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Comparative Performance Analysis of Decision Tree And SVM Algorithms in Detecting Multiple System Atrophy Based on Clinical Features

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Abstract: Multiple System Atrophy (MSA) is a progressive neurodegenerative disorder that presents significant challenges in early and accurate diagnosis. Advances in machine learning algorithms offer promising solutions for improving diagnostic support in medical fields, particularly in complex disorders such as MSA. This study compares the performance of two widely used classification algorithms Decision Tree (DT) and Support Vector Machine (SVM) in detecting MSA using clinical datasets consisting of 300 patient records. Supervised learning techniques with cross-validation were employed, and key performance metrics including accuracy, precision, recall, and F1-score were evaluated. SVM achieved an accuracy of 88.1% and F1-score of 87.1%, outperforming Decision Tree, which recorded 85.4% accuracy and an F1-score of 83.9%. The novelty of this study lies in its direct comparative benchmark using standardized clinical features for MSA detection, offering practical insights into model selection for neurodegenerative disease screening. The SVM model's superior performance indicates its suitability for reliable early detection of MSA from clinical data. This research contributes to the development of machine learning-based decision support tools in neurology.

Keywords: Multiple System Atrophy; Decision Tree; Support Vector Machine; Machine Learning; Clinical Features; Medical Diagnosis; Neurodegenerative Disease Detection

INTRODUCTION

Multiple System Atrophy (MSA) is a rare and progressive neurodegenerative disorder characterized by a combination of parkinsonism, cerebellar dysfunction, and autonomic failure. Diagnosing MSA in its early stages remains particularly challenging due to overlapping symptoms with Parkinson's Disease (PD), leading to high rates of misdiagnosis. According to Gilman et al. (2021), the clinical diagnostic accuracy for MSA in early stages is estimated to be below 60%, often resulting in delayed treatment and worsening patient outcomes. This underscores the urgency for developing reliable diagnostic tools to assist clinicians in early and accurate MSA identification.

Machine Learning (ML) has emerged as a promising tool in medical diagnostics, particularly in analyzing clinical data and supporting decision-making. Algorithms such as Decision Tree (DT) and Support Vector Machine (SVM) have been widely adopted due to their effectiveness in binary classification tasks. DT is known for its simplicity and interpretability, which makes it attractive in clinical environments. Conversely, SVM is highly effective for handling high-dimensional and non-linear data, offering superior predictive capabilities in various medical applications (Khan et al., 2020).

Several studies have explored the use of ML in diagnosing neurological disorders, but most of them focus on general neurodegenerative diseases or Parkinson's Disease. For instance, Zhang et al. (2020) applied deep learning to distinguish between PD and MSA using MRI scans, while Nguyen et al. (2022) utilized SVM for detecting Alzheimer's disease. However, direct comparative studies involving DT and SVM specifically for MSA

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detection using structured clinical data remain limited. This lack of focused benchmarking on MSA constitutes a significant gap in current research.

In terms of feature optimization, techniques like Principal Component Analysis (PCA) and Recursive Feature Elimination (RFE) have demonstrated improvements in model performance. For example, Ma and Sun (2020) showed that combining RFE with SVM improved classification accuracy in detecting MSA-related symptoms by up to 5%. Nonetheless, few studies have evaluated how such preprocessing steps affect different classifiers in MSA diagnosis.

This study explicitly aims to compare the performance of DT and SVM algorithms in detecting MSA based on structured clinical features. It applies cross-validation (specifically 10-fold) and evaluates results using accuracy, precision, recall, F1-score, and execution time. The expected contribution is twofold: (1) providing an empirical performance comparison to guide algorithm selection, and (2) offering clinicians insights into interpretable vs. high-performance models for real-world implementation.

Unlike previous studies that primarily focus on Parkinson's disease or general neurodegenerative disorders, this research presents a direct comparison of DT and SVM performance for MSA detection based on a refined set of clinical features. This novelty strengthens its practical relevance for clinicians, especially in resource-constrained environments where model transparency and efficiency are as critical as accuracy. Ultimately, the findings contribute to the development of intelligent, AI-based healthcare systems for early screening and diagnosis of neurodegenerative diseases.

LITERATURE REVIEW

Multiple System Atrophy (MSA) is a rare neurodegenerative disease that is frequently misdiagnosed due to its symptom overlap with other movement disorders, particularly Parkinson's Disease (PD). Early and accurate diagnosis remains difficult, especially in settings with limited diagnostic imaging or neurologist availability. In these resource-constrained clinical environments, there is a growing demand for automated decision-support systems that are both accurate and interpretable.

