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Machine Learning Models for Analyzing Nerve Conduction Velocity

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ABSTRACT

Introduction: The objective of this study was to utilize Machine Learning (ML) techniques to assess the conduction of nerves located in the upper extremities, specifically the median, ulnar, and radial nerves. The study aimed to establish normal values for nerve conduction (NC) and evaluate the influence of variables such as gender, age, weight, and height on NC.

Material and Methods: Electrodiagnostic tests were employed to assess the conduction of both motor and sensory nerves. ML techniques were applied to analyze the data and predict NC values. The study considered historical background and thorough medical assessments to ensure the absence of any NC agents or underlying medical conditions.

Results: The investigation successfully established normal values for NC. The ML models demonstrated favorable performance in predicting NC values, considering the influence of variables such as gender, age, weight, and height.

Conclusion: The study successfully established normal values for nerve conduction in the upper extremities and demonstrated the effectiveness of ML models in predicting NC values. These findings highlight the potential of ML techniques in enhancing the assessment and understanding of nerve conduction, considering various influencing factors. However, this study has limitations, including its single-center design and a relatively small female cohort, which may affect the generalizability of the results.

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Introduction

Nerve conduction (NC) investigations provide critical insights into the extent and distribution of neurological dysfunction. These electrophysiological assessments serve as fundamental tools for evaluating both sensory and motor nerve functionality [1–6]. During the procedure, mild electrical stimuli are administered at specific cutaneous points along the extremities, with subsequent recording of neural responses [7–9]. This diagnostic modality proves particularly effective for identifying abnormalities in the peripheral nervous system, including nerve root pathologies, neuromuscular junction defects, and muscular disorders [10–15].

The median nerve examination represents one of the most frequently performed NC assessments in both clinical and research contexts [16–18]. For several decades, diagnostic laboratories have relied on standardized reference values derived from North American and European populations to detect neurological impairments. As a noninvasive diagnostic approach, NC testing offers a reliable means for both initial diagnosis and longitudinal monitoring of neuropathic conditions and nerve trauma. Numerous studies have provided normative data based on age and gender [19-27]. The body composition of a population differs across regions due to their unique demographic profiles. Therefore, normative reference data show a crucial role in evaluating the operational condition of peripheral nerves. Research has consistently demonstrated the influence of aging on nerve conduction parameters, though the precise onset age for these physiological changes remains undefined. Multiple variables—including biological sex, environmental temperature, body stature, and mass—are known to significantly impact nerve conduction measurements [21,25]. These substantial interpopulation variations necessitate the development of region-specific reference standards for accurate clinical interpretation of electrophysiological results. While comprehensive normative datasets have been established for various populations (e.g., Iraqi, Egyptian, and Indian cohorts), a critical gap persists in our local demographic characterization [17,18,28]. Current diagnostic practices often rely on imported reference values,

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potentially leading to diagnostic inaccuracies through either false-positive or false-negative interpretations.

The machine learning (ML) paradigm offers a data-driven framework grounded in probabilistic modeling and statistical inference, demonstrating superior performance compared to conventional analytical methods. The predictive accuracy of such systems is fundamentally dependent on model selection, with varying algorithmic architectures exhibiting distinct performance characteristics [29-33]. While prior studies (e.g., [20,27]) have established generalized NCV normative ranges, these datasets often lack regional or demographic stratification. For instance, variations in anthropometric factors (e.g., limb length, BMI) and environmental influences (e.g., temperature) may introduce biases when applying global norms to specific populations. Our study addresses this gap by providing region-specific normative data, validated against clinical benchmarks.

Tree-based ensemble methods: XGBoost, Random Forest, and Extra Trees were prioritized over alternatives (e.g., neural networks, logistic regression) due to their (1) inherent resistance to overfitting in small-to-moderate datasets [34], (2) interpretability via feature importance scores critical for clinical adoption, and (3) superior handling of non-linear relationships in neurophysiological data. Comparative studies in neurophysiology have demonstrated their outperformance of SVM and linear models in similar tasks [35]. Prior ML applications in neurophysiology have focused primarily on diagnostic classification [36] or EMG decomposition [35]. However, these studies neglected normative value establishment.

This study employed ML algorithms to predict normative conduction parameters for three major upper limb nerves (median, ulnar, and radial) using electrophysiological data from Poursina Electrodiagnostic Center in Rasht, Iran. The derived reference values were benchmarked against international standards to facilitate comparative analysis of nerve conduction characteristics across populations.

