
Diagnosis of knee abnormalities with sEMG using MATLAB

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05 / 04 / 2024

Abstract— In this project it was used Surface Electromyography (sEMG) of 4 muscles to identify knee abnormalities. Using signals from 22 individuals (11 with and 11 without knee abnormalities) from the UCI repository, an algorithm was programmed in MATLAB that processes sEMG signals and helps to label whether the patient has healthy or abnormal signals. For the characterization the stages of feature extraction and feature selection were important. For each patient there are 3 movements, walking, knee extension and flexion, and the recording of 4 muscles; therefore, 12 signals were processed per person. In the pre-processing stage, Empirical Mode Decomposition (EMD) was used to obtain a new physical view of the features, thus decomposing each of the 12 signals into 8 new components. Five Time Domain (TD) features were extracted from each component, resulting in 480 characteristics that defined each patient. Since there are so many characteristics, there is a possibility that some of them are redundant, and therefore not all of them add value to the model. The goal is to have enough features to help differentiate the subjects and they should be the ones that contribute the most to the model. So Principal Component Analysis (PCA) was used for dimension reduction and the first 3 principal components were used and the 22 subjects with these components are visually represented to determine if the selected features help identify each patient. Then, with Back-Propagation Neural Networks (BPNN), a two-layer network is trained to determine in a 3D graph the areas where sEMG signals are most likely to belong to an individual with abnormalities and differentiate them from people with normal signals.

Keywords—sEMG, Characterization, EMD, PCA, BPNN.

I. INTRODUCTION

Electromyographic signals (EMG) are used in different applications such as diagnosing conditions (such as neuromuscular diseases) [1], monitoring the rehabilitation progress of a patient [2] and controlling prostheses; which is related to the recognition of movement intentions [3]. Currently, EMG signals are interpreted by manual analysis of the signal, which requires time and expertise on the part of the professional [4]. That is, from the moment the doctor visualizes the signal, he concludes and detects anomalies, which become significant if the signals come from areas such as the knees, as they raise suspicions of the existence of severe musculoskeletal diseases in the body [5]. Some knee conditions that are detected with EMG are injuries to the sciatic nerve, meniscus or cruciate ligament. So, if it is desired to assist in the diagnosis with EMG and if the signals are normally interpreted by a trained specialist and takes time, how can the diagnosis process be faster? One idea is for a computer to carry out the process of identifying the most significant characteristics so that the diagnosis is assisted; similar to what is done with a laboratory test that separates normal cases from abnormal ones by means of a variable.

In this sense, ways were investigated to ensure that a

computer is capable of identifying and interpreting an EMG signal by itself. A review including 203 papers analyses Surface Electromyography (sEMG) signals with Artificial Intelligence methods [2], and there it mentions that in general, the procedure to analyze and conclude from sEMG signals using AI has 4 or 5 stages. It begins by pre-processing the signal, then it is the feature extraction, and depending the feature sets it can jump into dimension reduction stage or go directly to classification, and finally the activity prediction, being the last stage a unique characteristic of HAR. Some examples using AI and EMG are the articles that proposed applications like stress detection [6], or the diagnosis of nephropathy muscle diseases [1], or to control upper-limb exoskeleton [7].

Likewise, with the use of sEMG, there are studies focused in knee anomalies detection. Rani et al. [4] proposed to automatically diagnosed knee abnormalities using the empirical wavelet transform (EWT) to decompose the signal then get entropy-based features and finally use 3 Machine Learning (ML) models; Naive Bayes (NB), Support Vector Machine (SVM) and K Nearest Neighbors (KNN); resulting in a level accuracy results of 89.6%, 93.5% and 96.4% respectively. On the other hand, Vijayvargiya et al. [8] uses Wavelet Denoising (WD), 11 Time Domain (TD) features and 6 different classifiers that have a 95% confidence interval for 100 randomized tests in an oversampling situation. Similarly, Erkaymaz et, al. [9] used Discrete Wavelet

