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Pre-whitening as a means to improve dimensionality reduction and simplify clustering in spike-sorters for HD-MEA recordings

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Spike sorting is the process to extract single neuronal activity from extracellular recordings. Spike sorting makes use of the fact that spikes of a single neuron feature highly similar waveforms, whereas spikes from different neurons have different waveforms. Clustering algorithms are used to find groups of similar spikes that putatively originated from the same neuron. However, since spike waveforms, especially in multi-electrode recordings, can have a high dimensionality, their dimensionality needs to be reduced before clustering. Principal component analysis (PCA) is one of the most commonly employed dimensionality reduction methods for this purpose [1]. The resulting reduced dimensions are those along which the variance of the data was high, which presumably are those along which the waveforms of different neurons strongly differed. However, if the noise is not uniform in all dimensions, high variability can also mean high noise, which would render a dimension useless for discrimination. We, therefore, propose an additional pre-whitening step before PCA and discuss two beneficial effects on the subsequent clustering. We illustrate these effects by using spikes from retinal ganglion cells recorded with high-density multi-electrode arrays (HD-MEA).

Pre-whitening is a method that is used to transform a set of data points that follow a multivariate Gaussian distribution with a given covariance matrix to make them follow a multivariate standard normal distribution after transformation. In the case of our HD-MEA recordings, the noise covariance is a strong contributor to non-spherical shapes of spike clusters, which means that pre-whitening significantly affects the cluster shapes.

The first beneficial effect of pre-whitening for spike sorting is that it leads to a better alignment of the first principal components with the directions that feature the largest between-cluster variance, as the noise is uniformly distributed over the dimensions after pre-whitening. Therefore, the cluster locations are now the main contributor to the variance in the data.

The second benefit of pre-whitening is that it simplifies the clustering problem. After pre-whitening, the clusters are roughly spherical with uniform standard deviation in all dimensions (This is not entirely true, since the noise covariance matrix used for pre-whitening does not capture all the variability of the spike waveforms, but we will show that the benefits of the procedure are still given). Knowing the approximate size and shape of the clusters, we can chose a fitting clustering procedure, which offers the possibility to employ unsupervised learning techniques that do not require subsequent manual curation of the clusters.

In conclusion, pre-whitening is a simple method to improve PCA analysis of multi-electrode array recordings and it simplifies the clustering problem for the spike-sorting algorithms. Thus, we believe pre-whitening before dimensionality reduction is an important tool towards the development of fully automatic spike-sorters.

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References

1. Lewicki MS. A review of methods for spike sorting: the detection and classification of neural action potentials. Netw. Comput. Neural Syst. 1998;9:R53–78.