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Direct feature extraction from multi-electrode recordings for spike sorting

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ABSTRACT

Information from extracellular action potentials (EAPs) of individual neurons is of particular interest in experimental neuroscience. It advances the understanding of brain functions and is essential in the emerging field of brain-machine interfaces. As EAPs from distinct neurons are generally not recorded individually, a process to separate them from the multi-unit recordings, referred to as spike sorting, is required. For spike sorting, the feature extraction step is crucial. Starting from acquired data, the task of feature extraction is to find a set of derived values or "features" that are informative and non-redundant to facilitate efficient and accurate sorting, compared with using the raw data directly. It not only reduces the dimensionality of the data but also the impact of noise. In this paper, two novel feature extraction algorithms for sorting multi-electrode EAPs are proposed. These algorithms can be seen as generalizations of principal component analysis and linear discriminant analysis, but the features that match the dominant subspaces observed in the multi-electrode data are obtained without the need for vectorizing a multi-electrode EAP or breaking it into separate EAP channels. These algorithms require no construction of EAP templates and are applicable to multi-electrode recordings regardless of the number of electrodes. Clustering using both simulated data and real EAP recordings taken from area CA1 of the dorsal hippocampus of rats demonstrates that the proposed approaches yield features that are discriminatory and lead to promising results.

1. Introduction

Extracellular action potentials (EAPs) of individual neurons, referred to as "single-unit activity," are of particular interest in neuroscience research. Information derived from these EAPs is essential in understanding how interconnected neurons cause sensation and create responses in a changing environment [1,2], or in restoring motor functions in those with severe paralysis [3–5]. However, EAPs from distinct neurons are generally not recorded individually. Even though an extracellular probe is small and can be directly inserted into biological tissue to accurately target a specific location, it typically acquires a superposition of activity from an unknown number of neurons [6,7]. In addition, the recordings contain various noise components, such as electrode noise and biological noise (*e.g.*, activity of distant neurons and ionic channel noise). As a result, a process referred to as "spike" sorting, is required to separate out the single-unit activity prior to many applications [8–10]. Spike sorting in practice may involve human intervention; however, variability in the sorted results can be significant from one operator to another [11]. Furthermore, manually dealing with large volumes of data can be extremely time-consuming. These factors make an automated spike sorting procedure indispensable.

A spike sorting algorithm (see Fig. 1) consists of three basic steps [7,8]: *EAP detection and alignment*, *feature extraction*, and *clustering*. EAP detection refers to determining the occurrence times of EAPs in the recordings, normally achieved by detecting changes in amplitude or energy in the data series or by template matching [9,12,13], assuming that the EAP waveforms of interest are known a priori. Temporal alignment refers to the process of arranging the segmented EAP waveforms so that they "line up" in time. This is often done by finding a point of maximum amplitude or maximum slope for each EAP, or for each set of EAPs within a multi-electrode recording [14]. Clustering refers to grouping the extracted features into clusters associated with different putative neurons, and can be achieved through manual cluster cutting or via automated methods such as the k-means or valley-seeking clustering algorithms [9,10]. Starting from acquired data, the task of feature extraction is to find a set of derived values or features that are informative and non-redundant to facilitate efficient and accurate sorting, compared with using the raw data directly. It not only reduces the dimensionality of the data but also the effect of noise in the detected

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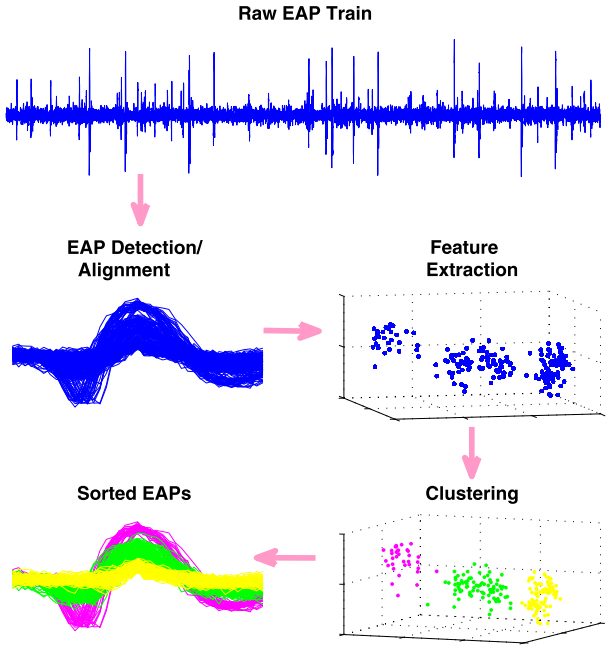

Fig. 1. Typical procedures for spike sorting.

EAPs. Since each neuron fires EAPs of a particular shape, features from EAPs are extracted to emphasize this point. Examples of these features include EAP shape-related features [10,15] such as height, width, peak-to-peak amplitude, principal components (PCs) [10], and wavelet coefficients [16,17]. With the help of an appropriate basis, the latter two feature categories can be extracted by directly projecting the EAPs onto the basis. Matching pursuit (MP) is another approach possessing similar properties [18].

