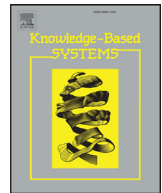




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Kernel density compression for real-time Bayesian encoding/decoding of unsorted hippocampal spikes

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ABSTRACT

To gain a better understanding of how neural ensembles communicate and process information, neural decoding algorithms are used to extract information encoded in their spiking activity. Bayesian decoding is one of the most used neural population decoding approaches to extract information from the ensemble spiking activity of rat hippocampal neurons. Recently it has been shown how Bayesian decoding can be implemented without the intermediate step of sorting spike waveforms into groups of single units. Here we extend the approach in order to make it suitable for online encoding/decoding scenarios that require real-time decoding such as brain-machine interfaces. We propose an online algorithm for the Bayesian decoding that reduces the time required for decoding neural populations, resulting in a real-time capable decoding framework. More specifically, we improve the speed of the probability density estimation step, which is the most essential and the most expensive computation of the spike-sorting-less decoding process, by developing a kernel density compression algorithm. In contrary to existing online kernel compression techniques, rather than optimizing for the minimum estimation error caused by kernels compression, the proposed method compresses kernels on the basis of the distance between the merging component and its most similar neighbor. Thus, without costly optimization, the proposed method has very low compression latency with a small and manageable estimation error. In addition, the proposed bandwidth matching method for Gaussian kernels merging has an interesting mathematical property whereby optimization in the estimation of the probability density function can be performed efficiently, resulting in a faster decoding speed. We successfully applied the proposed kernel compression algorithm to the Bayesian decoding framework to reconstruct positions of a freely moving rat from hippocampal unsorted spikes, with significant improvements in the decoding speed and acceptable decoding error.

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1. Introduction

Neural encoders and decoders are commonly used to study the relation between behavioral or sensory covariates and neural re-

sponses. Statistical inferences have played an important role in many encoding/decoding frameworks, e.g. [1–6]. Generally, the encoding model captures necessary properties from the recorded neural activities and constructs a model that maps to the observed behaviors or stimuli. The decoding model then employs the constructed relation to infer behaviors or stimuli based on the observed neural activity. For example, neural signals recorded from the action potentials (spikes) of pyramidal neurons in the CA1 region of the rodent hippocampus contain information that is correlated to spatial behaviors of the animal [7]. These cells are also known as place cells because spiking activities of certain place cells become more active when an animal is in

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a certain location [8]. In other words, the temporal patterns of spikes from different place cells are spatially tuned to different locations.

Most of existing neural encoders/decoders require sorted spikes to operate [9,10,11–18,2] (see [19] for a review). That is spiking activity of each single neuron has to be isolated from others and separated from background electrical noise before being handed over to the encoding/decoding model. This prerequisite step is called “spike sorting”. Many works have been contributed to the developing of fast and reliable spike sorting algorithms [20]. However, a study has shown that classification errors of assigning spikes to incorrect unit have various impact to information capacity of the resulting sorted spikes [21]. In addition, the objective of spike sorting to isolate and identify the cell that originated each spike is rather different from the goal of neural decoding which is to minimize the decoding error. Unclassified spikes during the sorting in attempt to minimize sorting errors could still convey information that can be extracted by the encoder/decoder.

To avoid the possibility of information loss and accumulation of errors from spike sorting, Bayesian encoding/decoding framework proposed in [22] has introduced a method to create a direct mapping between spike waveform features and the covariates of interest without a prerequisite step of spike sorting. The name “Bayesian” comes from the adoption of a statistical inference that utilizes Bayes’ theorem. More specifically, the decoding is obtained by the maximum posterior probability in Eq. (1), where the covariates are spatial behaviors of the animal, e.g. positions or head directions.

$$p(\text{covariates}|\text{spikes}) = p(x|s) = \frac{p(s|x)p(x)}{p(s)} \propto \frac{p(s|x)p(x)}{p(s)} \quad (1)$$

Outline of the Bayesian encoding/decoding framework [22] is illustrated in Fig. 1. The first stage (A) detects and extracts spike waveforms from extracellularly recorded multiunit activity from CA1 region of a freely moving rat in an open field. Next (B), waveform features, such as amplitudes, are extracted. At the same time (C), position of the animal is tracked using a video camera and forwarded together with the waveform features to the next stage (D), where the probability models $p(s,x)$ and $\pi(x)$ are modeled.

