up to 98% and achieve 0.95 areas under curve (AUC) performance. These results indicate that trustworthy models were built to fulfill the high demand for accuracy that is more or less commensurate with the cost of accuracy in the health sector relying only on vital information.

Keywords: Covid-19 · Vital information · EHR · Intensive care unit

1 Introduction

The declaration that happened on March 2020, by the World Health Organization (WHO) that the outbreak of a new corona virus disease (COVID-19), to consider as a pandemic has emerged as a major challenge for the health sector. Given the increase in the number of infections, the variation in symptoms and the patient's health status, there is an obvious burden on the medical staff in determining the optimal condition to follow up on patients. Especially, since the symptoms range from mild that can be treated at home, to intense that requires hospitalization. Without a doubt, due to the tremendous pressure caused by the pandemic, there is an undeniable gap between the number of infections and the ability to deal with them in term of the available resources. Early prediction of acute

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cases of covid-19 patients may contribute to saving their lives by contributing to the early preparation and management of resources in the ICU. Although there are many studies use machine learning to support decisions in the health sector, there is still a huge demand to work even more in this direction. There are real opportunities for ML to assist in taking the decision in clinics and hospitals during Covid-19 by using the vital and laboratory results from the rapidly growing EHR datasets. There are various healthcare aspects that ML can support. Healthcare generates massive datasets from medical follow-up results of patients that are updated daily or even hourly. ML can be utilized to process all these data to generate valuable information, evidence-based recommendations, or to make augmented tools for taking decisions [1]. One of the important aspects that ML support is the intensive care unit. Recently, and due to the current epidemic period, the interest in researches related to the ICU has increased. We use ML algorithms along with the statistical rules to build models that use the vital information of the covid-19 patients from available dataset to predict the ICU admission of severe cases. For this purpose, python was used as the programming language via Jupyter notebook.

This article has the following scheme, Sect. 2, which contains a literature review that synthesizes a basic view of the relevant works, and reviews the similarities and differences between this study and previous studies. After that, in Sect. 3, the dataset which used in this study is illustrated with a comprehensive description. The approach we used to initialize ML models to assist in predicting the ICU admission with overall structure in addition to the knowledge field discussion is shown in Sect. 4. In Sect. 5, we review and discuss the results in a purely analytical manner. A discussion of the limitations and the probable extensions is shown in Sect. 6. In Sect. 7, we provide the final remark in a brief conclusion.

2 Literature Review

In most of the previous works, researchers have been interested in finding tools to support the decision in clinics and hospitals based on medical records. There is no doubt that the healthcare industry is still struggling as studies are still hampered by the way these industries collect their records. Most of these records are unstructured data. There is an absence in enabling advanced analytics. However, early work has concentrated on training discriminative models according to an obvious target or output. For Instance, S. L. Hyland uses supervised ML techniques along with medical knowledge to predict the circulatory failure for patients in ICU [2]. Other works have focused on the intervention in ICU based on the EHR using unsupervised methods such as the work done by Massachusetts Institute [3]. So, the traction to automate the ICU and its decisions is not a new research field. There are a lot of researches on the topics of mortality prediction in ICU, management of ICU resources by suppressing false alarms in ICU, and prediction of ICU discharge and readmission [4, 5]. However, during the covid-19 period, the research on this matter has increased and several conferences were held to discuss these completed researches [6]. As stated in [7], they detect patients ready to be discharged from ICU by evaluating NLD criteria through machine learning classifiers trained on the MIMIC dataset. By stepping a little bit inside our scope of predicting covid-19 patients' ICU admission, there are also a not insignificant number of projects. In [8], the study focused on the results of laboratory blood tests to develop several analytic methods to predict covid-19 disease severity and mortality outcome with accuracy and precision for predictions that were above 90%. The study used two datasets of corona patients; the former contains samples of 89 covid-19 positive patients, and the latter is the same dataset that we used for this study. At first glance, what caught our attention is that they pointed out that this data set contains samples of 1,945 COVID-19 positive patients; however, this is a stateless consideration as we clarify that this data set contains five records for each 385 which results in 1925 samples. On the other hand, as this dataset -as will be briefly explained- contains a huge number of missing data they eliminated any record that contains at least one missing value. As a result of this elimination, they consider only 545 samples, and they did this kind of elimination after they made it clear that their trails of data imputation for the missing values resulted in poor performance. This is one of the clear differences between their study and ours, as we made it clear that filling in the missing data in the usual way will result in poor performance, but taking into account the points that we will be explained in the next sections will solve this problem. In [9], several classification methods were applied, including robust versions of logistic regression, and support vector machines, as well as random forests and gradient boosted decision trees to predict the following events: (1) hospitalization, (2) mortality, (3) need for ICU and (4) need for a ventilator. Their accuracy for ICU need event reaches, 80% and AUC of 0.54 without prior knowledge about the patient pneumonia and accuracy up to 82% and AUC of 0.63 with prior knowledge about pneumonia condition. Also, their accuracy, for the need of ventilator event inside ICU reached to 83% and the AUC to 0.77. In contrast to much of the works that were cited above, we built various models in an attempt to assist making the decision of admitting the patient to ICU only based on vital information. Taking into account special considerations of the used samples and features as will be explained in the coming sections. Three main factors are distinguishing our work from all works cited here, first: we use only the vital data which measured hourly to predicate the admission of a patient to ICU not the blood test results. The second difference is regarding the way of considering the samples and the way the data imputation was done. Finally, we relied on medical knowledge that was discussed in medical books and researches as illustrated in [10], by D. Silverstein, K. Hoppe that vital information is a strong predictor for the ICU. We aim to prove it through various machine learning techniques, and for each stage analytical explanations and various experiments were carried out to support this hypothesis.

