Automatic Detection of Myotonia using a Sensory Glove with Resistive Flex Sensors and Machine Learning Techniques

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***Abstract*—This paper deals with the automatic detection of Myotonia from a task based on the sudden opening of the hand. Data have been gathered from 44 subjects, divided into 17 controls and 27 myotonic patients, by measuring a 2-point articulation of each finger thanks to a calibrated sensory glove equipped with a Resistive Flex Sensor (RFS). RFS gloves are proven to be reliable in the analysis of motion for myotonic patients, which is a relevant task for the monitoring of the disease and subsequent treatment. With the focus on a healthy VS pathological comparison, customized features were extracted, and several classifications entailing motion data from single fingers, single articulations and aggregations were prepared. The pipeline employed a Correlation-based feature selector followed by a SVM classifier. Results prove that it's possible to detect Myotonia, with aggregated data from four fingers and upper/lower articulations providing the most promising accuracies (91.1%).**

***Keywords*—myotonia, SVM, hand, machine learning**

I. INTRODUCTION

The use of classification systems in medical diagnosis is gradually increasing. Recent advances in artificial intelligence have led to the emergence of expert systems and decision support systems (DSS) for medical applications. Moreover, over the past decades, computational tools have been designed to improve the experiences and capabilities of doctors and medical specialists in making decisions about their patients. Undoubtedly, the evaluation of patient data and expert decisions are still the most important factors in diagnosis. However, expert systems and different Artificial Intelligence (AI) techniques for classification have the potential to be good support tools for the expert. Classification systems can help increase the accuracy and reliability of diagnoses and minimise possible errors, and the main advantage of AI-enhanced medicine lies in its ease of deployment, its implementability in telemedicine solutions, its non-invasiveness and its real-time, low-cost characteristics. As a result, AI is used with promising results in many applications of medical signal analysis, from voice analysis [1]–[5] to movement [6], [7].

This study is focused on Myotonia, which is a disease of the muscular system characterised by an abnormal delay in the release of voluntary muscles after contraction, resulting in a variable degree of slowness and clumsiness in movement [8]. It affects several muscles, including phonatory and masticatory muscles, and especially hinders hand movement: the prehension movement of the hand is often followed by difficulty in the release (descent) mechanism. Several diseases, especially Steinert's myotonic dystrophy and congenital Myotonia, share the same symptomatology, although the underlying pathogenic dynamics are different: macroscopically, the patient is still defined as "myotonic". This creates, of course, additional difficulties in the diagnostic phase. Unlike some other muscle diseases, congenital myotonia does not cause weakness or atrophy of the muscles. The diagnosis of congenital myotonia is suspected on the basis of the child's characteristic appearance, inability to quickly relax the hand grip after closing it, and prolonged contraction when the doctor taps a muscle. To confirm the diagnosis, an electromyogram (an examination involving the recording of electrical impulses from muscles) is required. Sometimes a muscle biopsy is performed. Genetic tests can be performed to identify mutations in the gene that causes both forms. In this paper, we analyse data obtained from measurements taken from a sensory glove equipped with flex sensors on each finger, specifically focusing on the movement of sudden hand opening. In addition, comparisons are made between patients either by considering a single finger joint of the hand or by considering several joints simultaneously [9].

Not many attempts have been made at preliminarily identifying Myotonia with the aid of AI. Most notably, in 2019 Lin et al. [10] proposed a Deep Learning-based system for detecting Myotonia from the squeeze of the hand; in 2022 Bouma et al. [11] applied Machine Learning and statistics to a novel measurement instrument for non-invasively measure the clenching of the fist.

Thus, the following work is presented as a further aid to the treating physician in diagnosing and defining a clinical scale of progress or regression of the pathology under investigation. Moreover, a custom dataset has been used. Despite numerous examinations that the physician uses for a correct diagnosis of the pathology, it is still difficult to define a non-subjective scale of objective improvement or effectiveness of the proposed curative treatment.

