

# **Incremental Feature Selection and Interpretable Learning: An Application for Glioma Grading and Detection**

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## **Abstract**

This study presents a diagnostic framework for healthcare using explainable artificial intelligence and machine learning. Previous studies show that the ability of prediction models greatly depends on the relevance and independence of the feature set. Hence, various feature selection methods are presented in the literature. Moreover, the previous medical diagnostic models using neural networks offer accurate predictions, however, without generating explicit decision rules. A novel research framework with incremental feature selection and interpretable machine learning is proposed. First non-redundant and relevant features are selected. Further, the initial weights obtained during feature learning are fed to the interpretable neural network to obtain global and local explanations. This proposed research framework is demonstrated with an open-source medical dataset related to glioma, and the best-fit model is obtained. Moreover, an app for glioma grading is developed with the underlying predictive model to offer decision support to physicians and patients.

## **Keywords**

Medical diagnosis; Explainable artificial intelligence; Feature selection; Artificial neural network

## **1. Introduction**

Artificial Intelligence (AI) has revolutionized the field of medical diagnostics by recognizing the underlying pattern of medical conditions and symptoms that is beyond human cognition (Kumar et al. 2023). Diagnostic decision support systems enable clinicians to make accurate and timely diagnoses by mining rapidly growing patient data in a temporally evolving domain and further predicting the progression of health conditions across the recovery and treatment pathways (Sutton et al. 2020). Artificial neural network (ANN) is widely used in the development of robust decision support systems solving complex and unstructured problems with high predictive performance (Shahid, Rappon, and Berta 2019). However, the decision-making process and the inherent decision rules applied in making predictions for a patient are hidden to the clinicians and they design disease management program without this critical knowledge that are often not effective. Explainability and interpretability of machine learning (ML) models have unleashed the fullest potential of such systems and the decision rules generalized by the learned models help in better treatment delivery, recovery, and help providing timely preventive medicine (Joyce et al. 2023).

In this study, an intelligent interpretable framework for developing clinical decision support system which is illustrated using glioma dataset provided by UCI Machine Learning repository (Tasci et al. 2022). The independence and significance of the features are ensured by a filter approach that uses ant colony optimization (ACO) with mutual information gain as its fitness function. Then, the reduced data is taken further to explore various learners such as, Naïve Bayes (NB), decision tree (DT), random forest (RF) and support vector machine (SVM) that yield the best accurate prediction. Using wrapper approach, the least significant features are eliminated and the feature importance derived from the best fit model is further used as the initial weight vector while training a prediction model with artificial neural network (ANN) for early convergence and better performance. The predictive power with random and

derived weights is compared. Further, with local interpretable model-agnostic explanations (LIME), the surrogate model underlying the clinical decision support system becomes more transparent offering better man-machine interfacing. The proposed framework is presented in Figure 1.

