QUANTIZATION OF MOTOR ACTIVITY INTO PRIMITIVES AND TIME-FREQUENCY ATOMS USING INDEPENDENT COMPONENT ANALYSIS AND MATCHING PURSUIT ALGORITHMS

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*Abstrac*t- **It has been proposed that the segmental spinal nervous system may organize movement using a collection of force-field primitives. The temporal organization of primitives has not been examined in detail. Recent data examining muscle activity underlying corrections of motor patterns suggested that primitives might be recruited into motor programs as waveforms with a constant duration. Here we test the idea that each primitive or premotor drive comprising part of the motor patterns might be expressed as the combination of a small number of time-frequency atoms from some orthonormal basis. We analyze the temporal organization of pre-motor drives extracted from the motor pattern by the Bell-Sejnowski algorithm for independent component analysis. We then use matching pursuit cosine packet analysis to examine the time series of the activation waveforms of each of the independent components. The analysis confirms that the motor pattern can be described as a combination of a small number of time-frequency atoms. These atoms combine to generate the temporal structure and activation of the individual components or premotor drives that generate individual muscle activity.**
Keywords - **Primitives, electromyograms, force-fields, independent component analysis, time frequency atoms.**

I. INTRODUCTION

[*]The discovery of the (potentially low dimensional) structure underlying complex motor acts organized by animals and man is an issue of central importance to neuroscience. The organization of action impacts on sensory processing for action, learning, and development, and is significant for understanding of injury, disease, rehabilitation and biomimetic neurotechnologies or robotics. Motor acts organized by the spinal cord of lower vertebrates show complex adapted goal directed properties reminiscent of voluntary movement [1,2]. For example, after surgical preparation of a spinal frog by destroying the connection of medulla and rostral brain structures with the spinal cord, complex goal directed movement can be evoked from the spinal cord. The trajectories organized by the spinal frog to remove irritants from the skin share many properties with human voluntary movement [1] and exhibit rapid on-line corrections [2]. In the context of these on-line corrections, we observed that the activation of muscles for corrections and during other phases of the motor pattern exhibited a similar duration, regardless of context [2]. We also observed in a

different paradigm that isometric forces could be decomposed into fixed duration waveforms that were conserved across frogs [3]. These data relate generally to the idea of force-field primitives as a spinal basis for movement[2,3,4,5].

A. The hypothesis to be examined

Our data led us to speculate that the frog spinal cord constructs movement by a mechanism of combination of primitives, each primitive being of the following form:

$$\theta(r,\dot{r},t) = A.a(t)\phi_i(r,\dot{r})$$

(1)

A is a scaling factor, t is time and r a coordinate vector describing the limb configuration. We speculate that a(t) is similar in all primitives, resembling a fixed half cycle oscillation, or a fixed impulse response. If correct, this constrains the method of construction of a time varying force-field F(r,r,t) for generation of a behavior to the selection of the scalings A_i and the phasings τ_t of the component primitives in equation 2 below.

In this formulation the motion control field F is thus constructed as:

$$F(r,\dot{r},t) = \sum_i A_i a(t + \tau_i)\phi_i(r,\dot{r})$$

(2)

To test these ideas here we used analyses of electromyogram patterns in various behaviors. Our focus here will be on testing the conservation of timing properties (the function a(t)) across primitives.

II. METHODOLOGY

A. Electromyogram based analysis of primitives

In the earlier experiments referenced in [1,2,3] we examined waveforms by the methods historically used in Electroencephalography (EEG). We time aligned and amplitude normalized peaks of waveforms and examined deviations away from peak. Electromyograms (EMG) have the advantage over force records that they can be obtained during movement and that they more properly reflect the neural output of the central nervous system (CNS) than isometric forces, which depend on a combination of limb state and EMG. In our early examination of EMG we detected underlying groups of muscles and phases of activity by inspection and subtraction procedures [1,2,3]. Here, we sought a method to examine drives and temporal patterns in