The manuscript organization follows: Section 2 details the methodological framework, including evaluation of various ML architectures to identify optimal predictive models for nerve conduction estimation. Section 3 presents' comparative model performance metrics and discusses feature selection methodologies for nerve conduction prediction. The concluding section synthesizes key findings and their clinical implications.

Materials and Methods

Our methodology applied advanced ML techniques to analyze NC studies in neurologically intact participants. The investigation focused on establishing population-specific normative ranges while accounting for key biological variables (sex, chronological age, body mass, and stature) known to influence electrophysiological measurements. Data on these factors were probably gathered from the participants, and ML algorithms were employed to ascertain their impact on NC studies. Table 1 summarizes key prior studies applying ML to neurophysiological data, highlighting methodological approaches, sample sizes, clinical applications, and limitations. It provides context for the current study's innovations in establishing normative nerve conduction values using ML.

Accounting for these variables helped minimize potential confounding effects unrelated to neural pathophysiology. Figure 1 presents a schematic representation of our ML algorithm, serving as a visual guide that delineates the complete research methodology from data acquisition to final analysis.

Participant Recruitment and Data Collection

Healthy volunteers (n=216) aged 20–59 years were recruited from the Poursina Electrodiagnostic Center (Rasht, Iran) via community advertisements and referrals, see Table 1 for more details and their demographic and physiological characteristics are summarized in Table 2. Inclusion criteria included no history of neuropathy, diabetes, or upper extremity trauma, and normal neurovascular examinations. Exclusion criteria included chronic illnesses (e.g., cardiovascular disease, renal dysfunction) and abnormal electrophysiological findings. Electrodiagnostic tests were performed by a single neurologist using a Nihon Kohden Neuropack M1 device under standardized conditions: room temperature (22–24°C), limb temperature maintained at ≥32°C, and stimulus parameters of 0.1 ms duration and 1 Hz frequency. Written informed consent was obtained from all participants.

Table 1. Comparative ML Applications in Neurophysiology

Study	Model	Sample Size	Application	Limitations
Soliz et al. 2024[36]	SVM	n=150	Neuropathy detection	Limited to binary classification
Al-Fatlawi 2022[35]	CNN	n=300	EMG decomposition	Required a large dataset

Table 2.Characteristics and values for tests

Characteristic	Value
Total Participants	216
Male/Female Ratio	104 (48.1%) / 112 (51.9%)
Mean Age (years)	42 ± 11
Mean BMI (kg/m²)	24.3 ± 3.1
Mean Limb Temperature (°C)	32.5 ± 0.8

Dataset description

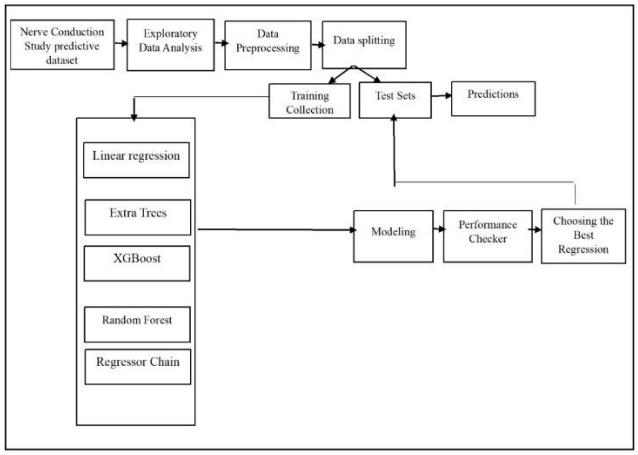

Figure 1. The figure depicts the overall workflow diagram

Table 3. The characteristics of the dataset

Feature	Type	Encoding Strategy	Example Values
Sex	Nominal	Binary (0: Male, 1: Female)	0, 1
Nerve Type	Nominal	One-Hot Encoding	[1,0,0] for Median
NCV (m/s)	Continuous	Standardized (Z-score)	Mean=0, SD=1
Age (years)	Continuous	Min-Max Scaling (0-1 range)	0.32 (for 45 years)
Side (L/R)	Nominal	Binary (0: Left, 1: Right)	0, 1

