

Comparison of machine learning algorithms to identify muscular atrophy and muscular dystrophy

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Article Info

Article history:

Received Jan 23, 2025

Revised Jun 11, 2026

Accepted Jul 9, 2026

Keywords:

Electromyography

Extreme gradient boosting

Gradient boosting

Muscular atrophy and dystrophy

Random forest

Support vector machine

ABSTRACT

Muscular dystrophy is a genetic disorder characterized by progressive muscle weakness and degeneration, while muscular atrophy involves the loss of muscle tissue due to pathological conditions. Accurate differentiation between these neuromuscular disorders is critical for effective clinical diagnosis and treatment planning. This study presents a machine learning-based framework for classifying muscular dystrophy and muscular atrophy using surface electromyography (sEMG) signals. sEMG data were acquired and processed to extract informative features with low computational complexity. Several machine learning classifiers several techniques were used and assessed, such as random forest (RF), support vector machine (SVM), gradient boosting (GB), and extreme gradient boosting (XGBoost). To further enhance classification performance, a novel ensemble learning approach combining multiple machine learning models was proposed. Experimental results exhibit that the suggested ensemble model completes significantly higher grouping accurateness and robustness compared to individual classifiers and existing methods reported in the literature. The results of this investigation indicate that ensemble-based machine learning techniques integrated with sEMG analysis provide a reliable and non-invasive diagnostic aid, with strong potential for early detection and improved clinical management of neuromuscular disorders.

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1. INTRODUCTION

Muscle weakness and gradual deterioration are hallmarks of a class of hereditary disorders known as muscular dystrophies. They are brought on by mutations in the genes that code for muscle proteins and are characterized by progressive degeneration of skeletal muscles [1]–[3]. Muscular dystrophies are progressive, systemic muscle diseases that typically arise due to malfunctioning or absent glycoproteins, such as dystrophin, in the muscle membrane [1], [2], [4]. The reduction of skeletal muscle mass is known as muscular atrophy, as shown in Figure 1. Factors such as immobility, ageing, malnutrition, drug usage, and various neurological or musculoskeletal disorders can contribute to muscular atrophy. Muscle atrophy leads to weakness and functional impairment [5]–[7]. A defining feature of all muscular dystrophies is the continuous cycle of muscle fiber degeneration and regeneration, as illustrated in Figure 2 [1], [8]. Medical professionals employ a variety of diagnostic techniques to identify myopathies and their underlying causes. These include electromyography (EMG) and blood tests to determine muscle enzyme levels to assess muscle function, and muscle biopsy for cellular-level examination of muscle tissue. In certain cases, particularly when hereditary myopathies are suspected, genetic testing [2], [7], [9] is also recommended.

Muscular atrophy and muscular dystrophy can be detected using EMG, as shown in Figure 3. EMG detects anomalies associated with muscular weakness, stiffness, and degeneration by measuring the electrical activity of muscles in response to nerve stimulation. Due to its non-invasive nature and ability to capture real-time muscle activity, EMG has become a valuable tool for neuromuscular disorder analysis [10]–[13]. Despite extensive research on EMG-based diagnosis, most existing studies focus on binary classification or rely on static datasets, limiting their applicability in real-time clinical scenarios [10]–[15]. Therefore, the primary research question addressed in this study is: can real-time EMG signals, when analyzed using machine learning and deep learning techniques, effectively distinguish between normal muscle condition, muscular atrophy, and muscular dystrophy. This study hypothesizes that advanced machine learning and deep learning models applied to real-time EMG data can achieve higher classification accuracy and robustness in differentiating these three muscle conditions compared to traditional static dataset-based approaches.



Figure 1. Muscular atrophy

Figure 2. Muscular dystrophy

Figure 3. Electromyography test

The significance of this discovery resides in its capacity to facilitate early, non-invasive, and real-time diagnosis of neuromuscular problems through the use of EMG signals, which can help doctors plan treatments and intervene promptly [2], [3], [16]. The suggested method improves diagnostic reliability by better reflecting physiological muscle function under dynamic conditions by utilizing real-time EMG data. Although EMG-based machine learning algorithms have been researched for neuromuscular problem diagnosis in the past, most current research concentrates on binary classification, single disease identification, or traditional standalone classifiers [10]–[15]. The proposed work extends the state-of-the-art by offering an ensemble learning framework that integrates random forest (RF), gradient boosting (GB), and extreme gradient boosting (XGBoost) models for the classification of muscular atrophy and muscular dystrophy using surface electromyography (sEMG) data. The ensemble approach blends the advantages of several classifiers. To increase robustness, lower prediction variance (VAR), and improve generalization ability across various feature representations, the ensemble technique leverages the advantages of several classifiers.