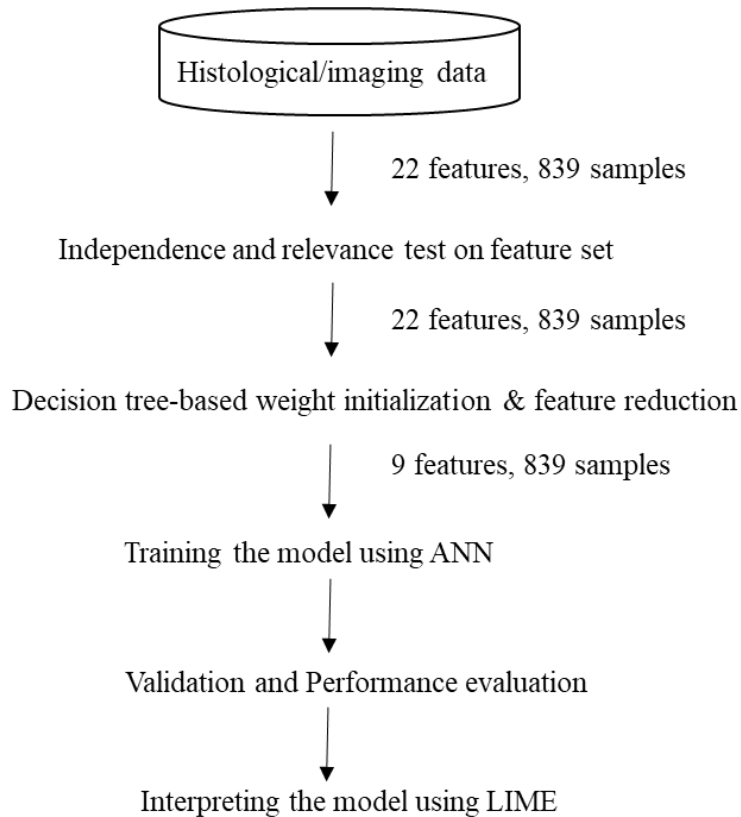


Figure 1. The framework

## 2. Literature review

While AI can control the treatment and recovery pathways of patients, it supports disease diagnosis, risk identification, drug discovery, treatment design, and recovery planning (Joyce et al. 2023; Kumar et al. 2023). Neural networks are widely used to offer diagnostic support in healthcare and have been used to detect diseases such as cancer, heart disease, Alzheimer, hepatitis, diabetes with high accuracy and robustness (Alkadri et al. 2021; Shahid et al. 2019). However, transparency in the human-computer interaction between the experts and decision support system is quite limited as they offer black box solution to the prediction problems preventing the experts to be aware about the connections among the predictors and the predicted variable (Messner 2023).

Explainable AI helps to uncover the opaque machine learning models and brings understandability, interpretability and explainability in these models (Joyce et al. 2023). Tree-based models are explainable by themselves and hence are used in developing decision-making rules while their predictive power is inferior to that of ANN-based prediction models (Gerlach et al. 2022). Explainable AI enabled ANN to model robust and interpretable prediction models that can reveal the complex relationships among predictors and predicting variable to the users which are often beyond human cognition, thus, improving the human-computer interaction.

Moreover, the feature selection before training a prediction model is critical to involve right predictors in decision-making (Meng et al. 2023). It improves the generalizability of the learners, conserves computing power, reduces convergence effort and expedites convergence. There are various approaches such as filter methods, wrapper methods and hybrid filter-wrapper approach to efficiently and effectively select features that are relevant and non-redundant. These methods stand differentiated from feature reduction methods that often can eliminate least significant but

relevant features. Filter methods estimate the importance of features with the available dataset and arrive at a reduced feature set with relevant, non-redundant and independent features (Sewwandi, Li, and Zhang 2024). Wrapper methods employ search to discover relevant and non-redundant features and then learn feature importance using well-known learners (Sivatha Sindhu, Geetha, and Kannan 2012). While filter methods perform well in high-dimensional problems, wrapper methods consume huge computing power and memory, however, compatible with the downstream learners enabling quick training. The hybrid approaches make an optimal trade-off and improve the predictive performance (Meng et al. 2023; Tasci et al. 2022; Zhou, Wang, and Du 2023). This paper presents the following addressing the aforementioned gaps in the literature. The drawbacks of both filter method and wrapper methods are addressed and features are selected without information loss. Both predictive performance and explainability of neural networks are to be examined with a suitable case application.

### 3. Materials and Methods

The framework presented in Figure 1 can be implemented to solve any prediction problem. The ability of the proposed framework in performing accurate predictive modelling using an open-source medical dataset is presented. The dataset used is taken from UCI Machine learning repository. Previous studies establish benchmark performance measures by exploring various feature selection methods and learners in developing predictive models for glioma detection using this dataset (Tasci et al. 2022, 2023). This study examines the application of the proposed framework to develop predictive models using the same dataset and the results are presented.

Glioma is a tumor that is exhibited with out-of-control growth of glial cells in brain or spinal cord. They manifest differently with different patients and vary in terms of symptoms, growth pace and malignancy. Generally, visual difficulty, headache, seizures, nausea, numbness are the symptoms of glioma. While there is 50% chance of gliomas being benign, they have to be treated as there is high chance of mutation of genes as the gliomas progress. Some cases are diagnosed with low grade glioma which are also monitored and treated to remove, control and manage further mutations and growth. The histological and imaging data of patients are used to extract information about 20 genes which could be mutated due to glioma. Table 1 presents the details of the dataset. The predictors are mostly binary except age and the predicted variable is also binary indicating low grade glioma or Glioblastoma Multiforme. The latter is generally due to poor prognosis at low-grade level. The dataset has 839 instances of which 487 instances show low grade glioma and remaining were of high grade.

Table 1. Dataset description

Feature	Description
Gender	Male/Female
Age	Patient's age at the time of diagnosis
IDH1	Isocitrate dehydrogenase (NADP(+)) 1 (mutated or not?)
TP53	Tumor protein p53 (Mutated or not?)
ATRX	ATRX - Chromatin remodeler protein (mutated or not?)
PTEN	Phosphatase and tensin homolog (Mutated or not?)
EGFR	Epidermal growth factor receptor (Mutated or not?)
CIC	Capicua (CIC) mutations present or not?
MUC16	Mucin-16 (Mutated or not?)
PIK3CA	Phosphatidylinositol 3-kinase Catalytic Subunit Alpha (Mutated or not?)
NF1	Neurofibromatosis type 1 (Mutated or not?)
PIK3R1	Phosphatidylinositol 3-kinase (Mutated or not?)
FUBP1	Far upstream element binding protein 1 (Mutated or not?)
RB1	Retinoblastoma protein Transcriptional Corepressor 1 (Mutated or not?)
NOTCH1	Neurogenic locus notch homolog protein 1 (Mutated or not?)
BCOR	B-cell lymphoma 6 corepressor (Mutated or not?)

