MSIAM – 2nd year research internship

Bayesian nonparametric models for hidden Markov random fields with medical applications

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This project will take place in collaboration with Grenoble Institut des Neurosciences (GIN) Stéphane Belin and Homaira Nawabi and Département de Chimie Moléculaire (DCM) Sabine Chierici.
Location of internship: Inria Mistis, 655 avenue de l'Europe, 38330 Montbonnot St Martin.

Allowance : about 550 euros per month
Duration: 5-6 months (starting in February)

Context:

The World Health Organization estimates that 250 000 to 500 000 new cases of spinal cord injuries occur each year. People suffering from those lesions endure irreversible disabilities, as no treatment is available to counteract the regenerative failure of mature Central Nervous System (CNS). Thus, promoting neuronal growth, repair and functional recovery remains one of the greatest challenges for neurology, patients and public health.

Our partners at GIN (Grenoble Institute for Neurosciences) demonstrated that doublecortin is a key factor for axon regeneration and neuronal survival. Short peptides could be used as a treatment to enhance axon outgrowth. To test their potential effect on axonal growth, embryonic neurons in culture are treated with those peptides. Neurons are then imaged and neurite length is quantified automatically. The analysis of such data raises statistic questions to avoid bias in testing the relevance of a given peptide, as illustrated in Fig. 1. All neuronal cultures are not the same. Particularly, the proximity between neurons is variable and likely to influence its intrinsic capability to grow. In such contexts, the usual test-based methodology to compare treatments cannot be applied and has to be adapted.

Tasks:

The aim of this M2 project is to establish a statistical methodology to correctly analyze data of neurite growth in a drug test assay. It will focus on both following points: 1) Characterize the effect of the density of neuronal culture on neurite length growth; 2) Define well-founded statistical tools to compare groups of neurons in presence of heterogeneity.

One promising idea is to model the data as a hidden Markov random field (HMRF) where each neuron is a node of the graph and the edges connect nearest neighbours in terms of their spatial locations. HMRFs have been widely used in image segmentation and more generally, for clustering data indexed by graphs [1,3]. Dependent hidden variables (states) represent cluster identities (in terms of density and neurite length). Assuming independent and identically distributed neuron features within clusters, statistical tests can then be built for comparing treatments. Permutation tests [2] seem to be a robust alternative to the analysis of variance.

The robustness of the results with respect to different strategies to build the dependency graph will be assessed.

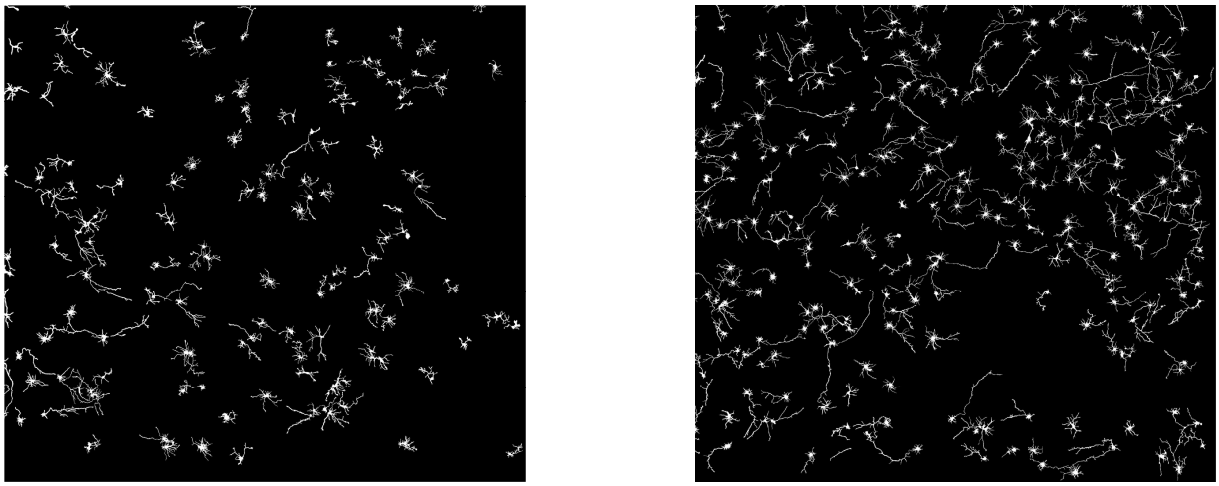

Figure 1: Examples of neurons cultures. Each neuron is identified with its nucleus and its dentrite. These two images illustrate the spatial difference observed between two cultures.

Prerequisites:

Multivariate statistical analysis, python programming.
Knowledge in Bayesian statistics and of the R software would be appreciated.

Related Master programs and tracks: MSIAM Data Science (research) or MoSIG Data Science

There is a possibility to pursue a PhD after the completion of the master project.

References:

[1] Albughdadi, M., Chaari, L., Tourneret, J.-Y., Forbes, F. and Ciuciu, P (2017). A Bayesian non-parametric hidden Markov random model for hemodynamic brain parcellation. *Signal Processing* **135**, 132-146.
[2] Good, P. (2005). *Permutation, Parametric and Bootstrap Tests of Hypotheses, Third Edition*. Springer Series in Statistics: New York, USA.
[3] Lü, H., Arbel, J., Forbes, F. (2019). Bayesian nonparametric priors for hidden Markov random fields. hal-02163046v2, https://hal.inria.fr/hal-02163046v2