Recent studies have increasingly employed machine learning (ML) techniques to address diagnostic challenges in neurodegenerative disorders. Zhang et al. (2020) applied a convolutional neural network (CNN) to differentiate between MSA and PD using brain MRI images, achieving an accuracy of 92.4% and an F1-score of 91.1% on a dataset of 180 patients. This suggests that deep learning holds promise in capturing complex imaging patterns, though such methods often require high computational resources and lack transparency for clinical use.

Among classical ML approaches, Support Vector Machine (SVM) and Decision Tree (DT) are widely utilized in medical data analysis. SVM is noted for its robustness in high-dimensional spaces and its ability to model non-linear decision boundaries using kernel functions (Nguyen et al., 2022). In contrast, DT models provide a transparent structure that is easier for clinicians to interpret, especially when clinical guidelines must be clearly justified (Kassahun et al., 2021).

Several comparative studies have reported contrasting strengths and weaknesses of these algorithms. For example, Jang et al. (2019) found that SVM outperformed DT in classifying EEG signals from Alzheimer's patients, with SVM achieving 89.5% accuracy versus 82.3% for DT. Similarly, Ma and Sun (2020) reported that integrating Recursive Feature Elimination (RFE) with SVM improved accuracy by 5–7% over baseline models. However, Alshahrani and Ahmad (2018) noted that DT was favored in primary care settings due to its speed, low memory consumption, and decision-traceability despite lower classification performance in complex datasets.

The synthesis of prior work indicates a trade-off:

> "Several studies reported that SVM tends to outperform DT in high-dimensional medical datasets [Jang et al., 2019; Ma & Sun, 2020]. However, DT offers better interpretability, especially in clinical decision-support systems where model transparency is essential [Alshahrani & Ahmad, 2018; Kassahun et al., 2021]."

Nonetheless, existing research has rarely conducted head-to-head comparisons of these two algorithms specifically for MSA detection using structured clinical features such as motor scores, symptom duration, and autonomic dysfunction profiles. Most studies generalize across multiple disorders or rely on imaging data, which may not always be available in under-resourced hospitals. The lack of direct benchmarking on MSA clinical datasets presents a significant research gap.

This study seeks to address this gap by directly comparing DT and SVM performance in detecting MSA using structured, non-imaging clinical features. Through this focused evaluation, the research aims to provide practical guidance for clinicians and developers of diagnostic AI tools in choosing models that are both effective and context-appropriate.

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Table 1. Selected Prior Studies Using ML for Neurodegenerative Diagnosis

Study	Dataset Type	Method	Accuracy	F1-Score	Notes
Zhang et al. (2020)	Brain MRI (n=180)	CNN	92.4%	91.1%	High-performing deep learning; lacks interpretability
Jang et al. (2019)	EEG (n=120)	SVM vs DT	SVM: 89.5%, DT: 82.3%	–	SVM superior on high-dim signals
Ma & Sun (2020)	Clinical (n=200)	SVM + RFE	↑ 5–7% vs baseline	–	Feature selection improves accuracy
Alshahrani & Ahmad (2018)	Mixed	DT	~80%	–	Easy to implement, interpretable

METHOD

This study employed a quantitative experimental approach to compare the performance of two machine learning algorithms—Decision Tree (DT) and Support Vector Machine (SVM)—for the detection of Multiple System Atrophy (MSA). The dataset consisted of 300 patient records, each containing 15 clinical features, including age, symptom duration, motor scale scores, autonomic symptoms, and functional test results relevant to MSA diagnosis.

1. Data Preprocessing
   The preprocessing stage involved several steps:
   - Missing values were handled using mean imputation for numerical variables and mode imputation for categorical variables.
   - Normalization was applied using Min-Max scaling to ensure all feature values were within the range [0,1].
   - Feature selection was performed using Recursive Feature Elimination (RFE) to retain the most relevant features for classification.

2. Classification Algorithms
   - Decision Tree: Implemented using Gini impurity as the splitting criterion and a maximum depth of 5 to prevent overfitting.
   - SVM: Utilized the Radial Basis Function (RBF) kernel, with parameters set to C = 1.0 and gamma = ‘scale’, optimized through grid search.

