RELEVANCE NETWORK MODELING FOR MUSCLE ASSOCIATION PATTERN IN REACHING MOVEMENTS

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ABSTRACT

Our purpose is to study how different muscles collaborate together to efficiently create a smooth, coordinated reaching movement. In the EMG literature, it has been commonplace to model the relationships between muscles using correlation and frequency-based measures such as coherence. Inspired by the observation that mutual information is a more general and reliable metric in revealing complex relationships between time series, we propose a relevance network framework for modeling temporally-aligned multivariate sEMG recordings. Such a network can identify functional muscle associations, providing insights into the underlying motor behavior. Here we demonstrate that relevance networks can: 1) detect the effects of handedness in normal subjects, and 2) robustly detect between the healthy and stroke subjects. Specifically, the structural features of muscle associations were sensitive to handedness and disease status yet relatively robust to differences across subjects – a longstanding goal in rehabilitation research. These results warrant further study to more fully determine the extent to which the Relevance Networks may elucidate the complex muscle interactions in reaching movements.

Index Terms: Biomedical signal analysis, reaching movement, relevance network, mutual information, muscle association.

1. INTRODUCTION

Analysis of simultaneously-recorded surface electromyographic (sEMG) signals is a topic of increasing research importance in the area of motor behavior. Although traditionally sEMG recordings have been examined in univariate fashion, it is well-known that sEMGs recorded from spatially distributed muscles may be correlated with each other [5]. Studies in muscle synergies suggest that the muscles are activated in a carefully coordinated fashion [6]. Therefore, a key challenge in motor control is to understand how different muscles collaborate together to efficiently create a smooth, coordinated movement.

To address this question, it has been investigated in the EMG literature to model the relationships between muscles using correlation and frequency-based measures such as coherence. However such measures are easily distorted by outliers, potentially biasing the estimates of muscle association. To better represent the synergy associations (or dependency patterns) between muscles, we propose to explore the relevance network (RN) framework for modeling multiple muscles, as this technique has been used successfully to model genetic regulatory networks [2]. We focus on utilizing mutual information (MI) to generate a relevance network, as MI is a more general, reliable metric in revealing complex relationships between time series. We also focus on addressing the issue of inter-subject variability, a fundamental research topic in rehabilitation science, by investigating the *structure features* of trained RNs in cross-subject classification. To our knowledge, this is the first work attempting to apply the concept of RN to model muscle associations and address the inter-subject variability using network structure features.

The paper is organized as follows. In Section 2, we describe the relevance network framework for learning muscle networks. A real case study involving sEMG recordings from normal and stroke subjects is described in Section 3. Finally, we conclude our paper with suggestions for future work.

2. METHODS

In this section, we first introduce the experimental procedure for recording sEMG data. We then describe the so-called mutual information relevance network approach, a technique that computes comprehensive pair-wise mutual information for all muscles in a sEMG data set, to identify functional muscle-muscle associations and thus generate a network of muscle associations during reaching movements. We also discuss the method for cross-subject classification.

2.1. sEMG Data Collection

In total, 20 stroke and 10 healthy subjects with ages ranging from 49 to 72 years were recruited. The severity of motor impairment of the paretic arm was assessed by upper extremity motor component of the Fugl-Meyer (FM) scale and by the Modified Ashworth Scale (MAS). During the test, each subject was first seated in a chair with their hands on the thigh and was instructed to reach and touch a fixed target after hearing an auditory cue. For every subject, the reaching movements were repeated five times on each side.

The electrical activity of seven muscles (the anterior and lateral deltoid, the triceps (long head and lateral), the biceps brachium, latissimus dorsi, and the brachioradialis) was recorded using surface electrodes. A bipolar montage was used to minimize the effect of crosstalk. The 7-channel sEMG signals were amplified, resampled at 600 Hz, and high-pass filtered at 20Hz. Pleaser refer to [4] for further experimental details.

