



Computational Neuroscience

A non-parametric Bayesian approach for clustering and tracking non-stationarities of neural spikes

Vahid Shalchyan^{a,b}, Dario Farina^{b,*}^a Department of Biomedical Engineering, Electrical Engineering Faculty, Iran University of Science and Technology (IUST), Tehran, Iran^b Department of Neurorehabilitation Engineering, Bernstein Focus Neurotechnology Göttingen, Bernstein Center for Computational Neuroscience, University Medical Center Göttingen, Georg-August University, Göttingen, Germany

HIGHLIGHTS

- We proposed two non-parametric Bayesian methods for tracking non-stationarities of neural spikes.
- The methods were tested and compared to Gaussian modeling approach using simulated and real data.
- The proposed method outperformed the parametric method in all simulated and experimental data tests.
- Non-parametric methods tracked varying cluster shifts over time better than the parametric approach.

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ABSTRACT

Background: Neural spikes from multiple neurons recorded in a multi-unit signal are usually separated by clustering. Drifts in the position of the recording electrode relative to the neurons over time cause gradual changes in the position and shapes of the clusters, challenging the clustering task. By dividing the data into short time intervals, Bayesian tracking of the clusters based on Gaussian cluster model has been previously proposed. However, the Gaussian cluster model is often not verified for neural spikes.

New method: We present a Bayesian clustering approach that makes no assumptions on the distribution of the clusters and use kernel-based density estimation of the clusters in every time interval as a prior for Bayesian classification of the data in the subsequent time interval.

Comparison with existing methods: The proposed method was tested and compared to Gaussian model-based approach for cluster tracking by using both simulated and experimental datasets.

Results: The results showed that the proposed non-parametric kernel-based density estimation of the clusters outperformed the sequential Gaussian model fitting in both simulated and experimental data tests.

Conclusions: Using non-parametric kernel density-based clustering that makes no assumptions on the distribution of the clusters enhances the ability of tracking cluster non-stationarity over time with respect to the Gaussian cluster modeling approach.

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1. Introduction

A microelectrode inserted within the cortex can record the activity of multiple neurons in the vicinity of the electrode tip. In these recordings, action potentials (also referred to as spikes) generated from multiple neurons can be classified and assigned to their corresponding neurons based on differences between the

waveform shapes. The process of assigning spikes to different neurons is referred to as spike sorting (Lewicki, 1998). A common general assumption in all spike sorting methods is that each individual neuron in close proximity of the recording electrode generates a distinct spike shape which remains stationary during a recording session. However, this assumption may be violated during long-term recordings. One source of non-stationarity is the slight drift in the position of the recording electrode relative to the cell body over time which causes gradual changes in the waveform shapes of the recorded spikes (Lewicki, 1998; Snider and Bonds, 1998). Heartbeat, respiration or mechanical perturbations by movements of the animal in awake preparations, can also cause non-stationarities (Snider and Bonds, 1998; Chakrabarti et al., 2012). Non-stationary may be caused by a process of electrode

* Corresponding author at: Department of Neurorehabilitation Engineering, Bernstein Center for Computational Neuroscience, Georg-August University of Göttingen, Von-Siebold-Str. 6, 37075 Göttingen, Germany. Tel.: +49 551 3920100; fax: +49 551 3920110.

E-mail address: dario.farina@bccn.uni-goettingen.de (D. Farina).

encapsulation by fibrous tissue and cell death in the vicinity of the electrode (Polikov et al., 2005). Non-stationarities make spike clustering complex since the clusters will be “smeared” over long time which may lead to geometrical shape change and overlapping of the clusters in the selected feature space. However if the recording is divided into short-time segments, the clusters can be considered as stationary within each segment (Emondi et al., 2004).

Assuming that the short-time stationary clusters may move in the multi-dimensional feature space smoothly (i.e., without any discontinuity). Snider et al. suggested an offline cluster linking method that uses a measure of linear change in density of points between clusters as a criterion for the cluster unification decision (Snider and Bonds, 1998). Emondi et al. proposed a method which performs manual clustering in each short time segment and uses a similarity threshold to automatically find the best match between clusters of the subsequent time frames (Emondi et al., 2004). Bar-Hillel et al. proposed an offline batch processing of a Bayesian framework in the clustering process, with the source neurons modeled as a non-stationary mixture of Gaussians; the candidate descriptions of the data and transition probabilities between candidate mixtures were computed for each short time-frame separately. A globally optimal clustering solution was found as the maximum a-posteriori solution of the resulting probabilistic model (Bar-Hillel et al., 2006). The drawback of the described approaches is that the batch processing for global optimization is associated with high computational cost and large memory footprint and cannot be implemented in online spike sorting applications (Linderman et al., 2008). Recently Wolf and Burdick (Wolf and Burdick, 2009) proposed a sequential extension of the expectation maximization (EM) algorithm (Dempster et al., 1977) to fit a Gaussians mixture model (GMM) in each time frame using the clustering results from the previous time interval as a prior. In particular, they used the cluster means obtained in one time frame to seed the EM algorithm in the next time frame, while still allowing for signal non-stationarity and changing numbers of recorded neurons in transition between time frames. While this approach is substantially faster than traditional EM for global optimization of mixture models and thus can be used for online applications, the assumption of Gaussianity for variability of individual single-unit waveforms is often not verified (Fee et al., 1996; Harris et al., 2000; Shoham et al., 2003; Schmitzer-Torbert et al., 2005; Delescluse and Pouzat, 2006).

