

Biologically realistic simulated extracellular potential data as benchmark for the evaluation of spike detection algorithms

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Abstract

Many spike detection and spike sorting algorithms are found in the literature. Their performance is either compared on the basis of experimental data or on the basis of synthetic data, mostly generated by the random distribution of spike templates in time and the addition of noise. But never before biologically realistic simulated extracellular potential data was used as benchmark, providing both, control and realistic features. We will describe the generation of our simulated test data within a biologically realistic network simulation and finally present some performance results of selected spike detection methods applied to our data.

A lot of spike detection and spike sorting algorithms can be found in the literature, ranging from thresholding methods in the time or frequency domain towards template matching and PCA. Authors compared the performance of several methods against each other, the problem being, however, that there doesn't exist a generally accepted set of test data. Either quality comparisons are carried out on the basis of experimental data the author has at hand, or on the basis of fully synthetic data. The experimental data has the disadvantage that it is always subjected to interpretations and experience of the viewer. Nobody can say for sure, how many spikes or even spike trains from individual cells are contained in extracellularly recorded data. Synthetic data provides the advantage of being perfectly controllable, but in most approaches this has to be paid for with a lack of biological reality. One frequently applied method is to extract spikes and chunks of noise from extracellular recordings, to distribute the spikes randomly in time and to add the noise sample [2], [8]. The disadvantage of this method is quite obvious. The randomly distributed spikes do not reflect any biologically realistic network behaviour and even no biologically realistic single cell behaviour. Nakatani [6] employs a peripheral nerve model in order to generate synthetic data. He adds a Gaussian noise process to the simulated signal. This method is comparable to ours, but lacks the presence of different interacting neurons within an elaborated network circuitry.

We generate controllable test data within a biologically realistic network simulation implemented in GENESIS 2.2 [3]. The simulation mimicks a tiny part of the CA3 region of the rat hippocampus. The network consists of 72 pyramidal cells [9], 9 feedforward and 9 feedback interneurons [10]. Details of the network circuitry can be found in [5]. In addition to slight changes concerning the cell connections, two main changes were performed compared to former implementations. First, the z-coordinates of the model neurons are randomized in a range of -50 to $+50$ μm in order to avoid having all cells lie in one plane. And second, the cells have a spacing of 10 μm \pm 3 μm only instead of 35 to 45 μm . This was made necessary by the small recording horizon of our simulated electrodes: Cells more distant than 15 μm are not trackable any more in the simulated extracellular potential data. Electrodes are simulated on the basis of an equation by Nunez [7] for the calculation of extracellular field potentials:

$$F = \frac{1}{4 \cdot \pi \cdot s} \sum_{i=1}^n \frac{I_i}{r_i}$$

Since recording distances of 20 μm [1] to 65 μm [4] are reported for experimental set-ups, we doubt in the suitability of the Nunez equation as basis for the simulation of extracellular recordings. Further electrophysiological and simulation work is under way to investigate this fact. We already improved the Nunez equation in that way, that we introduced a direction characteristic. The original equation allows to record from cells all around in an opening angle of 360°. By only taking into account the transmembrane currents of cells that lie within a certain sector as seen from the probe, the opening angle can be reduced to e.g. 120°, thus mimicking the case of a multi-site recording probe, where individual electrodes are fixed on an insulating carrier.

