



Wavelet thresholding estimation in a Poissonian interactions model with application to genomic data

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This paper deals with the study of dependencies between two given events modeled by point processes. In particular, we focus on the context of DNA to detect favored or avoided distances between two given motifs along a genome suggesting possible interactions at a molecular level. For this, we naturally introduce a so-called reproduction function h that allows to quantify the favored positions of the motifs and which is considered as the intensity of a Poisson process. Our first interest is the estimation of this function h assumed to be well localized. The estimator based on random thresholds achieves an oracle inequality. Then, minimax properties of the estimator on Besov balls are established. Some simulations are provided, allowing the calibration of tuning parameters from a numerical point of view and proving the good practical behavior of our procedure. Finally, our method is applied to the analysis of the influence between gene occurrences along the *E. coli* genome and occurrences of a motif known to be part of the major promoter sites for this bacterium.

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