Estimation of gene regulation during neuronal cell death

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The understanding of gene regulation of neuronal death in neurodegenerative diseases (Parkinson's disease, Alzheimer's disease and Huntington's disease) is very important for the development of efficient treatment strategies towards those diseases. Time series microarray array data could be used for estimation of gene regulation structure with statistical models such Bayesian networks and state space model. Especially, the space state model has the potential to infer gene regulation networks for large number of genes ranging from 10^2 to 10^4 using short length of the time series microarray data, e.g. less than 10. We estimated gene regulatory networks for 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) cell model of Parkinson disease using time series microarray data consisting of eight time points including time 0 (control) and 0.5, 1.5, 3, 6, 9, 12, and 24 h after exposure to MPP+, a metabolite of MPTP, with state space model. Gene expression data at each time point had three biological replicates and all replicated data were used for parameter estimation of state space model. The optimal dimension of state vector was determined by applying the maximum likelihood estimation and gene regulation structures were estimated for 999 genes showing significant differential gene expression profiles. In addition, the permutation tests were performed for evaluating the significance of the gene-gene connectivity.