II. Materials

A. Study Population and Tasks

The study population for the present work consists of an initial number of 44 subjects, of which 27 are myotonic (M) and 17 are healthy controls (H). The data gathering for the M subjects occurred in a hospital environment, and the presence and severity of the disease was medically validated, with Myotonia ranging from mild to moderate. The total time of the data gathering procedure was 6 months, during which subjects recorded more than one entry (but never more than three) in different timeframes.

With the aid of trained personnel, the subjects were fitted a sensory glove equipped with an array of Resistor Flex Sensors (RFS) [12] placed on the three phalanges of each finger (thumb excluded). RFS are elastic motion sensors made of a simple variable resistor designed to measure the amount of deflection experienced when bent. The resistance is maximum with a 90-degree angle and minimum when flat. The voltage output is converted by an ADC to a 12-bit digital signal with sampling frequency of 40 Hz, then elaborated on MATLAB ® (Natick, Massachusetts: The MathWorks Inc.).

The effectiveness of the RFS glove, in terms of accuracy/reliability and repeatability, have been proven in literature [13], [14] and specifically tested for the purpose of this paper under dynamic (versus quasi-static) conditions at various finger speed, as detailed in the study by Saggio et al. [15]. Test results show the RFS glove scoring an average accuracy range of $6.84° \pm 2.77°$ and an intraclass correlation coefficient (ICC) of 0.77 ± 0.14, with the slowest speed being the better in terms of reliability and repeatability. The results obtained under dynamic conditions are comparable to those obtained under static or quasi-static conditions, and the RFS glove outperforms inertial (IMU) devices within this environment.

With the glove being single-sized, a calibration procedure was necessary to ensure that the RFS measured the correct movements regardless of the physical characteristics of the subject. The calibration included the following tasks: the subject sets his fingers parallel to the surface, to set the minimum flex position; the subject holds a cylinder made of hard material with all fingers touching it snugly (two times, with two cylinders of diameter 6.3 and 5 cm); the subject is asked to form a firm fist with his hand to set the "closed finger" position.

The movement task measured after calibration was as follows: the subject is asked to firmly close his hand in a fist for a minimum of 5 seconds, and then to release, completely opening the hand the quickest they can.

This study is based on movement data from all fingers but the thumb, since its movements are too erratic, and in general with a different articulation than the other four fingers.

Three articulation points were captured for each finger, although the last one (closest to the tip) was not used in our analyses since its movement data involved negligible amplitudes and variability rates with respect to the other two.

After removing subjects or single records where data were noisy, badly recorded, or too erratic due to medical or logistic reasons, a final dataset of 60 instances from M subjects and 30 instances from H subjects was built. The inclusion criteria for deeming an instance worthy was identified as the full opening/closing motion signal being clear in its high-to-low evolution without unnatural peaks; moreover, annotations during the data gathering procedures allowed to identify possible artifacts or adverse phenomena such as an unbearable tremor in the subjects' hand or external forces hindering the measurement.

III. Methods

Each instance consists of two superposed signals (articulations) for each finger, which leads to a grand total of 8 signals per instance (2 articulations for 4 fingers). With each instance corresponding to a class label being either M (myotonic) or H (healthy), and with the grand division being between healthy and pathological subjects, binary classifications (healthy VS myotonic) were prepared at different levels and with different tasks:

- Comparison of each articulation of each finger, leading to 8 binary classifications thus prepared.
- Comparison of each finger, using data of both articulations, leading to 4 binary classifications.
- Comparison of each articulation, using data from all fingers each time, leading to 2 binary classifications (lower or upper articulation).
- Comparison of the whole hand, regardless of the finger or articulation, between M and H. This leads to a single binary classification task, healthy VS myotonic, employing the largest dataset.

Each file was manually trimmed to remove portions from the beginning and the end that are not related to the motion of the hand. The criterion for this was to simply trim the signal in a point ranging 10 ms before/after the "onset" (or offset), which is identified as the sudden peak after/before noticeably "silent" portions in which only the noise floor is detected. This allowed each instance to start exactly at the moment when the subject suddenly opened his hand.