2.2. Mutual-Information Based Relevance Network

Similar to the relevance network proposed in [2] for functional genomic studies (e.g. analyzing the functional gene clusters), our basic idea is to take data sets of sEMG measurements under different reaching movement conditions and generate networks of muscle-muscle interactions by performing pair-wise mutual information for all muscles. The relevance network for modeling associations among muscles includes two major components as follows:

- Calculating mutual information to evaluate muscle-muscle associations: Mutual information is a measure of the additional information known about one random variable when given another. Let X and Y be two random variables, the mutual information is expressed as

$$I(X,Y) = H(X) - H(X|Y), \tag{1}$$

where $H(X)$ means the entropy of a random variable X and $H(X|Y)$ means the conditional entropy. Since entropy is measure of the information content in a random variable, from its definition, the mutual information is a natural measure of the dependence between random variables. It is always nonnegative, and zero if and only if the variables are statistically independent. A higher mutual information between two muscles means that one muscle is non-randomly associated with the other. Thus the pair-wise mutual information takes into account the dependence structure of the two muscles and can be used as a metric between two muscles to represent their degree of independence. We believe that the higher a pairwise mutual information is, the more likely the two muscles have a coordination/association relationship.

In this study, assuming the discrete distributions, the pairwise MI is calculated as

$$I(X,Y) = \sum_{i=1}^{l_x}\sum_{j=1}^{l_y} P_r(x_i,y_j) ln \frac{P_r(x_i,y_j)}{P_r(x_i)P_r(y_j)}, \tag{2}$$

where l_x and l_y are the number of discrete values the variable X and Y can take, respectively. The above distributions are estimated using the corresponding histograms of the observations.

- Choosing a threshold and constructing relevance network correspondingly: Based on the M sEMG channel measurements (e.g. M=7 in our case), the electrical activity of all M muscles are compared against each other, resulting in M(M-1)/2 total pair-wise calculations of mutual information. Since it is biologically implausible to assume a fully connected network, we address this issue by setting a suitable threshold of mutual information (TMI) and reporting only those links between muscles that the corresponding pair-wise mutual information exceed the threshold. Setting an appropriate threshold warrants further consideration. One approach is simply to sort all the values of the pair-wise mutual information choose the largest N to represent the network. An alternative approach, similar to [2], is to utilize random permutations to estimate the MI values expected by chance and, based on this generated null distribution choose a suitable threshold. In this approach, the sEMG data are permutated n times (e.g. n=30) and a distribution of the new pair-wise mutual information is calculated. We utilized the latter approach.

So far, we did not consider the temporal information embedded in sEMG. Since sEMG are time-series data, and causality may exist between muscles as measurement of one muscle at time t could be associated with another muscle at a future time $(t+\tau)$, we intend to introduce temporality into Relevance Networks and take temporality into consideration in identifying the associations between muscles. To address this causality concern, we can calculate the mutual information by including the time factor. More specifically, for each pair of muscles, we determine the time-delay τ by

$$\hat{\tau} = \max_{\tau} I(x(t), y(t+\tau)). \tag{3}$$

Definite maxima in the above equation may imply that the estimated delay τ can be used to assign the causality relationship between pairwise muscles.

2.3. Cross-Subjects Classification

A fundamental research topic in rehabilitation science is the difficulty in quantifying "recovery" after, e.g., stroke. Inter-subject variability of recovery patterns complicates the ability to derive robust disease measures. To address this concern, an efficient and robust cross-subject classification method is needed. For instance, we may be interested in detecting whether a subject has an arm reaching pattern similar to stroke subjects and may want to estimate the severity of stroke from sEMG data. We believe that certain features of trained RNs are suitable candidates to serve this purpose and further to monitor recovery.