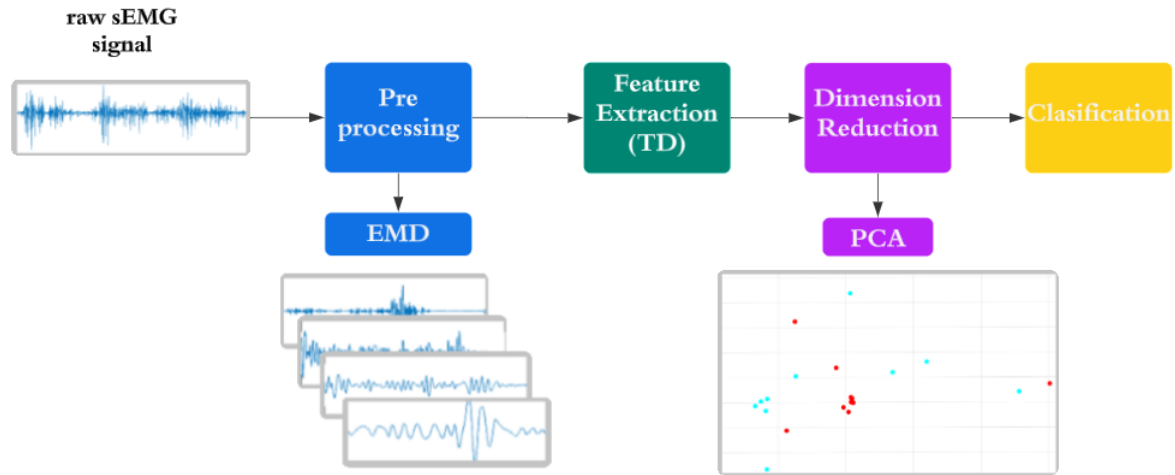


Fig. 1: Stages of the proposed approach for knee abnormalities detection.

Transform (DWD), TD feature extraction and Artificial Neural Network (ANN), particularly the Levenberg-Marquardt backpropagation algorithm, resulting in a good classification performance. Another classification accuracy of a multi featured set with six TD features is of 83.3% [10].

Another useful method to analyze signals is the Empirical Mode Decomposition, designed to handle non-stationary and nonlinear signals. This makes it suitable for analyzing signals that exhibit changes in both amplitude and frequency over time. Some current applications with biomedical signals are the respiratory rate monitoring [11], ECG signal enhancement [12] and EEG signal analysis [13].

From the diverse techniques that can be used in the processing of sEMG, which are mentioned in the review [2], this paper focus is on knee anomalies detection with an alternative tool, that also follows the procedure stated in the review, but addresses the need of improvement in classification performance. From each set of knee sEMG signals and using signal processing and machine learning techniques, it is enhanced the time signal with the use of EMD so that each raw signal is decomposed into several imfs and from the new signals 5 Time Domain (TD) features are extracted and analyzed using a supervised ML method to predict new sEMG; about which is more likely to be, normal or abnormal signals.

II. METHODOLOGY

Overview

The proposed approach for knee abnormalities detection is separated in stages as shown in Figure 1, one pre-processing stage to filter the signals, another stage to extract Time Domain Features, another stage for Dimension Reduction to sort the features that contribute the most to characterize each of the 22 participants, and a final stage to predict new the data.

Dataset

The dataset used in this project was obtained from UCI-sEMG [14] and it is one of the most employed for research work. The information was extracted from 22 male participants, 11 of whom have been previously diagnosed by experts

with knee abnormalities and the other 11 have normal knees. The atypical patients were injured in the sciatic nerve, the anterior cruciate ligament, the meniscus and six other ligaments. There is a folder containing all data of the 11 patients with knee abnormalities and another for the 11 healthy patients.

The dataset includes information of each subject with 3 different movements: march, leg extension in a sitting position and flexion of the knee while standing up. Each movement has information of the four knee muscles; vastus internus, semitendinosus, biceps femoris and rectus femoris; and also the goniometry of the knee. Figure 2 shows that there are 33 files with abnormal signals and 33 files with normal signals. Each file contains 5 signals, making it then 66 files and 330 signals. However, in this analysis only the sEMG signals will be used, leaving out of the analysis the gonometry of each movement, giving a total of 264 signals to be processed.