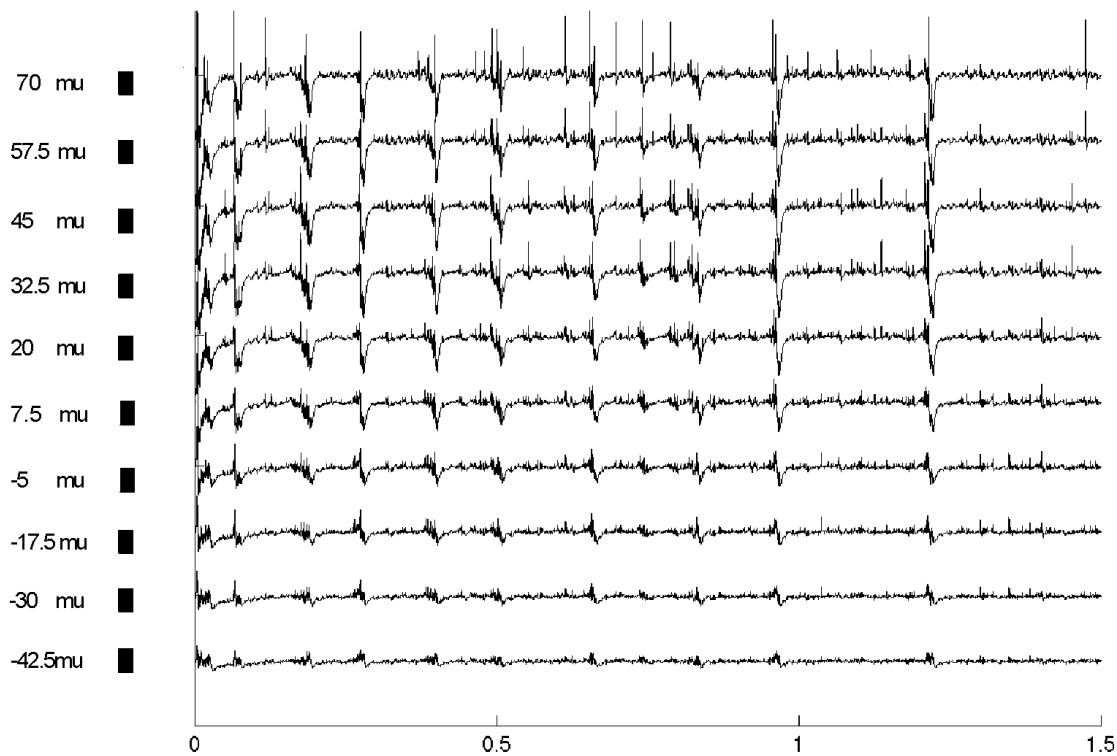


Figure 1: Simulated multi-site recording data. The numbers on the left refer to the z-coordinates of the individual recording sites.

Our simulated data (Figure 1) gets highpass filtered with a cut-off frequency of 500 Hz and white noise is added, that is supposed to represent thermal noise of recording devices. Background activity coming from cells farther away from the electrode is already contained in the simulated data. The simulated extracellular potential data resembles closely experimental recordings in spike shapes, firing rates and decay over distance. Many overlapping spikes, originating from synchronous activity of several neurons, are contained in the data – a tough problem for all types of spike train analysis known.

On the basis of the above described simulated data so far we tested the following spike detection methods: positive voltage threshold (pt), pt plus peak-to-peak amplitude threshold (pt + ppa), pt + ppa plus peak-to-peak time (pt + ppa + pp-time), peak-to-peak amplitude only (ppa-window), thresholding of the second derivative of a signal (sec_dev + pt), of the energy

(energy + pt) or of the by means of Discrete Wavelet Transform (DWT) denoised signal (dwt-denoising + pt). The notation in braces refers to Figure 2. This figure illustrates the results we obtained by applying the various approaches on the simulated data. The two bars on top in each case result from comparisons of the detection results with the spike times of two pyramidal cells only (70 spikes in total), the two bars on bottom from comparisons with the spike times of three pyramidal cells that are definitely contributing to the simulated extracellular data (112 spikes in total). The spike amplitudes of the third pyramidal cell are hardly above the noise level and are obviously difficult to detect. In the case of the pt method e.g., 24% of the 70 spikes originating from two pyramidal cells are missed, compared to 45% of 112 spikes originating from three pyramidal cells. However, even 24% of missed spikes are an alarmingly high value, and except thresholding of the denoised signal, none of the other investigated methods yields better results. Especially the investigation of peak-to-peak amplitude and peak-to-peak time in addition to the positive peak amplitude does not improve the performance. The ppa-window, sec_dev + pt and energy + pt methods predict much more than 50% false positives and thus should not be used as stand-alone detection methods. The presented results were achieved for a high SNR. We also tested simulated data with low SNRs, which can easily be achieved by properly scaling the added white noise. Under low SNRs, we got up to 85% false positives and 48% false negatives (of 70 spikes), not shown. The test of further spike detection and spike sorting algorithms is pending. Special attention will be paid to approaches that take advantage of multi-site recording data and to the performance on overlapping spikes.

