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ENHANCING EARLY PARKINSON'S DISEASE DIAGNOSIS THROUGH HANDWRITING ANALYSIS

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Abstract. *Parkinson's disease (PD) is a progressive neurological disorder that affects millions worldwide, leading to motor dysfunction and significant reductions in quality of life. Early diagnosis is pivotal for initiating timely treatment and improving long-term patient outcomes, yet existing diagnostic methods, which often rely on clinical evaluations and imaging, are prone to delays and varying accuracy. This study presents an innovative, non-invasive approach to early PD detection through the analysis of handwriting patterns, offering a potential alternative to traditional diagnostic techniques. Leveraging a publicly available and meticulously normalized handwriting dataset, our approach applies advanced data processing methods to identify subtle neuromotor impairments associated with PD. Through the integration of robust feature selection processes and cutting-edge machine learning models, we achieved a high accuracy rate of 83.02%, highlighting the method's reliability. The findings suggest that this approach could significantly enhance early PD detection, leading to more personalized therapeutic strategies that align with the stages of disease progression and potentially delaying the onset of severe symptoms.*

Keywords: Parkinson's disease, handwriting analysis, feature selection, machine learning, early diagnosis

POPRAWA WCZESNEJ DIAGNOSTYKI CHOROBY PARKINSONA POPRZEZ ANALIZĘ PISMA RĘCZNEGO

Streszczenie. *Choroba Parkinsona (PD) jest postępującą chorobą neurologiczną, która dotyka miliony ludzi na całym świecie, prowadząc do zaburzeń motorycznych i znacznego obniżenia jakości życia. Wczesna diagnoza ma kluczowe znaczenie dla rozpoczęcia leczenia w odpowiednim czasie i poprawy długoterminowych wyników leczenia pacjentów, jednak istniejące metody diagnostyczne, które często opierają się na ocenach klinicznych i obrazowaniu, są podatne na opóźnienia i różną dokładność. W niniejszym badaniu przedstawiono innowacyjne, nieinwazyjne podejście do wczesnego wykrywania PD poprzez analizę wzorców pisma ręcznego, które stanowi potencjalną alternatywę dla tradycyjnych technik diagnostycznych. Wykorzystując publicznie dostępny i skrupulatnie znormalizowany zbiór danych dotyczących pisma ręcznego, w naszym podejściu zastosowano zaawansowane metody przetwarzania danych w celu identyfikacji subtelnych zaburzeń neuromotorycznych związanych z PD. Dzięki integracji solidnych procesów selekcji cech i najnowocześniejszych modeli uczenia maszynowego osiągnęliśmy wysoką dokładność wynoszącą 83,02%, co podkreśla niezawodność tej metody. Wyniki sugerują, że podejście to może znacznie poprawić wczesne wykrywanie PD, prowadząc do bardziej spersonalizowanych strategii terapeutycznych dostosowanych do etapów postępu choroby i potencjalnie opóźniających wystąpienie poważnych objawów.*

Słowa kluczowe: choroba Parkinsona, analiza pisma ręcznego, selekcja cech, uczenie maszynowe, wczesna diagnoza

Introduction

Parkinson's disease (PD) is a severe neurodegenerative disorder affecting millions of people worldwide, characterized by progressive degeneration of dopaminergic neurons in the substantia nigra pars compacta of the brain [3, 12, 14, 28]. PD manifests with motor symptoms such as tremor, rigidity, bradykinesia, and postural instability, as well as non-motor symptoms such as cognitive impairment [31]. With an aging global population and increasing life expectancy, the prevalence of PD is expected to increase significantly, posing a significant challenge to healthcare systems worldwide [20]. Timely diagnosis of PD is crucial for initiating treatments promptly, which can alleviate symptoms, improve quality of life, and potentially slow disease progression [1, 6, 18, 26]. However, current diagnostic methods, primarily clinical assessments and imaging techniques, often struggle to accurately detect PD in its early stages [11]. These methods may lack sensitivity and specificity, resulting in diagnostic delays, misdiagnosis, and suboptimal patient care [10]. Due to the limitations of existing diagnostic techniques, there is growing interest in alternative approaches to enhance early PD detection. One promising method is handwriting analysis, a non-invasive tool capable of identifying subtle motor impairments associated with PD [25]. Handwriting involves intricate coordination of cognitive, motor, and sensory functions, making it a potentially sensitive indicator of early motor dysfunction [2]. By analyzing handwriting features such as velocity, pressure, and stroke duration, researchers aim to develop robust algorithms capable of distinguishing PD patients from healthy individuals [4]. This study explores the potential of handwriting analysis to improve early PD diagnosis. By critically assessing current diagnostic limitations and highlighting the importance of early detection, we underscore the need for innovative approaches in PD diagnostics. Through a thorough exploration of the rationale behind using handwriting analysis as a diagnostic tool, we aim to demonstrate its potential as a complementary method for early PD detection. Leveraging advanced data analysis techniques and machine learning algorithms, our research seeks to refine handwriting analysis methodologies for enhanced diagnostic accuracy and efficacy in early PD detection.

