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Title: A system for automatic on-line time detection and classification of neural spikes based on a digital signal processor and a FPGA controller

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Definition of single spikes from multiunit spike trains plays a critical role in neurophysiology and in neuroengineering as it does the question of how much information is encoded by single neurons in a neuronal network. Moreover, the possibility to develop a bidirectional communication between electronic devices and neuronal networks provides great perspectives in neuroengineering. Traditionally, the functional properties of neurons and neuronal networks have been investigated using conventional electrodes, such as glass micropipettes, thus allowing neurophysiologists to disclose a detailed picture about the single cell properties. Thirty years ago Micro-Electrode Array devices (MEAs) have been developed as tools providing distributed information about learning, memory and information processing in a cultured neuronal network. Recent applications of this technologies have the problem of the recording and storage of the huge amount of data processed. Here we describe a system based on a FPGA controller coupled to a Digital Signal Processor for the automatic single spike detection, sorting and classification. The first step involves FPGA: its inputs are 60 neuronal signals caming from the 60 channels of MEA and its outputs are time stamps for single electrode and templates of the spikes for single channel. At this level, an adaptative threshold method is used for spike detection. The second step involves the DSP: the principal components of previously recorded templates are computed. Spikes are classified using information about their shape, characterized by different features; the principal component analysis is one method for choosing these features automatically. The challenge is to accurately and reliably separate the spikes from a single neuron from spikes from other neurons and classify them. The on-line application of this method provides an efficient system to reduce the computation time and the space on the storage unit. Our aim is to estimate the number of neurons that are naturally interconnected in complex networks and to discriminate single template's shape of individual neuronal cell.

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