Additionally, the proposed framework offers a unified classification strategy that can discriminate multiple neuromuscular disorders utilizing a similar EMG analytic pipeline, in contrast to earlier research that mainly focuses on muscular dystrophy or muscular atrophy independently. In order to provide light on feature sensitivity and model stability, the study additionally examines classifier behavior under various feature dimensions (5, 160, and 181 features). These contributions enable the prospective use of EMG-based diagnostic systems in intelligent clinical decision-support environments and improve their dependability. Earlier research concentrated on machine learning or deep learning models using static datasets that included only muscular dystrophy or muscular atrophy cases. In contrast, the present study extends EMG-based analysis to three distinct muscle conditions by introducing machine learning and deep learning algorithms tailored for real-time EMG data during muscle movements.

The remainder of this paper is organized as follows. Section 2 presents the related work. Section 3 describes the proposed methodology. Section 4 presents the results and discussion. Finally, section 5 concludes the study.

2. RELATED WORK

Numerous studies have examined the use of EMG, medical imaging, genetic analysis, and machine learning approaches in the diagnosis and categorisation of neuromuscular illnesses, namely muscular dystrophy and muscular atrophy. Through machine learning and deep learning techniques, recent

developments in artificial intelligence have significantly increased the precision and effectiveness of illness diagnosis. In order to highlight current limits and provide motivation for the planned study, this section examines the most pertinent papers concerning EMG-based diagnostics, machine learning and deep learning techniques, and clinical investigations of muscular illnesses.

Askarinejad *et al.* [5] analyzed 25 sEMG readings captured from the biceps muscle, comprising 17 healthy and 8 atrophic samples, and employed a quadratic discriminant analysis (QDA) classifier to achieve improved classification accuracy. Vogel and Hagengruber [6] developed an sEMG-based interface that enables individuals with atrophic muscles to control a robotic manipulator with three degrees of freedom. Bao *et al.* [17] designed a four-class motor imagery-based brain–computer interface system for a subject with severe spinal muscular atrophy. Srivastava *et al.* [18] demonstrated that combining both quantitative muscle ultrasonography (QMU) and electrical impedance myography (EIM) data allows highly accurate classification of spinal muscular atrophy-affected muscles. Bittmann *et al.* [19] reported clinical test results from a case study involving a five-year-old girl diagnosed with spinal muscular atrophy. Hassan *et al.* [20] assessed and contrasted how well different machine learning algorithms classified data. Leung *et al.* [21] provided a thorough analysis of machine learning applications in genetic medicine, emphasizing accessible datasets and computational difficulties. Sathyavikasini and Vijaya [1] proposed a novel approach for muscular dystrophy classification using mutated gene sequences and positional cloning techniques.

Moreno *et al.* [4] using integrative analysis, a gene expression core signature for Duchenne muscular dystrophy was found, and promising therapeutic drugs were identified. Hetnarska *et al.* [7] introduced a diagnostic method based on creatine phosphokinase (CPK) activity for identifying spinal muscular atrophy. Nofal *et al.* [22] utilized network analysis and machine learning techniques to identify genes implicated in spinal muscular atrophy with high accuracy. Danowski *et al.* [9] investigated serum creatine kinase (CK) levels in muscular dystrophy and myotonia dystrophica to support disease identification. Kehri and Awale [10] proposed an EMG signal analysis method that uses artificial neural networks (ANN), support vector machines (SVM), and wavelet transform to diagnose muscular dystrophy. Nardo *et al.* [11] demonstrated the feasibility of a machine-learning-based method for predicting the onset and offset timing of muscular recruitment, achieving high performance despite significant variability in sEMG signals. Bitar *et al.* [14] proposed an EMG-based machine learning framework for the detection of Duchenne muscular dystrophy. Subasi *et al.* [12] created an automated approach for classifying EMG signals that uses bagging and discrete wavelet transform to diagnose neuromuscular diseases.

Kefalas *et al.* [15] assessed how well automated machine learning techniques performed in identifying normal and abnormal EMG data. Inam *et al.* [13] provided a concise review of strategies used for EMG signal classification. Szajewska and Kopeć [8] analyzed electromyographic patterns in Duchenne and Becker muscular dystrophy across different stages of muscle degeneration. Taghizadeh *et al.* [23] shown how deep learning techniques can be used to quickly and accurately quantify rotator cuff muscle degeneration using shoulder computed tomography (CT) datasets. Mastropietro *et al.* [24] suggested a deep learning model based on swin transformers that increases the accuracy of classifying various forms of muscular dystrophy using magnetic resonance imaging (MRI) pictures. Yang *et al.* [25] created a deep learning system with great diagnostic accuracy for identifying dystrophinopathies from thigh muscle MRI images. Garibaldi *et al.* [26] analyzed muscle MRI patterns in myotonic dystrophy type 1 (DM1) to refine muscle involvement characterization and support clinical trial design. Tobore *et al.* [16] reviewed deep learning–based interventions for addressing healthcare challenges, highlighting key considerations in biomedical applications.