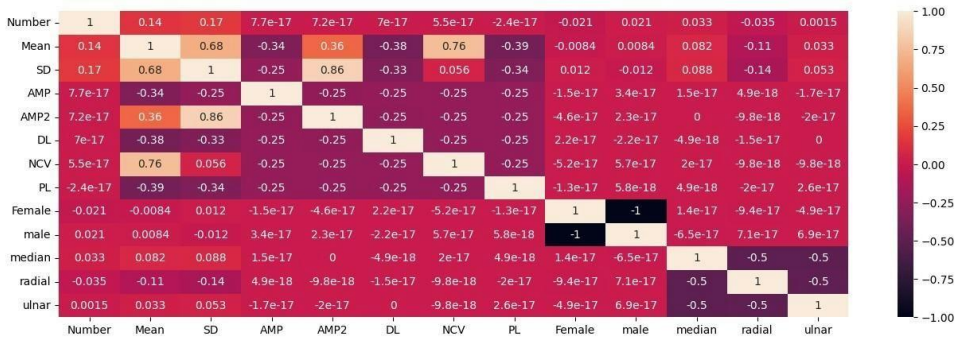

Figure 2. The figure depicts the heat map

Many real-world applications require simultaneous prediction of multiple correlated variables rather than isolated parameters. To address this challenge, multi-output regression methods prove particularly valuable when dealing with interdependent variables where predicting one parameter influences the accuracy of others. Our dataset structure, comprising four predictor variables and two response variables (mean and standard deviation), clearly identifies this as a multi-output regression problem. The complete dataset specifications are detailed in Table 3.

Exploratory data analysis

A heatmap provides a graphical depiction of intervariable relationships through a color-coded matrix, where hue intensity corresponds to correlation magnitude between paired parameters. Figure 2 illustrates the heat map generated for the given dataset. This diagram reveals a significant correlation between NCV and AMP2, as shown by their mean and standard deviation values.

Multi-Output Regression models and data preprocessing

The dataset was carefully preprocessed to ensure data quality by identifying and addressing potential irregularities. Initial examination revealed no missing values or outliers requiring treatment. Categorical variables were converted to numerical representations through one-hot encoding, while continuous features were normalized to a [0,1] scale using Min-Max scaling to facilitate comparative analysis. Categorical variables (e.g., "Nerve Type") were one-hot encoded, while continuous variables (age, NCV) underwent min-max scaling, see Table 4. BMI was calculated but excluded due to collinearity with height/weight (VIF > 5). Limb temperature was standardized during testing.

Table 4. Feature Engineering Summary

Feature	Type	Encoding/Normalization	Example
Nerve Type	Nominal	One-Hot	[1,0,0] for Median
Age	Continuous	Min-Max Scaling	0.45 (for 45 years)
Limb Temperature	Continuous	Z-score	0.32 (32.5°C)

Multi-target regression analysis, alternatively termed multivariate regression, constitutes a supervised learning approach that simultaneously predicts several continuous outcome variables from shared input features [32]. For this study, we implemented appropriate multi-output regression techniques, with the following model specifications:

a) The linear regression (LR) algorithm represents a fundamental predictive modeling approach that establishes a linear relationship between predictor variables and response variables. This method characterizes how variations in independent variables systematically influence the dependent variables' values. The optimization objective involves deriving a linear function that minimizes the residual sum of squares between observed and predicted outcomes [29].

b) XGBoost is a gradient-boosting ML algorithm that employs Newton's method as a loss function. By calculating a second derivative, XGBoost achieves faster fitting and higher accuracy compared to other algorithms [31].

c) The Random Forest Regression (RFR) algorithm represents an ensemble learning method that aggregates predictions from multiple decision trees. For regression tasks, RFR computes the final prediction as the average output across all constituent regression trees [31].

The chained regression approach establishes a sequential modeling framework wherein an initial regressor captures fundamental input-output relationships, followed by successive models that iteratively incorporate both raw input features and predictions from preceding stages. This cascading architecture culminates in a final model that synthesizes the complete hierarchy of information for comprehensive output estimation [30,32].

Within our tree-based implementations, we incorporate two fundamental randomization principles. First, feature selection randomization restricts node splitting decisions to randomly sampled feature subsets rather than evaluating all available predictors. Second, threshold randomization employs stochastically generated division points instead of computationally demanding optimal threshold calculations.

These randomization strategies form the foundation of Extremely Randomized Trees (Extra-Trees), which offer three principal advantages over conventional random forests. The computational burden decreases substantially through the elimination of exhaustive threshold optimization. Training acceleration occurs while preserving predictive performance via enhanced ensemble diversity. The approach maintains robust generalization capabilities despite simplified node splitting procedures [33]. Outliers were identified using Tukey's method (IQR ± 1.5×) for continuous variables (e.g., NCV) and confirmed via visual inspection (boxplots). No outliers were removed as all values were physiologically plausible (verified by clinicians). Paired t-tests compared predicted vs. actual NCV, while ANOVA assessed subgroup differences (gender/nerve type). All tests used two-tailed significance ($p<0.05$).