Report Documentation Page

Report Date	Report Type	Dates Covered (from... to)
25OCT2001	N/A	-

Title and Subtitle	Contract Number
Quantization of Motor Activity into Primitives and Timefrequency Atoms Using Independent Component Analysis and Matching Pursuit Algorithms	
	Grant Number
	Program Element Number

Author(s)	Project Number
	Task Number
	Work Unit Number

Performing Organization Name(s) and Address(es)	Performing Organization Report Number
Department of Neurobiology and Anatomy, MCPHU School of Medicine, Philadelphia	

Sponsoring/Monitoring Agency Name(s) and Address(es)	Sponsor/Monitor's Acronym(s)
US Army Research, Development & Standardization Group (UK) PSC 802 Box 15 FPO AE 0949-1500	
	Sponsor/Monitor's Report Number(s)

Distribution/Availability Statement
Approved for public release, distribution unlimited

Supplementary Notes
Papers from the 23rd Annual International Conference of the IEEE Engineering in Medicine and Biology Society, October 25-28, 2001, Istanbul, Turkey. See also ADM001351 for entire conference on cd-rom., The original document contains color images.

Abstract

Subject Terms

Report Classification	Classification of this page
unclassified	unclassified

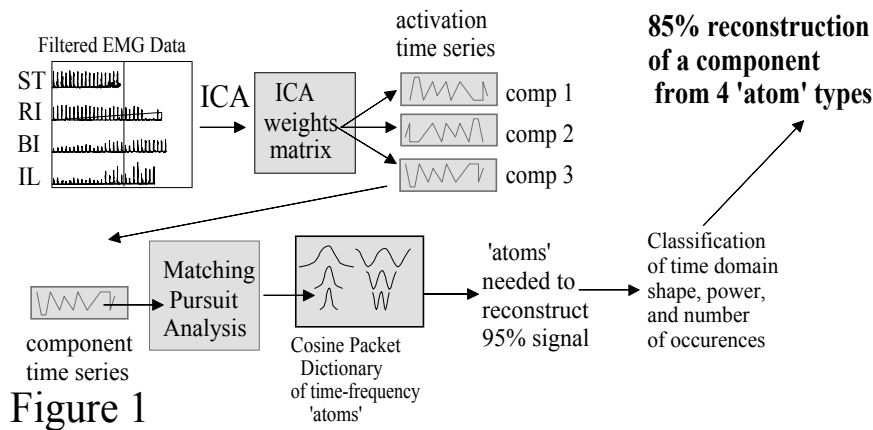| Classification of Abstract	Limitation of Abstract
unclassified	UU

Number of Pages
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Figure 1

Figure 1: Processing stream and data analysis. Raw EMG was rectified and filtered and used as input to the Bell-Sejnowski ICA algorithm. This generated an ICA weight matrix describing EMG contributions of each component or drive, and activation time series for each component. The activation time series were subject to Mallat and Zhang Matching pursuit cosine packet analysis and those time-frequency atoms required to achieve 95% signal reconstruction examined. See Figures 2-4

an hypothesis free manner, insofar as feasible. We sought to achieve two goals: (1) decompose the electromyograms into a set of premotor drives, (2) to examine the temporal behavior of these drives.

B. Extraction of premotor drives

To extract premotor drives representing primitives we used the Bell-Sejnowski algorithm for independent component analysis (See Figure 1). This infomax neural network algorithm has been applied extensively to EEG and maps naturally onto the problem of detection of primitives or drives in EMG patterns. Each EMG channel from a muscle can be considered a "microphone" listening to one or more premotor drives, in the manner of a person listening to multiple speakers conversing. Neurophysiological data provides support for the motor unit acting as an element which linearly sums premotor drives under most circumstances. Premotor drives and primitives are considered to be independently controllable contributors to movement. Extraction of premotor drives from EMG is thus likely to be a problem well suited to the Bell-Sejnowski Algorithm [6,7]. We first extracted the weight matrices for independent components and their associated activation waveforms through time using this algorithm in the MATLAB implementation of Scott Makeig[1] and then examined the time series behavior of these waveforms.