Thomas *et al.* [2] reported that the time to diagnosis of Duchenne muscular dystrophy has remained largely unchanged over a 15-year surveillance period. Quinlivan [3] emphasized the critical importance of early diagnosis in Duchenne muscular dystrophy in order to improve long-term patient outcomes. Yan *et al.* [27] enhanced adaptability across imaging tasks by the introduction of a foundation model for universal moving-object segmentation in medical images. Bushby *et al.* [28] highlighted clinical diagnostic delays by recognizing persistent shortcomings in the prompt detection of symptomatic Duchenne muscular dystrophy. Avanzo *et al.* [29] offered a comprehensive examination of machine learning and deep learning techniques used to radiomics for medical imaging. Although Huysmans *et al.* [30] developed an automated MRI-based method for quantifying muscle fat fractions in patients with muscular dystrophies, the study did not investigate real-time sEMG-based multi-class classification using machine learning or ensemble learning techniques.

Overall, prior research has demonstrated the efficacy of EMG, medical imaging, genetic analysis, and machine learning techniques in the diagnosis of neuromuscular illnesses. Using EMG signals, medical imaging, and machine learning techniques, numerous studies have examined muscular atrophy, muscular dystrophy, or spinal muscular atrophy [1]–[23]. Despite their positive outcomes, the majority of these studies concentrated on offline datasets, binary classification, or a single disease. Their use in real-time diagnosis is therefore restricted. Furthermore, very few research have taken into account the categorisation of muscular dystrophy, muscular atrophy, and normal muscle health within a unified framework. The suggested study

offers a real-time sEMG-based ensemble learning method for multi-class classification that makes use of RF, GB, and XGBoost in order to get beyond these restrictions. To increase classification accuracy and dependability, the suggested approach also assesses classifier performance using various feature dimensions.

3. METHOD

The suggested approach is displayed in Figure 4. The procedure of monitoring the electrical activity generated during muscle activation is known as EMG, or myoelectric signal. Any muscle's performance can be examined by recording this electrical activity. Machine learning techniques can be used to predict when muscle anomalies will occur.

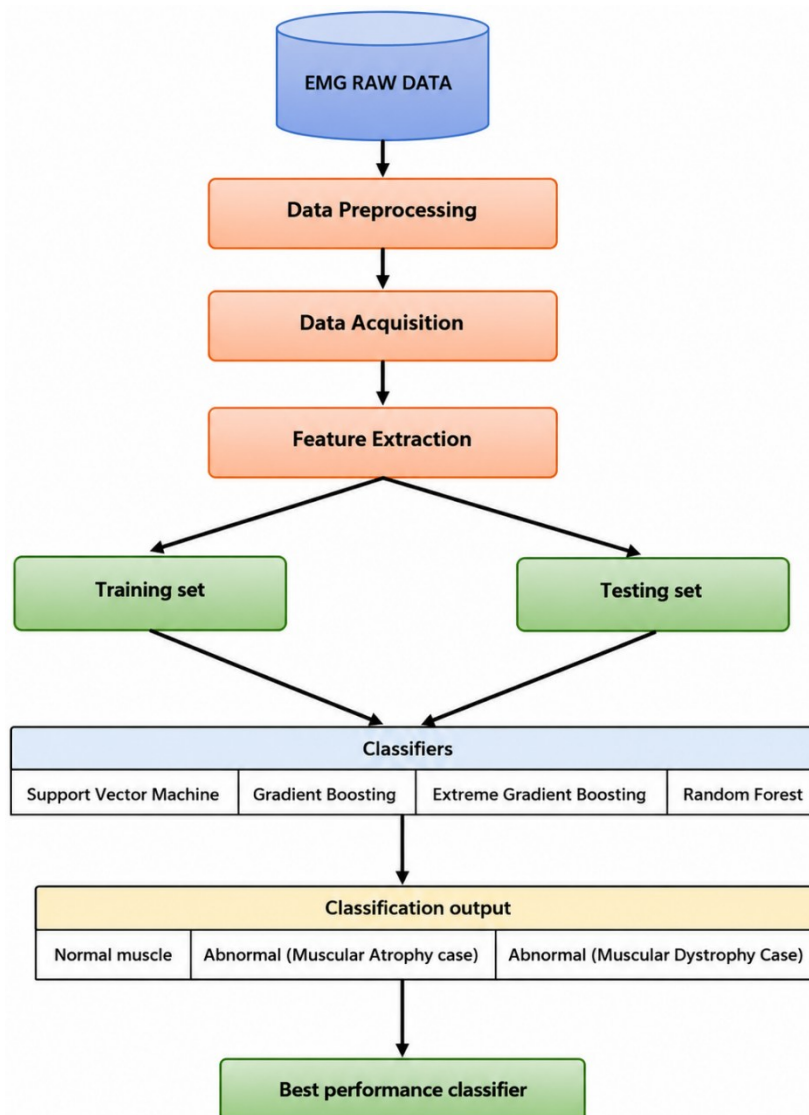


Figure 4. Block diagram of proposed method

3.1. Electromyography data acquisition

The UCI Machine Learning Repository's results provided the dataset that was utilized to train the predictive models. The National Science Foundation, a division of the Centers for Disease Control and Prevention (CDC), oversees UCI. The program uses a combination of physical tests and interviews to assess the health and nutritional status of Americans. Eleven of the twenty-two male individuals had a professional diagnosis of a separate knee abnormality. They performed three exercises to assess their knee muscle

behavior, walking, leg flexion up, and leg extension from a seated position. The acquisition process involved the use of a goniometer in the knee and four electrodes: the rectus femoris, biceps femoris, semitendinosus, and vastus medialis. Some sample datasets are shown in Table 1, which is related to abnormal and in Table 2 which is related to the normal position of the knee muscle.

