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NON-PARAMETRIC DYNAMIC MODELLING OF BIOLOGICAL TIME SERIES

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This talk illustrates the theory and application of a novel sequential non-parametric method for estimating the dynamics of time series models. This method provides a robust alternative to Bayesian state-space models which does not involve any parametric assumption on the form of the evolution of a model's parameters. Their dynamics are assessed within a hypothesis testing framework as a change-point problem. The Kullback-Leibler divergence between the posterior distributions of different sets of data under the same model is proposed as a test statistic. Posterior simulation is used to approximate the value of the KL divergence and its critical region under the null hypothesis of no change.

The main motivation of this work is to estimate the molecular and functional dynamics of biological systems using high throughput technologies such as microarrays and multi-electrode arrays. In this context, robust dynamic stochastic models are fundamental tools because little is known about the mechanisms regulating the evolution of many biological processes. This talk focuses mainly on the estimation of neuronal functional dynamics using multiple spike trains recorded in-vitro and in-vivo. The neuronal dynamics are shown to explain some aspects of a simple decision process and the onset of movements.