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Machine Learning in Medicine

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ABSTRACT: Machine learning approaches are garnering a lot of interest from medical academics and physicians after several noticeable triumphs on a variety of predicted tasks. The demand for addressing the capacity in building area through offering a conceptual machine learning introduction as well as a practical guide to testing prediction algorithms and constructing using publicly available information and open-source software. So far, most Machine Learning research has been focused on technology concerns and is primarily application-driven. The uses of machine learning and successful methods during the workshop presented on machine learning in applications of medical are summarised in this letter. The objectives of the workshops were to promote fundamental and research applied in the application of machine learning to methods of medical problem solving and research, to provide a reporting for a forum on significant findings, to define whether methods of machine learning can underpin the development of intelligent systems research for to identify areas where more research likely to yield advances. The agenda of research proposals were made, with both human-centered challenges and technical.

KEYWORDS: Algorithms, Machine Learning, Training the ML algorithms, Machine Learning analysis, Using R, Generalised Linear Models (GLMs)

I. INTRODUCTION

To do a wide range of computers are being utilized for tasks that are complicated with amazing precision, advances thanks in processing power, memory, storage, and the massive amounts of data creation. The duration of machine learning denotes for both businesses to promote and academia the creation of "intelligent products" that can accurate predictions to generate a variety of data sources and utilizing [1]. To date, those who were able to the industries and acquire this recruit the requisite people and data to alter their products have been the primary benefactors of the century of the twenty-first surge in big data availability, data science, and machine learning. Clinical research and medical research should benefit care greatly from the methods of learning established in and for these factors, especially clinicians increasingly as the use of electronic health information [2].

Unstructured text data to make sense of machine learning to be used in increasing conjunction by (NLP) Natural language processing. It has been able to gain research from new insights comments from social media activity, clinical event reports, reviews of doctor performance, and patients reports following cancer treatments successful by integrating algorithms of NLP and ML. For insight into safety, quality, and performance, but also early diagnosis, information is produced automatically and might be quite beneficial for unstructured data. A study of computerized records on free speech during in-person has shown interviews with the capacity to transition prediction and psychosis in a sample of high-risk 100% accuracy with teenagers[3].

In the learning healthcare development systems, machine learning will also play a key role. Learning healthcare systems are defined as settings where science, informatics, incentives, and culture are all aligned to promote continual improvement and innovation. These systems will mix different data sources with powerful machine learning algorithms of any size, from local group clinics to massive national providers. As a result, a steady stream of data-driven insights will be available to improve scientific research, public health, and healthcare quality.

1.1 Machine learning

Algorithms- that define the set of mathematical rules and the connection between underpinning – variables and machine learning approaches. The designing of the verification and the process of an algorithm to predict the sample of malignancy based on breast tissues and their features will be described in this study. In a variety of ways, though algorithms function depending on their kind, similarities are noticeable in how they are created. Machine learning algorithms of intricacies may look arcane, sometimes they exhibit more than a similarity to a passing and studies of traditional statistical[4][5][6].

In the subject of machine learning, on the other hand, the major aim is an accurate prediction; the 'what' rather than the 'how.' In image recognition, for example, the link between individual characteristics (pixels) and the outcome is unimportant provided the forecast is correct. Because the link between numerous inputs, such as pixels in an image or

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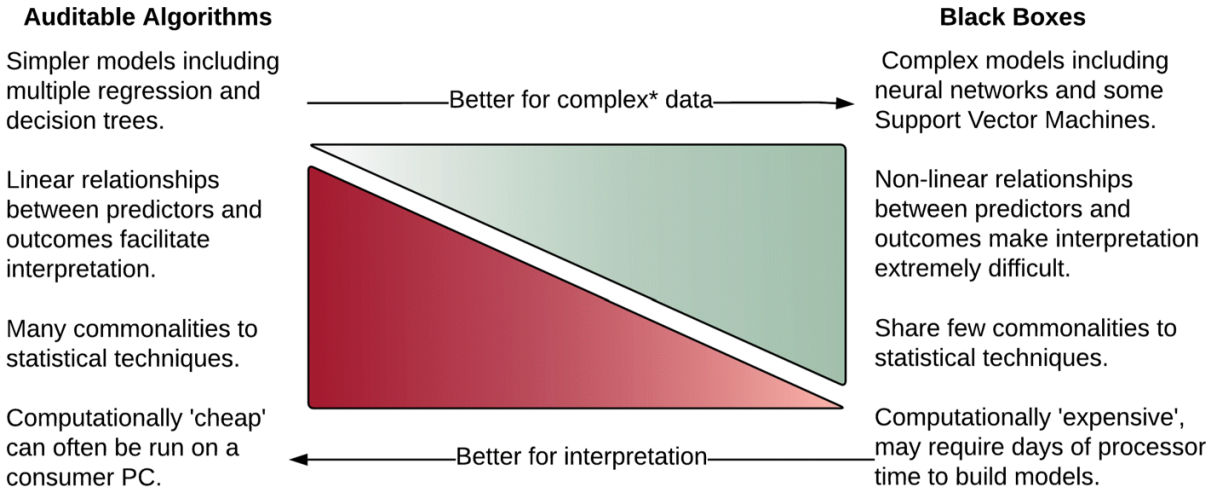
video and geo-location, is complicated and frequently non-linear, this is a fundamental aspect of ML approaches. When the connections between predictors and outcomes are non-linear and there are a huge number of predictors, each of which makes a little individual contribution to the model, it is extremely difficult to explain them in a meaningful fashion[7].

