A Comparison of Feature Selection Techniques for First-day Mortality Prediction in the ICU

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***Abstract*—First-day mortality prediction is a critical task in the Intensive Care Unit (ICU), as it can help clinicians identify which patients are at the highest risk for death and thus may need more intensive care. Many heuristic-based metrics for first-day mortality exist. However many signals exist in the Electronic Health Record (EHR) that are not used in these metrics. For the implementation of these metrics, it is important to keep the number of required signals as small as possible so that the user can quickly receive an assessment of their patient. In this paper, we leverage techniques from classical machine learning to compare sets of signals from a patients record (like demographic information, lab values, and vital sign measurements) to find the minimum feature set that best informs first day mortality. We compare several feature selection techniques to identify various feature sets with differing number of features. We found that Elastic Net was the overall best performing method and was able to reach the same performance as the current state of the art with less than half the features. This suggests that an optimal feature set is clinically meaningful.**

***Index Terms*—Machine Learning, Healthcare, Human-centred design.**

I. Introduction

The use of machine learning in today's healthcare systems is rapidly growing as many new techniques are being developed with applications including predicting illnesses, determining the most effective treatments, making quicker and more accurate diagnosis, and many more [1]. The growing demand for more personalized healthcare is becoming an increasingly pressing need. It is imperative that the methods created today are precise in their input. Until Electronic Health Record (EHR) integration can be achieved, we cannot expect users to enter large swaths of data for each prediction. The following research will focus on utilizing machine learning and various feature selection techniques in order to more efficiently and accurately predict mortality in the Intensive Care Unit (ICU).

Feature selection is the process of reducing the number of input signals such that the most relevant attributes are used to create a predictive model [2]. There are a total of 194 features within the eICU database [3]. Therefore, it is imperative that this number is greatly reduced to not burden the user. Having excess tests or features not only slows down the time it takes to collect and enter the data, but also can have a negative impact on the results of the prediction [4]. Having the ability to decrease the number of features used while maintaining a relative measurement of success is crucial for this experimentation and is the motivation behind using feature selection for this research.

Feature selection can be further classified as either supervised or unsupervised. In an unsupervised method, the function is provided inputs, but no target function. The goal is to identify the most relevant features in the input dataset. This can be achieved by calculating the correlation with the target variable, or by applying feature-specific statistical tests (such as t-tests). Supervised methods, on the other hand, have the goal of identifying the most relevant features in order to improve the performance of a target function. This can be done by using a training dataset, where the target output is known. The features that correlate with the target variable are identified and used to optimize the target function. In this work, the filter, wrapper, and embedded methods under supervised feature selection will be utilized.

Filter methods are those that are typically performed during the preprocessing stage of feature selection. For this method, the features are chosen based on certain characteristics or scores that they achieve in various statistical tests. Some of the most popular examples of filter methods include correlation, Chi-Square tests, and analysis of variance (also known as ANOVA) [5]. The features are then sorted based on their scores and a threshold is chosen either by heuristic or statistics to choose the final set of features.

Wrapper methods are those that evaluate various subsets and combinations of features in order to choose the one that produces the best result for the given algorithm. These methods are often referred to as greedy due to the fact that they search through all subsets and therefore can become computationally expensive and take a long time to execute. The benefit of this method is that it is guaranteed to provide the optimal set of features. The process of utilizing a wrapper

method starts with choosing a search method or technique in order to select an available subset of features. Once the subset is identified, the desired machine learning algorithm is trained on the chosen subset. The model is then evaluated and the process is repeated with various other subsets of features until the best model is identified. Popular search methods include forward selection, backward elimination, and bi-directional searches [6].

For embedded methods, as the name suggests, the feature selection is embedded within the training of the model. In the previous two methods, feature selection was performed before the model was trained. The process of the embedded method includes training a machine learning model and then deriving the feature importance from the model. As the model is being trained, the features that have the least impact on the prediction are discarded. Examples of embedded methods include lasso/ridge regression and decision trees [6].

The dataset utilized in this work is the eICU database [3]. This database is a synthesis of data collected from many critical care units throughout the United States. We have identified 194 different features of different types, such as: lab tests, demographic data, disease/disorder indicator variables, and vital signs. For this analysis we collected 145,000 instances along with their mortality outcome.

In this paper, we seek to build off of prior research in this area in order to identify the smallest set of features that can be used to predict mortality in ICU patients with high performance [7]. This work will be useful in determining high-risk patients who may benefit from closer monitoring or more aggressive treatment. We would like to use this work to challenge clinician opinion on the importance of several popular first-day metrics in determining mortality outcomes.

