# BAYESIAN NETWORK MODELING FOR DISCOVERING "DIRECTED SYNERGIES" AMONG MUSCLES IN REACHING MOVEMENTS

*Junning Li, Z. Jane Wang, and Martin J. McKeown*[2]
Department of Electrical and Computer Engineering, University of British Columbia
[2]Brain Research Centre, University of British Columbia, Vancouver, Canada

## ABSTRACT

Modeling the muscle activity patterns in coordinated reaching movements from surface Electromyogram (sEMG) recordings is a key challenge in motor behavior studies. Based on Bayesian Network (BN) modeling of sEMG data, this paper presents a framework for discovering and modeling muscle networks and identifying functional muscle groupings. The learned network is further explored for the purpose of classification. We demonstrate the proposed approach on reaching movements in stroke. We found that the specific muscle triples <anterior deltoid, biceps-brachium and lateral deltoid>, <biceps-brachium, triceps lateral and lateral deltoid> and <triceps long head, triceps lateral and lateral deltoid>, are selectively recruited during reaching movements and are differentially recruited after stroke. We call these computed muscle triplets "directed synergies" to contrast with synergies that are defined by traditional covariance methods. A BN trained on a single healthy subject completely classified and detected the affected side in all stroke subjects. The proposed approach appears a promising technique for muscle network and synergy analysis in motor control.

## 1. INTRODUCTION

An important goal of motor control is to understand how the central nervous system (CNS) co-ordinates the muscle activity patterns necessary to achieve a variety of natural motor behaviors [1]. To address this central goal, a key question to answer is how different muscles efficiently collaborate together for coordinated reaching movements. The concept of muscle "synergies", the coherent activations of a group of muscles, has been proposed in the literature as possible building blocks to analyze motor pattern behaviors (e.g. in frogs) [1]. However, identifying muscle synergies from all possible muscle patterns and the efficient decomposition of complex and variable motor behaviors into meaningful synergies remain challenging problems. So far, a muscle synergy is simply represented as the co-varying activation of different muscles and the reconstruction is based on simple linear combination of covariance-based synergies. These current approaches may not sufficiently represent the complexity and variability of muscle dynamics in higher animals such as humans.

In this paper, to better represent the complex collaborating relationships among muscles during reaching movements, we generalize the muscle synergy idea into the concept of a *muscle network*, defined as a set of muscles and *directed* interactions between them that are coordinated to achieve specific motor behaviors. From the overall muscle network meaningful functional muscle synergies (i.e. sub-networks or network-motif [2] representing interactions between specific muscles, referred as "directed synergies" in this study) can be revealed.

The surface Electromyogram (sEMG) signal, a semi-stochastic complex signal depending on anatomical and physiological properties of the contracting muscle, is recorded on the skin by the means of appropriate non-invasive electrodes [3]. As the sEMG signal can be obtained non-invasively, and it directly reflects the underlying muscle contraction, it has been widely applied in motor control studies. In this study, sEMG signals from several muscles were recorded simultaneously during reaching movements in both healthy and stroke subjects. The overarching goal is the identification of a common formalism able to model the sEMG data.

By employing similar techniques developed for network analysis in other areas, a wide variety of modeling formalisms can be used for inferring muscle networks from sEMG data [4], such as Boolean networks and Bayesian networks (BN) [5]. We are particularly interested in Bayesian networks (also known as directed graphical models) due to its popularity and success in many areas [6]. BN is a knowledge representation formalism at the cutting edge of knowledge discovery and data mining that can combine information and make probabilistic inferences. A BN represents the statistical structure of a data set through a graph of vertices (or nodes) and arcs (or edges) connected by rigorous statistical rules (see section 2).

Use of BN for modeling muscle networks is attractive because its modular nature makes it easily extensible to the task of modeling sEMG data and its solid basis in statistics enables it to deal with the stochastic and nonlinear aspects of sEMG measurements in a natural way. Moreover, Bayesian networks can be used when incomplete knowledge about the system is available, and further it can deal with dynamical aspects of muscles through generalizations like dynamic Bayesian networks.

The main contributions of this paper are as follows:

- To present a framework for learning the muscle networks during reaching movements based on the BN modeling of sEMG data.
- To conduct the pattern analysis and comparison of "directed synergies" between healthy and stroke subjects during reaching movements, and to identify specific three-vertex muscle directed synergies which provide insights into the underlying deficits seen in stroke.
- To explore a supervised classification approach to represent muscle profiles that characterize stroke, by extending the simple Bayesian network.

The paper is organized as follows. In Section 2, we describe the proposed BN framework for learning muscle

networks and analyzing the patterns of the functional muscle directed synergies. A real case study utilizing sEMG recordings from stroke and healthy subjects is described in Section 3. Finally, we conclude our paper and suggest some directions for future research.