Table 1. Sample EMG dataset related to abnormal condition of patient in gait

Recto femoral	Biceps femoral	Vasto medial	EMG semitendinosus	Flexo-extension
-0.0548	-0.0015	0.042	0.0285	-9
0.0795	-0.0256	0.078	0.0397	-9
0.084	-0.0293	0.069	0.0345	-9
0.0802	-0.0203	0.0525	0.0345	-9
0.0847	-0.0008	0.0412	0.0337	-9
0.0937	0.009	0.0382	0.0082	-9
0.0892	0.006	0.0315	-0.0315	-8.9
0.0877	0.0105	0.0165	-0.042	-8.8
0.093	0.018	-0.0091	-0.0263	-8.7
0.0937	0.0277	-0.0285	-0.0181	-8.7

Table 2. Sample EMG dataset related to normal condition of patient in gait

Recto femoral	Biceps femoral	Vasto medial	EMG semitendinosus	Flexo-extension
0.0007	-0.0083	0.0045	-0.0091	57.6
-0.0008	-0.0038	0.0007	-0.0046	57.5
-0.0008	-0.0068	0.0015	-0.0023	57.3
-0.0008	-0.0053	0.0045	-0.0038	57.1
0.0007	0.0015	0.0082	-0.0075	56.9
0.003	0.0052	0.009	-0.0083	56.7
0.0015	0.003	0.0067	-0.0038	56.5
0.0015	0.0022	0.0022	-0.0023	56.3
0.0015	0.003	-0.0008	0.0015	56.1
0.0022	0.0045	-0.0008	0.0082	55.9

3.2. Electromyography data instrumentation

Biometrics employed MWX8 datalog equipment with eight digital channels and four analog channels—four for sampling using sEMG and one for goniometry. A microSD card was used to store the data straight onto the computer's internal storage, and a Bluetooth adapter was used to transmit it to real-time datalog software. The program's sampling frequency was 1000 Hz, and its resolution was 14 bits. There are four electrodes in total, one for each channel (1–4) and one for the time series. For every subject, there are around five shares or motion repetitions in each series as shown in Figure 5.

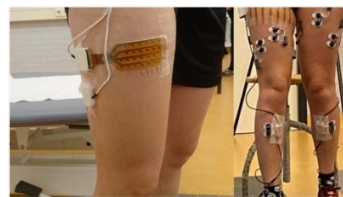


Figure 5. Multi-array EMG test

3.3. Electromyography signal preprocessing and feature extraction

The acquired sEMG signals were subjected to a preprocessing stage to improve signal quality and reduce the influence of noise and inter-subject variability. Initially, the raw EMG signals were inspected for missing values and outliers. Signal amplitudes were then normalized using min-max normalization, which scales the signal values into the range of 0 to 1 according to:

$$X_{\text{norm}} = \frac{X - X_{\min}}{X_{\max} - X_{\min}}$$

Normalization ensures that all features contribute equally during classifier training and prevents attributes with larger magnitudes from dominating the learning process. Each EMG channel had its informative properties extracted after normalization. Among the statistical and temporal characteristics considered were

mean absolute value (MAV), root mean square (RMS), VAR, standard deviation (STD), waveform length (WL), signal energy, maximum value, minimum value, and zero crossing rate (ZCR). These characteristics ensure a low computing cost appropriate for real-time execution while accurately representing patterns of muscle activation.

3.4. Feature selection

Using RF feature importance analysis, features were ranked based on their contribution to classification performance based on impurity reduction scores. The highest-ranked features were chosen to create reduced feature sets with 5, 160, and 181 features. This method reduces model complexity while maintaining the discriminative information required for precise classification of muscular atrophy and muscular dystrophy.

3.5. Reproducibility guidelines

Each machine learning model was implemented using Python and the scikit-learn module. In order to ensure objective performance estimation, ten-fold cross-validation was employed in the experiments. While preserving class balance, the dataset was randomly split into subsets for testing and training. To provide fair comparisons between classifiers, hyperparameter settings were maintained throughout the tests. The publicly accessible UCI dataset can be used to reproduce the entire workflow, this covers model training, evaluation, feature extraction, feature selection, and preprocessing.

3.6. Prediction models

Finding patterns in different features is one of the main goals of using machine learning algorithms on large datasets. Both muscular atrophy and muscular dystrophy criteria were used to label the data in this investigation. SVM, GB, XGBoost, and RF are the supervised learning methods used in this work. Python scikit-learn was used to implement each algorithm. This paper compares the algorithms which are provided better accuracy in the analysis of sEMG signals to identify muscular atrophy and muscular dystrophy diseases. By comparing the outcomes of these four classifiers using assessment parameters, the prediction accuracy rose. The best classifier is described by the experimental result in between them.

