

Improving Neural Spike Sorting Performance using Template Enhancement

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Abstract—This paper presents a novel method for improving the performance of template matching in neural spike sorting for similar shaped spikes, without increasing computational complexity. Mean templates for similar shaped spikes are enhanced to emphasise distinguishing features. Template optimisation is based on the separation and variance of sample distributions. Improved spike sorting performance is demonstrated on simulated neural recordings with two and three neuron spike shapes. The method is designed for implementation on a Next Generation Neural Interface (NGNI) device at Imperial College London.

I. INTRODUCTION

Neural recording is a fundamental technology for many emerging applications in neuroscience. Action potentials (or “spikes”) recorded invasively via intracortical electrodes can potentially enable the control of external devices (such as advanced limb prostheses) by direct neuronal signalling. Spikes from a single electrode can be separated into multiple distinct groups, corresponding to individual local neurons, so that the behaviour of individual neurons can be linked to larger scale neural network activity.

Fully implantable recording units, using wireless data transmission through the skull, will make long-term real-world recording applications possible. However, as electrode arrays with hundreds or thousands of channels become available [1], each channel recording digital samples at a minimal rate of 15kHz, the rate of data acquisition will exceed the capacity of wireless data transmission (due to bandwidth and power restrictions). One solution to this problem is online on-chip spike sorting, which would reduce the system output to a series of binary spike events (at most a few hundred Hz per channel).

The NGNI (next generation neural interface) device in development at Imperial College London is capable of recording from up to 1,024 channels based on off-the-shelf low power FPGA electronics [2]. The system implements a two stage spike sorting solution, proposed in [3] (see Fig. 1). In stage 1, clustering is performed off-chip on pre-recorded training data using any state-of-the-art algorithm to extract the mean template shape of each spike cluster. In stage 2, the cluster templates are used to perform simple and fast on-chip template matching on incoming spikes in real-time. This approach avoids the need to perform computationally intensive clustering on limited FPGA resources.

The system’s current template matching algorithm is sum of absolute difference (SAD) with mean templates (see Fig. 2(a)). This algorithm can achieve good online classification performance in many, but not all, cases. Summation of sample-wise differences between templates and recorded spike yields

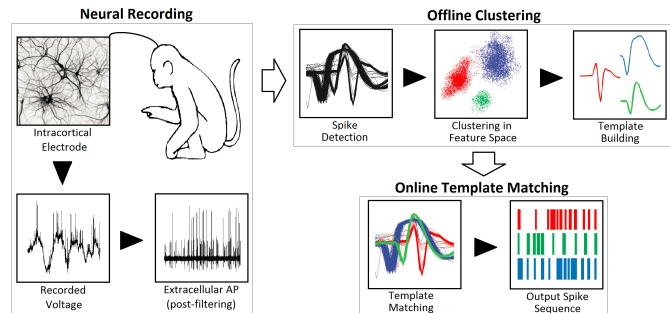


Fig. 1: Two stage spike sorting. Neural spike recordings are processed and clustered offline. Cluster templates are then used to perform real-time online template matching. Adapted from [2].

a set of distance scores, where the smallest score indicates the best template match. Due to noise and spike shape variations, each spike cluster will produce a distribution of scores, as seen in Fig. 2(b). The proximity of score distributions reflects template similarity. For similarly shaped spike templates, the corresponding distributions will be overlapping and difficult to distinguish, causing poor classification performance. An alternative algorithm is desirable for these difficult cases.

More complex online algorithms exist and could provide better performance, but their computational demands make them incompatible with the NGNI hardware. The aim here is to improve NGNI performance with minimal impact on hardware. Improving performance will involve more efficiently using the information provided by the spike samples.

Several attempts have been made to implement spike sorting based on concepts of information content and statistical probabilities. [4] develops a Bayesian approach based on electronic hardware filters, but is not compatible with the NGNI system

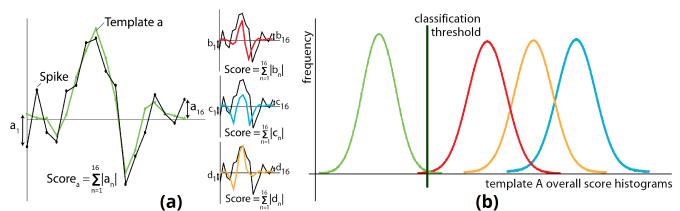


Fig. 2: Sum of absolute distance (SAD) template matching. (a) Individual samples distances are summed into a single distance score for each template. (b) The smallest distance score for a given spike reflects the most likely classification cluster. Distribution colours in (b) correspond to template spike groups in (a). Adapted from [2].