Many of the correlations of interest in medicine are quite basic, such as those between BMI and diabetes risk or cigarette use and lung cancer. As a result, their interactions can typically be described rather effectively using relatively basic models. Understanding the link between characteristics and outcomes is less important in many common ML applications, such as optimizing navigation, translating papers, and detecting objects in films[8]. This enables complicated non-linear algorithms to be used. Given this crucial distinction, researchers may find it beneficial to think of algorithms as a continuum between those that are easily interpretable (i.e., Auditable Algorithms) and those that are not (i.e., Black Boxes), depicted visually in Figure 1.



* 'Complex' data could refer to data which do not have a linear relationship with the outcome, such as a pixel in an image, the frequency of a wave in a sound bite, or movement data captured by a smart phone.

Figure 1:- The complexity/interpretability trade-off in machine learning tools

When a traditionally statistical approach becomes a machine learning technique, interesting concerns remain. We will show how various computational modifications to standard statistical approaches, such as elastic net regression, allow these algorithms to perform effectively with massive data in this paper[8]. However, a more detailed examination of the parallels and differences between machine learning and traditional statistics is beyond the scope of this work. Interested readers are referred to publications that expand on the concepts presented here. It's also worth noting that, while the 'Black Box' notion applies to models that use non-linear transformations, such as neural networks, work is being done to make feature detection in complicated algorithms easier[9][10][11].

The bulk of machine learning methods may be divided into two categories: supervised and unsupervised learning approaches. Both are discussed in the sections that follow[12][13].

II. WHAT THIS PAPER WILL ACHIEVE

This study shows how to use supervised machine learning algorithms to extract classifications from a dataset with numerous inputs. Regularized logistic regression, the first approach we describe, is quite similar to multivariate logistic regression[14][15][16]. The application of a regularisation function minimizes the number of features in the model while also reducing the magnitude of their coefficients. Regularization is thus appropriate for datasets with a large number of variables and missing data (also known as high sparsity datasets), such as the term-document matrices used to represent text in text mining research[17].

The second approach, a Support Vector Machine (SVM), has gained traction in the machine learning field because of its high accuracy in predicting outcomes in scenarios where the link between variables and outcomes is non-linear. It employs a mathematical method known as the kernel trick, which we'll go over in more depth later.

Finally, we offer an Artificial Neural Network (ANN), which has found broad usage in a variety of hard applications, including image and video recognition, due to its complicated design and highly adjustable parameters. Specialty neural networks, such as recurrent or convolutional networks, have been combined with ANNs to provide outstanding

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results on a variety of tasks. ANNs are prone to over-fitting since they are highly parameterized models. A regularisation approach, such as DropConnect, can help them function better.
The ultimate purpose of this paper is to provide physicians and medical researchers with a fundamental knowledge of machine learning (ML) and how it may be applied in medicine, as well as the practical abilities to create, assess, and compare their algorithms to solve prediction issues.

2.1 How should I proceed with this paper?
We include a conceptual overview as well as step-by-step guidance using code created for the R Statistical Programming Environment, which can be readily adapted and used for different classification and regression problems. This code will serve as a foundation for academics to build their own machine learning experiments. The models described here may be fitted to a variety of data formats and are appropriate for text and picture analysis with simple adjustments[18].
Preparing data, training algorithms, verifying algorithms, measuring algorithm performance, and applying fresh data to learned models are all covered in this work.
Examples of R code used to execute the analysis are supplied throughout the publication. Additional file 1 contains the whole code. Addition file 2 contains the data that was used in these studies[19].