Since the RNs reveal the graphical features between muscle nodes, structure features of RNs (e.g. whether an edge exists or not) can be used as the input classification features for a given classifier. Based on the learned RN, we represent the input features by a binary vector with length n, where n means the total number of possible pair-wise connection edges, and each element value 1 means an edge exists. For instance, since 7 muscles are considered in our problem, we have $n = 21$ representing all possible pairs. In this study, a classification tree (CT), also known as decision tree because decisions about class membership are represented at the leaf nodes, is chosen to classify the binary vectors. Classification trees have been proposed in statistics, artificial intelligence, and machine learning [7]. Classification tree is learned through a binary recursive partitioning process, which is an iterative process of splitting the data into partitions. We choose a CT as our classifier because of two reasons: first, CT is especially suitable for categorical data as an adjacent matrix is in our problem; secondly and most importantly, CT is a good choice when the goal is to generate rules that can be easily understood and explained, and its meaning can be explicitly interpreted in terms of muscle interactions, as in our case. A CT selects the most informative features and explicitly gives the conditions of predicting an input be to a class. Based on our categorical input vector (e.g. binary in our case), CT is built by selecting those pair-wise interactions that are most important in determining an outcome, and then is used to assign/predict the class membership of coming inputs. CT can also provide the measure of confidence that the classification is correct.

To prevent over-fitting the data, the performance of RN-based classifiers were evaluated with cross-subject validation. The strategy of cross-subject validation is illustrated in Fig. 1. In our experiments, each subject was asked to perform a reaching movement several times with each side of arm. In cross-subject validation, the trials of one arm side of one subject are left aside as the testing data, and all the other data are used to train a classifier which then is used to predict the stroke state and hand dominance of the testing subject. The testing trials all have the prediction results and they vote which group type the tested data set belongs to. In this way, all the trials of each arm being tested are used to predict its group membership. This procedure is repeated and each time a different subject arm side is selected as the testing data. Cross-subject validation evaluates whether data sets of the same group type share common features while data sets of different group types have distinguishing features.

3. RESULTS

In this section, we study the performance of the proposed relevance network approach by examining the sEMG data collected during the reaching movements. Our purpose is to investigate whether certain muscle associations and dependency patterns revealed by MI-based RNs are consistently different between the dominant and non-dominant hands of subjects, and between healthy and stroke sub-

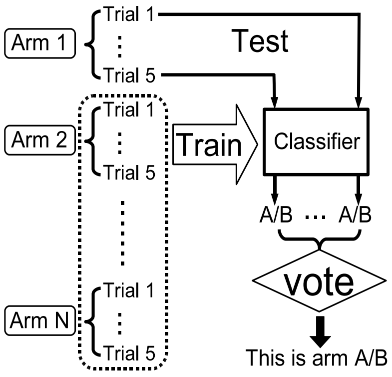


Fig. 1. The procedure of leave-one validation in cross-subject classification.

jects.

3.1. MI-based RNs

Since each reaching movement was repeated 5 times by each subject, we explored the reliability of the proposed idea by investigating the consistency in the computed networks. From our results, it is encouraging to note that the derived structures of each trial are similar, and demonstrated trial-to-trial reliability. Therefore, in the following we concatenate data from all 5 trials together and report the overall learned network.

We compare the learned relevance networks in Figure 2. The three networks are of the same task, but for different subjects and arms. We can see that, for all three networks, the muscle 1-and-7 association (i.e. the association between Anterior Deltoid and Lateral Deltoid) has the largest MI value, as would be expected as they represent two heads of the same muscle. Comparing Figure 2A and 2B, we note that the dominant and non-dominant sides share some major association patterns, although there are more muscle associations observed in the dominant side. Also, muscle 3 (Triceps:Long Head) seems playing a more important role in the dominant side, indicating a more complicate muscle collaboration pattern in the dominant side for a healthy subject.

To get some insight into the pattern difference between healthy and stroke status, we compared Figure 2A and C. For the dominant arm, the healthy subject indicates more associations than that of the stroke subject (i.e. the more affected arm), which suggests that stroke may damage the cooperation of muscles, especially of muscle 6 (Latissimus Dorsi). An interesting observation about muscle 3 (Triceps: Long Head) and 4 (Triceps: Lateral) may suggest a possible alternative strategy in stroke patients. In Figure 2A, muscle 3 is connected with many muscles while muscle 4 is lightly connected. From Figure 2C, certain connections with muscle 3 are missing in stroke, while in stead muscle 4 plays a more significant role in the movement task.