C. Examination of time series behavior of premotor drives

We tested two methods for decomposing the time series of independent component activation into a small number of wavepackets or elements. Both are well established and available in the Wavelab MATLAB extension. Both are means of selecting a small orthornormal basis from an overcomplete set of bases or wavepacket dictionaries of size 2^N, where N is the time series length. The best basis algorithm of Wickerhauser and Coifman performs a globally optimal decomposition into a basis than minimizes entropy. The matching pursuit algorithm of Mallat and Zhang [8] uses a greedy algorithm to locate a small number of locally optimized time-frequency 'atoms' (ibid.) from the wavepacket

dictionary. In this paper we will focus on the use of the matching pursuit algorithm[2]. We chose the subset of atoms from the wavepacket dictionary built by the matching pursuit algorithm that gave reconstruction of 95% of the signal variance of the activation time series. We then examined the time-frequency atoms in this subset in more detail.

III. RESULTS

A. Similarly shaped time-frequency atoms dominate the significant independent components in a frog

We present data for matching pursuit analyses from 2 frogs, showing analyses of 3 components in one frog and a similar example of a component in a second frog for comparison.

In figure 2 we summarize part of the analysis of a typical set of components from such a data set. Time frequency atoms were classified in the time domain into groups and the groups ranked in terms of frequency of occurrence in the decomposition. In the top row (figure 2A) we show the number of occurrences of specific impulse shapes for the three components accounting for the highest fractions of EMG variance in frog 1. The corresponding tapered cosine shapes were normalized to a peak amplitude of 1. In the figure in row 2B the normalized waveforms are displayed over the 100 point (400ms) intervals examined in a time domain classification of the atoms. The same two waveforms (the first two in each row) were most frequent in all 3 components. In 2C we show the mean amplitude of each of these waveform classes in the reconstruction. To generate the graphical display of the data shown in 2C the wave in 2B was amplitude modulated according to its mean peak amplitude in the reconstruction. In general the first waveform was the highest mean amplitude. The exception was in component 2 in which the 9th was. However, this waveform was only used once in the reconstruction (presumably) for some unusual
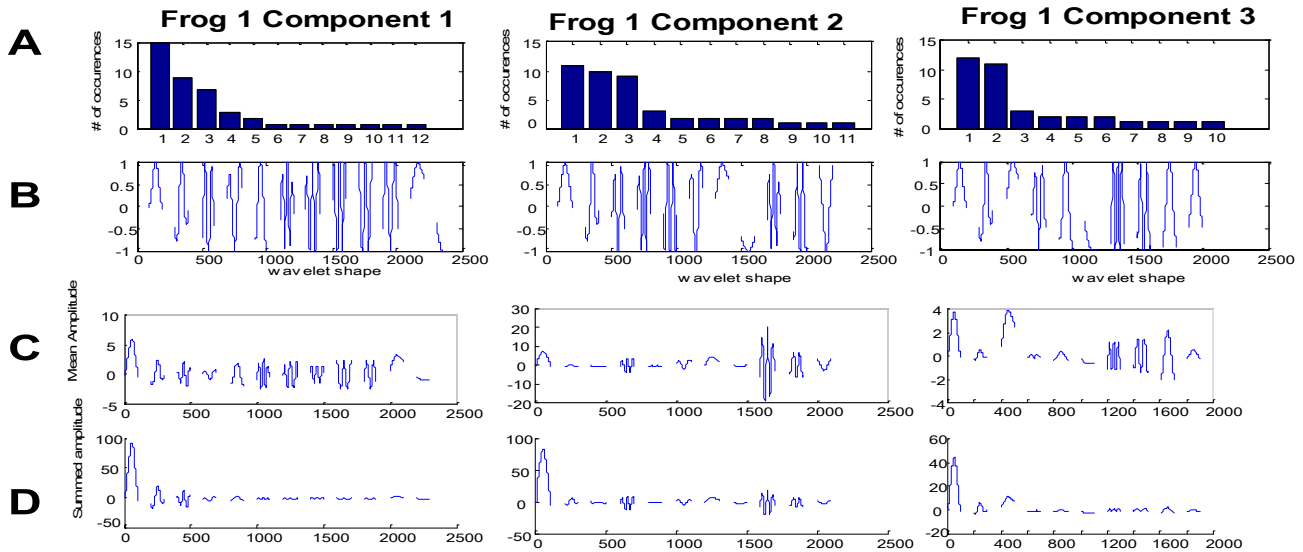