2.2 Methods
The Breast Cancer Wisconsin Diagnostic Data Set was used in this study. The Machine Learning Repository at the University of California, Irvine (UCI) has made this dataset freely available. It is made up of the properties, or features, of cell nuclei, extracted from breast tumors using fine-needle aspiration (FNA), a popular oncology diagnostic method. From January 1989 to November 1991, clinical samples were collected for this collection. The methods outlined were used to extract relevant information from digitized pictures of FNA samples. Figure 3 shows an example of one of the digitized pictures from an FNA sample[20][21].

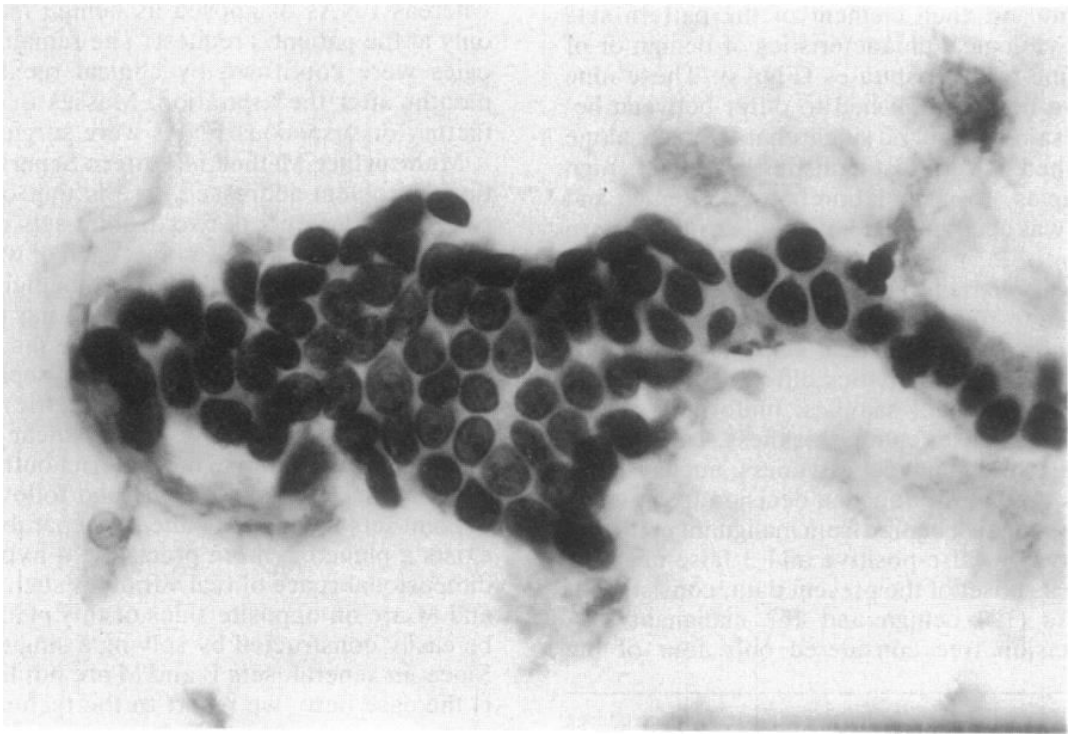

Figure 2:- An example of an image of a breast mass from which dataset features were extracted

Characteristics detected or computed from each FNA picture make up the dataset's features. This dataset contains nine attributes, each of which is rated on a scale of 1 to 10 for each occurrence, with 1 being the most benign and 10 being the most malignant. Uniformity of Cell Size and Uniformity of Cell Shape are descriptors of cell features, whereas Clump Thickness and Marginal Adhesion are more sophisticated cytological qualities.

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Because this dataset is basic, it is computationally efficient. Because of the small number of characteristics and instances, the analysis presented in this work can be completed on most current PCs in a reasonable amount of time[22]. Using huge datasets to train Machine learning algorithms may be computationally costly and, in some situations, take many days to finish, although the principles are the same as those explained throughout the rest of this work. The principles outlined here can be applied to any size dataset. Figure 4 lists all nine attributes, as well as the Instance No., Sample I.D., and Class. The entire dataset is a 699 x 12 matrix (one identification number, nine features, and one outcome per instance).