3 Data

To satisfy the purpose of this study, the data of positive covid-19 patients from the Hospital Sírio-Libanês, São Paulo, and Brasilia were acquired from an open-access repository to be used [11]. Three main classes of information can be extracted from this dataset: demographic information, blood test results, and vital information results. It contains anonymous records for patients. There are 1925 samples gathered from 385 4 patients, and each one has 5 records. Along with 231 columns that contain the features, however, there are huge numbers of the missing values that range from 511 to 1140 per column which makes this dataset suffer from sparsity. Unfortunately, some features do not have a description available from the dataset provider. Some of those features are: “disease grouping 1, disease grouping 2, other “etc.

4 Methods

Taking into consideration what we have mentioned in the description of the data in the previous section, our method of processing the missing data and adopting the samples constituted an important stage in the overall process of building the proposed model Fig. 1 shows the overall scheme of the method proposed by us and in the following sub-sections, we will discuss each phase in detail.

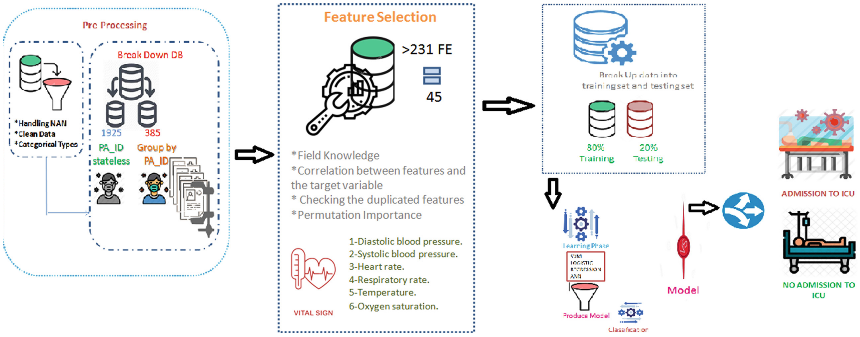


Fig. 1. The overall scheme of the proposed methodology

4.1 Data Pre-processing

In this stage, firstly we deal with the categorical types; hence, one hot encoding is used to put dummy numeric values which result in the binary vector representation of the “age_percentil” and “window columns” which contributed to adding new columns represented these two categorical columns. Then, we cleaned the data by filling in the missing values. In the following section, we will illustrate the consideration we take into account for this purpose.