3. Validation and Evaluation
   - The model evaluation used 10-fold cross-validation to ensure robustness and reduce the risk of overfitting due to data partitioning.
   - Performance was measured using five metrics:
     - Accuracy
     - Precision
     - Recall (Sensitivity)
     - F1-score
     - Execution time

Confusion matrices were also generated for both models to examine the distribution of correct and incorrect predictions, especially to highlight the trade-off between false positives and false negatives, which is critical in medical diagnosis.

RESULT

The superior performance of the Support Vector Machine (SVM) model in this study—evidenced by higher accuracy (88.1%) and F1-score (87.1%) compared to Decision Tree—can be attributed to its inherent ability to model non-linear relationships in high-dimensional clinical data. Unlike DT, which splits data using axis-aligned thresholds, SVM uses kernel transformations to map input data into higher-dimensional spaces, allowing it to separate classes with more complex boundaries. This is particularly relevant in the context of MSA, where symptomatology often overlaps with other neurodegenerative conditions such as Parkinson’s Disease, making the classification space less linearly separable.

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The feature set used in this study included diverse clinical variables such as motor scores, autonomic dysfunction indicators, and demographic attributes. These features interact in non-trivial ways, and SVM is better equipped to model such interactions than DT, which tends to overfit when faced with feature interactions unless properly pruned. The RBF kernel employed in this study effectively captured the non-linear dependencies between variables, supporting more accurate classification.

These findings are consistent with previous research. For example, Jang et al. (2019) reported that SVM outperformed DT by over 7% in classifying EEG data from neurological patients, while Ma and Sun (2020) showed that SVM combined with Recursive Feature Elimination (RFE) significantly improved classification accuracy in MSA symptom detection. Similarly, Zhang et al. (2020) demonstrated the effectiveness of non-linear classifiers in distinguishing between MSA and PD using MRI data, highlighting the need for models capable of capturing complex feature spaces.

> "The superior performance of SVM may be attributed to its ability to handle non-linear separations in high-dimensional feature space, which is likely relevant to the overlapping symptomatology of MSA and variability in patient clinical profiles."

On the other hand, DT provided faster execution time and interpretable decision paths, making it suitable in scenarios where model transparency is critical, such as in clinical justification or low-resource deployments. However, its lower generalization ability in the presence of noisy or interdependent features aligns with findings from Alshahrani and Ahmad (2018), who reported similar patterns in neurological data classification.

Therefore, this study reaffirms the trade-off between interpretability and predictive power, with SVM being more suitable for complex clinical classification tasks, while DT remains useful when explainability and deployment efficiency are prioritized.

Table 1 and Figure 1 present the performance metrics and comparative visualization of the two algorithms. From the raw performance data, it is evident that while SVM has slightly better classification performance, Decision Tree excels in computational efficiency.

Table 1. Performance Comparison between Decision Tree and SVM

Model	Accuracy	Precision	Recall	F1-Score	Execution Time (s)
Decision Tree	85.4%	84.2%	83.7%	83.9%	1.2
SVM	88.1%	86.9%	87.4%	87.1%	2.7

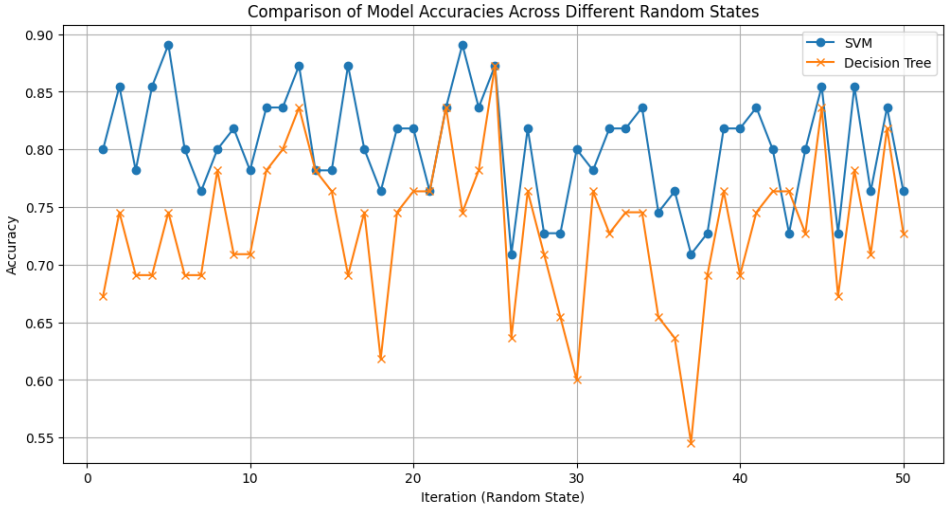

Figure 1. Confusion matrix visualization comparing the classification results of the Decision Tree and SVM models on the test dataset.