CSMD3	CUB and Sushi multiple domains 3 (Mutated or not?)
SMARCA4	SWItch/Sucrose Non-Fermentable chromatin-remodeling complex (Mutated or not?)
GRIN2A	Glutamate Ionotropic Receptor N-methyl-D-aspartate Type Subunit 2A (Mutated or not?)
IDH2	Isocitrate dehydrogenase (NADP (+)) 2 (mutated or not?)
FAT4	FAT atypical cadherin 4 (Mutated or not?)
PDGFRA	Platelet-derived growth factor receptor alpha (Mutated or not?)

#### 4. Results and Discussion

Firstly, feature selection is performed. An incremental two-level feature selection is carried in which non-redundant features are extracted using ACO search algorithm using mutual information gain (Manzoor, Kumar, and others 2017) as a fitness function. Further, wrapper approach is carried out to extract relevant features using gini index learned using decision tree learner. The predictive power of learners such as NB, ANN, DT, RF, SVM are obtained and the prediction modelling using decision tree yielded accurate results. Hence, the ability of features in discriminating all data instances is measured and used to represent the significance and relevance of the features. While filter method could not eliminate dependent features in this dataset, wrapper method using decision tree learner removed 13 irrelevant features. Further, the reduced dataset is used train the model. The instances are randomly split into training and testing instances. While the former is used to train the model, the latter is used to validate the prediction model. The initial weights for ANN are derived from the purity measure of features obtained from wrapping process. The prediction accuracy of the model yielded by ANN after feature selection using ACO based filtering and decision tree-based wrapping is increased by 7%. The results are presented in Table 2.

Table 2. Prediction accuracy of different learners

Learner	Average Accuracy
NB	0.784
ANN	0.8795
DT	0.9005
RF	0.8751
SVM	0.8565
ACO-DT-ANN	0.9405

The accuracy measure obtained by ACO-DT-ANN has outperformed that presented in the previous studies (Tasci et al. 2022, 2023). The results are obtained after performing hyper parameter tuning and 16-fold cross validation and the average performance is presented in Table 2.

Further, the model developed by this methodology is interpreted using local interpretable model-agnostic explanations (LIME) (Ali et al. 2023; S Band et al. 2023). In this process, the basis in which prediction is made for each instance and the decision rule constructed with features are presented. Interpretation of the prediction made for four instances is presented in Figure 2.