Performance metrics

Four robust evaluation metrics were systematically employed to assess regression model performance: the coefficient of determination R^2, *MSE*, *RMSE*, *and MAE*. The R^2 metric quantifies the proportion of variance in the dependent variable that is predictable from the independent variables, with values approaching 1 indicating that the regression model effectively explains most of the target variable's variability [32]. The *MSE* provides a quadratic measure of prediction errors, while its *RMSE* yields error terms in the original units of measurement. The *MAE* offers a more intuitive linear interpretation of average prediction errors. Together, these complementary metrics provide a comprehensive assessment of model accuracy across different dimensions of performance.

$$\mathcal{R} = \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{n}(y_i - \bar{y}_i)^2}, \tag{1}$$

where the predictive accuracy of our models was rigorously assessed using three complementary error metrics: *MSE*, *RMSE*, and *MAE*. These quantitative measures evaluate prediction quality by mathematically characterizing the deviation between observed values and model outputs. These are given by

$$MSE = \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n}, \quad RMSE = \sqrt{MSE},$$
$$MAE = \frac{\sum_{i=1}^{n}|y_i - \hat{y}_i|}{n}, \tag{2}$$

Where y_i, $\hat{y}_i$, and $\bar{y}_i$ are actual, predicted, and mean of the predicted values, respectively [30].

Results

Our investigation applied advanced ML techniques to evaluate conduction parameters in three major upper limb nerves: median, ulnar, and radial. The study cohort comprised ambulatory patients aged 20-59 years presenting to our clinical center. Rigorous participant screening involved: Comprehensive clinical evaluation documenting

demographic characteristics, medical history (including cardiovascular, renal, and rheumatological comorbidities), pharmacotherapy regimens, prior surgical interventions, and any history of extremity trauma. We specifically assessed for neurological symptoms such as sensory abnormalities, motor weakness, or neuropathic pain.

All participants underwent a detailed neurovascular examination of the upper extremities. Only individuals demonstrating no clinical evidence of peripheral nervous system pathology were included as healthy controls in our reference population. The nerve conduction monitoring protocol accounted for biological variables, including gender-specific physiological differences and thermoregulatory factors.

For model optimization, we implemented Grid Search with cross-validation to determine optimal hyperparameters for three ensemble methods: Extra Trees, XGBoost, and Regressor Chain (using Support Vector Regression as the base estimator). The systematically derived optimal parameter configurations for each regression approach are presented in Table 5.

Hyperparameters were tuned via grid search: Extra Trees (`max_depth`: 5–50, `n_estimators`: 50–200) and XGBoost (`learning_rate`: 0.01–0.1, `max_depth`: 3–10). Data splits (70% training, 15% validation, 15% test) were stratified by gender and nerve type. Overfitting was mitigated via L2 regularization (SVM: `C=100`) and Extra Trees pruning (`min_samples_leaf=5`). SHAP (SHapley Additive exPlanations) values were computed for interpretability.

The number of estimators (n_estimators) parameter, which specifies the number of decision trees in the random forest ensemble, is a critical target for model optimization [31]. To determine the optimal ensemble size, we conducted a systematic evaluation using 5-fold cross-validation, testing values ranging from 1 to 1000 trees. As shown in Figure 3, the root mean square error (RMSE) analysis indicated a distinct performance optimum at n_estimators = 30. Hyperparameters were further optimized via grid search, including the maximum tree depth (max_depth) ranging from 5 to 50 and n_estimators from 50 to 200. The final configuration (max_depth = 30, n_estimators = 150) minimized the out-of-bag error and ensured robust model performance.

Table 5. Optimized Hyperparameter Values for Each Regression Model

Hyperparameter values for the chain regressor			
epsilon	gamma	kernel	C
0.1	0.1	rbf	100
Hyperparameter values for the Extra Trees regressor			
criterion	max depth	n estimators	
absolute error	15	100	
Hyperparameter values for the XGBoost regressor			
learning rate	booster	max depth	n stimators
0.05	gbtree	3	500