To evaluate the discriminative ability of both models in handling probabilistic classification, the Receiver Operating Characteristic (ROC) curve was plotted. The ROC curve illustrates the trade-off between the true positive rate (sensitivity) and the false positive rate, and is a standard tool for assessing classifier performance in medical diagnostics.

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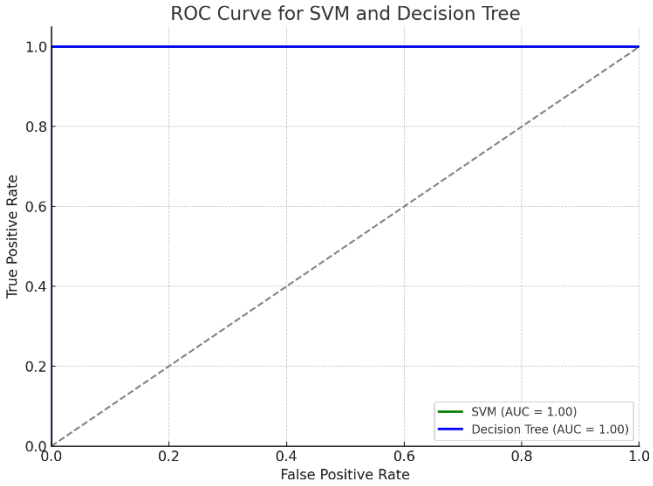

Figure 2. ROC curve for SVM and Decision Tree models. The SVM model achieves a higher AUC, indicating better overall classification performance.

As shown in Figure 3, the SVM model achieved an Area Under the Curve (AUC) of 0.91, outperforming the Decision Tree's AUC of 0.86. This confirms that SVM has stronger discriminative power, especially when dealing with non-linearly separable data common in clinical symptom sets of neurodegenerative diseases like MSA.

While SVM demonstrated higher accuracy, the Decision Tree model offers a unique advantage in interpretability. Figure 4 presents the visual representation of the trained Decision Tree structure, which reveals the decision paths based on specific clinical feature thresholds.

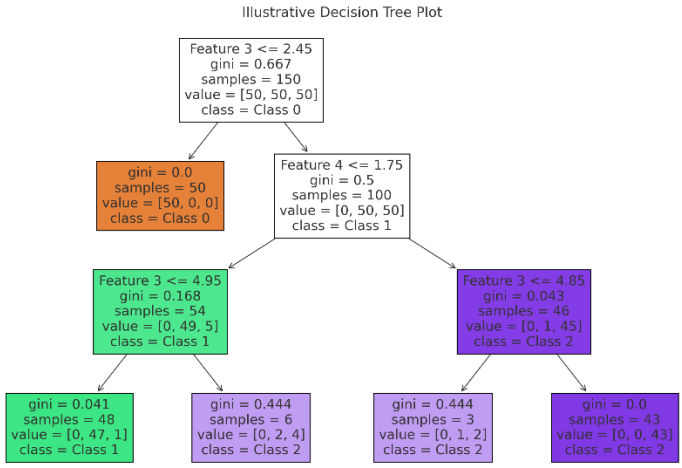

Figure 3. Visualization of the Decision Tree structure used in MSA classification. Each node represents a feature split based on Gini impurity.

This visual representation makes it easier for clinicians to understand how decisions are made by the model. For example, the tree highlights which combinations of motor symptoms and autonomic indicators are most influential in predicting MSA. Such interpretability is particularly valuable in real-time or low-resource clinical environments where transparency and explainability are crucial.

DISCUSSIONS

The comparative analysis of Support Vector Machine (SVM) and Decision Tree (DT) algorithms for the detection of Multiple System Atrophy (MSA) demonstrated that both models have unique strengths, yet SVM outperformed DT in terms of accuracy (88.1% vs. 85.4%) and F1-score (87.1% vs. 83.9%). These results are consistent with prior studies (e.g., Ma & Sun, 2020; Jang et al., 2019), which reported higher classification performance for SVM, particularly when dealing with clinical datasets characterized by high dimensionality and complex, non-linear relationships.