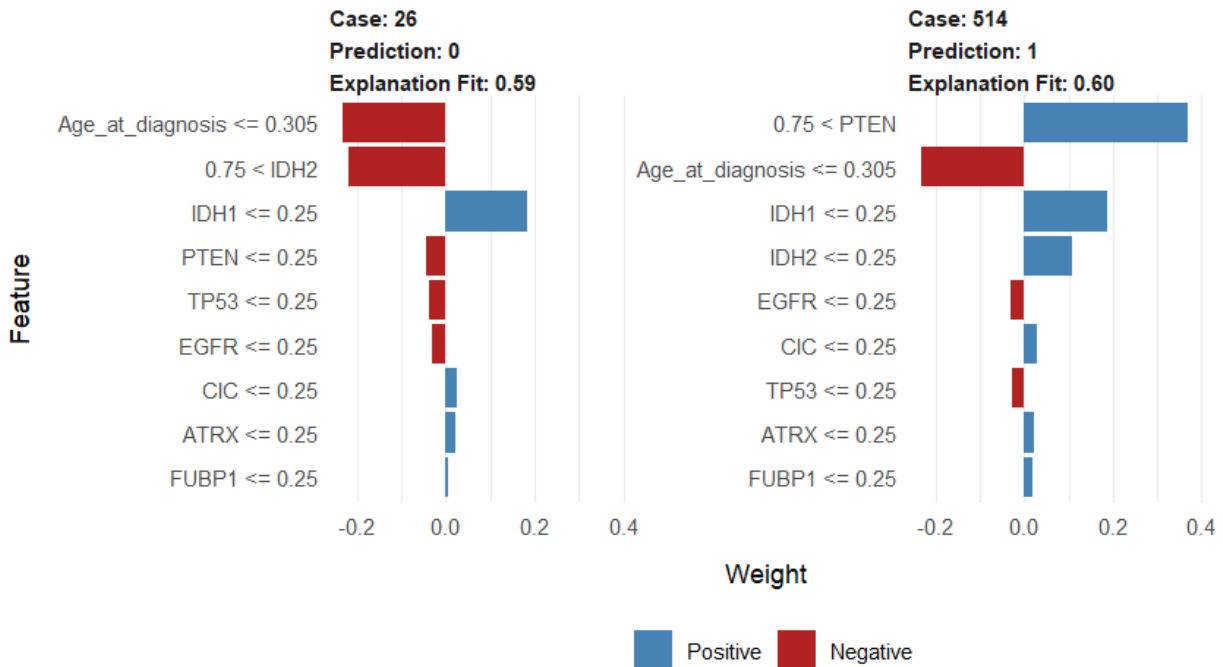


Figure 2. Partial result from LIME

Conventionally, the neural network yields these global explanations and the decision rules behind are hidden to the users. Using LIME, we can derive the local explanations for prediction that has been made. Figure 2 shows both local and global explanations for two sample test instances. The test instances are unlabeled and are provided to the best-fit model with values for each feature. For the first instance, the model predicts glioma negative and for the second instance, the model predicts glioma positive. The explanation fit shows the extent to which the local explanations are revealed for the problem. It can be observed that the positive predictions are explained upto 60% and the negative predictions are explained upto 59%. The weightage of each feature in making the predictions is presented for each instance which shows the discriminating power of features in detecting glioma positive or negative individuals. In this case, for glioma negative decision, age and IDH2 play important roles, while for glioma positive PTEN and age play significant role with high discriminating power. The decision rules that explain the final prediction for an instance are also presented. For instance, PTEN less than or equal to 0.25 indicates glioma negative when if greater than 0.75 indicates glioma positive. Such results offer domain information to patients to understand the importance of these features and their thresholds that categorically discriminate glioma positive and negative individuals. This also helps medical practitioners to validate their diagnostic rules analytically.

## 5. Implications

The study has significant implications to practice. From the prediction model generated for automatically detecting glioma, a web application is made as presented in Figure 3.

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## Glioma Grading - Clinical Decision Support System

Age

Isocitrate dehydrogenase (NADP(+)) 1 (mutated or not?)

Tumor protein p53 (Mutated or not?)

Isocitrate dehydrogenase (NADP(+)) 2 (mutated or not?)

ATRX - Chromatin remodeler protein (mutated or not?)

Capicua (CIC) mutations present or not?

Epidermal growth factor receptor (Mutated or not?)

Far upstream element binding protein 1 (Mutated or not?)

Phosphatase and tensin homolog (Mutated or not?)

You are diagnosed with Glioblastoma Multiforme. Please meet Doctor immediately!

Figure 3. Web Application for Glioma grading

The underlying model behind this application is developed based on the proposed approach. This can be used as an informal screening mechanism which can be further validated and investigated by clinicians.

The study has significant research implications. The role of incremental feature selection and precomputing initial weights for ANN in improving the prediction performance of ANN-based prediction model is demonstrated. Results of the proposed approach outperformed those presented in the previous studies.

## 6. Conclusions

This study presents incremental feature selection and interpretable learning using neural network. The proposed framework is demonstrated using glioma dataset and the results are compared with the benchmark performance measures. It is found that the proposed method outperformed other feature selection methods, learners and their different combinations of these. This framework is applicable for performing prediction modelling in any problem domain. Future researchers can deploy this framework to solve prediction problems with varying number of dimensions and instances. However, the choice of the feature selection method should be based on the dimensionality and heterogeneity of the instances. An app has been developed with the trained and validated model and can be used

as a decision support tool. The dataset used for training is collected from patients in a particular geographical region. The model should be further trained with cross-country dataset for wider use.

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### **Biography**

**Jinil Persis** is currently working as Assistant Professor at Indian Institute of Management (IIM), Kozhikode, India in quantitative methods and operations management area. Prior to this, she worked at IIM, Mumbai in Operations and supply chain management area. She obtained her Ph.D. and Masters in Engineering with Industrial Engineering specialization from College of Engineering, Guindy (CEG), India in 2015 and 2011 respectively. Her research interests include Evolutionary computation, Artificial intelligence and Machine learning applications. She has published her research articles in journals of international repute such as IEEE Transactions on Engineering Management, Production Planning and Control, Annals of Operations Research, Journal of Cleaner Production, Journal of Environmental Management and Wireless Personal Communication.