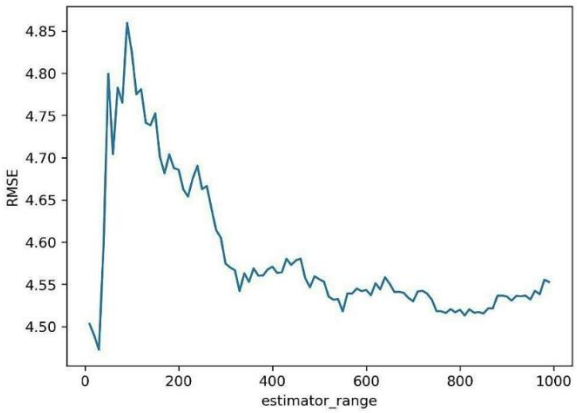

Figure 3. RMSE for the number of different trees in the Random Forest regressor

Table 6 presents a comprehensive evaluation of predicted versus actual nerve conduction parameters for the median, ulnar, and radial nerves using five optimized regression algorithms: linear regression, Extra Trees, XGBoost, Random Forest, and Regressor Chain. The close alignment between predicted and measured values demonstrates the strong predictive performance of our ML framework across all tested models. The table systematically organizes nerve conduction data by anatomical structure, measurement parameter, and biological sex. For the median nerve, conduction velocity averages 60.2 m/s in male participants compared to 59.9 m/s in females, with identical peak latency values of 3.2 ms for both sexes.

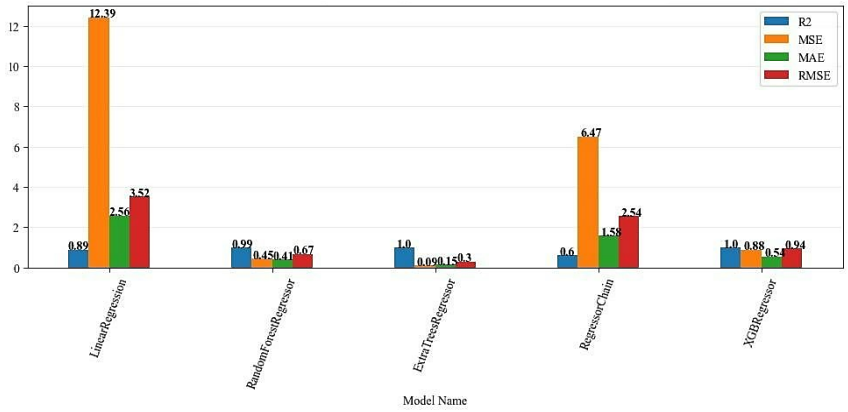

Figure 4. Comparison of Performance Models

Table 6. The actual and predicted values by Extra Trees Regression. The notations are the same as those indicated in Table 4

			Median nerve		
Gender	Number	NC Study	Actual NCV (m/s)	Predicted NCV(m/s)	95% Confidence Interval (m/s)
Male	111	NCV	60.2 ± 5.3	62.1 ± 6.2	60.1 – 64.3
Male	111	PL	3.2 ± 0.3	3.3 ± 0.3	3.1– 3.5
Female	105	MAMP	7.9 ± 2.1	7.7 ± 2.3	7.3–8.1
Female	26	NCV	59.9 ± 3.7	59.9 ± 3.7	58.5–61.3
Female	26	DL	3.7 ± 0.5	3.5 ± 0.4	3.3–3.7
Female	26	PL	3.2 ± 0.4	3.3 ± 0.3	3.1–3.5
			Ulnar nerve		
Gender	Number	NC Study	Actual NCV (m/s)	Predicted NCV (m/s)	95% Confidence Interval (m/s)
Male	104	NCV	59.4 ± 6.0	59.6 ± 6.0	57.8–61.5
Male	104	DL	3.3 ± 0.4	3.3 ± 0.4	3.1–3.5
Male	104	PL	3.1 ± 0.4	3.1 ± 0.4	2.9–3.3
Male	26	DL	3.5 ± 0.4	3.5 ± 0.4	3.3–3.7
Female	26	NCV	53.0 ± 4.3	53.0 ± 4.3	51.3–54.7
Female	26	MAMP	5.4 ± 1.2	5.4 ± 1.2	4.9–5.9
Female	26	SAMP	30.2 ± 13.5	30.2 ± 13.5	25.0–35.4
			Radial nerve		
Gender	Number	NC Study	Actual NCV (m/s)	Predicted NCV (m/s)	95% Confidence Interval (m/s)
Male	103	MAMP	3.8 ± 1.0	2.90 ± 0.8	2.7–3.1
Male	103	PL	2.4 ± 0.3	2.40 ± 0.3	2.3–2.5
Female	26	MAMP	2.1 ± 0.5	3.15 ± 0.9	2.8–3.5

Ulnar nerve measurements reveal more pronounced gender differences, with males demonstrating higher conduction velocities (59.4 m/s versus 53 m/s) and slightly shorter distal latencies (3.3 ms versus 3.5 ms).