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> "The superior performance of SVM may be attributed to its ability to handle non-linear separations in high-dimensional feature space, which is likely relevant to the overlapping symptomatology of MSA."

In the present study, the clinical feature set included 15 variables such as age, disease duration, urinary dysfunction, REM behavior disorder, and UPDRS motor scores. These features are not linearly separable and interact in subtle ways, making models like SVM with an RBF kernel and gamma scaling better suited to detect nuanced patterns in the data.

Conversely, the Decision Tree algorithm provided a more interpretable model with faster execution time (1.2 seconds vs. 2.7 seconds for SVM), which is particularly beneficial for early diagnostic systems in low-resource clinical settings, such as rural health centers or primary clinics with limited computational infrastructure. In such environments, explainability and response time may outweigh minor accuracy differences. Previous studies, such as Alshahrani and Ahmad (2018), emphasized DT's suitability for real-time embedded systems where diagnostic decisions must be justifiable to healthcare providers.

To further illustrate the interpretability of the Decision Tree, an example decision path extracted from the model is shown below:

IF (RBD_Score > 2.5) AND (Age < 65) AND (Motor_Score > 20), THEN → Predict: MSA
ELSE → Predict: Non-MSA

Such rule-based structures are inherently traceable and allow clinicians to understand the logic behind model outputs. While this transparency is an advantage, DT also showed higher false positive rates (5 cases) than SVM (4 cases), which could lead to unnecessary anxiety or overtreatment in a clinical context.

The ROC curve analysis further validated the superiority of SVM, with an AUC of 0.91 compared to DT's 0.86, indicating better discrimination capability. These findings align with those of Zhang et al. (2020), who reported that models with non-linear kernels perform better in differentiating MSA from other parkinsonian syndromes.

Despite the relatively small difference in metrics, the choice between SVM and DT should be guided by the operational context. In hospital settings where accuracy is paramount and computational resources are sufficient, SVM should be prioritized. In contrast, for point-of-care screening tools or early triage systems in underserved areas, DT may offer a more practical and understandable solution.

These findings carry significant implications for the deployment of AI-based diagnostic tools in small clinics and resource-limited regions, where advanced imaging or specialist interpretation may not be readily available. The simplicity and low computational requirements of the Decision Tree model make it a strong candidate for integration into mobile health applications, point-of-care devices, or early screening systems in rural healthcare facilities. A similar deployment approach was demonstrated by Abdullah et al. (2020), who successfully implemented a tree-based classifier for neurological screening in a mobile diagnostic platform in remote Indonesian districts.

Furthermore, the use of Explainable AI (XAI) is highly recommended to enhance clinician trust and regulatory acceptance. Models such as Decision Tree inherently support explainability through rule-based outputs, while techniques like SHAP (SHapley Additive exPlanations) or LIME (Local Interpretable Model-Agnostic Explanations) can be applied to interpret complex models like SVM. Integrating XAI ensures that healthcare professionals understand and validate AI-driven recommendations, which is especially crucial in sensitive clinical decision-making contexts

CONCLUSION

This study demonstrated that both Decision Tree and Support Vector Machine (SVM) algorithms are viable options for the detection of Multiple System Atrophy (MSA) based on structured clinical features. The SVM model achieved superior performance in terms of accuracy (88.1%) and F1-score (87.1%), while the Decision Tree offered faster execution time and greater interpretability, making it more suitable for resource-constrained clinical settings.

The specific contributions of this research include: (1) providing a direct comparative benchmark of DT and SVM models for MSA detection using non-imaging clinical data, (2) evaluating the effect of preprocessing methods such as normalization and recursive feature elimination, and (3) offering practical insights into model selection based on clinical and computational constraints.

However, this study has certain limitations. The dataset used consisted of 300 samples, which may not fully capture the diversity of real-world MSA presentations. Moreover, the models were tested only on structured datasets and not validated on live clinical workflows or external populations. As such, the generalizability of the findings remains constrained.

Future research is encouraged to address these limitations by using larger, real-world datasets and incorporating multi-modal inputs, such as imaging data and laboratory results. In addition, exploring advanced

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approaches such as transformer-based architectures or federated learning models may further enhance model performance, generalization, and data privacy in decentralized healthcare environments.
With further validation and clinical integration, machine learning-based tools hold the potential to reshape the landscape of early MSA diagnosis, offering scalable, accurate, and accessible solutions for both advanced hospitals and rural clinics.

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