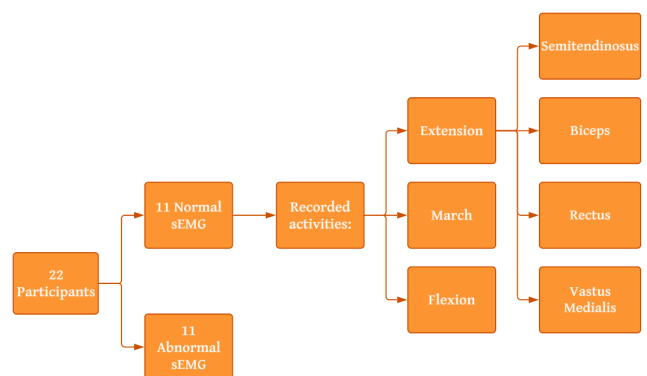


Fig. 2: Dataset explanation.

A set of signals of any patient, doing one of the three movements is exemplified in Figure 3, where the EMG provides information about a specified muscle activity. The called "flexion of the knee" indicates when the muscles were activated due the movement the subject is doing. illustration corresponds to a flexion movement, in which there is a change in angle while the muscles are activated simultaneously.

A. Pre-processing

Skeletal muscles are made up of collections of motor units (MUs), each of which consists of a motor neuron, its axon, and all muscle fibers innervated by that axon. When stimulated, each motor unit contracts and causes an electrical signal that is the summation of the action potentials of all of its constituent cells, and it is called single-motor-unit action potential (SMUAP). A surface acquired EMG is the sum of several SMUAP trains. It can be represented as a function of time and muscular force produced. Spatiotemporal summation of the MUAPs of all of the active motor units gives rise to the EMG of the muscle and one EMG signal indicates the level of activity of a muscle [3]. The EMG signal can be obtained via intramuscular (iEMG) or on the surface (sEMG).

Huang et al. [15] introduced in 1998 the Empirical Mode Decomposition (EMD). Individually, decomposition is the separation of the signal into components to gain new insight into inherent features. And mode is the name of the components obtained from the decomposition, a portion of the complete signal. Empirical stands for not being based on a prescribed system, so the data itself describes the decomposition. Some other decomposition methods as Fourier Transform (FT), Wavelet Transform (WT), Singular Value Decomposition (SVD) or Dynamic Remote Decomposition (DMD) are used but are better suited for linear and stationary data. Unlike them, the EMD ability to process non-linear and non-stationary data makes it then its most important feature because EMG, like several biomedical signals, is non-linear and non-stationary. Such property is achieved by using an adaptive basis system, which is dictated by the data itself, and the modes are additively biased towards locally dominant frequencies for time dependant signals. This allows to extract physical meaningful modes.

The decomposition of the original signal into components that should help analyze the features of the data it is of utter importance because these components reflect physical features. And EMD unlike the other modes, that produce mathematically meaningful modes, produces physical significance so the conclusion drawn from it is hardly misleading.

The modes produced from EMD are called Intrinsic Mode Functions (IMFs). The algorithm to get IMFs is to

1. Find the local extrema of the signal.
2. Fit envelop through the founded maxima E_{up} and an envelop through the minima E_{low} . All envelops must cover all data between them.
3. Determine mean of upper and lower envelop.

$$E_{mean}(t) = \frac{E_{up} + E_{low}}{2}$$

4. Determine a residual $res(t)$, by subtracting the mean from the original signal.

$$res(t) = f(t) - E_{mean}$$

5. Check stopping criterion to determine if it is an IMF.

$$\sum_t = \frac{[res(t) - f(t)]^2}{f(t)^2} < \epsilon$$

Which is the standard deviation normalized, that compares the result with a threshold called ϵ

6. If the stopping criterion is true then $imf(t) = res(t)$ And the original data is then updated as $f(t) = f(t) - imf$.

This is an iterative process to obtain as many IMFs are needed and it is stopped when the residual approaches a monotonic function.

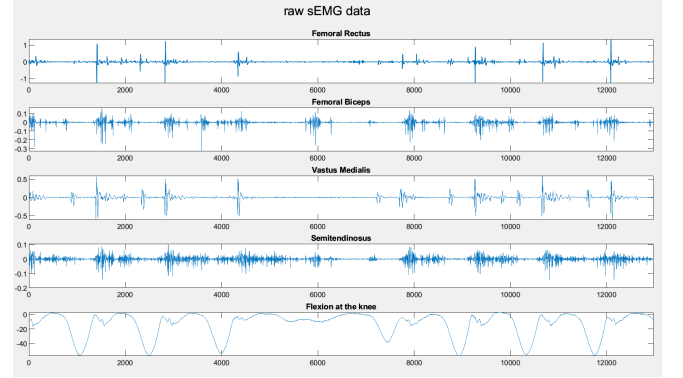


Fig. 3: Patient information at one movement.