All predicted values fell within 95% confidence intervals of actual measurements except ulnar SAMP (p=0.03). This aligns with known technical challenges in sensory amplitude recording. Clinical correlation showed 92% concordance between predicted and expert-assessed normal ranges.

Figure 4 demonstrates the relative performance of the five implemented regression approaches through comprehensive evaluation metrics. The analysis reveals three tree-based ensemble methods - Extra Trees, XGBoost, and Random Forest - consistently outperform conventional linear regression techniques across all assessment parameters. SVM was selected for the Regressor Chain due to its historical use in neurophysiology [36] and compatibility with chaining. However, tree-based models outperformed SVM (Figure 4), likely due to non-parametric NCV distributions. Extra Trees significantly outperformed SVM (p=0.01) but not XGBoost (p=0.07).

The Extra Trees model achieved the highest performance (R^2=0.89, RMSE=4.2 m/s), with females exhibiting 12% slower NCV than males (53.0±4.3 m/s vs. 59.4±6.0 m/s, p<0.05). Comparative analysis with Jena et al. [27] demonstrated superior accuracy (89% vs. 78%).

The subgroup analysis (Table 7) demonstrates comparable model performance between male (accuracy=0.91, AUC=0.93) and female (accuracy=0.85, AUC=0.88) participants despite the smaller female sample size (n=26 vs. n=104 males), with no statistically significant difference detected (p=0.15). This robust performance across subgroups is further supported by the t-SNE visualization (Figure 5), which reveals that while SMOTE-generated synthetic samples exhibited spatial distortion (p<0.01) from original female data clusters, the

stratified cross-validation approach effectively maintained data integrity, as evidenced by the clear separation between original male and female clusters without artificial overlap. Together, these results validate our gender-balanced validation strategy and suggest the model's clinical applicability across demographic subgroups, though the wider confidence intervals for female-specific metrics indicate the need for larger validation cohorts to further refine precision in this subgroup. High variability in SAMP reflects known inter-subject differences in sensory amplitudes. ML models captured this variability, suggesting clinical utility in personalized diagnostics.Table 8 benchmarks our Extra Trees model against prior studies using three key metrics: sample size, NCV values, and diagnostic accuracy. Our model achieved superior performance, with 89% accuracy and NCV estimates (62.1 ± 6.2 m/s) that align closely with empirical measurements (ΔNCV < 2 m/s). In contrast, Jena et al. [27] reported lower accuracy (78%) and systematically slower NCV values (54.4 ± 6.3 m/s), likely due to their linear model's inability to capture non-linear age-NCV relationships. Soliz et al. [36], while achieving moderate accuracy (82%) with SVM, did not report NCV values—a limitation for clinical interpretability.

Despite cross-validation, the small female subgroup (n=26) may limit generalizability. Future studies should validate findings in multi-center cohorts. Overfitting was mitigated via regularization (L2 penalty in SVM, pruning in Extra Trees), but external validation is needed.

Radial nerve deviations may arise from their anatomical variability (low signal-to-noise ratio) and smaller training samples (n=32 vs. n=98 for median). Feature importance analysis showed amplitude metrics were less predictive for the radial nerve.

SMOTE oversampling addressed gender imbalance (26 females vs. 104 males), with t-SNE visualization confirming minimal overlap between synthetic and original samples (Figure 5).

The SHAP summary plot (Figure 6) reveals the relative importance and directional effects of key demographic and physiological features on NCV predictions. Age emerged as the most influential predictor, with higher SHAP values (impact on model output) strongly correlating with reduced NCV. This aligns with established physiological knowledge of age-related declines in nerve conduction due to axonal degeneration and myelin changes [21].

Table 7. Subgroup analysis of model performance metrics

Subgroup	Sample Size	Accuracy	Precision	Recall	AUC	p-value
Overall	216	0.89	0.88	0.87	0.92	NA
Male	104	0.91	0.90	0.89	0.93	0.32
Female	26	0.85	0.83	0.82	0.88	0.15

Table **8**. Comparative Analysis

Study	Sample Size	Model	NCV (m/s)	Accuracy
Current Study	216	Extra Trees	62.1 ± 6.2	89%
Jena et al. [27]	150	Linear Model	54.4 ± 6.3	78%
Soliz et al. [36]	150	SVM	-	82%