II. Methods

Our analysis consists of three components. First, an evaluation of the dataset with all 194 features is done. Second, a 1-1 comparison is made with our prior work by selecting the 20 features using each feature selection technique. Lastly, a quantitative and qualitative study of the performance of each feature selection method is compared. The following techniques were evaluated: variance threshold, Analysis of Variance (ANOVA), Mutual Information (MI), Recursive Feature Elimination (RFE), Elastic Net, and Principle Component Analysis (PCA).

The variance threshold method is a simple, baseline approach to feature selection. It removes any feature that has a variance less than a chosen threshold. By default, this technique eliminates features with zero variance, but can be changed to any desired threshold value. Features with little to no variance may often not contain much significant information and can in some instances reduce the overall performance of a model. Since this method is dependent on the statistics of the feature, this method must be performed before standardizing the data [8].

The Analysis of Variance method, often referred to as ANOVA, is a widely popular filter method. For this project, the ANOVA f-test statistic was utilized. The ANOVA technique is used to determine how similar or different the means of two or more variables are to each other. It can also be utilized to realize the correlation between an independent variable and the dependent variable. Using the ANOVA method, f-scores are assigned to each feature where the higher the f-score indicates a higher correlation between that particular feature and its impact on the output [5].

Shannon Mutual Information between two random variables is defined by conditional entropy. Entropy of the class variable, Y, is desired to be very low in order to maximize classification performance. For a given feature X, Mutual Information between X and Y is a measure of the change in entropy of Y due to the presence of X as defined in Equation 1. In this equation, $p(xy)$ is the joint probability of x and y and $p(x)$ and $p(y)$ are the marginal probabilities. Therefore, a high Mutual Information between a feature and the class label indicates that the feature is a good predictor of the class label [9].

$$I(X;Y) = \sum_{x \epsilon X} \sum_{y \epsilon Y} p(xy) \log \left(\frac{p(xy)}{p(x)p(y)} \right) \tag{1}$$

Recursive Feature Elimination (RFE) is a wrapper-type feature selection algorithm. It operates by first building a model on a dataset containing all features and then computing an importance score for the features using the model (ROC AUC for our case). Next, a set of features are removed, the model is retrained and the outputs are an updated importance score on the reduced feature set. This process is then repeated until all the least important features, determined by the importance score from the model, are eliminated. RFE requires two inputs to operate; number of k features to keep and an estimator model with a built-in importance score [8].

TABLE I
STATISTICS FOR CLASSIFIER TRAINED ON ALL 194 FEATURES.

Measurement	Mean	Standard Error
Accuracy	0.855106	0.002542
Precision	0.260902	0.003493
Sensitivity	0.819577	0.008339
Specificity	0.857289	0.002884
ROC AUC	**0.918066**	**0.002748**
PRC AUC	0.507141	0.009412
Balanced Accuracy	0.838433	0.003765

To find the k number of features to keep, RFE with cross validation (RFECV) can be utilized. RFECV keeps track of a score computed from the model for a given number of features. Using logistic regression as the model for RFECV and tracking the ROC AUC score, the number of features to keep was based on the specifications from previous Work [10].

The following parameters were used; a five-fold stratified for cross-validation, logistic regression as the estimator and the area under the receiver operating characteristic curve (ROC AUC) for scoring the performance of the estimator. The dataset was divided into 33% testing (for scoring) and the remaining was used for training the estimator.

Elastic net is an embedded type feature selection algorithm that combines LASSO and RIDGE regression. Both LASSO and RIDGE Regression use regularization to avoid overfitting. Regularization achieves this by penalizing complex models by adding a penalty to the following cost function, W in Equation 2. In this equation, y_i is the target class for instance i, x_{ij} is the feature value for instance i and feature number j and w_j is the corresponding weight value.

$$W = \sum_{i=1}^{N} \left(y_i \ - \sum_{j=0}^{M} w_j \, x_{\,\mathrm{ij}} \right)^2 \tag{2}$$

RIDGE regression uses L2 regularization, which modifies the cost function by adding a penalty term to the residual sum of squares. Equation 3 shows the added penalty term of lambda times the sum of square of weights, where N is the total number of training instances and M is the total number of input features.

$$W = \sum_{i=1}^{N} \left(y_i \ - \sum_{j=0}^{M} w_j \, x_{\,\mathrm{ij}} \right)^2 + \lambda \sum_{j=0}^{M} w_j^2 \tag{3}$$

For Least Absolute Shrinkage and Selection Operator or LASSO regression, L1 regularization is used. This modifies the cost function by adding a penalty term of lambda times the sum of absolute value of weights to the residual sum of squares. This is shown in Equation 4.

$$W = \sum_{i=1}^{N} \left(y_i \ - \sum_{j=0}^{M} w_j \, x_{\,\mathrm{ij}} \right)^2 + \lambda \sum_{j=0}^{M} |w_j| \tag{4}$$

