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A novel framework for feature extraction in multi-sensor action potential sorting

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HIGHLIGHTS

- Multi-sensor extensions of conventional single-sensor feature extraction algorithms.
- Spatio-temporal features are extracted simultaneously from multi-sensor AP measurements.
- Spatial information is extracted without a need for a forward propagation model.
- Temporal information is extracted without predefined AP templates.

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ABSTRACT

Background: Extracellular recordings of multi-unit neural activity have become indispensable in neuroscience research. The analysis of the recordings begins with the detection of the action potentials (APs), followed by a classification step where each AP is associated with a given neural source. A feature extraction step is required prior to classification in order to reduce the dimensionality of the data and the impact of noise, allowing source clustering algorithms to work more efficiently.
New method: In this paper, we propose a novel framework for multi-sensor AP feature extraction based on the so-called Matched Subspace Detector (MSD), which is shown to be a natural generalization of standard single-sensor algorithms.
Results: Clustering using both simulated data and real AP recordings taken in the locust antennal lobe demonstrates that the proposed approach yields features that are discriminatory and lead to promising results.
Comparison with existing method(s): Unlike existing methods, the proposed algorithm finds joint spatio-temporal feature vectors that match the dominant subspace observed in the two-dimensional data without needs for a forward propagation model and AP templates.
Conclusions: The proposed MSD approach provides more discriminatory features for unsupervised AP sorting applications.

1. Introduction

Direct measurement of neuronal action potentials (APs) with extracellular electrodes placed in the vicinity of active neurons has become an indispensible tool in experimental neuroscience. A typical goal in these experiments is to record the APs (spikes) of individual neurons, often referred to as "single-unit activity." Since specific brain behaviors emerge from the interaction of individual neurons, identifying single-unit activity in large populations of neurons remains a high priority in experimental neuroscience (Buzsáki, 2004). In addition to advancing understanding of brain function, information from these recordings is increasingly important in the emergent field of brain–machine interfaces (Carmena et al., 2003), which may potentially restore motor function in those with severe paralysis. Despite their small size and high precision of placement (Cham et al., 2005), signals at extracellular electrodes often contain the superposition of the activity from several neurons. In addition, these signals invariably contain various noise components, such as electrode (thermal) noise, biological noise (activity of distant neurons), and ionic channel noise (Benitez and Nenadic, 2008). The process of separating out the activity of individual neurons from this so-called multi-unit activity measurements is often

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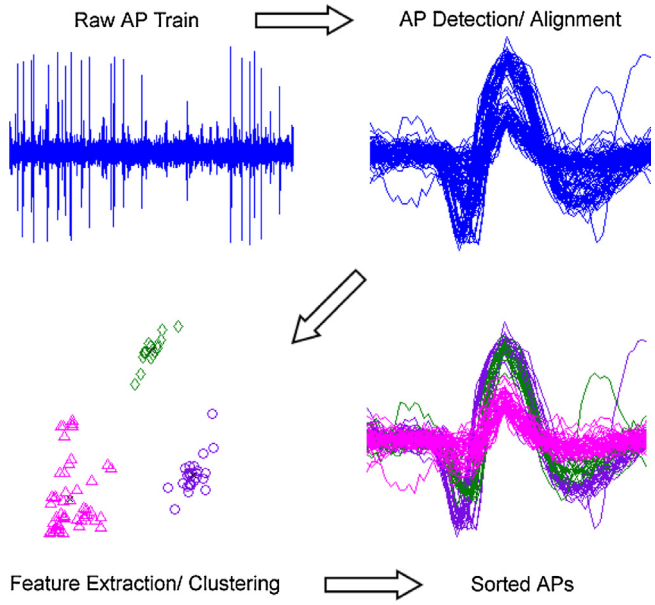

Fig. 1. Automated procedures for AP sorting.

referred to as AP sorting or spike sorting (Fee et al., 1996; Abeles and Goldstein, 1997; Lewicki, 1998; Gibson et al., 2012; Micera et al., 2010).

Manual sorting of APs in large volumes of experimental data may be prohibitively time-consuming, and so automated AP sorting procedures have become essential. An automated AP sorting algorithm (see Fig. 1) typically entails three steps: (1) *AP detection and alignment*, *i.e.*, determining the locations of APs in the electrode time series and arranging the segmented AP waveforms so that they "line up" in time, (2) *feature extraction*, *i.e.*, finding a low-dimensional representation of detected APs, that facilitates AP discrimination according to their neuronal sources, and (3) *clustering*, *i.e.*, grouping the extracted features into clusters associated with individual neurons. The feature extraction step is crucial since it reduces the effect of noise and removes redundant information in the input data so that clustering algorithms can work efficiently. The three most common feature categories discussed in the literature are: (1) AP shape-related features (Lewicki, 1998; Yang et al., 2009), such as AP height, width, peak-to-peak amplitude, inter-AP interval, and first-order derivative, (2) wavelet coefficients (Yang and Shamma, 1988; Letelier and Weber, 2000; Hulata et al., 2000, 2002; Quiroga et al., 2004; Nenadic and Burdick, 2005), and (3) principal components (PCs) (Gray et al., 1995; Lewicki, 1998; Csicsvari et al., 1998; Harris et al., 2000). A common characteristic of the above features is that they only capture temporal information since they are extracted from single-sensor measurements. However, temporal features are suboptimal for AP sorting since neurons of the same class located at roughly equal distances to the electrode can generate similar AP waveforms (Buzsáki, 2004), and therefore similar features.