Data Imputation

Missing data presents a real challenge as it makes the data analysis problematic and implies efficiency reductions, however, imputation is seen as a way to avoid pitfalls involved with these problems [12]. Imputation preserves all cases by filling the missing values with the result of estimation other related available values. In our case, we go into three directions for data imputation. First, we fill the missing value of each column by the mean of all its other values and then through trial and error, we built a hypothetical model, and in any case, even with the features selection, the results of that hypothetical model were not good enough and could not be adopted, so we moved to the second method of filling in the data which is filling the missing values of each patient from its mean values. This second way which built upon the fact that each patient in the dataset has 5 records so, we just filled in each column with the values of that patient, however, there was no improvement in the accuracy of the model. This prompted us to think about a possible hidden problem in the recorded data and the way that they were recorded. We thought that there might be some data for each patient that was not registered with the correct considerations, which causes noise in the data. In another word, there is no proven explanation of which values in which record of vital information from the five records of each patient led to the ICU admission. For example, assume patient x was admitted in his third record from his hospitalization time, the time of admission may be not accurate and his data in the first or the second record is the one that contributed to his admission not the data of the third record. As we cannot be sure of this information and any problem in the data set might be caused by the data of the people who experienced the ICU in one of their five records. As a consequence, we looked for the data that we considered clean, reliable and of course, those data are for patients who had either never been to intensive care or who had been to intensive care in all of their five records. Thus, the answer to the following question: “Has the patient ever experience the ICU in any of his records?” made us fill in the data with the mean values of each column of those patients’ types separately. In other words, we consider only those patients who were never admitted in all of their five records or those who were admitted to ICU in all of their five records then we fill in the missing values by using the mean value of each column separately. Figure 2 shows this process of considering the data of the 190 patients whom never admitted to ICU in all 5 records and the data of 32 patients who were admitted in all of their records.

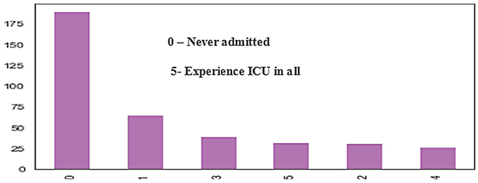


Fig. 2. Patient ICU experience

Data Sampling

Sampling is a process used in statistical analysis in which a predetermined number of observations are taken from a larger population [13]. For our study, sampling is an important consideration whether we will rely on patients’ data as being stateless or will we rely on collecting patient data and grouping them. Here we will try the two considerations and compare their results.

Stateless Data

The stateless consideration approach is one way to deal with the samples in the dataset. As discussed in Sect. 3, the dataset contains 1925 samples as a result of five records for each one of the 385 patients specified by unique patient identifier. When considering data as stateless means that these records are independent of each other and save no information of the previous records. Thus, the identifier for each patient is neglected. Each sample is considered as belonging to a different patient. However, only 1110 samples from 222 patients were taken into account based on Sect. 4.1. There are four reasons that encourage us to handle the as a stateless data. First, the main goal for this study is to use the features without adopting the patient's demographic information such as gender, age, or any medical history records. Therefore, we do not intend to study a specific patient's case. Secondly, depending on the literature as in [8], which considers the data as stateless, however, this method was used to increase the number of samples in the dataset. Finally, data imputation which was considered in this study led to consider only the records of patients who never entered the ICU or the data of patients who experienced ICU in all their five records. Thus, there is a state of stability in the values of records, either being normal or abnormal values, and therefore we drop from them the possibility that the previous record affects the current record state, and so on.

Grouped Data

Samples in the dataset can be divided into groups based on the identifier of each patient. Each patient in the dataset has five records; hence, it's possible to calculate the mean of the representative values of each patient to get a single record for each one. For this purpose, the records were grouped by paitent_identifier, and then the mean was calculated for all other values and kept as a new record for that patient in a dataset that we express as grouped data. Unfortunately, the process discussed in Sect. 4.1 to consider only 1110 samples cannot be used to generate the grouped data. Because, after the process of gathering these samples based on the patient's identifier and calculating the mean of the representative values the number of samples in the dataset is 222. However, this dataset can be considered an imbalanced dataset. As shown in Fig. 3 it contains 85.6% of samples for patients who have never been admitted to ICU compared to 14.4% who were admitted to ICU. Obviously, this will cause poor performance in prediction, especially for the class of those who have been admitted to ICU, and therefore it cannot be adopted.

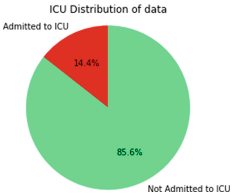


Fig. 3. Distribution when considering 222 samples

As a result of the foregoing, we have increased the samples in an attempt to make the two classes of the target variable as balanced as possible in the dataset, by adopting the data of the 385 patients with some considerations. First: The initial 1925 samples were taken and the missing data were filled by using the mean value of each column of all patients. Then, the samples were gathered by using the paitent_identifier. Subsequently, the mean of all of the representative values of each column of the five records for each patient was calculated for the gathered data to get a single record. Finally, if the patient has experienced the ICU even once in one of his five records, his target value of the ICU column is set to 1. But if he does not experience the ICU in all of his five records, the value of the target variable becomes 0. As a result of this process, the numbers of samples are 385 now. As shown Fig. 4 that 49.3% of patients were not admitted and 50.7% were admitted to ICU and this is a balanced dataset and can be considered.