Using non-parametric clustering methods is a preferable choice for spike sorting in general (Hill et al., 2011). However traditional non-parametric clustering methods, such as hierarchical clustering (Fee et al., 1996; Kaneko et al., 1999; Geng et al., 2010; Shalchyan et al., 2012), are usually not suitable for online sorting and tracking variability of the spike waveforms over time. The aim of this study was to compare the use of a non-parametric Bayesian approach and the parametric (GMM) Bayesian approach for tracking non-stationarities of the clusters over long-term recordings. Two Kernel-based methods were used for non-parametric estimation of the cluster probability density functions (PDFs) in each short time frame. Various synthesized datasets were generated to simulate non-stationarity of the spike waveforms over long-term data. The methods were tested on both synthesized and experimental data and compared to the sequential cluster tracking method based on Gaussian cluster PDF estimation by using the EM algorithm.

2. Methods

2.1. Overall view

The method described in the following was specifically designed to compare the effect of non-parametric versus parametric cluster

PDF estimation in tracking waveform non-stationarity over time. Therefore, we did not intend to propose a complete and stand-alone algorithm for spike detection and clustering. It was assumed that the spikes were detected and aligned in an appropriate manner prior to the spike sorting task. For feature extraction, principal component analysis (PCA) (Glaser and Marks, 1968) was used because PCAs capture the largest variation of the data in ordered orthogonal vectors (i.e., principal components) and provide relatively good cluster separation in low dimension among ordinary feature extraction methods (Wheeler and Heetderks, 1982; Rutishauser et al., 2006). However, the proposed method can be applied in any other feature space. The long-term recording was divided into short time segments (e.g., 10 s) in which the stationarity was considered as a valid assumption, as in previous studies (Emondi et al., 2004; Bar-Hillel et al., 2006; Wolf and Burdick, 2009). The spike waveforms in the first time segment projected into their two-dimensional PCA basis and this PCA basis was fixed for extraction of features from spike waveforms of all time frames to the end of the recording to track cluster shifts on the same basis. It was also assumed that the spike features were reliably classified into their neuronal sources in the first time segment by using a manual or an automatic spike sorting method (for review on spike sorting methods see (Lewicki, 1998)). This assumption is necessary for the sequential clustering method because it classifies the current data based on previous cluster priors. In the following sections, the methods are described in details.

2.2. Non-parametric cluster tracking

The PDFs for each cluster were estimated by using kernel-based density estimation methods, as described in the next section. The estimated PDFs of the clusters in each time segment were used to classify the data in subsequent time segments using a Bayes classifier (Mitchell, 1997). The clusters and their PDFs were updated by adding new classified data in each and keeping up to $N=100$ newest members in every cluster for the next PDF estimation. The procedure was repeated for each new time segment to the end of recording.

Kernel density estimation is a smoothing method which allows estimation of the underlying PDF for an unknown distribution by summing kernel functions centered at each observed data point (see Bowman and Azzalini, 1997, for details). Given n sample data points $x_i, i = 1, \dots, n$ drawn from an unknown PDF, the kernel density at the point x is estimated as follows:

$$\hat{f}(x) = \frac{1}{nh} \sum_{i=1}^n K\left(\frac{x-x_i}{h}\right) \quad (1)$$

where h is the bandwidth and $K(x)$ is the smoothing kernel function. In this study, the Gaussian kernel function was used as in Bowman and Azzalini (1997). The estimated PDF is given by:

$$\hat{f}(x, h) = \frac{1}{n\sqrt{2\pi}h} \sum_{i=1}^n e^{-(x-x_i)/2h^2} \quad (2)$$

The optimal value for the bandwidth parameter h was computed by the following formula suggested by Bowman and Azzalini (1997).

$$h = \left(\frac{4}{3n}\right)^{1/5} \sigma \quad (3)$$

where σ denotes the standard deviation of the distribution which was robustly estimated as in Bowman and Azzalini (1997) by:

$$\sigma = \frac{\text{median}(|x_i - \text{median}(x_i)|)}{0.6745} \quad (4)$$

Considering the two-dimensional PCA basis, the projection of cluster samples into every principal component was used for the

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