

Bayesian Inference for Diffusion Processes with Applications in Life Sciences

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Diffusion processes are a promising instrument to realistically model the time-continuous evolution of natural phenomena in life sciences. However, approximation of a given system is often carried out heuristically, leading to diffusions that do not correctly reflect the true dynamics of the original process. Moreover, statistical inference for diffusions proves to be challenging in practice as the likelihood function is typically intractable.

This talk contributes to stochastic modelling and statistical estimation of real problems in life sciences by means of diffusion processes. In particular, it presents a framework of existing and novel techniques for the correct approximation of pure Markov jump processes by diffusions. Concerning statistical inference, it explains and further develops a well-known Bayesian approach which introduces auxiliary observations by means of Markov chain Monte Carlo (MCMC) techniques. This procedure originally suffers from convergence problems which stem from a deterministic link between the model parameters and the quadratic variation of a continuously observed diffusion path. This talk shows a neat modification of the above approach for general multi-dimensional diffusions and provides the mathematical and empirical proof that the so-constructed MCMC scheme converges.

The potential of the newly developed modelling and estimation methods is demonstrated using the example of the in vivo binding behaviour of proteins in cell nuclei.