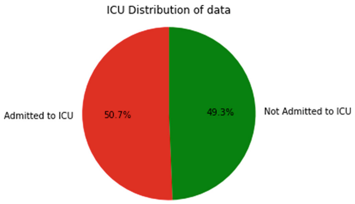


Fig. 4. ICU distribution when considering 385 samples

4.2 Feature Selection

For this dataset, numerous conceivable features can be chosen. Taking into account that we have a large number of algorithms that perform this task, we had to define our primary goal, which is to study the vital signs of patients and their impact on the admission process for ICU, and whether they are already sufficient alone. Therefore, we decided to make two copies of this data, one with the application of feature selection and the other without it, and compare the performance as will be clear in the next parts. To make the feature selection, we relied on the following:

Field Knowledge

As known in the medical field, abnormal vital signs are strong predictors for intensive care unit admission. As pointed in [10, 14], abnormal vital signs are strongly associated with adverse outcomes and significantly associated with ICU admission. This is reinforced by what was stated in the study published in the Journal of Acute Disease. This study shows that the presence of any of the specified trigger vital signs, although representing only a small proportion of the total population, was strongly associated with admission to the ICU [14]. Vital Signs that are available in the dataset that we used are the Body Temperature, Pulse Rate, Respiration Rate, Blood Pressure, and Oxygen Saturation. These signs were extended by calculating the mean, median, min, max, and differences of each sign. Figure 5 shows the results of plotting the variance of each column of vital signs measurements between 222 patients who either have been admitted or not to ICU in all of their five records.

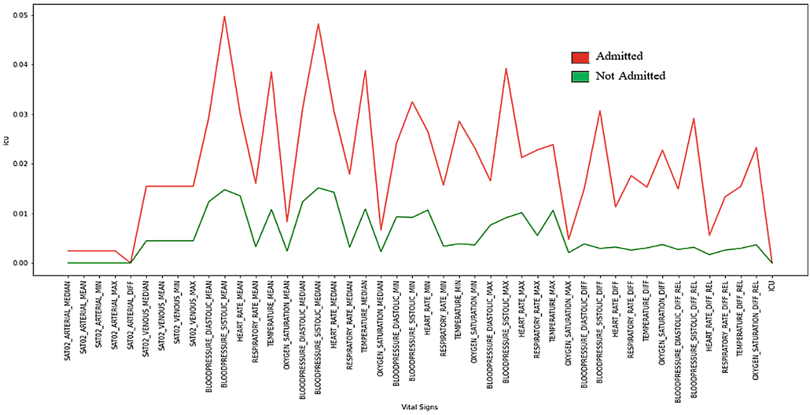


Fig. 5. Vital signs and ICU admission

It shows clearly that there is a clear difference between the vital values for both parties. Obviously, the vital values of the admitted patients vary radically compared to the values of the not admitted patients. Relying on these scientific facts, we can go towards the fact that our assumption of using only vital signs is correct and sufficient, but we will also test this choice for our dataset in the next sections as well to increase our certainty.

Pearson Correlation Coefficient

Pearson correlation coefficient examines the strength and direction of the linear relationship between two continuous variables. The higher the absolute value of the coefficient, the stronger the linear relationship between the variables. The correlation coefficients denote three relationships: positive, negative, and no relationship. For the Pearson correlation, an absolute value of +1 indicates a perfect positive linear relationship. When the coefficients are greater than 0 then this is a positive relationship in which if one variable increases the other will increase as well vice versa [15]. However, it's not worthy for our case as it shows that lactic highly correlated with ICU, but according to the medical knowledge we can say that covid-19 patients suffer from an excessive increase in lactate levels in the blood which means that the disease or condition a person has is causing lactate to accumulate. In general, a super increase in lactate indicates more severity of the condition. As pointed by [16], "When associated with lack of oxygen, an increase in lactate can indicate that organs are not functioning properly". However, this is not a direct or indirect reason for the ICU admission. It's just some of the main abnormalities found in the blood testing results of covid-19 patients. Thus according to this method that is shown in Fig. 6 the relevant features which have higher than 0.5 were the different LACTATE and RESPIRATORY_RATE values. The discussion held before is not enough for this study thus we move to the next method.