Finally, when combining the two penalty terms from LASSO and Ridge in Elastic-Net, an additional α term is added that determines the ratio of L1 to L2 regularization. The Elastic-Net cost function is given in Equation 5.

$$W = \sum_{i=1}^{N} \left(y_i \ - \sum_{j=0}^{M} w_j \, x_{\,\mathrm{ij}} \right)^2 + \alpha\lambda \sum_{j=0}^{M} |w_j| + (1-\alpha)\,\lambda \sum_{j=0}^{M} w_j^2 \tag{5}$$

The values of α and λ for Equation 5 can be computed using elastic net with a cross validation (ElasticNetCV) function. A list of α values was provided and the value of λ was picked automatically from the ElasticNetCV function [8]. The value of α was then chosen by performing a grid search on the interval $[0, 1]$. The following parameter values were found to be optimal: λ = 4.317e-4, α = 0.995.

Principal Component Analysis, more commonly known as PCA, is an unsupervised method that can be used for dimensionality reduction while having a maximum variability. The overall goal is to make sure all of the of the transformed features are linearly independent, as well as, finding components in order of highest importance. The PCA approach can be defined as the eigendecomposition of the covariance matrix $\mathrm{X^TX}$.

TABLE II
COMPARISON OF FEATURE SELECTION TECHNIQUES. THE TOP 20 FEATURES ARE CHOSEN FROM EACH METHOD FOR A DIRECT COMPARISON OF THE CLINICIAN CHOSEN FEATURES FROM THE PREVIOUS STATE-OF-THE-ART [7]. THE METRIC REPORTED IS THE MEAN ROC AUC FROM THE 10-FOLD CROSS VALIDATION AS WELL AS THE 95% CONFIDENCE INTERVAL.

Method	ROC AUC
Clinician Chosen [7]	0.8564 ± 0.002748
Variance Threshold	0.7661 ± 0.00747
ANOVA	0.8901 ± 0.00309
Mutual Information	0.8365 ± 0.00554
PCA	0.8980 ± 0.00302
ElasticNet	$\mathbf{0.9056 \pm 0.00336}$
Recursive Feature Elimination	0.8512 ± 0.00415

TABLE III
MINIMUM NUMBER OF FEATURES REQUIRED TO HAVE STATISTICALLY SIGNIFICANT PERFORMANCE INCREASE OVER PREVIOUS STATE-OF-THE-ART [7].

Method	Number of features
Variance Threshold	102
ANOVA	13
Mutual Information	30
PCA	3
ElasticNet	6
Recursive Feature Elimination	26

There are five steps to complete the process of principal component analysis. To begin with, the data must be standardized using Equation 6, where μ is the mean and σ is the standard deviation of all features.

$$x_{\mathrm{stand}} = \frac{x - \mu}{\sigma} \tag{6}$$

The standardized data would then have a mean of 0 for each feature while having a standard deviation of 1. Doing this will scale all features properly and prevent skewing in the results. Step 2 involves finding the covariance matrix of the standardized data. Equation 7 was used to find the covariance matrix where $\bar{x}_i$ is the mean of the ith column, $\bar{x}_j$ is the mean of the jth column, x_{im} is the ith column and x_{jm} is the jth column.

$$\mathrm{Cov}\,(i,j) = \frac{1}{n-1} \sum_{m=1}^{n} (x_{\mathrm{im}} - \bar{x_i})\,(x_{\mathrm{jm}} - \bar{x}_j) \tag{7}$$

The resultant covariance matrix will be a square matrix $\mathrm{X^TX}$. The next step was to find the eigenvectors and eigenvalues using eigendecomposition. After finding the eigenvalues, the fourth step is to sort them and its corresponding eigenvectors in descending order. The fifth and final step is to choose the number of components to keep from the highest importance to then transform the standardized data into a transformed matrix using Equation 8.

$$T_R = XW_R \tag{8}$$

In Equation 8, T_R is the transformed matrix, W_R are the loadings or eigenvectors, X is the standardized data, and R itself is the number of components chosen.

TABLE IV
TOP 10 FEATURES SELECTED BY EACH METHOD AS COMPARED TO CLINICIAN OPINION. FR - FEATURE RANK.