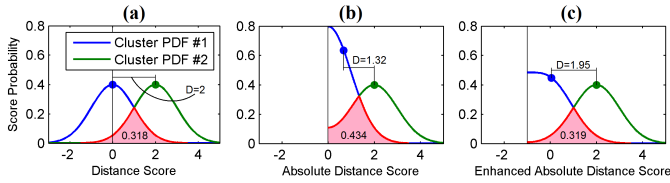


Fig. 3: Separation of cluster distributions. (a) shows overlap in general space, (b) shows overlap after computing absolute distance from the centre of cluster #1, and (c) shows the effect of template enhancement. The numbers above the curves are the cluster centre distances. The numbers inside the shaded zones are the areas of overlap.

design. [5] implements template matching with samples scaled according to noise content, but is intended specifically for cases where two spike groups have different variances (which is not necessarily the case). [6] uses estimation of Gaussian noise in the data to actively increase the functional information of each spike sample, but is focused on spike clustering and isn't directly applicable to template matching.

This paper presents a novel method for optimisation of template matching performance: enhanced templates. Mean template shapes are distorted according to the relationship between noise distributions of adjacent spike clusters, so that the distinguishing features of similar spike groups are emphasised. For SAD, this method optimises performance without affecting computational complexity. The efficacy of this method is demonstrated here for simulated spike data.

This paper is structured as follows: Section II describes the concept of template enhancement; Section III details procedures for performance testing and template optimisation; Section IV presents simulated performance; and finally Section V summarises our findings.

II. TEMPLATE DISTORTION

For SAD template matching, the distribution of absolute distance between a spike cluster and a template is calculated by folding the original distribution around the template value. However, folding may produce increased overlap between distributions of different clusters. Measuring absolute distance can make two adjacent distributions appear more similar than they truly are, in particular when they are close together.

Fig. 3 illustrates this concept. In Fig. 3(a), two spike clusters are close together, so that significant overlap occurs. In Fig. 3(b), the clusters are folded around the mean point of cluster #1, which increases the overlap and decreases separation of the cluster centres. This is the effect of SAD template matching using mean cluster templates. When calculating the absolute distance of multiple clusters from one mean template value, information is wasted because the clusters will appear less distinct than they are in reality. Using a template distance measure that avoids this problem would be likely to improve spike sorting performance.

The concept of 'template enhancement' is proposed in order to reverse the observed increase in distribution overlap. Instead of using cluster mean templates, the templates are exaggerated to be more different from each other (as illustrated by Fig. 4). Fig. 3(c) shows spike clusters folded around an 'enhanced template' point, where the template position of cluster #1 has been shifted one standard deviation farther away from cluster #2. This is a relatively small change, the template value remains within the central part of cluster #1, but the

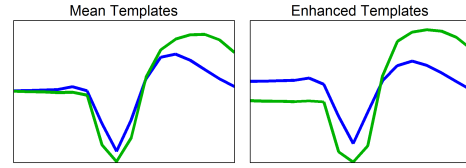


Fig. 4: Illustration of template enhancement concept. Distinguishing features of similar mean templates are exaggerated in the enhanced version.

overlap and separation of the clusters have been restored to near optimal values. Template modification can produce more favourable sample distribution spacing such that clusters can be more easily distinguished. Cumulatively, better sample score spacing will improve overall SAD distribution spacing, producing better classification performance.

This concept can also be stated in terms of classification probabilities. Calculating the distances between a spike and set of templates is equivalent to determining which template has the highest probability of having produced the spike. When sample distributions are folded and the separation between distributions is reduced, the relative classification probabilities are transformed. For example, a spike which based on unfolded distributions has 90% probability of originating from template A might appear, based on folded distributions, to have only 70% probability. Loss of information allows noise to produce more classification errors. Template enhancement ensures that the relative classification probabilities are close to ideal.

III. METHODS AND MODELS

This section is divided as follows: Subsection III-A describes the performance testing program for spike sorting of simulated datasets; Subsection III-B outlines the sample distribution model; and Subsection III-C discusses the procedure for calculating optimised template values.

A. Performance Testing

Performance testing of template matching focused on simulated datasets because of known ground-truth. Spike data was generated using open-source NeuroCube software [7], which produces realistic extracellular spike recordings by modelling individual neurons in three-dimensional space relative to a virtual electrode. Datasets were created featuring two and three different single-unit neurons, against increasing levels of Gaussian noise and background spiking. Simulated datasets were 3 minutes long, with approximate firing frequencies of 5 Hz per neuron. Nine two-spike datasets were tested, with each dataset having a different level of spike shape similarity and with the most similar shaped datasets being the most challenging and relevant. Data processing and spike properties were determined by NGNI system parameters: bandpass filtering between 300 Hz and 3 kHz, 15 kHz sampling, 16 samples per spike for template matching.

Initial clustering was performed on each dataset using WaveClus [8], a wavelet-based superparamagnetic clustering algorithm. The cluster mean templates from each dataset were then used for template matching and for calculating enhanced templates. This procedure mimics the two stage spike sorting solution of the NGNI system.