## 2. METHOD

### 2.1. The framework

The EMG signals of muscles in a movement are modeled as a vector-valued stochastic process $X(t)=[X_1(t),\ X_2(t)\dots\ X_n(t)]^T$ where $X_i(t)$ is the signal of the $i$th muscle and $n$ is the number of the muscles. A BN is applied to model $X(t)$, to represent the cooperation pattern of the muscles. Different types of BNs may be applied, depending on researchers' interest and prior knowledge. For example, a BN may be static or dynamic.

Features of the BN can be extracted to characterize the network. Widely known features include the number of arcs in or out from vertexes, or the path length from one vertex to another. To go beyond the vertex and the arc levels, we can use as the feature the "network motifs" [2] which are the connection patterns recurring frequently in the sub-networks of the whole network. Due to our specific interest in muscle synergies at the sub-network level, the network motifs are a suitable choice.

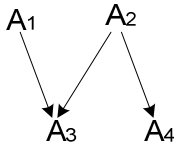
In addition, the BN model built from supervised learning can be extended to classify different cooperation patterns of muscles.

Therefore, the proposed framework includes three main components: Bayesian network learning, sub-network pattern analysis, and the BN-based classification. We will discuss these components in detail as follows.

### 2.2. Brief introduction of Bayesian networks

As shown in Figure 1, a BN consists of a graph, conditional probability distributions for the random variables, the joint probability distribution, and conditional independencies. It is a directed acyclic graph (DAG) of vertices representing random variables and arcs representing dependence relations among the variables. If a vertex $A_i$ has incoming arcs from vertices ($A_1$, $A_2\dots A_m$), it depends on ($A_1$, $A_2\dots A_m$). ($A_1$, $A_2\dots A_m$) are called the parents of $A_i$ and are denoted as pa ($A_i$). $A_i$ is associated with a conditional probability distribution $P(A_i|\ \text{pa}\ (A_i))$. If a vertex $A_i$ has no parents, it is associated with an unconditional probability distribution $P(A_i)$. A BN can represent the joint distribution of all the random variables ($A_1$, $A_2\ \dots\ A_n$) as

$$P(A_1 \dots A_n) = \prod_{\text{pa}(A_i)\neq\phi} P[A_i \mid \text{pa}(A_i)] \prod_{\text{pa}(A_i)=\phi} P(A_i) \cdot$$




$P(A_1)$, $P(A_2)$
$P(A_3A_2A_1)=P(A_3|A_1A_2)P(A_2)P(A_1)$
$P(A_4A_2)=P(A_4|A_2)P(A_2)$
$P(A_1A_2A_3A_4)$
$=P(A_4|A_2)P(A_3|A_1A_2)P(A_2)P(A_1)$

**Figure 1**. An example of Bayesian network. Vertexes $A_1$ and $A_2$ have no parents and they are associated with unconditional probability distributions. Vertexes $A_3$ and $A_4$ have parents and they are associated with conditional probability distributions.

### 2.3. Training Bayesian networks

For simplicity, we consider static BNs, assuming that the muscles cooperate in a same pattern through the whole movement and that the signals at different time points are mutually independent. This assumption probably oversimplifies the truth, but it could provide a sufficient profile of muscle interactions during reaching movements. Therefore, based on the assumption, we use the signals at times $t_1$, $t_2\dots t_k$ as $k$ i.i.d samples, *i.e.* $X(t_i)\sim X=[X_1, X_2\dots X_n]$, to learn a static BN of $X_1$, $X_2\dots X_n$. Furthermore, we assume that $X$ is a Gaussian random variable, though it can be extended to more general distribution models.

Training a BN includes two steps: learning the structure of the DAG and estimating the parameters of the conditional distributions. Several algorithms, for instance, hill climbing (HC), Kutato2 (K2)[7], Inductive Causation (IC)[8], Markov Chain Monte Carlo (MCMC) have been developed to learn the structure. To avoid local minimums found by greedy algorithms (such as HC and K2) and to avoid time-consuming exhaustive search, we use MCMC to learn the structure, with Bayesian Information Criterion (BIC) as the score function which is defined as Equation (1), where $D$ is the observed data, $N$ is the size of $D$, $M$ is the statistical model and dim($M$) is the number of free parameters in the model.

$$BIC(M \mid D) = \log P(D \mid M) - 0.5 \dim(M) \log N \quad (1)$$

Based on the learned structure of the BN, the parameters of the conditional distributions are estimated via the Maximum Likelihood criterion. In this study, we use the software Bayes Net Toolbox (BNT) [9] for Matlab in our analysis.