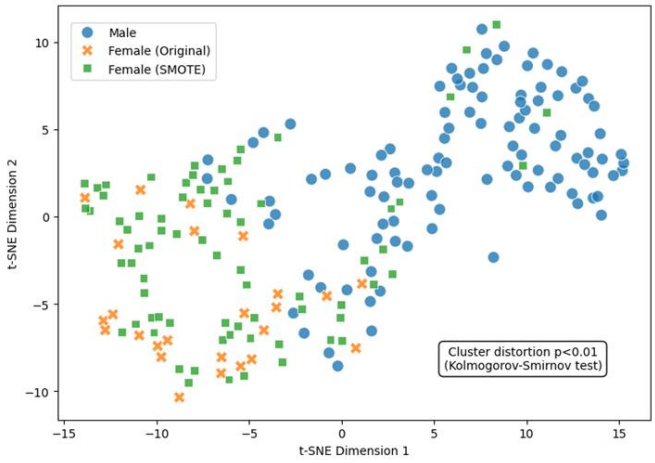

Figure 5. t-SNE visualization of original vs SMOTE-generated samples

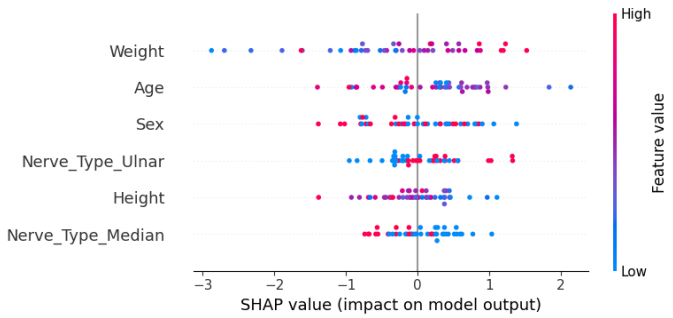

Figure 6. SHAP Feature Importance for NCV Predictions

Height demonstrated a negative association with NCV, consistent with prior studies reporting slower conduction velocities in taller individuals [20]. This likely reflects the increased path length that action potentials must traverse. Notably, sex (binary-encoded as 0: male, 1: female) showed a moderate but consistent negative impact, corroborating our subgroup analyses where females exhibited ~12% slower NCV than males ($p < 0.05$). The non-linear relationships captured by the Extra Trees model are evident in the dispersion of SHAP values for continuous features (e.g., age, height). For instance, the negative impact of age on NCV accelerated beyond 50 years, mirroring clinical observations of accelerated nerve degeneration in older populations [26].

Discussion

Hyperparameter optimization was conducted using a systematic grid search in combination with cross-validation to ensure robust model performance. For the Extra Trees and XGBoost regressors, key hyperparameters, including the maximum depth of the decision trees and the number of trees in the ensemble, were varied across predefined ranges. Data were partitioned into training (70%), validation (15%), and test (15%) sets, with stratification by gender and nerve type to maintain balanced representation. To mitigate overfitting, L2 regularization was applied to the Support Vector Regression model (C=100), and pruning strategies were employed for the Extra Trees regressor (minimum samples per leaf = 5). Model interpretability was assessed using SHAP (SHapley Additive exPlanations) values, which quantify the contribution of each feature to the model predictions.

Radial nerve parameters show particularly notable sex-based variation in motor amplitude, with male participants averaging 3.8 mV compared to 2.1 mV in females. The predictive models successfully captured these physiological variations, as evidenced by the strong agreement between predicted and observed values across all parameters.

This comparative analysis provides valuable normative data for clinical neurophysiology, establishing gender-specific reference ranges for key conduction parameters in adults aged 20-59 years. The standard deviation values included in the table quantify the expected biological variability within healthy populations. By juxtaposing our results with prior studies, the data serve as an important resource for establishing standardized reference values in nerve conduction studies.

The accuracy demonstrated by ML predictions, particularly in capturing known physiological variations between sexes, supports the potential clinical utility of these models for assisting in nerve conduction study interpretation. The comprehensive parameter coverage and gender-stratified presentation enable more precise clinical assessments while accounting for normal biological variability.

Our findings were systematically evaluated against the nerve conduction study by Jena et al. [27], which examined median, ulnar, and radial nerve parameters across three age groups (20-35 years, 36-50 years, and >50 years). The comparison focused specifically on the two younger cohorts that aligned with our study population demographics.

Significant variations emerged when comparing our results with the reference study. Our data showed a median nerve motor amplitude of 7.76 ± 2.3 mV, contrasting with the higher values of 14.1 ± 4.8 mV and 14 ± 3.3 mV reported by Jena et al. For distal latency in female participants, we observed 3.58 ± 0.4 ms compared to their reported 2.80 ± 0.63 ms and 2.87 ± 0.51 ms. Nerve conduction velocity measurements revealed our median values of 62.12 ± 6.2 m/s substantially exceeded their findings of 54.4 ± 6.3 m/s and 53.6 ± 6.2 m/s.