3.6.1. Support vector machine

It is a method for regression and classification. Each data point in SVM is plotted in n-dimensional space, where the number of dimensions corresponds to the attribute or feature count as shown in Figure 6. The number of attributes is denoted by n. Every attribute's value corresponds to a specific coordinate, and the decision function is represented as shown in (1).

$$y = w^T x + b \quad (1)$$

The hyperplane equation is given by (2).

$$w^T x + b = 0 \quad (2)$$

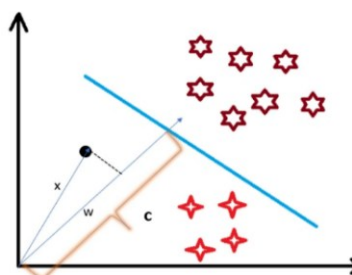


Figure 6. Support vectors machine

3.6.2. Gradient boosting

One of the most popular types of machine learning models is the prediction model. In machine learning, the GB algorithm stands out for its accuracy and speed of prediction, especially when working with big and complicated datasets. The mathematical representation of GB is shown in (3).

$$F_m(x) = F_{m-1}(x) + h_m(x) \quad (3)$$

The classification problem's loss function is defined in (4).

$$L = \sum(y_i - F(x_i)) \quad (4)$$

3.6.3. Extreme gradient boosting

A state-of-the-art machine learning technique noted for its exceptional prediction abilities is XGBoost. The formula for loss function or mean squared error (MSE) is as shown in (5).

$$F_m(x) = \arg \min_{\gamma} \sum_{i=1}^n (y_i, \gamma) = \arg \min_{\gamma} \sum_{i=1}^n (y_i, \gamma)^2 \quad (5)$$

3.6.4. Random forest

To generate predictions, each tree is voted across using the RF algorithm, a powerful tree learning technique in machine learning. Both classification and regression tasks make extensive use of them. The formula for calculating the feature importance is defined in (6).

$$\text{Feature Importance} = \sum(\text{decrease in impurity}) \quad (6)$$

3.7. Evaluation parameters

Accuracy, precision, recall, and F-measure are a few data mining evaluation measures. Where FP, FN, TP, and TN stand for false positive, false negative, true positive, and true negative, respectively. As stated in (7), accuracy is calculated by dividing the number of correctly identified instances by the dataset's overall number of instances.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (7)$$

According to (8), precision is defined as the mean likelihood of pertinent retrieval.

$$\text{Precision} = \frac{TP}{TP + FP} \quad (8)$$

According to (9), the average likelihood of full retrieval is the recall.

$$\text{Recall} = \frac{TP}{TP + FN} \quad (9)$$

As indicated in (10), the F-measure is computed utilizing both precision and recall.

$$\text{F-measure} = \frac{2 \times (\text{Precision} \times \text{Recall})}{\text{Precision} + \text{Recall}} \quad (10)$$

4. RESULTS AND DISCUSSION

4.1. Datasets

The EMG dataset mentioned in Section 3.1 was used for the experimental evaluation. Three feature sets (5, 160, and 181 features) were produced for classification after preprocessing and feature extraction. Both the suggested ensemble model and the individual machine learning models were trained and tested using these feature sets. Standard criteria, such as accuracy, precision, recall, and F1-score, were used to assess each classifier's performance and compare how well it identified normal muscle condition, muscular atrophy, and muscular dystrophy.

The accuracy, completeness, and volume of data in the UCI database are well-known. The superior performance of the proposed ensemble-based framework demonstrates the effectiveness of combining complementary learning strategies for EMG signal classification. The ensemble technique benefited from lower VAR and better generalization across various feature subsets, whereas individual classifiers like SVM and GB produced competitive results. In comparison to independent machine learning models, the finding suggests that ensemble learning can more accurately capture the intricate and non-linear patterns linked to muscle atrophy and muscular dystrophy, enhancing diagnostic reliability.

4.2. Machine learning classifiers

Four classification techniques are used in this study and are implemented in Python. Prediction is enhanced by the usage of these models. To determine which classifier best predicts a patient's likelihood of

developing muscular atrophy and dystrophy illnesses, several classifiers are compared. A brief explanation of these categorization methods and classifiers is provided as follows:

- i) SVM: the SVM classifier performance was evaluated using ten-fold cross-validation. The obtained classification results based on accuracy, precision, recall, and F-measure are presented in Figure 7.
- ii) GB: the classification performance of GB was evaluated using the same evaluation parameters. The obtained accuracy performance is presented in Figure 8.
- iii) XGBoost: the performance of XGBoost in classifying muscular atrophy and muscular dystrophy using sEMG signals is presented in Figure 9.
- iv) RF: the RF classifier performance was evaluated using the same experimental setup. The obtained accuracy results are presented in Figure 10.

