



## *Emerging Topics in Biological Networks and Systems Biology*

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*Detecting Change-points in the Structure of a Network: Exact Bayesian Inference*

### **Abstract:**

We consider the problem of change-point detection in multivariate time-series. We are typically interested in detecting changes in the interaction structure between a set of genes or in the connexion pattern between brain regions. The data at hand are typically time-course gene expression data or multivariate EEG signals. The multivariate distribution of the observations is supposed to follow a graphical model, whose graph and parameters are affected by abrupt changes throughout time. We demonstrate that it is possible to perform exact Bayesian inference whenever one considers a simple class of undirected graphs called spanning trees as possible structures. We are then able to integrate on the graph and segmentation spaces at the same time by combining classical dynamic programming with algebraic results pertaining to spanning trees. In particular, we show that quantities such as posterior distributions for change-points or posterior edge probabilities over time can efficiently be obtained. We illustrate our results on both synthetic and experimental data arising from molecular biology and neuroscience.

### **About:**

I am a senior researcher in statistics at the INRA (French national research institute in agronomics). My research are devoted the development of novel statistical methodologies with application in life sciences. I have been mostly involved in applications to molecular biology and bioinformatics but, more recently, I got interested in evolution and ecology. From a statistical point-of-view, I am interested in latent variable models, change-point detection, network models using both frequentist and Bayesian inference, with an emphasize on variational approximations.