

Bayesian networks in neuroscience

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Neuroscience is a scientific domain with many challenging problems to be solved. The development of new recording technologies has caused an increase in size and complexity of neuroscience datasets. Data driven methods allowing the discovery of complex interactions between the brain and behavior and the development of tools for the diagnosis and prognosis of neurological disorders and psychiatric diseases are becoming an important issue in computational neuroscience.

Bayesian networks are computational models that represent the conditional independence relationships among the variables in a given domain. They allow for any kind of inference, from predictive or diagnostic to intercausal, bidirectional and also total and partial abduction. In addition, there exist some methods for learning Bayesian networks from data. This type of probabilistic graphical model has been applied in a large number of neuroscience problems due to its transparency and computational properties (Bielza and Larrañaga, 2014, *Frontiers in Computational Neuroscience*). During this talk, some Bayesian network applications developed inside the Human Brain Project, whose aim is to decipher the most highly organized piece of excitable matter in the known universe --the human brain-- will be presented.

Bayesian classifiers will be used for solving a supervised classification problem with imprecise labels for discriminating among different types of interneurons. The problem of classifying and naming neurons has been a topic of debate since the original findings of Santiago Ramón y Cajal, more than 100 years ago. The dataset was obtained by means of a web-based interactive system that collected data about the terminological choices for a set of 320 cortical interneurons by 42 experts in the field (DeFelipe et al. 2013, *Nature Reviews Neuroscience*).

Morphology of dendritic spines appears to be critical from the functional point of view. Although many different classifications of spines have been proposed, the most widely used categorization is still that of Peters and Kaiserman-Abramof, which traditionally groups spines into four types (thin, mushroom, stubby and filopodium). We will introduce a quantitative and objective method to clustering dendritic spines based on finite mixture models where each component of the mixture factorizes according to a Gaussian Bayesian network, that incorporates linear and directional variables. More than 7000 individually 3D reconstructed dendritic spines from human cortical pyramidal

neurons to cluster spine morphologies have been used in the experiments (Luengo et al, 2017, in preparation).

Neuron morphology is crucial for neuronal connectivity and brain information processing. Computational models are important tools for studying dendritic morphology and its role in brain function. During the talk, an approach based on Bayesian networks will be used for modeling and simulation of more than 350 layer III pyramidal dendritic trees from three different regions of the neocortex of the mouse (Lopez-Cruz et al. 2011, Neuroinformatics).

Multilabel classification based on multidimensional Bayesian network classifiers applied to a real-world data set containing 488 Parkinson's disease patients will be presented in the last part of the talk. The aim is to predict the European Quality of Life-5Dimensions (EQ-5D) from the 39-item Parkinson's Disease Questionnaire (PDQ-39) (Borchani et al. 2012, Journal of Biomedical Informatics).