Evaluating ANOVA F-Value selected features:

SVM Results with 160 features:

Accuracy: 0.7593

	precision	recall	f1-score	support
0	0.83	1.00	0.91	10
1	0.58	0.70	0.64	10
2	1.00	0.11	0.20	9
3	0.87	1.00	0.93	13
4	0.70	0.78	0.74	9
5	0.75	1.00	0.86	3
accuracy			0.76	54
macro avg	0.79	0.76	0.71	54
weighted avg	0.80	0.76	0.71	54

Figure 7. Accuracy performance of SVM

Gradient Boosting Results with 160 features:

Accuracy: 0.8333

	precision	recall	f1-score	support
0	1.00	1.00	1.00	10
1	0.89	0.80	0.84	10
2	1.00	0.56	0.71	9
3	0.86	0.92	0.89	13
4	0.78	0.78	0.78	9
5	0.43	1.00	0.60	3
accuracy			0.83	54
macro avg	0.83	0.84	0.80	54
weighted avg	0.88	0.83	0.84	54

Figure 8. Accuracy performance of GB

Extreme Gradient Boosting Results with 160 features:

Accuracy: 0.8704

	precision	recall	f1-score	support
0	0.91	1.00	0.95	10
1	0.91	1.00	0.95	10
2	1.00	0.44	0.62	9
3	0.92	0.92	0.92	13
4	0.80	0.89	0.84	9
5	0.60	1.00	0.75	3
accuracy			0.87	54
macro avg	0.86	0.88	0.84	54
weighted avg	0.89	0.87	0.86	54

Figure 9. Accuracy performance of XGBoost

Random Forest Results with 160 features:

Accuracy: 0.8519

	precision	recall	f1-score	support
0	1.00	1.00	1.00	10
1	1.00	1.00	1.00	10
2	1.00	0.56	0.71	9
3	0.91	0.77	0.83	13
4	0.62	0.89	0.73	9
5	0.60	1.00	0.75	3
accuracy			0.85	54
macro avg	0.85	0.87	0.84	54
weighted avg	0.89	0.85	0.85	54

Figure 10. Accuracy performance of RF

4.3. Comparison of machine learning algorithms

The overall accuracy performance of the methods is shown in Figure 11, such as SVM as in Figure 11(a), GB as in Figure 11(b), XGBoost as in Figure 11(c), and RF as in Figure 11(d). Figures 12 to 14 show the performance of various evaluation parameters in the prediction of muscular atrophy and muscular dystrophy diseases. The experimental results show the comparison of GB, XGBoost, SVM, and RF classifiers and evaluate the performance on the bases of accuracy, precision, recall, and F-measure.

In terms of accuracy, precision, recall, and F-measure for the classification of muscular atrophy and muscular dystrophy using sEMG signals, the experimental findings show that the RF classifier performs better than SVM, GB, and XGBoost. The capacity of RF to manage high-dimensional data and successfully capture non-linear correlations is responsible for this higher performance. These results align with earlier research that has been documented in literature. For example, Subasi *et al.* [12] showed that ensemble-based

methods greatly increase classification accuracy in neuromuscular disorder identification by proposing an EMG-based classification system employing discrete wavelet transform and bagging techniques. The efficacy of ensemble and tree-based models was also demonstrated by Kefalas *et al.* [15], who demonstrated that automated machine learning techniques produce dependable performance in differentiating between normal and pathological EMG data. Additionally, the authors [10], [14] have reported good classification accuracy when using machine learning approaches like SVM and ANN for EMG signal analysis.