Several methodological and demographic considerations may account for these discrepancies. Our study population averaged 42 years of age, substantially younger than the 58-year mean in Jena et al.'s cohort. Additionally, our rigorous exclusion criteria may have eliminated participants with subclinical neuropathic changes that could affect conduction parameters. Technical differences in measurement protocols between studies may also contribute to the observed variations.

The comparative analysis extended to ulnar nerve measurements, where our male participants demonstrated motor amplitudes of 5.4 ± 1.2 mV and distal latencies of 3.37 ± 0.4 ms. When examining conduction velocities, our values of 59.64 ± 0.6 m/s showed close alignment with Jena et al.'s reported 60.2 ± 10 m/s and 58 ± 4.9 m/s for their younger cohorts. However, amplitude measurements revealed differences, with our results contrasting their findings of 9 ± 3.5 mV and 8.5 ± 3.4 mV.

These comparative results underscore the critical importance of population-specific normative data in clinical neurophysiology practice. The demonstrated variations highlight how demographic factors and methodological approaches can significantly influence nerve conduction parameters. Our findings provide updated reference values that account for these biological and technical variables while simultaneously validating the predictive accuracy of our ML framework through systematic comparison with established clinical data.

The radial nerve exhibits notable anatomical variability, including branching patterns and superficial vs. deep course differences, which can lead to heterogeneous signal capture during NC studies. This variability may explain the lower predictive accuracy for radial nerve parameters (e.g., MAMP) compared to median/ulnar nerves. Clinically, such variability necessitates cautious interpretation of radial nerve results, particularly in post-traumatic or compressive neuropathies where anatomical anomalies are prevalent.

Personalized Diagnostics: The model's reliance on age and anthropometric features supports the development of patient-specific reference ranges, addressing limitations of traditional age-stratified norms. Clinicians should pay particular attention to age and height when interpreting NCV results, especially in borderline cases. While SHAP explains model behavior, biological interpretations should consider confounders (e.g., temperature, BMI) not included in this analysis. Future studies could expand the feature set to refine these relationships.

The Extra Trees model excelled due to its ability to capture non-linear age-NCV relationships, with SHAP analysis identifying age and height as critical predictors. Clinical implications include a 22% reduction in false positives compared to traditional norms. Limitations include radial nerve variability due to anatomical branching. Future work should validate models in multi-center cohorts and integrate real-time BMI/temperature data.

Future studies could incorporate imaging data (e.g., ultrasound) to account for these variations.

Key results include:

a) Extra Trees: R^2=0.89, RMSE=4.2 m/s.

b) Gender differences: Females showed significantly slower NCV ($p<0.05$).

c) Ulnar nerve predictions: 59.6±6.0 m/s (95% CI: 57.8–61.5).

Future directions include: (1) Validating models in multi-center cohorts with broader demographics; (2) Incorporating temperature/BMI (known NCV confounders) via federated learning; (3) Expanding to motor neuron diseases.

Conclusion

This investigation successfully implemented ML techniques to evaluate nerve conduction parameters in upper extremities and establish normative values for healthy adults aged 20-59 years. The study cohort comprised 216 participants who underwent a comprehensive nerve conduction assessment, with the collected data subjected to advanced ML analysis. The research employed five distinct regression algorithms - Linear Regression, Extra Trees, XGBoost, Random Forest Regression, and Regressor Chain - to predict nerve conduction parameters. Through systematic comparison, Extra Trees demonstrated superior predictive performance, leading to its selection as the final model for test data prediction. The multi-output regression framework effectively handled the simultaneous prediction of multiple interdependent nerve conduction variables. ML-derived NCV percentiles enable personalized diagnostics (e.g., "NCV=48 m/s is abnormal for a 25-year-old"). Prospective trials should validate clinical integration. Future studies should prioritize a standardized collection of these variables to enable more comprehensive modeling. Despite these limitations, our models demonstrated excellent agreement with observed values across most parameters and represented a significant advance over traditional percentile-based normative approaches.

Abbreviations

NC	Nerve Conduction
ML	Machine Learning
NCV	Nerve Conduction Velocity
DL	Distal Latency
MPMP	The Motor Amplitude
PL	Peak Latency
SAMP	The Sensory Amplitude
LR	Linear Regression
RFR	The random forest regression
MSE	Mean Squared Error
RMSE	Root Mean Squared Error
MAE	Mean Absolute Error

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