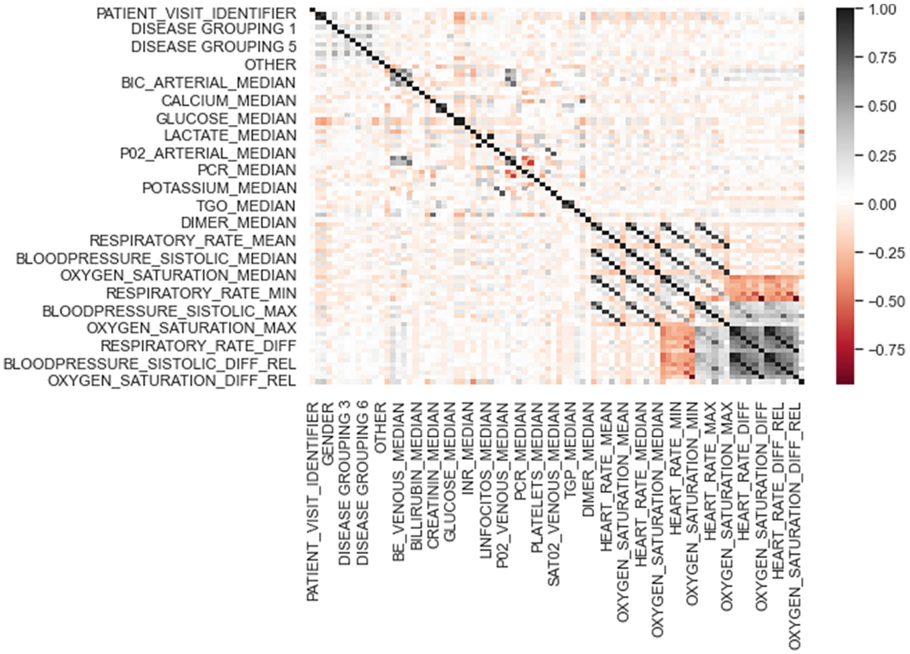


Fig. 6. Heat map shows features correlation

Permutation Importance
In Sect. 4.1 we have illustrated that we have built a hypothetical model, and this was a key decision to compare different models' results with and without the application of feature selection. In this trial and error direction, as we will explain in the next section, we found that one of the ML algorithms, which is the kernelized RBF-SVM, achieved high accuracy. This prompted us to wonder, what are the most influential features on the prediction of this classifier? Feature permutation importance is a model-agnostic global explanation method that provides insights into a machine learning model's behavior [17]. The permutation_importance function calculates the superiority feature of estimators for a given dataset in the training stage of the ML. The n_repeats parameter sets the number of times a feature is randomly shuffled and returns a sample of feature importance. Two results that we reached after obtaining the results of plotting the permutation importance; first of all, a large number of features in the dataset do not contribute to any impact on the prediction. Second: vital signs which are shown in Fig. 5 are the main influence, in addition to lactate values all contribute more than blood tests results.

4.3 Model Selection and Estimation

No doubts that the dataset prosperities are crucial aspect and has a huge impact on the selected models. As each model adjusts its parameters based on the available data that it learns from in the training phase. It was explained in Sect. 3, the dataset is imbalanced and suffers from sparsity. With the methods that were presented in the Sect. 4.1 so and so to improve dataset characteristics, choosing the appropriate model remains important to achieve the purpose of the study. After taking into consideration type of problem, size of the dataset, the number of features, and by considering the studies that have good results in the literature as in [8, 9]; we chose different machine learning algorithms to build the binary classifier which are Logistics regression, SVM with linear and RBF kernels, and ANN. As stated in [9, 7], logistic regression and SVM are very common in health care applications because of the high interpretability of their output and their simplicity. According to many experiments in literature that SVM even without further tuning can provide very accurate prediction in healthcare relevant problems [18, 19, 9, 20]. For ANN a sequential, fully-connected layered architecture are used in which each input neuron is connected to every neuron in the next layer. It consists of one input layer and three hidden layers a long with the output layer. The sigmoid is used as the activation function of the output layer whereas the ReLU (Rectified Linear Activation Unit) is used as the activation function for all hidden layer. The model trained with 0.0001 learning rate in 90 epochs using the Adam optimization function with binary_crossentropy as the lose function.