Figure 2: Matching Pursuit Analysis of three ICA components in a single frog. A: numbers of uses of a time frequency atom of the type shown in B. B: normalized time-frequency atom types shown over 400ms intervals. C: mean amplitude of each time-frequency atom in the 95% reconstruction. (Waveforms in row B multiplied by mean amplitude of waveform). D: total amplitude of all time-frequency atoms of each type. (Waveforms in B multiplied by total amplitude).

wave structure. In figure 2D we use a similar graphical device to show the summed amplitude of each wave type used in the to show the summed amplitude of each wave type used in the 95% reconstruction and the contribution of the first type of atom can be seen to dominate. The normalized waves in figure 2B were amplitude modulated according to their total summed amplitude in the reconstruction to generate this graphical display. It can be seen that in every instance power was concentrated in the first and most frequent wave shape. Taken together these analyses indicate that in this frog a single wave shape and similar frequency cosine packet accounted for most of the signal power of each independent component, drive or primitive extracted by ICA. This observation was in keeping with a fixed duration of activity for each type of primitive, as hypothesized above.
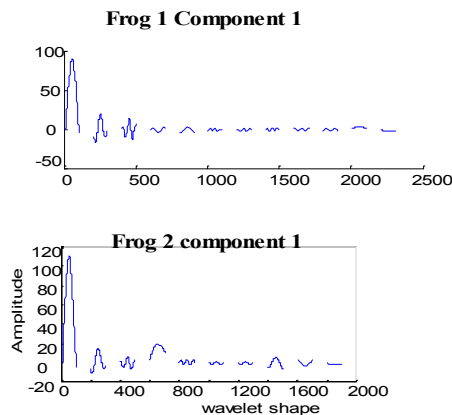

cosine packets used: 1 5 2 11 Reconstruction % = 84.836

Figure 4 Reconstruction of 85% of the variance of component 1, frog1. This was achieved with 4 types of time-frequency atoms (indicated by asterisks in part A). A: Mean amplitude of each time frequency atom (see Figure 1 and text) and atoms used. B: total amplitude of each atom type. C: original ICA component activation time series, extracted by Bell-Sejnowski algorithm. D: 85% reconstruction.

Figure 3 Comparison of matching pursuit analyses among components in two frogs. Although there are 12 'types' of waves in Frog 1 and 10 in Frog 2, most power is concentrated in a similar wave shape and the first three most frequent time-frequency atoms are similar.
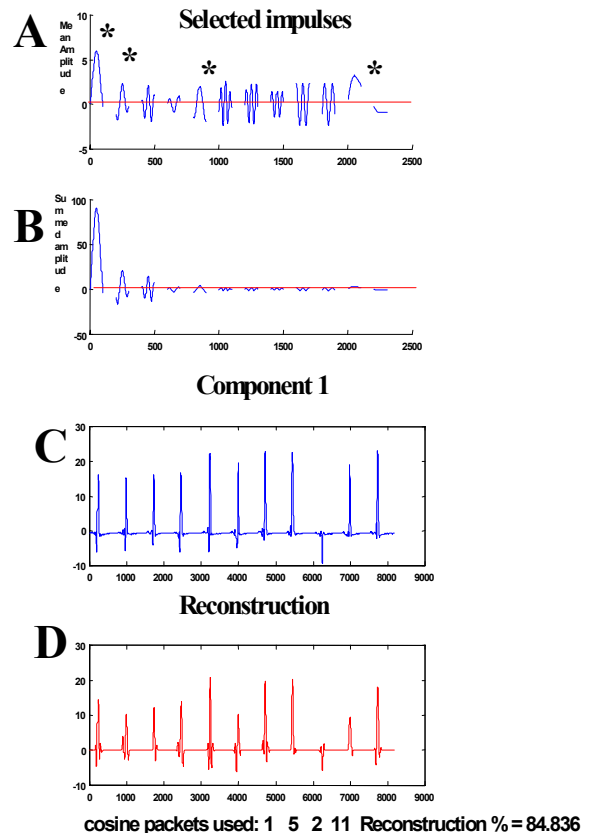
B. Similarly shaped time-frequency atoms dominate in significant components among frogs