We also proceed to assign causality between muscles by taking the temporal information into consideration. For example, the time-delay between Muscle 2 and 7 is estimated as -2, meaning that Muscle 7 at time t is associated with Muscle 2 at a future time (t+2). This is reasonable since muscle 7 (lateral deltoid) is a more proximal muscle than muscle 2 (biceps). Using the dominant side of the healthy subject as one example again, we note that more links are identified if the same MI threshold 0.09 is used.

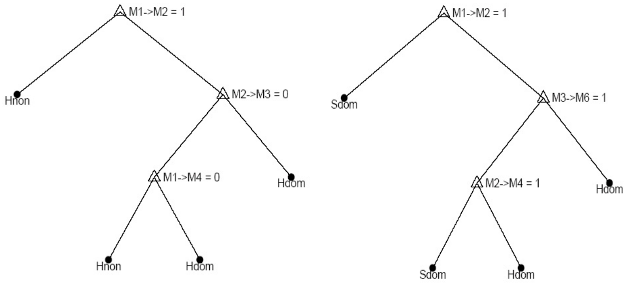
Table 1. The error rates of cross-subject classification by using pair-wise edge features as the classification feature inputs.

No. of edges	1	2	3
HD vs. HNd	0.28	0.22	0.16
HD vs. SD	0.14	0.07	0.00
HNd vs. SNd	0.29	0.18	0.12
SD vs. SNd	0.15	0.08	0.08

3.2. Cross-subject classification

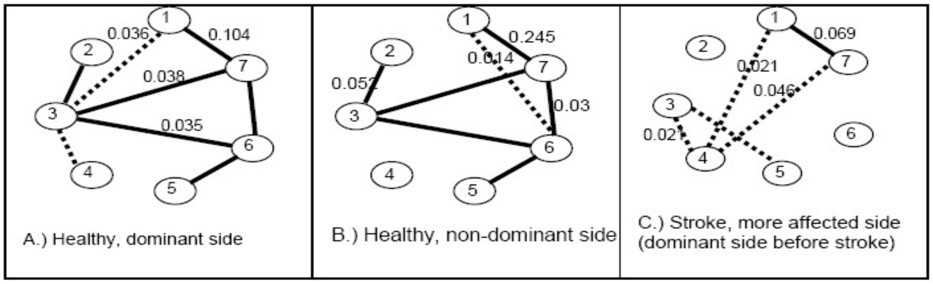
In this study, we are interested in the effects of two factors on muscle association patterns revealed by sEMG recordings, namely stroke status and hand dominance. Therefore, the sEMG recordings were grouped into four experimental conditions: healthy dominant case (i.e. notated as HD), healthy non-dominant case (i.e. notated as HNd), stroke involving the dominant hand case (i.e. notated as SD), and stroke involving the non-dominant hand case (i.e. notated as SNd). To study the effects of different factors, we explore four pair-wise cross-subject classifications. The comparisons, HD versus HNd and SD versus SNd are studied to examine the effect of hand dominance; and the comparisons, HNd v.s. SNd and HD v.s. SD, are studied to examine the effect of stroke status. To have a fair comparison, for each sEMG sample, top 10 edges are used to build a RN representing the particular reaching movement operation.

For each classification problem described above, a classification tree was built based on the structure features of RNs. For simplicity and for avoiding possible over-fitting, we restricted that the classification trees use no more than three elements (i.e. three pair-wise connection features from the input feature vector). The cross-subject classification performance was shown in Table **??** by using the leave-one cross-validation. A subset of edges of RNs represented by a binary vector are used as the inputs to a classification tree to classify two experimental groups characterized by different hand dominance and stroke status. The performances (from the second row) of the best subsets composed of a certain number of edges (the first row) are reported. For the detail of the best classification trees, please refer to Fig. 3. It is noted that classification trees based on the structures of RNs can classify well the four types of experimental groups. Also, it is noted that, as the number of the used edge features increases from one to three, the classification error rate decreases. Using 3 edge features seems a good choice in this study.