Using the MATLAB emd function, it is possible to obtain the IMFs of the sEMG. But given its property of being an univariate approach, the function is applied on one sEMG signal at a time, which does not guarantee that the sEMG signals are decomposed into the same number of modes and would cause the number of extracted functions characterizing each individual to vary.

To decide the number of modes to extract, it is extracted all the possible IMFs per sEMG and stored. Then the number of IMFs per sEMG are counted and finally the extracted modes are adjusted to the smallest number there were. The smallest number of IMFs was 8. So from each sEMG the first 8 modes were saved. The process did not prove futile as there were sEMGs from which up to 10 IMFs were derived.

B. Feature Extraction

The analysis in time domain involves indicators based on statistical approaches to make up the features while the EMG signal is treated as a function of time, making it more intuitive and with a low computational burden [2]. Instead of using all the information found in the signal, some variables will be extracted that are descriptive of what happens, which are a finite set of characteristics of the different knee muscles. The selected features to extract are:

- Mean value

$$\frac{\sum_{i=1}^n x_i}{n}$$

- Variance

$$\sigma^2 = \frac{\sum_{i=1}^n (x_i - \bar{\mu})^2}{n - 1}$$

- Skewness

$$\frac{\sum_{i=1}^n (x_i - \bar{\mu})^3}{(n - 1) \times \sigma^3}$$

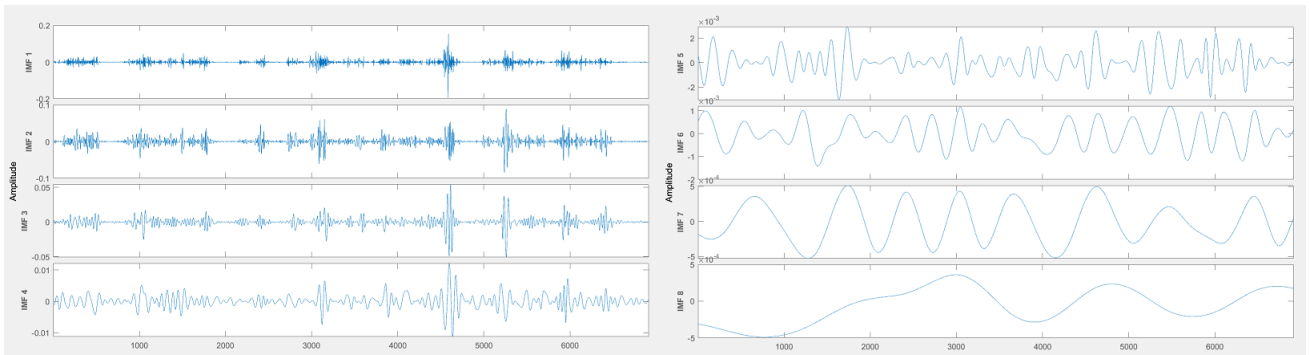


Fig. 4: IMF components derived from data shown in Figure 5.

- Kurtosis

$$\frac{1}{n} \sum_{i=1}^n \left(\frac{x_i - \mu}{\sigma} \right)^4$$

- Energy

$$\sum_{i=1}^n |x(n)|^2$$

Five features were extracted from each IMF.

C. Dimension Reduction

And with the union of the decomposition in empirical mode and the extraction of characteristics in time, a time-frequency analysis is obtained. Where it must be guaranteed that the characteristics obtained must be representative in the sense that they help to discriminate between a population that does not have anomalies and a population that does.

Classical datasets often consist of many features, making dimensionality reduction methods particularly appealing. PCA, that stands for Principal Component Decomposition is a straightforward frameworks to that goal and it is hard to find a domain in machine learning or statistics where it has not proven to be useful. PCA considers new decorrelated features by computing the eigendecomposition of the covariance matrix. PCA transforms the data into a new coordinate system where the greatest variances by any projection of the data come to lie on the first coordinates (principal components), the second greatest variances on the second coordinates, and so on, in other words, PCA reduces the number of variables in a dataset by identifying the most important features that capture the majority of the data's variability [16].