To overcome this problem, multi-sensor extracellular probes capable of recording time-aligned data from multiple spatial locations have been used (Harris et al., 2000; Takahashi et al., 2003; Emondi et al., 2004; Chelaru and Jog, 2005). The simplest way to extract features from multi-sensor measurements is to apply standard feature extraction techniques to individual channels, and then combine the extracted features into a single feature set. For example, in Csicsvari et al. (1998) and Harris et al. (2000), the first three PCs are calculated for each 4-sensor probe (tetrode) channel, and a 12-dimensional feature vector is created by projecting the data in each channel onto each of the three PCs later. Other approaches utilize spatial information in multi-channel measurements to extract features for clustering. Examples include estimating neuron locations (Chelaru and Jog, 2005; Szymanska et al., 2013) or calculating independent components (Takahashi et al., 2003, 2003; Brown et al., 2001). To localize a neuron with multi-sensor measurements, a "forward model" describing the propagation of APs through extracellular media is typically adopted. Monopole transmission represents the simplest forward model (Gray et al., 1995; Jog et al., 2002; Chelaru and Jog, 2005; Lee et al., 2007), but it may lack the flexibility needed to describe complex field patterns seen experimentally. Consequently, this may lead to a high variance in source localization and in turn to poor clustering outcomes. Independent component analysis (ICA) separates a multivariate signal into additive subcomponents. While ICA has been useful in resolving temporally overlapping spikes, it requires strong assumptions regarding the non-Gaussianity and independence of the APs. In addition, a feature extraction step is still required to identify the source of the recovered AP waveform. Finally, if propagation delays in the mixing medium cannot be neglected, the performance of ICA will degrade unless a more sophisticated time-delay model is employed (Takahashi et al., 2002; Shiraishi et al., 2009).

In this paper, we propose a novel framework for multi-sensor AP feature extraction based on the so-called Matched Subspace Detector (MSD) (Scharf and Friedlander, 1994; Kay, 1998; Parker and Swindlehurst, 2003). The MSD can be viewed as a multidimensional generalization of the ubiquitous matched filter. It is used to uncover an unknown low-dimensional subspace of data to which the signal of interest is typically confined. It has been applied to a variety of multivariate signals ranging from radar (Parker and Swindlehurst, 2003) to functional magnetic resonance imaging (Liu et al., 2001) data. Unlike multi-sensor PCA and algorithms based on location estimates, which respectively allow only temporal or spatial information to be extracted, our MSD approach provides joint spatio-temporal feature vectors that are more efficient for differentiating APs of individual neurons. With a multi-sensor probe, each AP is naturally recorded as a two-dimensional (space *vs.* time) data matrix, and each AP signal has an intrinsic spatial structure or "spatial signature" related to the location of the neurons relative to the probe. This spatial information can used to differentiate between the APs since the neurons where the APs originate are in different locations relative to the probe. The MSD, on the other hand, not only takes advantage of the spatial information, it also exploits the same temporal information used by previous algorithms, and thus is more discriminant. Extracting features directly from data matrices to preserve the structural information has also been exploited in the field of facial recognition (*e.g.*, see Yang et al., 2004), although the formulation and treatment of the problem are different from the proposed MSD approach. Furthermore, spatial information is extracted by the MSD method without the need for a forward propagation model as required by location-based methods. While we will focus on using the MSD approach assuming each AP results in a rank-one signal at the electrode array (*i.e.*, point source models), the technique can also be generalized for higher-rank signals, where point source models are unable to provide an accurate description of the measured patterns. This is an advantage compared with ICA-based methods, which have only been proposed under the assumption of instantaneous point source mixtures. Higher-rank signals, in practice, may be due to the fact that at close range the AP sources appear to be distributed rather than point sources, or they may be caused by dendritic current distortion (Somogyvári et al., 2005; Shiraishi et al., 2009). Finally, the MSD algorithm has no need for AP templates, and thus is suitable for unsupervised AP sorting.

The remainder of the paper is outlined as follows. In the next section, we present the data model and underlying assumptions. Section 3 reviews several popular feature extraction techniques, and the proposed MSD-based feature extraction algorithm is then