The dataset then endured a pipeline that is comprised of the following steps, better detailed in the corresponding subsections:

1) *Feature Extraction*
2) *Feature Selection*
3) *Classification*

Due to the limited dataset and to the small number of features, although feature selection was attempted for each classification approach, it only brought valuable results for the aggregated comparisons involving instances from all fingers. This will be better detailed in the "Results" section.

B. Feature Extraction

A total of 29 different features were extracted from each instance with the aid of custom MATLAB routines.

Each signal was segmented in the following sections: the upper part corresponding to the closed hand, the descent section corresponding to the opening of the hand and the final section after the descent, corresponding to the open hand at rest. We first qualified the descent part by defining for each patient, using the first derivative, an initial descent sample, hereon defined as "DS", a sample corresponding to the first decrescent part of the signal, identifying the start of the opening of the hand (EOF1) and a end-of-descent (ES) sample corresponding to a fully opened hand. Two samples were necessary to define the whole hand opening procedure because of the gradual nature of it, and because some patients with myotonia may also have problems holding their hand open at rest.

Once these samples had been defined, linear regression lines were fitted: one line regarding the upper part of the function up to the first sample before descent (R1); one considering the sample before descent and the first sample at the end of descent (R2); a line passing through 2 points considering the sample before descent and the first sample at the end of descent (R2b); a line passing through 2 points considering the sample before descent and the second sample at the end of descent (R3); and finally a line considering the first and the second sample at the end of descent (R4). Figure 1 details this segmentation procedure.

Let the reader be reminded that the "amplitude" of the signals is defined in terms of resistance, which in turn quantifies the flex of the RFS. After mathematically defining the three relevant sections (closed hand – descent movement – open hand), features were extracted. From the descent part (defined by the three samples DS, EOF1 and ES) the following features were extracted:

- yStart: Amplitude of the descent sample (DS).
- yPPP: Amplitude of the EOF1 sample (first sample after descent).
- yEnd: Amplitude of the ES, corresponding to the opening of the hand.
- Start2PPP: Length measured in number of samples from the DS to the EOF1.
- Start2End: Length measured in number of samples from the DS to the ES.
- PPP2End: Length measured in number of samples from EOF1 to ES.
- ratioTimes: Ratio of Start2PPP to PPP2End.
- ratioTimesRec: Ratio of PPP2End to Start2PPP.
- ratioSNs: Equals to (yStart - yPPP) / (yPPP - yEnd).
- m1fit: Angular coefficient of the R1 line (closed hand).
- q1fit: Known term of the R1 line (closed hand).
- m2fit: Angular coefficient of the R2 line.
- q2fit: Known term of the R2 line.
- m2rp2p: Angular coefficient of the R2b line.
- q2rp2p: Known term of the R2b line.
- m3rp2p: Angular coefficient of the R3 line.
- q3rp2p: Known term of the R3 line.
- m4fit: Angular coefficient of the R4 line.
- q4fit: Known term of the R4 line.

From the "still" traits of the signal, corrisponding to a fully closed hand (before descent) and a fully opened one (after descent), the following features were extracted:

- flatness: Difference, in terms of amplitude, between the maximum and minimum value within the trait.
- varianceOsc: Variance of the oscillations of the signal detected as deviation from the linear regression line.
- averageModuleosc: Average absolute value of the amplitude of the oscillations.
- ZCROsc: Crossing rate of the oscillations with the regression line.
- AreaOsc: Area of the oscillations, better displayed in Figure 2.
- TPPS: Distance (on the y-axis) between the last sample estimated by the regression line, and the DS sample, which corresponds to the beginning of the movement. This specific feature was only extracted for the first trait of the signal (hand closed to descent).

All of the abovementioned features but TPPS were extracted from both the initial (closed) and final (open) trait, with the latter having features with a "2" suffix (e.g., "varianceOsc2"). A graphical explanation is given in Figure 2.