Researchers findings demonstrate that extracting PCA is also helpful for classification. To classify the time-domain properties of the EMG signal researchers made a scatter plot [17] by using (PCA) to reduce the number of features and have been proved to be very accurate. The MATLAB function "pca" was used with each with each dataset, healthy and abnormal signals, and the scores were obtained and then plotted to contrast and have a visual representation of the dataset.

D. Backpropagation

Machine Learning (ML) is an algorithm that can take new information to adjust the architecture of an ANN. It aims to create a computer system that can learn and respond based on previous observation; this process can be supervised or unsupervised [2].

Back-Propagation Neural Networks (BPNN) is a multi-layer, feedforward neural network which consist of an input layer, hidden layer and output layer. The input and output layers serve as nodes to buffer input and output respectively, while the hidden layer provides a means for input relations to be represented in the output. The initial output might not be accurate. The network needs to learn from its mistakes and adjust its weights to improve. And Back-Propagation is essentially an algorithm used to train neural networks, applying the principle of error correction. So after forward propagation, the output error, which is the difference between the network's output and the actual output, is computed. Back-propagation adjusts the weights and the biases of the network to minimize that error, and the objective here is to improve the accuracy of the networks output during subsequent forward propagation, in essence is a process of optimization [18, 19]. BPNN was used to determine the spaces where the features were most likely to belong to patients with or without abnormalities according to the points obtained from each dataset. After training the Neural Network, a prediction was made, based on simulating 3000 new points (which served as new patients) and classifying them according to their similarity to the 22 known patients. This divided the geographical space into zones belonging to normal sEMG signals and zones for abnormal sEMG.

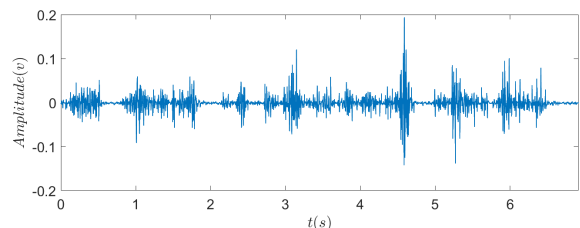


Fig. 5: Patient 11 normal sEMG, walking movement, semitendinosus muscle.

III. RESULTS AND DISCUSSION

Figure 5 shows an example of data that was used in this investigation. The decomposition of the original signal into components help analyze the features of the data because these components reflect physical features. Figure 4 illustrates the ways in which a signal was decomposed. It can be seen how a higher mode number contains, smaller frequencies. EMD was applied to all 22 patients in their 3 movements. Given that each patient has 3 movements, which are recorded from 4 muscles that originate the sEMG, to which EMD is applied

to obtain 8 IMFs per signal and to each component 5 features are calculated, then it can be said that there are 480 features that distinguish each patient.

$$\text{Number of features} = 3 \times 4 \times 8 \times 5 = 480$$

PCA is used to take into account only the features that add value to the model. From PCA it is obtained the principal components, which are the linear combinations of the observed variables.

To demonstrate that the proposed analysis in the time-frequency domain is better with the use of EMD, time features were extracted from EMG signals without using EMD. This caused 60 characteristics to be obtained that were later treated with PCA and the result was presented in a graph.

As can be seen, there are too many features so there is a possibility that some are redundant and do not add value to the model. Since it is not possible to simply eliminate variables arbitrarily.

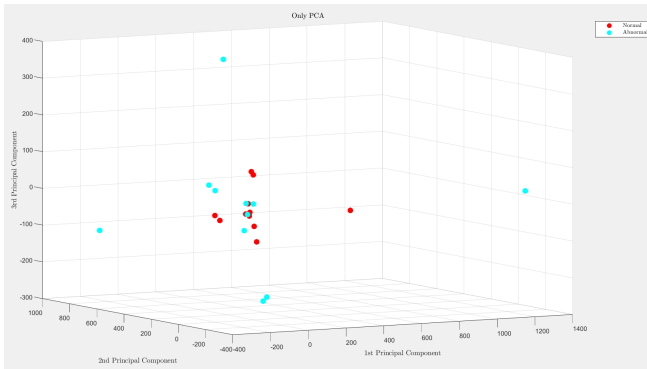


Fig. 6: Time Domain

In the ?? and 7 figures, the 22 points corresponding to the subjects to which the signal sEMGs belong are presented. In both figures there is a 3D plot of the first, second and third principal components, which in this case represent 80% of the original data. Eleven red dots and eleven blue dots are observed, representing patients with normal and abnormal signals respectively. The ?? figure is the result of treating the signal without EMD and the 7 figure includes the analysis with EMD. The comparison between these figure is that in 7 figure is clearer the distinction between patients with abnormalities and patients without abnormalities.