		Features									Outcome
Instance	Sample		Cell	Cell		Epithelial	Bare	Bland	Normal		Class
No.	I.D.	Thickness	Size	Shape	Adhesion	Size	Nuclei	Chromatin	Nucleoli	Mitoses	(Diagnosis)
1	1000025	5	1	1	1	2	1	3	1	1	2
2	1002945	5	4	4	5	7	10	3	2	1	2
3	1015425	3	1	1	1	2	2	3	1	1	2
.											
.											
.											
699	897471	4	8	8	5	4	5	10	4	1	4

Figure 3:-Because this dataset is basic, it is computationally efficient. Because of the small number of characteristics and instances, the analysis presented in this work can be completed on most current PCs in a reasonable amount of time. Using huge datasets to train Machine learning algorithms may be computationally costly and, in some situations, take many days to finish, even though the principles are the same as those explained throughout the rest of this work. The principles outlined here can be applied to any size dataset[23].

III. USING R

The R Statistical Programming Language was created as an extension of the S language and is an open-source tool for statistics and programming. R has a big community of active users and numerous good machine learning packages that are both versatile and simple to use. R is a computationally efficient language that is easy to understand even if you don't have a background in computer science. Many other statistical programming languages, such as MATLAB, SAS, and STATA, are similar to R. The Comprehensive R Archive Network organizes R packages into multiple task perspectives. Nearly 100 packages related to machine learning and statistical learning are now listed in the Machine Learning and Statistical Learning task view.
The R environment is accessed by many, if not all, R users via RStudio, an open-source integrated development environment (IDE) meant to make working in R easier. We propose that readers of this article download the most recent versions of R and RStudio and use the RStudio program to access the environment. R and RStudio are both free to use and licensed under an open-source license.

IV. CONDUCTING A MACHINE LEARNING ANALYSIS

4.1 ML algorithms are being trained.
We can start training our algorithms now that we've organized our dataset in a usable manner. The machine learning algorithms we'll employ are mentioned below and explained in-depth in the next section[24].

Logistic regression using L1 Least Absolute Selection and Shrinkage Operator (LASSO) regularisation using Generalized Linear Models (GLMs).

4.2 Support Vector Machines (SVMs) with a radial basis function (RBF) kernel.
Single-hidden-layer Artificial Neural Networks (ANNs).
4.3 Regularised regression using Generalised Linear Models (GLMs)
Regularised General Linear Models (GLMs) have excelled at predicting individual traits from online digital footprints, classifying open-text reports of doctors' performance, and detecting prostate cancer using desorption electrospray ionization mass spectrometric imaging of small metabolites and lipids[25].

When fitting GLMs with datasets with a large number of features and significant sparsity, model performance may be improved by reducing (or penalizing) the contribution of each of the included features to the model through

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regularisation, a technique that also decreases the danger of over-fitting. Regularisation decreases the number of coefficients in the model as well as their magnitudes, making it particularly ideal for large datasets with more features than occurrences. The Least Absolute Shrinkage and Selection Operator guide feature selection in this case (LASSO). Ridge Regression and the Elastic Net are two further regularisation methods available (which is a linear blend of both Ridge and LASSO regularisation). A concise, up-to-date overview of LASSO and other regularisation methodsis given in Ref [26][27][28].

The glmnet package in R is used to operationalize regularised GLMs. The GLM method is fitted to the training dataset using the code below. The regularisation parameter in the glmnet package is selected by a numerical value called alpha. A value of 1 picks LASSO regularisation, whereas a value of 0 selects Ridge regularisation. A value between 0 and 1 selects the Elastic Net, which is a linear combination of the two approaches[29][30][31].

The ideal value of lambda (), the regularisation parameter, is determined via tenfold cross-validation. The glm model$lambda.min object stores the value of () that minimizes prediction error[32][33]. The stronger the influence of regularisation on the number of features in the model and their related coefficients, the smaller the value. Figure 8 depicts the impact of various log(values.) The vertical broken line (seen here at x = -5.75) indicates the ideal value of log(). The most parsimonious value of log() is within 1 standard deviation of the absolute lowest value, as indicated by the rightmost dotted line. Because of the random nature of cross-validation, log() results may vary somewhat between investigations.The integers (0-9) in the table above refer to the number of features in the model. The code in Fig. applies the GLM method to the data and extracts the minimal value of and the coefficient weights[34][35][36].