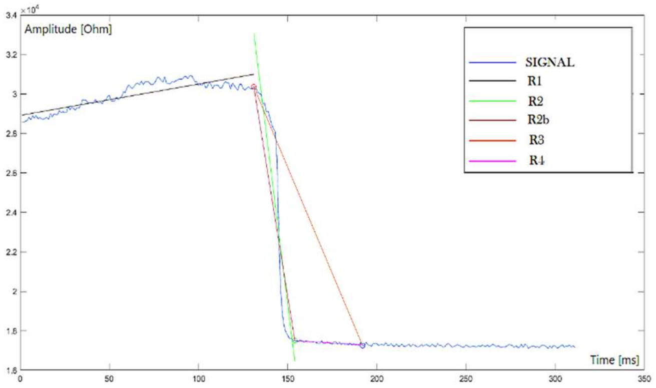

Fig. 1. Example of a trimmed instance and its regression lines R1, R2, R2b, R3 an R4 as defined in the "Feature Extraction" section.

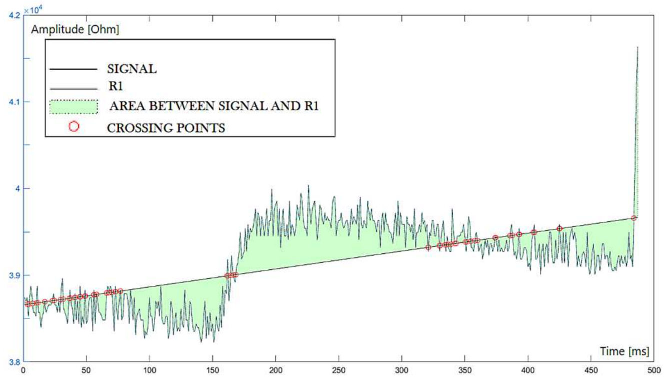

Fig. 2. Example of the first trait of the signal, from the beginning to the first descent sample (S1), and its oscillation above the R1 line.

C. Correlation-based Feature Selection

The next step after the extraction employed a feature selection based on Hall's Correlation-based Feature Selector (CFS) [16] that takes into account the importance of each feature for detecting between classes, and the redundancy of a given subset of features, according to the following formula:

$$M_S = \frac{k*\overline{r_{fc}}}{\sqrt{k+k(k-1)*\overline{r_{ff}}}} \qquad (1)$$

Where k is the number of features in a subset S, $\overline{r_{fc}}$ is the average correlation between features and the class label, and $\overline{r_{ff}}$ is the average correlation between pairs of features in the subset. Merit factors are computed incrementally and the best subset is found using a Forward Greedy Stepwise search method [17]. The number of features retained for each comparison is not predefined.

D. Classifier: Linear SVM

After feature selection, we trained several linear SVM classifiers chosen due to their performance and generalization power on medium-to-small datasets due to their generalization power. A general SVM is a binary classifier based on finding the optimal separation hyperplane between the two nearest examples of opposite classes, called "support vectors" by solving the the Lagrange dual formula [18]. When data are not linearly separable, it is possible to project on a higher dimension to find a suitable hyperplane; however, by choosing a linear kernel, the best separation hyperplane still lies within the dimensionality of the data, and out-of-bounds classification is made possible by "softening" the margins introducing a parameter C called "Complexity", which penalizes classification errors during training according to their distance from the support vectors [19].

We used a soft-margins linear SVM, solved with Platt's SMO algorithm, with the parameter C set as 1. A 10-fold Cross-Validation was used to produce the end results, by averaging. Each classifier was trained on a portion (9/10) of the respective dataset, in accordance with the definition of cross-validation. According to the list of prepared classifications detailed in the "Methods" section, each sub-dataset entailed a binary classification (healthy VS myotonic) containing data from either a single finger with a single articulation, a single finger regardless of articulation, upper/lower articulation regardless of fingers, or all data from healthy subjects VS all data from myotonic subjects regardless of fingers or articulation. Classification and the feature selection algorithms were implemented on Weka® (University of Waikato) [20].