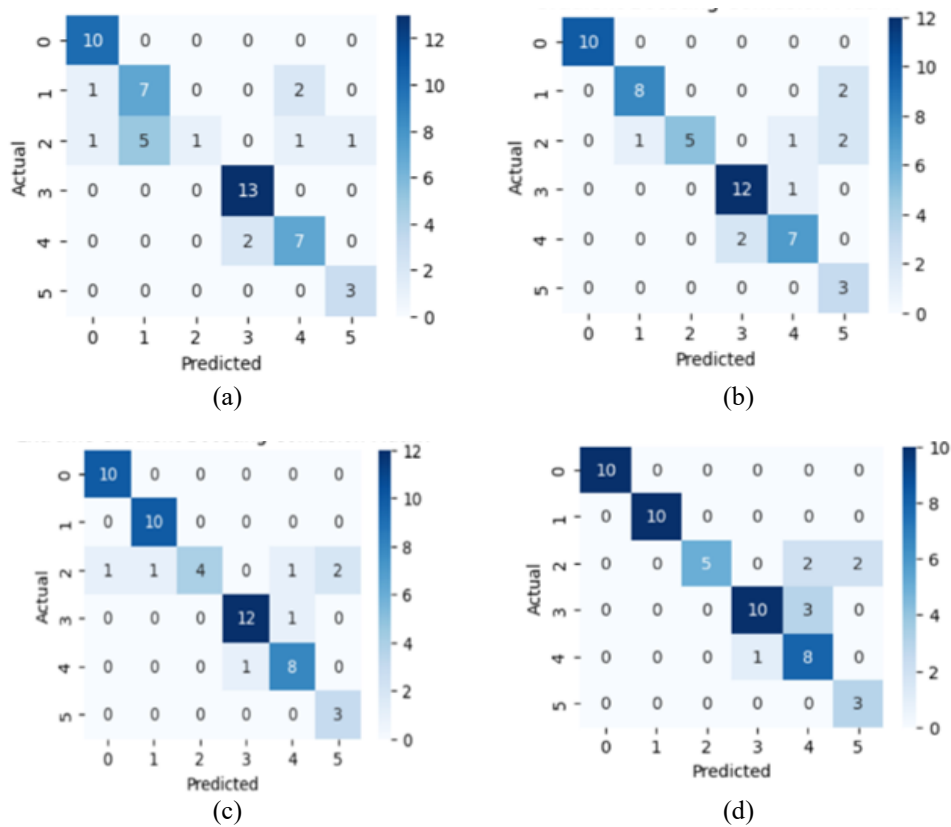


Figure 11. Confusion matrix of classification results: (a) SVM, (b) GB, (c) XGBoost, and (d) RF

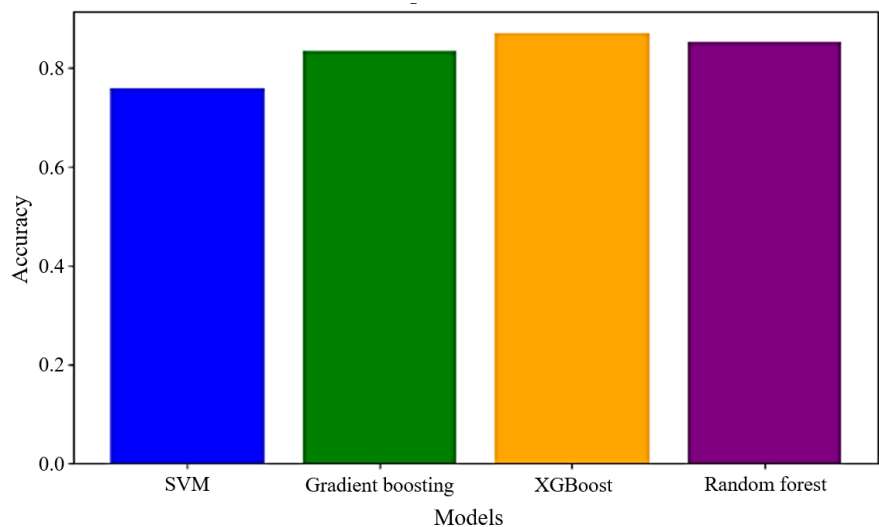


Figure 12. Model comparison for 160 features

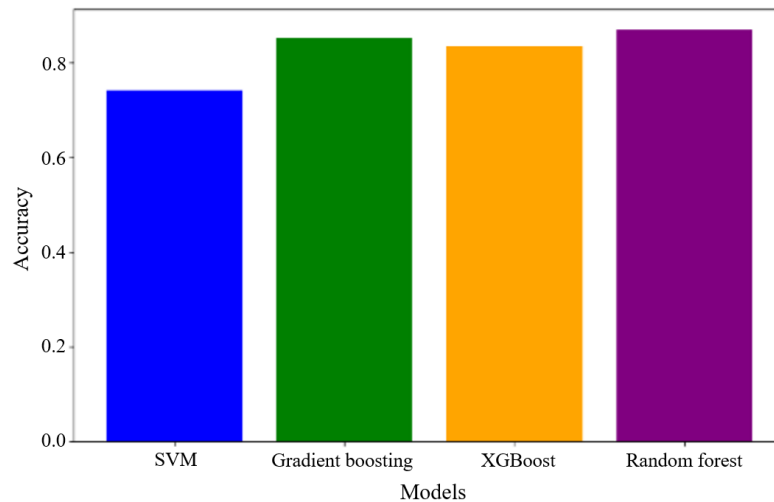


Figure 13. Model comparison for 181 features

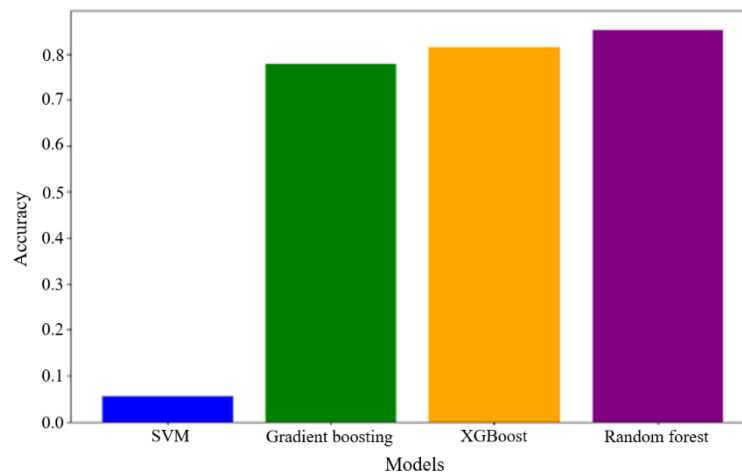


Figure 14. Model comparison for 5 features

However, the current work expands the analysis to several circumstances, boosting complexity and clinical importance, whereas prior research mostly concentrated on binary classification problems. The results of Hassan *et al.* [20], who emphasized the robustness of boosting algorithms in classification tasks involving complicated datasets, are consistent with the performance enhancement seen with GB and XGBoost in this study. RF, on the other hand, showed superior generalization and stability over various feature sets (160, 181, and 5 features), making it more appropriate for this use case.