Training Phase

Taking into account the considerations that we have discussed regarding the samples and the features; we decided to make four comparisons between two partitions of two different considerations of the dataset samples. Firstly, we will consider the dataset as stateless which results in 1110 samples according to the preprocessing that we discussed in Sect. 4.1. Also, to consider it as grouped data with only 385 samples by grouping the data using the patient identifier as illustrated in Sect. 4.2. Secondly, for each part, we will examine them under two more considerations one with feature selection and the other part without feature selection. In all cases, 80% were used for the training and 20% for the testing. This process is held before training any classifiers and is shown in Fig. 7 given below.

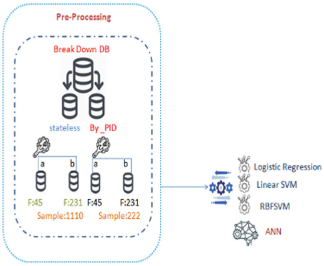


Fig. 7. Preparing dataset

Models Performance and Estimations

As an initial step, we plotted the confusion metric to see how the models perform in predicting each class. In order to measure each model's performance, we have used three main metrics. Firstly, we measure the models testing accuracy to evaluate the percentage of the correct prediction that was made for the testing data. Then, we rely on calculating the True Positive (TP) among TP to False Positive (FP) which defines the precision. The third metric that we define is the recall, as the sensitivity or the True Positive Rat TPR. Actually, the last two matrices are extremely crucial and take the trade-off between precision-recall so, we get an insight of the model relevancy and from the latter, we get a clue of the model competence. As also as an initiative way of judging the model performance is to get AUC interpretation for the classifiers. We plotted the receiver operating characteristic curve ROC and make AUC interpretation for the classifiers that showed better performance compared to the other classifiers under the same pre-training considerations.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{2}$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{3}$$

5 Results and Discussions

After training the models with the different partitions that we have mentioned in Sect. 4.3. We find that we have been effectively able to build a model that predicts the need for intensive care based on vital information. Overall, the trained models' results range from moderate to accurate prediction results. The results imply that there is a strong relationship between the abnormal vital signs results and the ICU admission. The results show that logistic regression and support vector machines generate better models in terms of accuracy. Classification accuracies reached 98% for predicting ICU admission with the RBF-SVM for both pre-training data considerations. The analysis shows that the most important preconditions for making the predictions for the four models derived are: receiving stateless data, perform data imputation based on the patients' ICU experience, and selecting vital information as we explained in Sect. 4, and evaluating samples correctly before making the data imputation. Figure 8 shows the overall accuracy between all of the used classifiers. And from that plot, we can say that all the classifiers achieved performance nearly the same for the stateless data with and without the feature selection due to the way we chose the samples and the way we make the data imputation. One important observation about liner SVM and RBF-SVM is that both share comparable performance when utilized with the stateless consideration of the samples in conjunction with the feature selection as discussed in Sect. 4.2. The best performance is achieved by RBF-SVM with stateless sample consideration and elaborating the feature selection. This is clear as the AUC reaches 95%, hence, it is considered the best model in performance as it shows good generalization capabilities. This model can be deployed in the healthcare decision systems to help in the early prediction of the ICU admission and therefore help in the early allocating of the resource using vital sign results which are very affordable, easy, and inexpensive. Linear SVM showed high performance with stateless data along with the feature selection it scored 95% in accuracy. However, it performs slightly lower with the grouped data with and without feature selection and scored 81% inaccuracy. ANN showed good performance for the stateless data and achieved 97% even without feature selection. Nerveless, it showed poor performance with the grouped data probably due to the limited number of the samples in the trained dataset. As mentioned above, the highest AUC is scored by RBF-SVM and both logistic regression and linear SVM scored 91% and 93% respectively under the same consideration. Whereas the linear SVM and logistic regression imposed poor comparable performance without feature selection as the dataset experienced some non-linearity which makes finding the best hyperplane that best segregate the two classes not visible this this made clear by analyzing their AUC results. Figure 9 shows the AUC graph for those classifiers.