IV. Results

In this section, classification results are presented for each binary comparison. Each finger is referred with its name: Index, Ring, Anular and Pinky. The articulation may be abbreviated as "art." and the two possibilities are "lower" or "upper". Results are reported in terms of classification Accuracy (Acc), Sensitivity (Sens) and Specificity (Spec). Sensitivity, which is defined as the True Positive Rate, is the ratio between the "true" positives - M subjects correctly identified as such - and all of the instances identified as positive, i.e. the sum of true positives and false negatives (H subjects wrongly identified as sick). Specificity is the ratio between true negatives and the sum of all instances identified as negative (true negatives plus false positives). Table I displays the results of the comparisons that involve single fingers with single articulations.

TABLE I. Results with single fingers and articulations

Comparison	***Acc (%)***	***Sens (%)***	***Spec (%)***
Index, art. lower	67.8	68.7	57.1
Index, art. upper	68.5	73.1	54.5
Middle, art. lower	78.9	78.1	82.3
Middle, art. upper	75.6	80.7	64.3
Ring, art. lower	76.7	75.3	84.6
Ring, art. upper	75.6	76.4	72.2
Pinky, art. lower	76.7	76	80
Pinky, art. upper	74.4	76.1	68.4
Mean	74.275	75.55	70.425

Table II displays the results of the comparisons that involve single fingers with both articulations.

TABLE II. Results with single fingers, all articulations

Comparison	***Acc (%)***	***Sens (%)***	***Spec (%)***
Index, all art.	76.7	80	68
Middle, all art.	91.1	100	78.9

Ring, all art.	85.6	88.5	79.3
Pinky, all art.	77.8	79.4	72.7
MEAN	82.8	86.975	74.725

Table III and Table IV display the results of the aggregated comparisons: the first two comparisons involve all fingers with two articulations, and the last is the fully-aggregated one. This is the only case in which feature selection brought detectable benefits, also due to the number of initial features being proportionally larger thanks to the aggregation. Each single task brings out 29 features, which leads to the grand total of 232 features for the fully-aggregated comparison. Feature selection, when applied to the other comparisons only brought slightly lower accuracies trying to reduce an already limited feature set.

TABLE III. AGGREGATED RESULTS, WITHOUT FEATURE SELECTION

Comp.	Without Feature Selection			
	Acc (%)	*Sens (%)*	*Spec (%)*	*Number of Features*
All fingers, art. lower	78.9	82.5	70.4	116
All fingers, art. upper	78.9	87.3	65.7	116
All fingers, all art.	85.6	89.8	77.4	232

TABLE IV. AGGREGATED RESULTS AFTER FEATURE SELECTION

Comp.	After Feature Selection			
	Acc (%)	*Sens (%)*	*Spec (%)*	*Number of Features*
All fingers, art. lower	82.2	83.3	79.2	11
All fingers, art. upper	67.8	71.2	52.9	16
All fingers, all art.	91.1	100	78.9	28

V. DISCUSSION AND CONCLUSION

Looking at the tables displaying accuracies, it is evident that the best results are obtained when several joints are considered at the same time, whether of the same finger or of different fingers. This is because by having more diverse features to use for classification, reconstruction of a proper classification map, and thus discrimination between the two classes is easier.

This is also the case with regard to feature selection, because when there are few starting features as in the case of single joints, feature selection is ineffective, worsening the results in all 8 cases, as it tends to select few features (from a minimum of 4 to a maximum of 7). A similar point of view can be made for the comparisons of the fingers, since only in the case of the pinky there is a slight improvement in accuracy (of about 1%), with a number of features selected ranging from a minimum of 9 to a maximum of 11. On the other hand, with regard to the joints considered simultaneously, in particular the first and the first together with the second, there is a clear improvement in the performance of the classifier after having carried out the feature selection, with improvements ranging from 4% to 6% [21].