Previous research extensively examines the use of handwriting analysis as a diagnostic tool for Parkinson's disease, analyzing various handwriting features to identify distinct patterns associated with PD symptoms [8]. For example, Smith et al. [7] conducted a comprehensive review of existing literature on handwriting analysis for PD diagnosis, synthesizing findings from multiple studies and discussing the strengths and limitations of different approaches. Handwriting analysis offers several advantages as a non-invasive method for PD diagnosis, demonstrating its potential to detect subtle motor impairments in PD patients, even in the early stages of the disease. Additionally, handwriting analysis can be easily integrated into routine clinical assessments, providing a cost-effective and accessible diagnostic tool [24]. The use of machine learning algorithms has enabled researchers to develop predictive models based on handwriting features, enhancing diagnostic accuracy [19]. Despite these strengths, handwriting analysis for PD diagnosis also presents certain challenges. One significant issue is the variability in handwriting patterns among individuals, which can complicate the identification of specific markers associated with PD [5]. Factors such as age, gender, and education level can influence handwriting characteristics, necessitating careful consideration in diagnostic algorithms [30]. Moreover, the lack of standardized protocols for handwriting analysis poses challenges for reproducibility and generalization of findings across different studies [4, 7]. Further research is essential to advance handwriting analysis for PD detection. Larger, more diverse datasets are needed to train and validate machine learning models, ensuring their robustness and applicability [9]. Longitudinal studies are crucial to monitor handwriting changes over time and their correlation with disease progression [12, 27]. Exploring novel technologies, such as digital pens and tablet-

based assessments, may further improve the sensitivity and specificity of handwriting analysis for PD diagnosis [14]. Addressing these research gaps will contribute to the development of more effective and reliable methods for early PD detection using handwriting analysis.

The paper is structured as follows: the first section presents the introduction. The second section explores the dataset and methodology employed. The third section presents the results, the fourth section covers the discussion, followed by a summary of conclusions in the fifth section.

1. Dataset and methodology

1.1. Dataset description

For our study, we used the NewHandPD dataset, a detailed collection of handwriting samples created specifically for Parkinson's disease (PD) research. This dataset is publicly available from the Botucatu Medical School, affiliated with the State University of São Paulo in Brazil. The handwriting samples were collected at this medical school, where participants were asked to fill out a form containing four spirals and four meanders. The dataset consists of two groups: (i) the healthy group and (ii) the patient group, which includes individuals diagnosed with Parkinson's disease (PD). It contains handwriting samples from 66 participants, 35 in the Healthy Group and 31 in the Patient Group [22, 23].

The dataset is structured as a CSV file comprising 16 columns and 265 rows, containing extracted features from images of spirals and meanders. The characteristics of these features are elaborated in table 1.

Table 1. Features of the NewHandPD dataset [21]

feature name	description
ID_EXAM	Unique identifier for the handwriting examination
IMAGE_NAME	Filename of the image
ID_PATIENT	Unique identifier for the patient
CLASS_TYPE	Classification type: 1 for control group, 2 for patient group
GENDER	Gender: M for male, F for female
RIGH/LEFT-HANDED	Handedness: R for right-handed, L for left-handed
AGE	Age of the individual
RMS	Root Mean Square, calculated as described in Equation 3 of the referenced paper [24]
MAX_BETWEEN_ET_HT	Maximum difference in radius between the Exam Template (ET) and the Handwritten Trace (HT), based on Equation 4 of the referenced paper [24]
MIN_BETWEEN_ET_HT	Minimum difference in radius between the ET and HT, based on Equation 5 of the referenced paper [24]
STD_DEVIATION_ET_HT	Standard deviation of the radius difference between ET and HT
MRT	Mean Relative Tremor
MAX_HT	Maximum radius of the HT
MIN_HT	Minimum radius of the HT
STD_HT	Standard deviation of the HT radius
CHANGES_FROM_NEGATIVE_ TO_POSITIVE_BETWEEN_ET_HT	Count of times the radius difference between ET and HT switches from negative to positive or vice versa