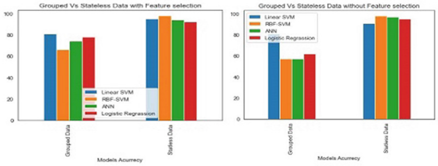
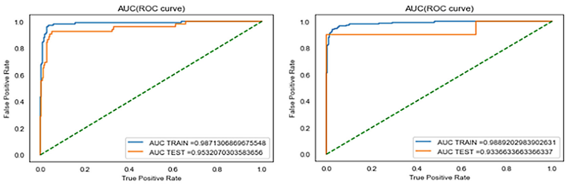


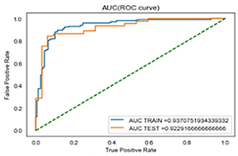
Fig. 8. Overall results of models accuracies with different considerations

We believe that the one who contributed to this result is the method of adopting samples and filling in the missing values. As were mentioned previously, without such consideration, the results of the models were not good enough. The detailed classification report is shown in Table 1 and the precision and recall all are shown for only the ICU admission class. Additionally, we got better precision and recall for the not admitted class but this is quite as expected due the supported number of samples in the dataset. On the other hand, the grouped data achieved unreliable results for both cases with and without feature selection; however, grouped data with feature selection shows slightly better performance.



A) SVM RBF

B) Linear SVM



C) Logistic Regression

Fig. 9. The AUC for different classifier

Table 1. Overall results

DATA	Feature Selection	Evaluation Matrices	Linear SVM	SVM RBF	Logistic Regression	ANN
Stateless	✓	Accuracy	95%	98%	92%	94%
		AUC	0.93	0.95	0.91	
		Precision	0.93	1.0	0.91	
		Recall	0.74	0.88	0.88	
		F1-Score	0.83	0.93	0.89	
Stateless	✗	Accuracy	91%	98%	95%	97%
		AUC	0.88	0.91	0.87	
		Precision	0.77	0.90	0.94	
		Recall	0.77	0.27	0.77	
		F1-Score	0.77	0.42	0.85	
Grouped	✗	Accuracy	%81	57%	62%	57%
		Precision	0.84	0.56	0.66	
		Recall	0.74	0.80	0.57	
		F1-Score	0.79	0.66	0.61	
Grouped	✓	Accuracy	81%	66%	78%	74%
		AUC	0.84	0.77	0.62	
		Precision	0.74	0.80	0.75	
		Recall	0.91	0.55	0.82	
		F1-Score	0.82	0.65	0.78	

6 Limitation and Potential Extensions

One of the most critical problems that we encountered during our work on this study is the number of samples that are available. Taking into account the fact that this data is actually for 385 patients only, and each patient has 5 records that extend the samples up to 1925. This imposes limitations in dealing with it and that thing what mainly pushes us to consider the data as stateless. Some information we wished the dataset would provide, such as the patient's discharge status and the patient's detailed time record. Such information did not affect our study or its results, but it prevented us from going to another dimension in the study. Actually, there is no information, including whether the patient has yet been released from the intensive care unit, as the data makes it clear that once the patient enters the intensive care unit, he remains in it. Moreover, there is not enough information regarding the time. Since if such information were added (i.e. the patient has been admitted to ICU in the current record, and for example, the same patient in the next record has an improvement and left the ICU). With such information will be able to add other dimensions to our study and search for values that contribute to the improvement of the patient's condition and thus it is possible to predict the patients who may be discharged from ICU. Also predicting the time when something like this is expected to happen. If it is possible to add such information and increase the size of the data samples and add time in a more detailed way, we will be able to go further in building a new and more powerful model.

7 Conclusion

In light of the corona pandemic, the pressure on the intensive care unit has increased. Vital information provides great opportunities to rely on to enhance decision-making in hospitals and clinics, which may relieve pressure, especially at this stage. For this study, we make a critical study of the process of selecting the features and even verifying the correctness of our hypothesis to use only the vital signs. Then, we trained supervised ML algorithms using the patient's vital signs after processing the data under two assumptions as stateless and as grouped data taking into consideration feature selection decisions. Then, we use different evaluation matrices to measure the models performance, completeness, and sensitivity. We have achieved so good results for the stateless data with accuracy up to 98% and the estimated AUC is 0.95 for RBF-SVM. This indicates clearly that we can rely on the vital signs for the covid-19 patients as a strong indicator for ICU admission.

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