The study was carried out using a publicly available UCI dataset with a small number of participants, despite the suggested framework achieving encouraging classification results. The dataset's size and controlled acquisition conditions may not accurately reflect the variability found in actual clinical settings, even though it offers a helpful benchmark for comparing machine learning techniques. EMG features can be greatly influenced by a number of factors, including patient age, disease severity, muscle group variances, electrode placement changes, and signal noise. As a result, the published findings ought to be regarded as a preliminary validation of the suggested framework. To further examine the model's robustness, generalizability, and clinical reliability, future research should use larger, more varied, and clinically validated EMG datasets gathered from several healthcare facilities.

Additionally, this study has an edge over previous research that used static datasets because it uses real-time EMG data. According to Nardo *et al.* [11], machine learning models need to be resilient to the considerable variability in EMG signals. This variability is handled well by the suggested method, which improves diagnostic performance. Overall, the results support current research trends and show that ensemble-based machine learning models—RF in particular—are highly effective in classifying EMG

signals. In addition to achieving competitive performance, the proposed framework expands the scope by tackling real-time, multi-class classification, which has received less attention in previous research.

4.4. Practical deployment in clinical and rehabilitation environments

The suggested sEMG-based machine learning paradigm offers a great deal of promise for practical clinical use. The framework can function as an intelligent decision-support tool for doctors during neuromuscular disorder assessment because sEMG acquisition is non-invasive, inexpensive, and able to record muscle activity in real time. The method can help medical personnel with early diagnosis, disease monitoring, and treatment planning by automatically categorizing patterns of muscle atrophy and muscular dystrophy. The framework can be combined with wearable EMG sensors in rehabilitation settings to continually track muscle activation while performing physiotherapy activities. Therapists would be able to objectively assess patients' progress and modify rehabilitation regimens using quantitative muscle performance markers thanks to this integration. Additionally, wearable EMG equipment and edge computing technologies can facilitate remote patient monitoring, enabling medical professionals to monitor the course of a patient's illness outside of hospital settings.

Additionally, telemedicine platforms, assistive devices for patients with neuromuscular impairments, and smart healthcare ecosystems can all use the suggested architecture. Clinicians and patients may receive instant feedback from real-time categorization results, enhancing therapy effectiveness and enabling customized rehabilitation plans. These real-world application possibilities show how machine learning-based EMG analysis can be applied outside of the lab.

5. CONCLUSION

This study shows how well machine learning-based EMG data analysis can classify muscle dystrophy and atrophy. The RF model regularly outperforms other methods, demonstrating its aptitude for representing the complex, non-linear properties of EMG data, according to a comparative examination of several classifiers. The findings highlight the potential of EMG-based intelligent systems for early, non-invasive, and economical diagnosis of neuromuscular disease. From a clinical standpoint, the suggested framework can lessen the need for invasive treatments while supporting decision-making in diagnostic and rehabilitation contexts. Opportunities for early detection, ongoing monitoring, and individualized therapy planning for neuromuscular illnesses are presented by the capacity to automatically and reliably evaluate sEMG signals. However, the controlled manner of data collection and the comparatively modest size of the UCI dataset constrain this study. Before widespread clinical implementation, more validation using bigger and clinically validated datasets is required, even though the experimental results show the efficacy of RF and ensemble-based learning techniques. Future research will concentrate on gathering data from several centers, incorporating a variety of patient demographics, and conducting assessments in actual clinical settings. In order to facilitate real-time diagnosis and ongoing patient monitoring in real-world healthcare settings, integration with wearable sEMG devices, edge computing platforms, rehabilitation monitoring systems, and telemedicine applications will also be investigated.

FUNDING INFORMATION

The authors state that there was no funding.

AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Ganga Bhavani Billa	✓		✓	✓		✓		✓	✓					✓
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Peddada														

C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project administration

Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

No conflicts of interest are disclosed by the authors.

INFORMED CONSENT

This is not a pertinent section. This study did not involve any human subjects, personally identifiable information, or circumstances requiring individual informed consent because it only used publicly available datasets, computational simulations, and machine learning algorithms without violating participants' privacy rights or requiring written consent.

ETHICAL APPROVAL

This section is not relevant. The study was exempt from review by an institutional review board, ethics committee, or adherence to the Helsinki Declaration because it did not use human subjects or animals and instead relied only on non-biological computational techniques like optimization algorithms and data analysis.

DATA AVAILABILITY

The data that support the findings of this study are available on request from the corresponding author, [GBB].

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