1.2. Methodology

The methodology section outlines the steps followed to analyze the NewHandPD dataset, from data preprocessing to model evaluation.

1.2.1. Data preprocessing

The preprocessing phase included the following steps:

- Data Cleaning: This step involved removing any incomplete or corrupted samples to ensure data quality and integrity. Incomplete data can introduce biases and inaccuracies in the analysis, so only complete and valid samples were retained.
- Normalization: Handwriting samples were normalized to a consistent scale to remove variability due to different writing instruments, paper sizes, and individual writing styles. Normalization ensures that the features extracted from the handwriting samples are comparable across all participants, facilitating accurate analysis.
- Feature Extraction: Although feature extraction was initially performed by the dataset creators, ensuring that the dataset includes relevant features such as Root Mean Square (RMS), Mean Relative Tremor (MRT), and the minimum difference between HT and ET radius, these features were verified and standardized during preprocessing.

1.2.2. Feature selection methods

Feature ranking serves as a crucial preprocessing technique aimed at identifying significant features within a dataset. Utilizing an optimal feature selection method presents two primary advantages: it reduces data dimensionality and improves model performance. In this study, we employ four feature ranking methods, leading to the selection of 4 features out of a total of 16. Below, we elaborate on the feature ranking methods integrated into our proposed system.

Correlation analysis: This method evaluates the relationship intensity and direction between each feature and the target variable, which in this study is the health status. Correlation coefficients help in understanding the dependencies among variables and their influence on the outcome, as noted in earlier research [1].

Analysis of Variance (ANOVA): ANOVA was used to identify features that show significant variation between groups, specifically PD patients and healthy controls. This method enables the identification of statistically significant differences in the means of independent groups, as documented in the literature [17].

LASSO regression: The Least Absolute Shrinkage and Selection Operator (LASSO) regression method was employed to select a subset of features by applying a penalty proportional to the absolute value of the coefficients. This technique effectively mitigates overfitting by shrinking less important feature coefficients to zero, as highlighted in previous studies [29].

Principal Component Analysis (PCA): Linear PCA was applied to transform the original features into a smaller set of uncorrelated components. This method reduces dimensionality while preserving as much variance as possible, facilitating the selection of key features that contribute significantly to the overall variance in the dataset.

1.2.3. Machine learning algorithms

To evaluate the effect of feature selection, we compared the performance of three classifiers using both the full feature set and various reduced subsets. The characteristics of these classifiers in our methodology are as follows:

Support Vector Machine (SVM): is a powerful supervised learning algorithm used for classification and regression tasks. Its main strength lies in identifying a hyperplane that optimally separates different classes in the data set. This hyperplane is determined by maximizing the margin, which is the distance between the hyperplane and the nearest data points (support vectors) from each class. In many real-world scenarios, data is not perfectly separable by a linear hyperplane in lower dimensions. To deal with this, SVMs use the kernel trick, which transforms the data into a higher-dimensional space where the separation becomes clearer. For this study, we used the sigmoid function as the kernel function for SVM .

Random Forest (RF): is a versatile supervised learning algorithm that can handle both regression and classification tasks. It employs ensemble learning by constructing a large number of decision trees based on different subsets of data. Each tree provides its prediction, and the final output is derived by either majority voting (for classification) or averaging (for regression).

This method reduces the reliance on any single tree, resulting in more accurate and robust models. Increasing the number of trees typically improves accuracy and reduces the risk of overfitting, which occurs when a model performs well on training data but poorly on unseen data. Random forests mitigate overfitting by introducing diversity through multiple trees and different training subsets [16].