During the decoding phase (e), a sequence of spikes is partitioned into bins. For each decoding bin, the posterior probability is computed and the behavior is decoded. The likelihood $p(s|x)$ of the stimulus x given a set of spike features s models the relation between spiking patterns (modulation of spike amplitudes and firing rates) and behaviors by assuming spatiotemporal Poisson statistics as follows:

$$p(s|x) = \Delta t^n \left[\prod_{i=1}^n \lambda(s_i,x) \right] e^{-\Delta t \lambda(x)}, \quad (2)$$

where the decoding bin containing n spikes has a size of Δt time interval. Rate parameter $\lambda(s_i,x)$ which is the fraction of the occurrences of certain spike features s_i coinciding with certain stimulus x divided by the total time stimulus x (*occupancy*(x)) is presented as follows:

$$\lambda(s_i,x) = \frac{\text{spikecount}(s_i,x)}{\text{occupancy}(x)} = \frac{N}{T} \frac{p(s_i,x)}{\pi(x)} = \mu \frac{p(s_i,x)}{\pi(x)}, \quad (3)$$

where N is the total number of spikes and T is the total time from all the decoding bins. $p(s_i,x)$ is the joint probability distribution of

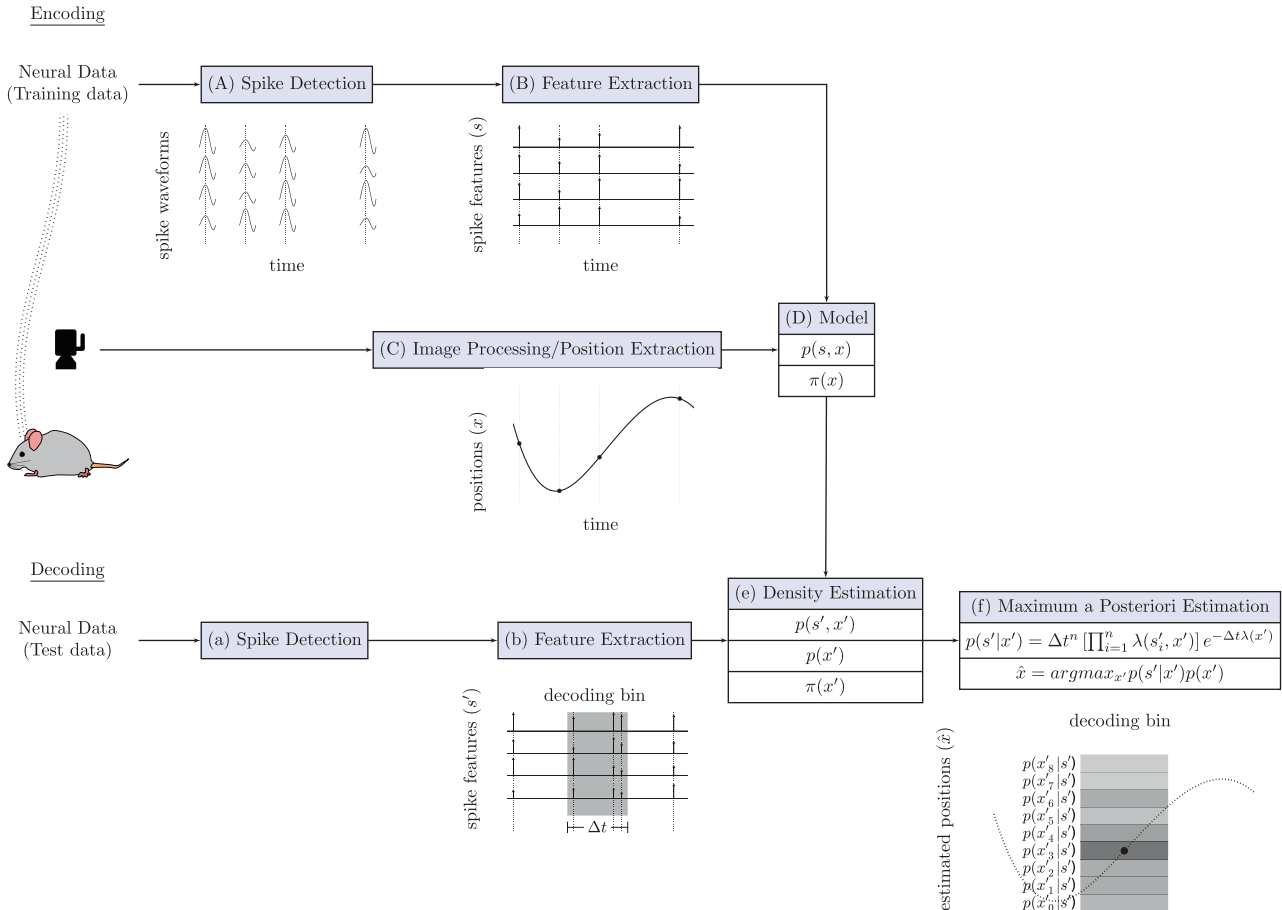


Fig. 1. Bayesian decoding using unsorted spikes in the rat hippocampus.

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