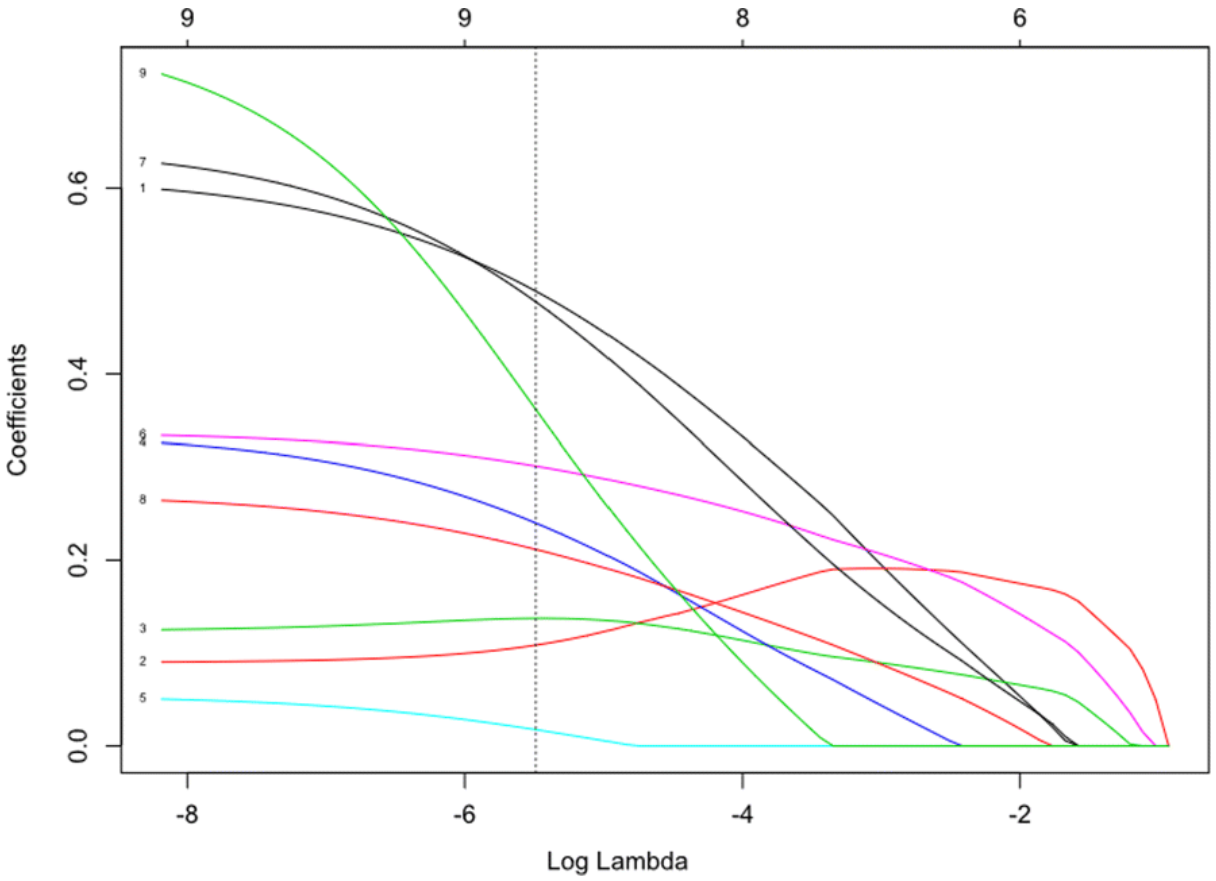

Figure 4:- The GLM model's regression coefficients. The coefficients for the 9 model features for various log(values are shown in the graph[37][38]. The number of features in the model is presented above the picture, with log() values on the lower x-axis. The number of variables in the model (i.e. those having a nonzero coefficient) rises as the size of log() decreases, as does the magnitude of each feature. The vertical dotted line denotes the log() value at which the forecast accuracy is highest[39][40][41].