Naïve Bayes (NB): NB is a popular classification algorithm that uses Bayes' theorem to predict class labels. It is favored for its simplicity and efficiency and is used in various applications such as spam filtering, document classification, and disease diagnosis. The core assumption of NB is class conditional independence, meaning that the presence of a particular feature in a class is independent of other features. NB computes the posterior probability, P(m|n), which is the probability that an object with feature 'n' belongs to class 'm'. This is computed using Bayes' theorem, where P(n|m) is the probability of features 'n' given class 'm', P(m) is the prior probability of class 'm', and P(n) is the total probability of features 'n' [15]. This is done using the following equation:

$$P(m|n) = \frac{P(n|m)*P(m)}{P(n)} \quad (1)$$

Here, P(n|m) signifies the probability of features 'n' being associated with class 'm'. P(m) represents the prior probability of class 'm' existing even without considering the features. Finally, P(n) denotes the prior probability of the features 'n' appearing in general, regardless of the class [13].

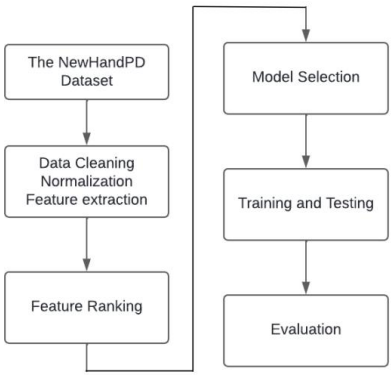

Fig. 1. Flowchart of the NewHandPD dataset processing and analysis pipeline

1.2.4. Experimental setup

The experimental setup was carefully designed to thoroughly evaluate the performance of the classification models:

Training and testing data splits: The data set was divided into training and testing sets, with 80% allocated to training and 20% to testing. To maintain the class distribution within each subset, stratified sampling was used to ensure proportional representation of both PD patients and healthy individuals. In addition, stratified 5-fold cross-validation was used to validate the models. This technique involves dividing the data into 5 equal parts (folds). Each fold serves as a validation set once, while the remaining four are used for training. This rotation ensures that every data point is used in both training and validation, increasing the robustness of the model evaluation.

Evaluation metrics: Several metrics were utilized to thoroughly assess the performance of the models, offering a detailed understanding of their strengths and weaknesses:

- Accuracy: This reflects the overall correctness of predictions

$$Accuracy = \frac{Correct\ Predictions}{Total\ Predections} \quad (2)$$

- Precision (Positive Predictive Value – PPV): Precision evaluates the relevance of positive predictions by determining the ratio of true positives (correctly identified positive cases) to all predicted positive cases.

$$Precision = \frac{True\ Positives}{Total\ Predictions} \quad (3)$$

- Sensitivity (Recall): is also known as True Positive Rate (TPR). This metric assesses the model's ability to accurately identify true positives, representing the proportion of actual positive cases correctly predicted as positive.

$$Recall = \frac{True\ Positives}{Total\ actual\ Positives\ cases} \quad (4)$$

- F1_Score: is a metric that combines precision and recall into a single value, thereby providing a balanced view of the classifier's performance. The harmonic mean of precision and recall is a metric that penalizes significant disparities between these metrics.

$$F1\_Score = \frac{2*Recall*Precision}{Recall+Precision} \quad (5)$$

Parameter tuning: Hyperparameter tuning was conducted using grid search and randomized search methods to identify the optimal parameters for each classification algorithm. This step was crucial for enhancing the model's performance and ensuring the generalizability of the results.

2. Results

The findings of this study provide a comprehensive analysis of the effectiveness of handwriting features in distinguishing between individuals with Parkinson's Disease (PD) and healthy controls. By employing various feature selection methods and classification models, the results demonstrate the significant role of specific kinematic and dynamic handwriting characteristics in early PD diagnosis. The subsequent tables and figures detail the performance of these methods, highlighting the accuracy, precision, recall, and F1 scores achieved across different tasks and classifiers. These outcomes offer valuable insights into the potential of handwriting analysis as a diagnostic tool in clinical settings.