Advances in microfabrication technology have enabled the production of multi-electrode extracellular probes with several closely spaced recording sites. Their use facilitates better sorting quality and increases the number of correctly identified neurons [19–21]. While multi-electrode probes are capable of providing better insight into the spatiotemporal nature of the signals produced by each recorded neuron, the resulting massive volumes of data unquestionably pose challenges to revealing discriminant information required for spike sorting. The simplest approach for exploiting multi-electrode recordings is to apply the above feature extractors (*e.g.*, EAP shape-related features) electrode-by-electrode to form a concatenated feature set [22–24]. With this approach, a large-dimensional space is created where sorting must be performed [25]. Applying multivariate matching pursuit (MMP) [18], a computationally efficient multichannel extension of MP, to feature extraction for sorting multi-electrode EAPs is also feasible. However, issues such as how to determine the dictionary for a given set of EAPs, shortening the searching time for the best atom functions, and reducing the size of the concatenated feature vectors need to be well considered before applying it to real spike sorting problems. Efforts have also been made to utilize spatial information [26–28] or independent components [29,30] for clustering. Examples of spatial information include neuron locations [26,27] and spatial signatures [28]. However, the estimation of neuron locations requires a "forward model" (*e.g.*, the monopole model) to describe the propagation of EAPs through the extracellular media [31]. The spatial signature, on the other hand, can be extracted without the need for a forward model, but its performance is sensitive to noise. Spatial signatures are also seen in the application of locating cerebral sources in electroencephalograms [18]. Independent component analysis (ICA) is a blind source separation technique that is able to resolve temporally overlapping EAPs, but it requires assumptions about the non-Gaussianity and independence of the EAPs. Moreover, the observed data are modeled to be a linear mixture of signals [29], and the number of electrodes needs to be greater than the number of neurons [9,30,32]. As the application of these approaches for unveiling discriminant information in multi-electrode recordings may not satisfactorily achieve the desired performance, the search for new methods continues.

To elicit the spatiotemporal information contained in the multi-electrode recordings for the spike sorting application, two block projection based feature extraction algorithms are proposed in this paper. The extraction process begins by identifying two different discriminant subspaces in the recordings. Features are then extracted by directly projecting the multi-electrode data block corresponding to each EAP onto these subspaces. Unlike the above mentioned feature extractors that are applied electrode-by-electrode, the proposed algorithms allow the features to be extracted while maintaining the structure of the data between electrodes so that the relative spatial information between them can be preserved for clustering. To avoid losing this spatial information, one may directly apply principal component analysis (PCA) to the vectorized multi-electrode data block, a technique that will also be covered in Section 3.2. The proposed algorithms can be used for higher-rank signals, where point source models are unable to provide an accurate description of the measured EAPs. This higher-rank property is due to the fact that at close range the EAP sources appear to be distributed rather than point sources, or it may be caused by dendritic current distortion [31,32]. The ability to exploit higher-rank models is an advantage compared with the ICA-based methods which have been proposed under the assumption of instantaneous point source mixtures. With a further dimensionality reduction, the ultimate feature vectors of the proposed algorithms can have dimension as low as that in typical spike sorting applications. Finally, the algorithms are applicable irrespective of the number of electrodes used for the extracellular recordings, and have no need for EAP templates.

The remainder of the paper is outlined as follows. In the next section, we present the data model and underlying assumptions. The PCA based feature extraction techniques and our proposed algorithms are given in Section 3. The results of simulations and real experiments are then discussed in Sections 4 and 5, respectively. Finally, some conclusions are offered in Section 6.

2. Data model and assumptions

To focus on the feature extraction problem, we assume that the EAPs on one of the electrodes have been detected using existing approaches (*e.g.*, [10]), and that the multi-channel, time-aligned data segments are isolated accordingly based on these detected EAPs. For the situation where the EAPs from a specific neuron are only seen by a subset of the electrodes in an electrode array, this process may need to be repeated from one electrode to another. This is because any selected electrode whose recordings are used for EAP detection may not contain the EAPs from that specific neuron, and repetition is used to avoid this situation. Assuming there are m electrodes and n samples per segment, the data corresponding to the i-th detected EAP forms an $m \times n$ matrix $\mathbf{X}_i$, which is hereafter referred to as an "EAP bundle."[1] Assuming that each bundle consists of an EAP from a single neuron (similar to most of the methods described in [10], the proposed algorithms are not intended to handle the overlapping EAP problem). Moreover, the EAPs from that specific neuron are assumed to be seen by more than one electrode in this bundle. An appropriate model for $\mathbf{X}_i$ can be expressed as

[1] $\mathbf{X}_i$ is also known as a "multi-electrode waveform" in, for example, [12,33,34].