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```
install.packages("glmnet")
require(glmnet)
glm_model = cv.glmnet(x_train, y_train, alpha=1, nfolds=10)
lambda.min = glm_model$lambda.min
glm_coef = round(coef(glm_model,s= lambda.min),2)
```

Figure 6:- shows the cross-validation curves for different levels of log(λ). This figure can be plotted using the code in Fig.

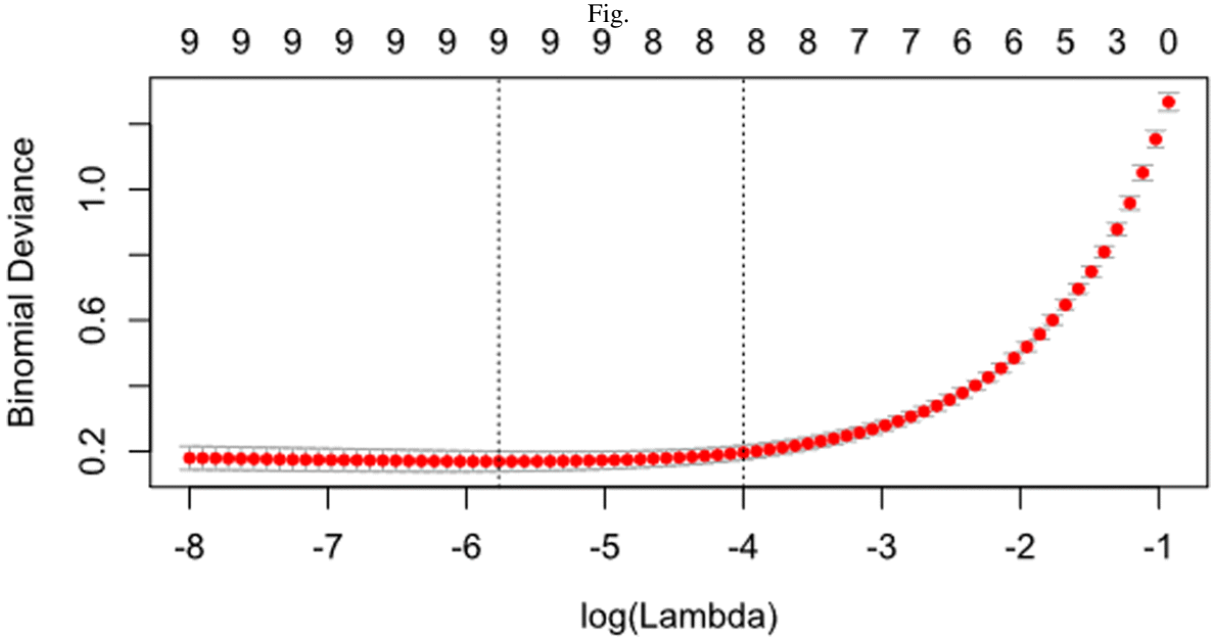

Figure 5:- The GLM model's cross-validation curves. The cross-validation curves are represented as red dots in the picture, with higher and lower standard deviations indicated as error bars[42][43][44].

The GLM model's cross-validation curves. The cross-validation curves are represented as red dots in the picture, with higher and lower standard deviations indicated as error bars[45][46][47].

```
plot(glm_model)
```

Figure 6:-Plot the cross-validation curves for the GLM algorithm

Figure 8 With varying values of log(), illustrates the magnitude of the coefficients for each of the variables inside the model[48][49]. The value of log() that minimizes the mean squared error established during cross-validation is indicated by the vertical dotted line[50][51][52]. The line() method can be used to add a dotted vertical line representing the value of log(), as illustrated in Fig. 12.

```
plot(glmnet(x_train,y_train, family="gaussian", alpha=1),"lambda",label=T, main="")
abline(v=log(lambda.min), lty=3)
```

Figure 7:- Plot the coefficients and their magnitudes

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V. CONCLUSION

The strategy we've used in this research has some major advantages and disadvantages. We selected to work with a publicly available dataset that had a limited number of inputs and cases. The data is organized in such a manner that people with a background in medicine will be able to readily draw comparisons between traditional statistics and innovative machine learning approaches. Furthermore, the little dataset allows for fast calculation on practically all current processors. Many of the subtleties and intricacies of ML studies, such as sparsity or high dimensionality, are not adequately reflected in the data, which is a drawback of this technique.Despite the absence of these typical aspects of an ML dataset, we are optimistic that users who have followed the examples here and worked with the code in the appendix will be well-equipped to work on more complicated datasets utilizing the scalable code framework we provide. Furthermore, this data supports an essential ML principle: more sophisticated algorithms do not always result in more relevant predictions[53][54].

We envision a future in which the potential of machine learning will significantly improve medical research and practice.We hope that by publishing this article, excitement for new and transformational machine learning techniques will be tempered by a critical understanding of how they function and the hazards they may bring[55].

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