Journal de la Société Française de Statistique
Vol. 157 No. 1 (2016)

Editorial for the special issue on Statistics and Neurosciences

Titre: Éditorial du numéro spécial sur la statistique et les neurosciences

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The neurosciences are nowadays undergoing a fast development driven mainly by new experimental techniques (Luo, 2015, Chap. 13). Large data sets containing the simultaneous activities of many (10 - 1000) neurons are becoming common. Anatomical data revealing the morphology together with part of the expressed genes at the single neuron level but for large brain regions are produced every day. Such data are clearly presenting attractive challenges for statisticians, probabilists and any mathematically oriented scientists. The problems range from experimental methods improvement–something falling into the category of *pre-processing* for experimentalists–to stochastic model formulation and exploration / resolution not to speak of more classical experimental design.

In the large realm of neuroscience, we have chosen to focus on problems taking the neuron as the elementary level of analysis in a given small population of neurons, in contrast to more macroscopic approaches where neuronal populations are taken as elementary–as is frequently done when analyzing electroencephalographic (EEG) or functional magnetic resonance imaging (fMRI) data or more microscopic levels such as gene or synapses. This choice was clearly not motivated by a lack of interesting statistical questions at the other levels–far from that!–but as editors, we aimed at giving a unity to the present opus as well as at focusing on our present area of expertise. We have also chosen topics that would most readily appeal to neurobiologists, or people interested in theoretical models in neuroscience as well as statisticians, hoping that some of them will venture into these pages, as opposed to topics dealing with specific experimental recording techniques and the data processing problems they generate. In other words, the stochastic modeling–in time or space–was privileged over the "pre-processing" issues despite of the fundamental importance of the latter.

The first two articles, Samson and Ditlevsen and Galves and Löcherbach are motivated by the "stochastic" or "irregular" behavior of neurons *embedded in a network*. Samson ans Ditlevsen consider a single neuron and model a two dimensional process with a stochastic differential equation (SDE) – a stochastic version of the Morris-Lecar model. One component of the 2D process can be identified with a membrane potential, a quantity familiar to cellular neurophysiologists. Stochastic

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modeling of membrane potential can be traced back to Gerstein and Mandelbrot (1964), but the vast majority of the literature in this domain does not explicitly model the action potential: a SDE is used below a threshold and every time the threshold is reached an action potential is emitted and the membrane potential is reset to a "resting" level, this is the now classical integrate-and-fire model, see Burkitt (2006a,b) for a review. Samson ans Ditlevsen are presenting a richer but more complex model with the inference challenges it generates. Galves and Löcherbach tackle the next level: given a large population of coupled stochastic neurons, what can be said *and analytically computed* about its macroscopic properties? This is obviously a typical issue in theoretical / computational neuroscience; the originality of the Galves and Löcherbach model is that by imposing a small restriction–the relevant history for the prediction of the action potential occurrence for a given neuron goes back to *the last action potential* of that neuron–they are getting a variable-order Markov model from which many properties can be analytically derived. They then review many classical macroscopic properties of neural networks from the viewpoint of their model. As mentioned this is a vast topic than cannot possibly be covered in a single review and the interested reader looking for another "popular" approach in that field can start with Cocco et al. (2009).

The last article by S. Eglen presents–at the editors' request–two topics: a spatial stochastic model for photo-receptor types localization in the retina together with a *fully reproducible* description of the analysis. These two topics are currently actively explored in neuroscience. A good introduction to the known quantitative aspects of neuro-anatomy is the the book of Braitenberg and Schüz (1998). Until recently, anatomical data have mainly been used to constraint network models (like the one of Galves and Löcherbach), Eglen article presents a new trend in the field were generative models are considered. This approach presents clearly natural bridges with dynamic–like developmental (Luo, 2015, Chap. 5 and 7) and memory / plasticity (Luo, 2015, Chap. 10)–issues making it particularly attractive. The second topic, the explicit description of the analysis with all the codes in R and access to the data, addresses a pressing issue for any "outsider", like a statistician, interested by new scientific problems. It is all too often very long–and painful–to figure out what was precisely done to the data and to compare a too vaguely described analysis with a newly proposed method. By advertising an approach, *reproducible research*, that is making progress in neuroscience, we hope to convince data eager statisticians that contemporary neuroscience has lot of fascinating and challenging problems to offer, on which it is actually possible to work. It is definitely a great time to work at neuroscience / statistics interface!

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