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Inference of the complex system via particle filtering approach

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In biochemical systems, the stochastic modelling is the unique method that can capture the random nature of the actual biological processes when the exact number of molecules in the reaction is known. This model can be applied to the systems via three major approaches, namely, Langevin, Fokker-Plank and diffusion approximation. Among them, the first and the third one indicate the same mathematical model and their parameters can be inferred by typically Bayesian methods. On the other hand the second approach is not used commonly since its parameters can be estimated merely for toy systems. In this study the discretized version of the diffusion approximation, named as the Euler-Maruyama approximation, in a partially observed time-course dataset was implemented. In inference of the model parameters, i.e., reaction rate constants, MCMC methods are performed along with data augmentation to decrease the bias due to the discretization. Moreover the particle filtering approach to both estimate parameters and missing states simultaneously are applied. In literature it is shown this method is successful in dealing with the high dependency in the sequential updates of the reaction rates and missing states in toy systems. Here, as the novelty, we perform it in a realistically large system, selected as the MAPK/ERK pathway, by considering all possible sources of dependency caused by high dimension. The data are generated via Gillespie algorithm when the biological activation of the system is described by 51 proteins and 66 reactions. Finally the results with respect to their accuracies and computational time are compared.

Biography

Vilda Purutcuoglu has completed her BSc, MSc degree in Statistics and minor degree in Economics at METU and her PhD in Statistics at Lancaster University. Then she has been the instructor and Assistant Professor at METU. She has also worked as the visitor Researcher in Groningen University and Researcher in Glasgow University. Currently she has been working as the Associate Professor in the Department of Statistics at METU. Her research is in the fields of bioinformatics, systems and computational biology. Currently she has been co-authoring on a monograph about statistical modelling and inference in genomic networks.

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