### 2.4. Patterns of sub-networks

Milo and Shen-Orr [2] reported that a few connection patterns are dominant in the networks in the real world, and that different types of networks are distinguished by different dominant connection patterns. Thus, they proposed using the dominant connection patterns (called network motif) to characterize complex networks. Since the dominant connection pattern may be functional, we adopt a similar idea to discover the functional muscle synergies from BNs.

Given a DAG, we can scan all of its $m$-vertex sub-networks, and record the number of the occurrences of each connection pattern. Since several different DAGs may determine the same statistical model, before we scan the patterns, the DAG of a learned sub-network is converted to the essential graph (EG) [10] which uniquely determines the statistical model and which

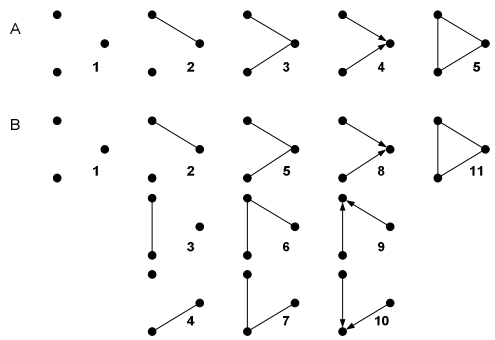



**Figure 2**. Connection patterns of 3-vertex essential graphs (EG). Sub-figure A ignores the order of the vertexes and sub-figure B considers the order [10].

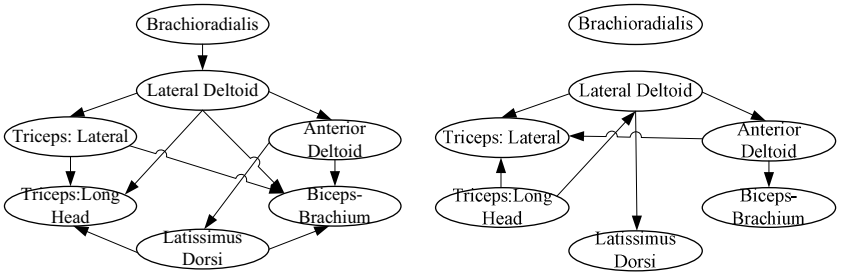



**Figure 3**. Example of the learned Bayesian learned. Both graphs are of the same subject and the same task. The left graph is for the less-affected and the right graph is for the more-affected side.

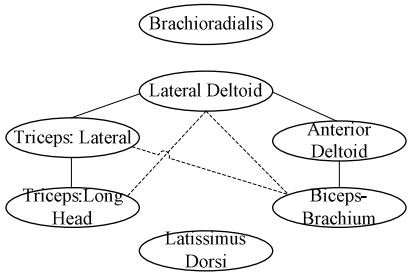



**Figure 4**. The consistent connection patterns of a few specific muscles of a subject. All the arcs appear in the less affected side while the dashed do not in the more affected side.

may have undirected arcs. In the present study, we studied connection patterns of triples ($m$=3) whose possible patterns are shown in Figure 2A [10]. The count of the connection patterns provides an insight to the EG features.

While the general network motif patterns give information in the overall connectivity of the network, we are also interested in sub-networks between *specific* muscles, because these specific muscles may cooperate in similar synergies during different movement tasks. Thus, Figure 2B also shows all the possible connection patterns of 3-vertex EG however the index and order of the vertexes are now considered [10]. For a given subject, several EGs may represent different movement behaviors and therefore we can count the dominant interaction patterns between specific muscles. The significantly recurring patterns may represent the functional muscle synergies.

### 2.5. Classification

We now describe an extension of Bayesian networks to classification, as one goal of our studies in sEMG data is the discovery of a muscle behavior profile for stroke diagnosis or prognosis.

Our intuition is that different subjects use their non-paretic sides similarly while their paretic sides are diseased in different ways. Thus, the BNs associated with the non-paretic sides are expected to be similar across subjects. Suppose that the common joint statistical model of the non-paretic side is $M_0$ and that $D$ is the coming data of an unknown side, and then the likelihood $P(D|M_0)$ represents how much the data $D$ fit the model and thus can be used as a decision value to classify the data. The larger $P(D|M_0)$ is, the more likely $D$ belongs to the non-paretic side. Due to the dimension issue, to make a fair comparison, we used the mean log likelihood (MLL) $\log(P(D|M_0))/N$, with $N$ being the sample size of $D$, as the criteria for classification.

## 3. RESULTS AND DISCUSSIONS

### 3.1. sEMG data sets

The sEMG data were collected from three stroke patients, recording the activities of the following seven muscles: the anterior and lateral deltoid, the triceps (long head and lateral), the biceps brachium, latissimus dorsi, and the brachioradialis. A bipolar montage was used to minimize the effect of crosstalk. The 7-channel sEMG signals were amplified, high-passed filtered at 20 Hz to reduce movement artifact, and sampled at 600 Hz. Since each stroke subject had only one arm predominantly affected the other arm was used as a comparison. For each subject, six reaching movements were performed 5 times repeatedly on each side.