The spike sorting functionality of the NGNI FPGA device was translated into Matlab for testing. Initial baseline testing was carried out on the device's current SAD algorithm. Results

from the enhanced algorithm are compared to the baseline performance to determine improvement.

For a given dataset and given noise level, performance is described here in terms of specificity and sensitivity. Specificity is calculated as: true spikes / (true spikes + false positives). Sensitivity is calculated as: true spikes / (true spikes + false negatives). True spikes are those which are correctly classified.

These performance metrics reflect type I and type II errors (false positives and false negatives, respectively), relative to the known identity and timing of all spikes in the simulated datasets. Results are provided for each individual spike cluster. To facilitate comparison of results between mean and enhanced template matching, curves were produced which reflect the robustness of performance as noise increases.

B. Sample Distribution Analysis

Optimisation of sample-specific template distance scores requires knowledge of the distribution for each spike cluster at each template sample. It has been shown that spike sample distributions can be approximately modelled as Gaussian [6]. In theory, channel noise is expected to be stationary, so template samples should have equal variance. However, spike occurrence and data sampling may not be synchronous. The peak of the sampled spike may not be the true peak of the waveform. This is problematic because template matching requires alignment of spikes by peak location. Most template matching algorithms use interpolation to improve accuracy of peak identification, but the NGNI system does not (due to computational cost). As a result, spike values are distorted by ‘sampling jitter’, in addition to noise. On both simulated and recorded neural data, observed spike sample distributions were found to be modelled acceptably well by approximation as Gaussian with variance dependent on both channel noise and the derivative of template shape.

C. Template Design

Template optimisation was investigated in Matlab by measuring the change in centre distance (separation) between two folded Gaussian distributions as the folding point (template position) shifts. The effect of template shifting depends on the true distance between distributions and on the ratio of standard deviation. In the general case, separation has an approximately logarithmic relationship with template shift, such that a modest shift (up to one standard deviation) produces the majority of separation improvement. Beyond this range, incremental gains are small. The potential benefits are greatest when the distributions are relatively close together and have similar variance. When variance is mismatched, the more diffuse cluster will benefit more from shifting but will require a larger shift to maximize separation.

In the final enhancement algorithm, templates were optimised on a sample-by-sample basis. For each template sample distribution (see Fig. 3) in the test datasets, the separation from adjacent distributions (quantified in terms of mean distance) was calculated over a range of ± 2 standard deviations. The point of maximal separation over this interval is the ideal distortion. However, because the majority of improvement is produced by the initial shift, enhanced template positions were selected as the minimum shift producing a separation at least 90% of the maximum. This approach ensures near maximal improvement with optimally efficient distortion. A

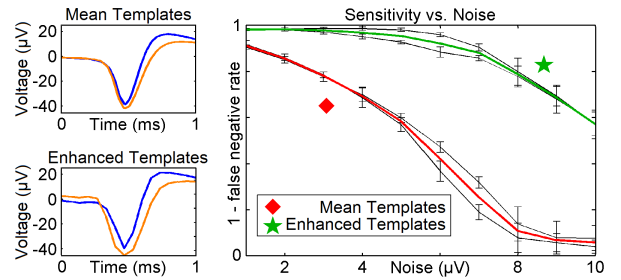


Fig. 5: Spike sorting performance for simulated dataset with two single-units. The red curve shows the sensitivity results for SAD with mean templates and an imposed specificity of 95%. The green curve shows the sensitivity results under the same conditions, but using enhanced templates. The black lines show cluster-specific performance and standard deviation, while the coloured curves are averages for both clusters.

lower threshold (80%) would decrease improvement without greatly affecting distortion. A higher threshold (95%) would significantly increase distortion for a minimal performance gain. For expected recording noise conditions (4-6 μV), the largest distortion in the test datasets was 15 μV (approximately equal to the maximum sample variance, since sample variance is a function of both noise and template slope).

Of course, very large template shifts would produce ideal separation between distributions, but might cause misclassification problems in the presence of a third distribution (either another single-unit or a general multi-unit cluster). This is why template enhancement should be kept to a minimum. Datasets with three single-units were tested to verify that enhancement is effective when more than two spike distributions are present. Cluster separation between all three distributions was taken into account when determining optimal template enhancement for these datasets. Optimized distortions were therefore generally smaller for three-spike datasets than for two-spike datasets, but the enhancement effects were still significant.

IV. RESULTS

This section presents template enhancement performance results for simulated data with two single-unit spikes (Subsection IV-A) and three single-unit spikes (Subsection IV-B).

