Plenary Lecture - Reinhart Heinrich Award, Friday, July 1, 17:40

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Approximate Bayesian Computation for parameter inference and model selection in systems biology

Mathematical modelling has become an important tool in the biological sciences. Due to the overwhelming complexity of biological systems, it is not straightforward to determine the structure of the models. Moreover, the majority of parameter values are unknown and despite technological advances, these parameters are often difficult to measure experimentally. Therefore, statistical and computational techniques are needed to distinguish the good models from the unsuitable ones and to estimate unknown parameters.

In this talk we present a novel algorithm for parameter estimation and model selection of dynamical systems. The algorithm is based on Sequential Monte Carlo framework, and belongs to the class of Approximate Bayesian computation (ABC) methods. ABC methods can be used in situations where the evaluation of the likelihood is computationally prohibitive. They are thus ideally suited for analysing the complex dynamical models encountered in systems biology, where knowledge of the full (approximate) posterior is often essential.

The algorithm is applied to a variety of stochastic and deterministic biological models. We apply the model selection algorithm to distinguish between differential equation models of MAP kinase phosphorylation dynamics, the JAK-STAT signalling pathway, and the influenza infection outbreaks.