FR	Clinician Survey [7]	Variance Threshold	ANOVA	Mutual Information	Recursive Feature Elimination	Elastic Net
1	Age	CPK	Lactate	Lactate	Potassium	Lactate
2	Immunosuppresion	AST (SGOT)	GCS Motor	Mechanical Ventilation	paCO2	GCS Motor
3	HepaticFailure	Lymphs	GCS Eyes	GCS Eyes	pH	paCO2
4	Lactate	ALT (SGPT)	GCS Verbal	GCS Motor	Myglobin	Bicarbonate
5	Metastatic Cancer	FiO2	Intubation	GCS Verbal	Lactate	Fio2
6	Creatinine	Glucose	Ventilator	Albumin	Glucose	BUN
7	Leukemia	Platelets	AST (SGOT)	Age	Respiratory Rate	WBC
8	Platelet	Akaline	PT-INR	Creatinine	Chloride	Mechanical Ventilation
9	Bilirubin	PaO2	Anion Gap	BUN	Albumin	Sodium
10	Aids	Glucose	ALT (SGPT)	INR	TV	Age

III. EXPERIMENTAL PROTOCOL

For our first and second analyses, missing data was assumed to be missing at random and features with missingness at 70% or greater were dropped from the dataset. Next, features with pair-wise Pearson correlations greater than 0.9 were also discarded. The data was then standardized and imputed with multiple imputation [11]. To correct for the 95%-5% class imbalance, we apply the Synthetic Minority Oversampling (SMOTE) technique [12]. For each 20-feature set, we perform a 10-fold cross validation and determine the mean ROC AUC and 95% confidence interval. The classifier is a multi-layer perceptron (MLP) with 2 hidden layers and SELU activations [13]. The model is trained for 127 epochs using full-batch stochastic gradient descent with a learning rate of 0.03104 and Nesterov momentum of 0.4204 [14]. The hyperparameter values were obtained by performing Bayesian Optimization using ROC AUC as the target metric [7].

For our third analysis, we want to consider all features. Therefore we do not drop features based on missingness and correlation. For each method, we choose an increasing number of features and perform 10-fold cross validation to collect a ROC AUC and 95% confidence interval. The rest of the preprocessing procedure remains the same as the previous analyses. This process results in 194 ROC AUC means and 95% confidence intervals. To quantitatively measure which method performs the best, we compute the area under the ROC AUC vs number of features curve. In addition, for each method, we determine the minimum number of features that can provide a statistically significant result over the work in [7]. Lastly, we provide a qualitative measure of performance by comparing the top selected features from each method compared to clinician opinion [7]. Our baseline measure of performance is to consider using all features. The performance metrics for this baseline can be found in Table I. A link to our code has been provided[1].

IV. RESULTS AND DISCUSSION

In Table I, we show the target performance by using all 194 features. Next, we reduce the number of features to what was used in the previous state-of-the-art [7], which is 20 features. The results for each method is shown in Table II.

[1]https://github.com/jrepifano/FeatureSelectionInTheICU

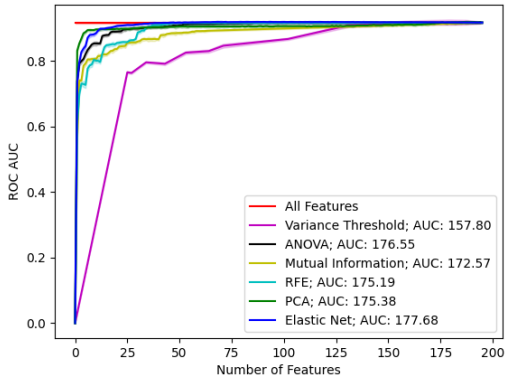

Fig. 1. 10 fold cross validated ROC AUC as a function of number of features selected. The best performing method will have the highest area under the curve.

Here, we observe that the top methods are ANOVA, PCA and ElasticNet. When looking at the number of features required to outperform the opinion of the clinicians (as in Table III), we show that PCA and Elastic Net vastly do better than other methods. This trend continues in Figure 1. The PCA approach is quick to rise to a ROC AUC value of 0.89 but has trouble increasing as more components are added. The best performing method overall is Elastic Net due to it having the highest ROC AUC value as features are increased as well as consistent performance across the other experiments.

In Table IV, we show the top 10 features chosen by each method and compare them to what is selected by ICU clinicians. In the clinician column, we observe a large amount of indicator variables as opposed to the columns selected by feature selection. There are also many common features/feature sets that are selected by multiple methods. These include: lactate, GCS scores (Eyes/Motor/Verbal), mechanical ventilation, and age. We postulate that this difference can be attributed to clinician focus on comorbidities with our machine learning models having no knowledge of diagnosis and patient history. It is possible that the optimal feature set lies somewhere in the combination of these methods. We defer the use of a meta set of features selected by multiple methods for future work.

V. SUMMARY AND CONCLUSIONS

In our study, we provide a quantitative and qualitative assessments of feature selection methods on the eICU first

day mortality dataset. We conclude that Elastic Net is the overall top performing method and requires the fewest number of features to match clinician performance while retaining the original features. Finally, we conclude that there is a significant difference in the types of features chosen by humans versus machines. Humans tend to choose features that indicate the presence of disease or comorbidities and the machines tend to choose continuous lab based features. We postulate that the optimal feature set may lie in the intersection of the sets of features selected by these various methods.

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