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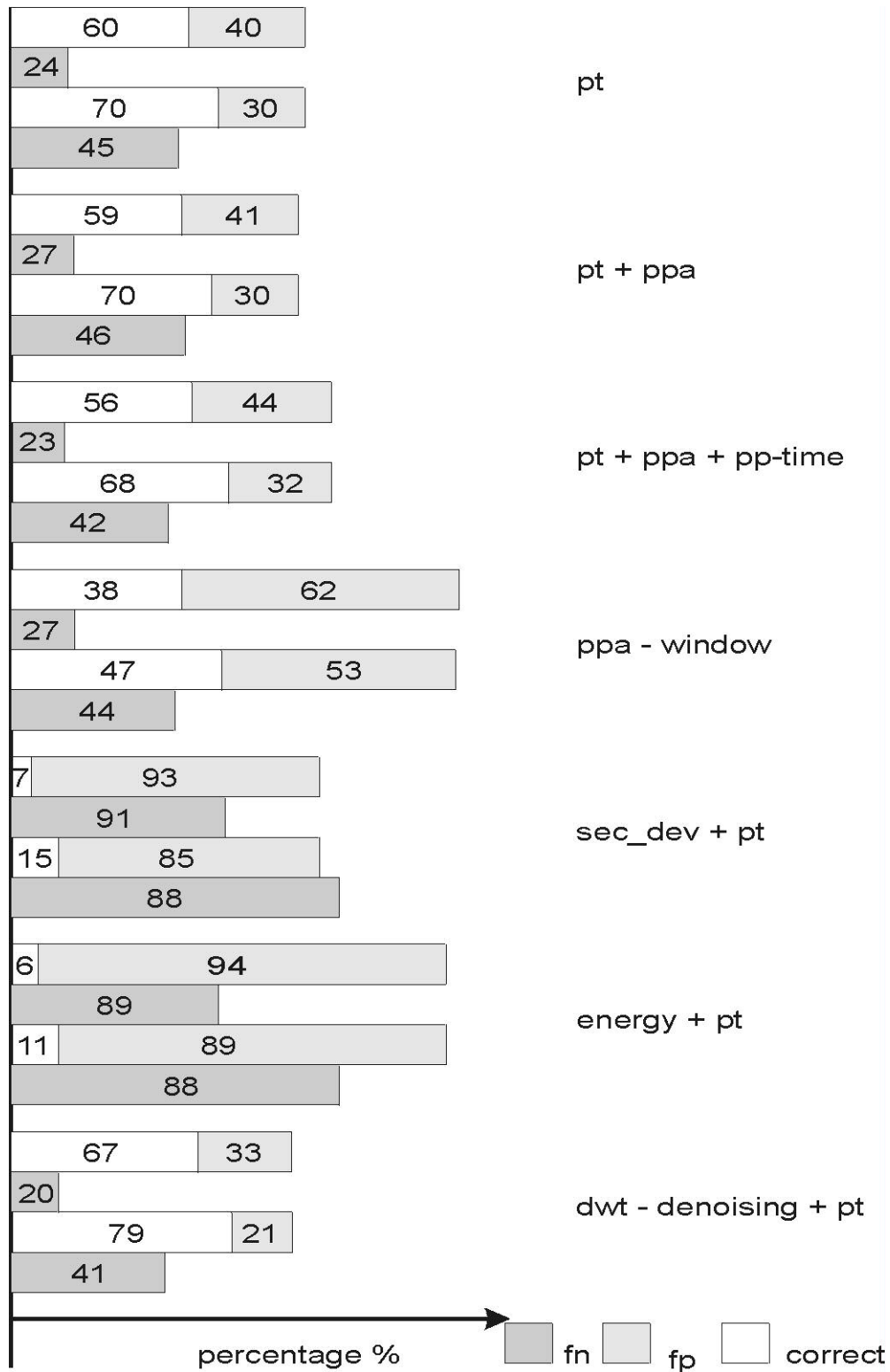


Figure 2: Percentage of correctly detected spikes (correct) and false positives (fp) are calculated on the basis of all detected spikes. False negatives (fn) are given as percentage of 70 or 112 spikes, respectively, see text.