In figure 3 we show that signal power was concentrated in specific and similar time-frequency atoms and wave shapes in two frogs. We display the summed amplitude measure, which graphically indicates both wave type and power content for the time frequency atoms accounted for 95% of signal variance in the two most important independent component in two frogs. This figure corresponds to Figure 2 row D. Note the close similarity of the first three wave types and especially the first high amplitude component. We found this similarity of wave shape or impulse in most frogs in which independent components different from EMG channels were readily obtained.

C. Selection of a few time frequency atoms reconstructs 85% of signal variance for an independent component.

We found that selecting a few of the time-frequency atom types (<4) from the dictionary used in the reconstruction allowed us to reconstruct ~85% of the independent component variance and to substantially reconstruct the original EMG signal. In figure 4 we show the mean (4A) and summed (4B) amplitudes of atoms. The types of time-frequency atoms selected are shown in A with asterisks. In figure 4C the time series of the independent component activation directly obtained from the ICA analysis is shown. In 4D we show the reconstruction using four time-frequency atom types indicated by asterisks in figure 4A. The substantial variance captured by this reconstruction is in keeping with a description of the behavior of individual independent components as comprised of a series of amplitude and phase modulated pulses of similar waveform.

IV. DISCUSSION

The notion of intermittency and time quantized elements in human and animal movement construction has been suggested by many sets of experiments e.g. from Ghez, Krebs and Hogan, Flash, Milner and others. The decomposition of EMG into principal components, or factors has been used to examine the dimensionality of drive or control variables underlying the motor pattern, or kinematic production. Independent Component Analysis is a superior method for this decomposition, although not the primary focus of this presentation. Use of ICA to extract lower dimensional and significant representations of EEG or other biological signals has been thoroughly explored. Such components might be used as a basis for neuroprosthetic control [9]. In this study the relation of components to the basis of motor action may be far more direct than in previous studies. However the drives extracted by ICA need not possess similar timing structures among themselves, indeed it might be speculated they would not. The extraction of similar frequency impulse structures underlying the more significant components is thus both potentially surprising and important. If components represent premotor drives or primitives, this analysis implies these are not passive followers of arbitrary imposed control

signals but possess intrinsic dynamics or filtering properties. Further, we can speculate that the imposed control signals are either fairly discrete impulses or else the circuitry of primitives organizes the incoming control signals into pulsed actions by their intrinsic dynamics. These data also support a separation of a rhythm generating or a pulse timing system in the spinal cord from a set of execution modules or primitives. This is a departure from the conventional fully integrated central pattern generator systems suggested by invertebrate systems like the stomatogastric ganglion but in keeping with frameworks suggested by ourselves, by Schaal and Sternad, by Prochazka and some engineering decompositions used in robotics. In our opinion these data and our other analyses of reflex trajectories do not support any explicit central equilibrium path or other trajectory specification, therefore resembling the descriptions of Todorov [10] at a non-cortical level. Based on our analyses we believe there is good reason to suppose the formulation of equation 2 in the introduction may capture the essence of spinal construction of movement. Issues then become whether descending controls can modify the intrinsic dynamics or structure of primitives so as to alter field structure or time dilate or contract the impulses which appear to drive movement at the spinal level.

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