Table 2. Feature selection results for spiral and meander tasks

task	feature ranking method	features selected	feature name
Spiral	Correlation	4	STD_HT, RMS, MRT, CHANGES_FROM_NEGATIVE_ TO_POSITIVE_BETWEEN_ET_HT
	ANOVA	4	STD_HT, RMS, MRT, CHANGES_FROM_NEGATIVE_ TO_POSITIVE_BETWEEN_ET_HT
	LASSO Regression	4	STD_HT, RMS, MAX_BETWEEN_ET_HT, MIN_BETWEEN_ET_HT
	Linear PCA	4	RMS, MAX_BETWEEN_ET_HT, MIN_BETWEEN_ET_HT, STD_DEVIATION_ET_HT
Meander	Correlation	4	MRT, STD_HT, MAX_BETWEEN_ET_HT, RMS
	ANOVA	4	MRT, STD_HT, MAX_BETWEEN_ET_HT, RMS
	LASSO Regression	4	MRT, STD_HT, RMS, MAX_BETWEEN_ET_HT
	Linear PCA	4	RMS, MAX_BETWEEN_ET_HT, MIN_BETWEEN_ET_HT, STD_DEVIATION_ET_HT

Table 3. Performance metrics for different classifiers

classifier	task	features	accuracy	precision	recall	F1-score
SVM	spiral	Selected by Linear PCA	72.33%	76.15%	72.33%	72.24%
	meander	All features	67.92%	80.60%	67.92%	64.50%
RF	spiral	Selected by Linear PCA	83.02%	83.31%	83.02%	83.08%
	meander	Selected by ANOVA	73.58%	66.67%	92.31%	77.42%
NB	spiral	Selected by Linear PCA	69.81%	76.49%	69.81%	69.25%
	meander	Selected by ANOVA	62.26%	57.14%	92.31%	70.59%

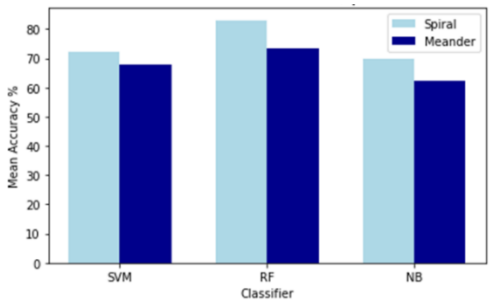

Fig. 2. Mean accuracies for different classifiers (spiral and meander)

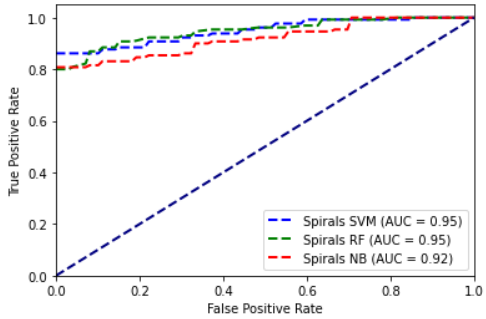

Fig. 3. Average ROC curves for spirals

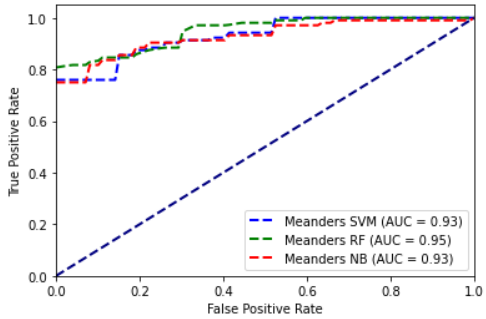

Fig. 4. Average ROC curves for meanders

3. Discussion

The results from the feature selection methods (table 2) and classifier performance metrics (table 3) provide a comprehensive understanding of the effectiveness of handwriting analysis in early Parkinson's disease (PD) diagnosis. This analysis is particularly relevant when comparing spiral and meander tasks.

3.1. Feature selection and importance

The feature selection methods yielded consistent results, with features such as Standard Deviation of Handwriting Task (STD_HT), Root Mean Square (RMS), and Mean Response Time (MRT) being highlighted across Correlation, ANOVA, and LASSO regression methods. These features are crucial as they capture the variability and dynamic aspects of handwriting that are indicative of motor dysfunction in early PD.

The fact that different feature selection methods – ranging from simple statistical methods like Correlation and ANOVA to more sophisticated approaches like LASSO regression and Linear PCA – selected overlapping features suggests that these features are robust indicators of the underlying motor dysfunctions associated with early PD. For instance, RMS and STD_HT are related to the consistency and variability of handwriting pressure and speed, which can reflect the subtle motor impairments characteristic of the disease. The dynamic features, particularly those related to extrema points (e.g., MAX_BETWEEN_ET_HT and MIN_BETWEEN_ET_HT), are likely critical in distinguishing between healthy individuals and those with early PD.