(a) HD vs. HNd (b) HD vs. SD

Fig. 3. The best classification trees by using three RN edge structures as the classification features. For each node, a label specifies its group membership. For a branch, its label is the decision rule. For the performances of these trees, please refer to Table 1.



A.) Healthy, dominant side

B.) Healthy, non-dominant side

C.) Stroke, more affected side (dominant side before stroke)

Fig. 2. The examples of learned relevance networks. The solid lines indicate the shared links between all networks, and the dashed lines indicate the special links for each network. For comparison, for each network, the largest 4 MI values are marked in the plots. The index of muscles are as following: 1-Anterior Deltoid, 2-Biceps Brachium, 3-Triceps:Long Head, 4-Triceps: Lateral, 5-Brachioradialis, 6-Latissimus Dorsi, and 7-Lateral Deltoid.

As an illustrative example, assuming using three edge features, examples of the best classification trees for the pair classification problems are illustrated in Figs. 3. In the figures, for each branch node, the left child node corresponds to the satisfying condition (i.e. YES condition), and the right child node corresponds to the unsatisfying condition (i.e. NO condition). The index such as $M1$ means Muscle-1. These trees include connections between agonist-antagonist pairs (e.g. long head of triceps, biceps), muscles with similar actions (e.g. biceps, brachioradialis), and muscles with no obvious similarity of function but might be part of larger synergies (e.g. brachioradialis and latissimus dorsi).

In contrast, Fig. 4 shows that even the amplitude of the most distinguishing muscle cannot easily separate the four experimental groups. Yet most of current studies on sEMG emphasize the amplitude of one muscle for classification. Our classification trees are based on the “carrier” signal (see subsection **??**) which is usually lost by the traditional rectification, smoothing and other preprocessing methods, but they perform very well and offer visible interpretations. The impressive classification performance is unlikely related to over-fitting because the error rate is estimated with cross-subject validation. This cross-subject classification results also indicate that the MI-based RN can be a promising tool to examine the sEMG recordings.

4. CONCLUSION

Performing a reaching task is a complex coordination between muscles. By calculating comprehensive pair-wise mutual information between muscles, a relevance networks can be constructed by displaying links above a threshold to find functional muscle associations during reaching movements. We have demonstrated significant effects of handedness in normal subjects. By applying the relevance network approach to sEMG recordings from reaching movements in stroke subjects, we notice certain muscle association and dependency patterns are consistently different between the healthy and stroke subjects. These results warrant further study to more fully determine the extent to which Relevance Networks may elucidate the complex muscle interactions in reaching movements.

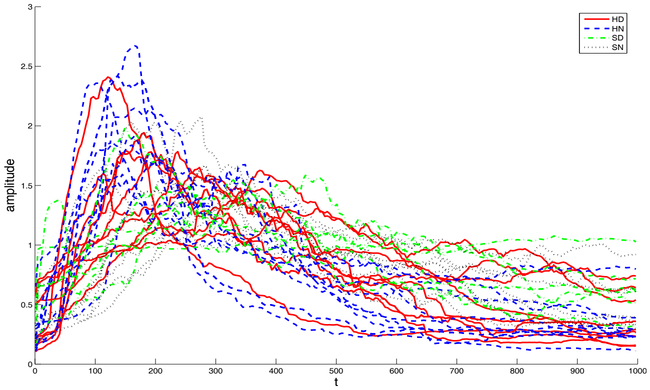


Fig. 4. The sEMG amplitudes of the most distinguishing muscle as selected visually (the lateral head of the triceps). The mean of all the trials from each arm and each subject are shown. Though amplitudes are typically emphasized sEMG studies, the amplitudes cannot separate the different conditions easily. in this study.

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