A. Two Spikes

Two-spike datasets were tested using mean templates and enhanced templates. In order for the results to be directly comparable, classification thresholds for all cases were set to impose a minimum specificity level of 95%. Fig. 5 above shows the comparison of results for the most difficult of nine simulated datasets. The mean spike shapes are differentiated only by small differences at a few samples. Using mean templates, sensitivity is poor such that at 6 μV noise only about 40% of spikes are classified correctly. Using enhanced templates, the gain in sensitivity is large and sustained across all noise levels. At 6 μV noise over 90% of spikes are classified correctly. The enhanced algorithm continues to perform well even at noise levels where the original algorithm failed completely. Only the sensitivity plots are shown here because the specificity levels are the same. Comparable results were achieved for all challenging datasets tested.

The results of Fig. 5 offer strong support for template enhancement as a useful technique. For the targeted case of difficult datasets, where two spike shapes are very similar and

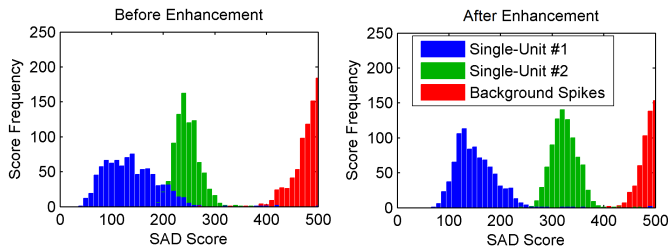


Fig. 6: Effect of template enhancement on overall SAD histograms. Increased cluster spacing produces improved spike sorting performance.

the probability of classification error is high, this method has significant performance benefits.

Another way to observe SAD performance improvement is by looking at the score histograms. Datasets with poor performance will have spike histograms which overlap, leading to the possibility of misclassification. Fig. 6 shows how template enhancement affects the SAD histograms for one illustrative noise level ($4 \mu\text{V}$). The SAD score histograms for the two different spike groups have much better separation in the enhanced template case than in the mean template case. In fact, the enhanced case has no histogram overlap at all. Decreasing distribution overlap at each sample results in a cumulative effect on the summed score, such that overall cluster separation is much improved.

Notably, the position of the background spike histogram does not change significantly. This suggests template enhancement can safely be used when other spikes are present, without increasing the number of falsely detected background spikes. In theory, classification errors for strong multi-unit activity can be worsened by template enhancement (if an enhanced template becomes too similar in shape to the background spikes). In simulated data, this has only been observed when single-unit spike magnitudes are made unrealistically small.

B. Three Spikes

Fig. 7 demonstrates that template enhancement is also beneficial for datasets with more than two single-units. The simulated dataset shown here contains two very similar single-unit shapes and a third with the same amplitude but a different

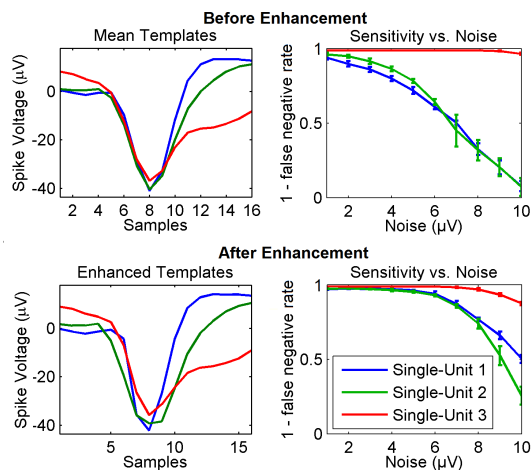


Fig. 7: Spike sorting performance for simulated dataset with three single-units. Each colour represents the templates and performance curves for one single-unit.

shape. With mean templates, sensitivity is poor for the two similar spikes. After template enhancement, the blue and green performance curves have improved significantly and the red curve continues to exhibit good performance.

Testing on datasets with three single-units supports that the technique can be generalised, but there are limits. Enhancing the performance of two similar spikes in the presence of other non-similar spikes is very feasible. Enhancing the performance of three or more very similar spikes may be problematic. However, given that this is an unlikely case where most other spike sorting algorithms would also perform poorly, this is a reasonable limitation.

V. CONCLUSION

This paper presented the novel method of template enhancement for improving SAD template matching performance without affecting computational complexity. The aim of this work was specifically to improve spike sorting performance of the NGNI device. Template enhancement will be incorporated into future versions of the system. Key concepts were:

- SAD with mean templates decreases separation between adjacent spike clusters.
- Template enhancement optimises cluster separation.
- Template enhancement consistently improves classification performance for datasets with two similar shaped spike templates.
- Template enhancement is also effective for datasets with more than two spike shapes.

ACKNOWLEDGEMENTS

This work was supported by UK EPSRC grants EP/K015060/1 and EP/M020975/1.

Portions of this work were submitted as a requirement of the first author's Master's program, BioMedical Engineering - Bioengineering and Innovation in Neurosciences (BME-BIN). The Master's degree is awarded jointly by Université Paris Descartes and ESPCI Paris.

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