### 3.2. Learned Bayesian networks

At first, a BN of every trial was learned with a 100-step MCMC. In order to create a more robust BN representing the subject's performance, separate BNs were trained on each trial and later combined. If a given arc across all single-trial BNs occurred greater than 60 % of the time, that arc was selected for the final BN. In order to verify the above procedure, the data from each trial were permuted (each channel separately) and the robust BN network was recalculated to ensure that no significant arcs survived.

Examples of the learned DAGs, extracted from the computed BNs are shown in Figure 3. The two DAGs are of the same patient, the same task, but different sides. It is noted that the unaffected side has more arcs than the affected side, suggesting that stroke may damage the cooperation/interaction of muscles, especially of the biceps-brachium. The lateral deltoid and lateral triceps were highly connected with other muscles, indicating that they play central roles in the cooperation between muscles in this reaching movement.

### 3.3. Sub-network Patterns and Muscle Synergies

The sub-network pattern analysis revealed that the connection patterns of the stroke affected side were quite different from that of the unaffected side. As one example, considering one reaching task and all subjects, Figure 5 shows the distribution of the five possible 3-vertex patterns (as seen in Figure 2A) in the EGs representing the unaffected and affected sides, respectively. The histogram indicates that connection pattern 2 is dominant in both sides; while connection pattern 5 is dominant only in the unaffected sides and pattern 1 is dominant only in the affected sides. Recall that pattern 5 means a full interaction between 3 muscles while pattern 1 means no active interaction. Thus, it is suggested that stroke may damage the cooperation capability between muscles, by a tendency of movement towards a pattern 1.

A few specific muscle triples appear consistently in different reaching movements. Figure 4 shows the combined graph of these functional muscle connections of a patient. The muscle triple <Anterior Deltoid, Biceps-Brachium and Brachioradialis>

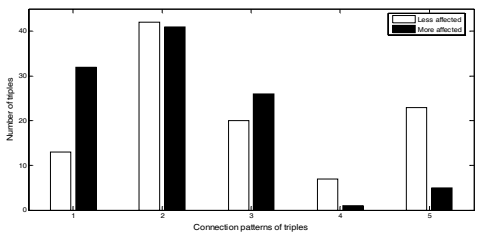



**Figure 5**. The count of the connection patterns.

cooperate in the same consistent pattern on both sides. However muscle triples <anterior deltoid, biceps-brachium and lateral deltoid>, <biceps-brachium, triceps lateral and lateral deltoid> and <triceps long head, triceps lateral and lateral deltoid> cooperate in one consistent pattern on the unaffected, but another consistent pattern on the affected side. These triples can be identified as the functional muscle synergies and they warrant further investigation.

### 3.4. Classification Performance

The data of one patient's unaffected side in one movement task were picked out to train the BN. Then, the data of other patients' were used to test the classification performance of the BN. The test data contains different trials, different arms and different tasks.

Figure 6 shows that the unaffected side and the affected side are completely separated. We note that the MLL of the unaffected sides across all subjects is higher than that of the affected sides, and that the BN used for classification was trained on a single subject's unaffected side. This suggests that the BN-classification method can gracefully deal with intersubject variability.

## 4. Conclusions

In this paper, we have developed a framework for discovering and modeling muscle networks in motor control. By applying these methods to sEMG data collected from reaching movements in healthy and stroke subjects, we demonstrated that Bayesian network modeling provides a powerful tool to model and to analyze sEMG data. We have demonstrated that analyzing the sub-networks of BNs is a promising way of identifying functional muscle directed synergies (specific interacted small muscle groups). Analysis of BNs at different levels can provide different insights into the underlying muscles' functions. Network analysis suggests that stroke disease may damage the effective cooperation between a few specific muscles during reaching movements.

As BNs can be generalized in various ways, dynamic BNs will be explored in the future to study the dynamics of the muscle networks. Hidden vertexes can also be included to represent the neural cells in modeling the motor control.

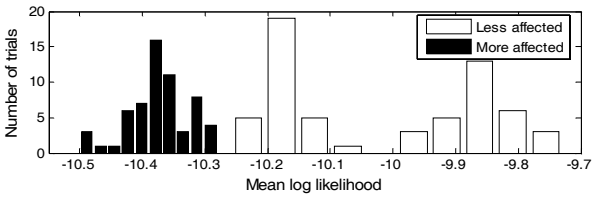



**Figure 6**. The mean log likelihood (MLL). The MLL is of different subjects, different tasks and different arms.

## 5. ACKNOWLEDGEMENTS

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