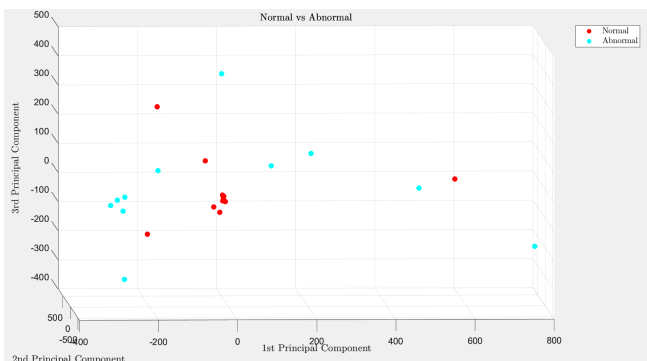


Fig. 7: Domain Time-Frequency

Figure 7 shows that mostly normal points are spatially contained within the abnormal signals, which means that the characteristics of people with abnormal knee sEMG

are distanced from a certain pattern that people without abnormalities do have, as the points are scattered throughout the space. This demonstrates that with EMD, TD features and PCA it was possible to characterize and differentiate both sets of patients in a way that is visually understandable.

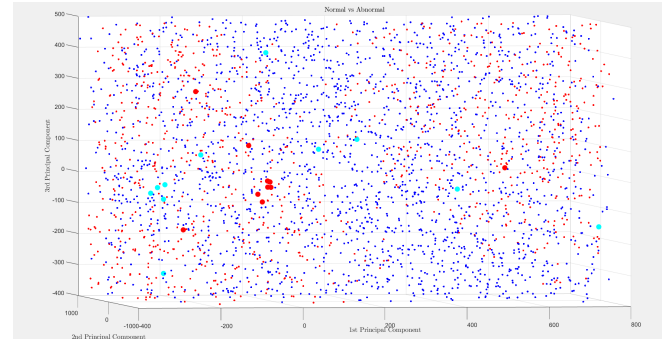


Fig. 8: Qualitative appreciation of Neural Network

The neural network fundamentally comprises multiple layers of neurons interconnected by weight. There is an input layer, two layers in the middle as hidden layers and the layer on the end here that is the output layer. These neurons are all interconnected with each other across the layers, so each neuron is connected to each other neuron and the weights define the strength of the connections between each of the neurons. The accuracy of predicting knee abnormalities depends on the quality of the extracted features, in other words, whether they distinguish one set of patients from the other.

The extracted features, which are the 1st, 2nd and 3rd Principal Components, were used to train the neural network. Twenty hidden neurons were used in the algorithm.

To evaluate the algorithm, 3000 random data were introduced and, based on the training of the network, the algorithm predicted based on the probability to which class the data belonged. The result is Figure 8, which spatially demonstrates how likely it is that the data is a patient with knee anomalies (blue dots) or without anomalies (red dots). And like the result from PCA stage, shows that overall the blue dots enclose the red dots that corresponds to abnormal knee principal components. It shows potential as a tool for signal visualization, because after the linear PCA transformation, if an expert looks at the location of patient features, he can conclude from whether the signal is in an abnormal or normal region.

IV. CONCLUSIONS

This paper presents a unique approach that uses knee sEMG data with EMD to improve knee features identification significantly. The recommended methodology achieves a visually good distinction by combining Time Dimension features, PCA for dimension reduction, and EMD for noise reduction and physical meaningful features. This contribution has the potential to improve the perception of the results in a graphical way and by incorporating mathematical performance tools there is a possibility to boost effectiveness and accuracy of knee abnormalities diagnosis. Characteristics that define the patients were obtained, it was shown that the time domain frequency is better than the time domain to extract features. Future research work can be carried out by enhancing classification accuracy in the back propagation algorithm along

with the response time in order to be a helpful medical tool.

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