Furthermore, the consistent selection of these features across tasks (spiral and meander) reinforces the notion that these motor dysfunctions are not task-specific but rather represent generalized motor impairments that can be detected through various handwriting tasks.

3.2. Classifier performance

The performance metrics of the classifiers, as shown in table 3, reveal that the Random Forest (RF) classifier outperformed the Support Vector Machine (SVM) and Naive Bayes (NB) classifiers across both tasks. The RF classifier's highest accuracy of 83.02% for the spiral task, using features selected by Linear PCA, underscores the effectiveness of this method in handling the complex interactions between the selected features. This finding is significant as it suggests that RF's ensemble learning approach is particularly well-suited for early PD detection through handwriting analysis.

The SVM classifier, with its strong performance in high-dimensional spaces, achieved an accuracy of 72.33% for the spiral task and 67.92% for the meander task. Although these results are lower than those achieved by RF, they still demonstrate that SVM can be a viable option, particularly if further optimization of hyperparameters or the use of alternative kernel functions is explored.

The NB classifier, while being computationally efficient, showed the lowest performance, especially in the meander task, where it achieved an accuracy of only 62.26%. This lower performance might be due to the assumption of feature independence in NB, which may not hold true for the complex, interrelated features derived from handwriting analysis.

3.3. ROC curve analysis and additional insights

The ROC curve analysis, depicted in Fig. 3 and 4, further validates the superior performance of the RF classifier. The high area under the curve (AUC) values (0.95 for both spiral and meander tasks) indicate that RF consistently achieves a high true positive rate while maintaining a low false positive rate. This is crucial in clinical settings where false positives can lead to unnecessary anxiety and further tests for patients.

Interestingly, despite the lower overall accuracy, the NB classifier still demonstrated respectable AUC values (0.92 for spiral and 0.93 for meander), particularly in the context of the meander task. This suggests that NB might still be useful in specific contexts, especially when used as part of an ensemble method where its strengths can complement those of other classifiers.

An additional insight from this analysis is the potential role of hybrid models. Combining the strengths of RF's robust performance and SVM's adaptability to complex feature spaces could lead to even more accurate diagnostic tools. Exploring ensemble methods that incorporate these classifiers, or even integrating deep learning models, could further enhance early PD detection.

Moreover, the consistent selection of features across different tasks and methods suggests that these features could be used to develop a standardized set of diagnostic criteria for early PD. This could facilitate the development of automated diagnostic tools that are both accurate and generalizable across different patient populations and handwriting tasks.

4. Conclusion

This study demonstrates the potential of handwriting analysis as a powerful, non-invasive tool for enhancing early Parkinson's disease (PD) diagnosis. By applying advanced feature selection techniques like LASSO Regression, ANOVA, and Linear PCA, we identified key handwriting characteristics that correlate with early neuromotor impairments in PD patients. Our approach, which integrates these features with sophisticated machine learning classifiers, achieved a notable accuracy of 83.02% using the Random Forest classifier on spiral tasks, underscoring the method's robustness and precision.

The findings reveal that specific handwriting features – such as variability in pressure and speed, and dynamic changes between extrema points – are critical indicators of early PD. The consistent performance across various tasks and classifiers emphasizes the versatility and reliability of this approach. Particularly,

LASSO Regression and Linear PCA were instrumental in optimizing classifier performance, making them valuable tools in the feature selection process.

This research contributes significantly to the development of non-invasive diagnostic methods, providing a promising alternative to traditional, often delayed, diagnostic techniques. By enabling earlier and more accurate detection of PD, this approach could lead to more timely interventions, potentially delaying the progression of severe symptoms and improving patient outcomes. Future work should focus on expanding this methodology by incorporating additional data sources, such as sensor data or genetic information, and validating the approach in clinical settings through rigorous trials to ensure its practical applicability and reliability.

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Data availability statement

The dataset used in this study is publicly available and can be accessed at [27].

Declarations

Conflict of Interest: The authors declare no competing interests.

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