Using a high number of features with respect to the number of data can often bring overfitting, according to the principles of the "Curse of Dimensionality": data are over-represented by too many indicators, which make the reconstruction of a proper feature map harder for classifiers, in turn worsening generalization [22].

For single-finger tasks, the initial number of features is lower (29) because there is no aggregation, and the number of instances is lower accordingly: this partly explains why feature selection is ineffective. On the other hand, it brings noticeable improvements when considering sets with a higher number of instances and features, like the aggregated ones.

Analysing the confusion matrices of the various comparisons, it can be seen that in general, the classifier tends to misclassify more controls by classifying them as myotonia patients than the other way around, having instead a better accuracy for myotonia patients. In fact, the worst results are obtained when the classifier gets all the controls wrong. This may probably be due to the fact that the data collected during the measurements of the controls are more similar to those of the myotonia patients than they should be, due to several factors: the correct execution of the test by each control is variable and subjective, the glove made to fit differently according to the palm size of the persons tested, problems related to an incorrect sampling of the measured signal, etc.

In the end, the best classification results are obtained considering both joints of the middle finger and all 8 joints of the four fingers.

As far as features are concerned, it is already stated that, due to the limited amount of data and features, selection on single tasks did not bring relevant results. In general, with regard to the eight joints taken individually, mostly features inherent to the angular coefficients and known terms of the drawn lines were selected. With regard to the index and middle finger, there are also a good number of features inherent to the oscillations. In particular, for the first joint of the middle finger, we have the two features considered most important in this table, i.e. q4fit and yEnd, indicating that probably the final part (open hand at rest) of the measurement is of particular importance for discrimination with this joint. With regard to the two joints considered together of each finger, a greater importance is noted for the features related to the first joint, especially in the index, middle and ring fingers. For the middle finger in particular, q4fit and yEnd were again the most important, as was the case when only the first joint of the same finger was assessed. In general, again, there is a majority of features related to the five regression lines.

The present work has made it possible to highlight the importance of motion analysis in the recognition and characterisation of myotonia, demonstrating that such analysis can represent an additional tool for better understanding the abnormalities of hand movement in this pathology. In fact, the main aim of our study was to demonstrate that by means of classification techniques based on machine learning algorithms, it is possible to construct classifiers that can discriminate measurements belonging to subjects with myotonia and healthy subjects [23]. All of the algorithms employed in the pipelines are not dependant on the number of instances per class, i.e., they are insensitive to unbalances. Soft margins, linear SVM

Of the 8 joints analysed, we have shown that the best results are obtained when considering the features of several joints at the same time, in particular those related to the first joint of the middle finger and also the ring finger are most effective. In general, however, the classifier performs better when it has a number of features that is not too small for the dataset provided to it, making it also sensible and effective to apply a feature selection algorithm, which, as seen above, manages to improve some results. In any case, this study can be expanded by considering additional features that highlight the difference between the hand movement of a myotonia patient and a control, as well as trying to consider the thumb and third joints of each finger and see if the accuracy results could improve. A better balance of the dataset between the number of controls and myotonia patients may also help in the correct classification of the two classes, in addition of course to the fact of measuring and sampling well the movements performed by each patient, so as to minimise sensor-induced differences or other external factors not directly related to the disease [24]. Additional limitations of this study include the reduced amount of training data, the possibility of adding more custom features, the inherent characteristics of the employed sensors and the nature of the (only) movement task employed.

Clearly, considering the variety and quantity of tests that have been carried out on each patient, this is only a small part of all the work that can be done to try and demonstrate that it is possible to extract features that are particularly discriminating for this disease, perhaps even obtaining better results than those obtained by analysing this particular exercise. Additional future implementations will entail addressing class imbalances, with solutions like oversampling or the usage of weighed classifiers, and using more accuracy metrics such as leave-one-out validation.

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