



Thesis Topic (B.Sc / M.Sc)

Entropic matching to approximate filtering distributions of chemical reaction networks

The rational design of genetic circuits in synthetic biology requires robust mathematical models describing their behavior – in particular when embedded in the cell or in a cell-free environment leading to perturbations and so-called context effects on the circuit.

We model reaction networks by continuous time Markov chains and distinguish between a network of interest (subnet) and an environmental network. The chemical master equation describes the evolution of the probability of the entire network to be in a specific state, so it gives the evolution of a probability distribution on the product space of subnet and environment states.

Applying model reduction techniques like marginalizing the joint network with respect to the environment yields a description of the subnet only. The filtering distribution of the environmental state, given the history of jumps in the subnet, occurs in this description. This filtering distribution is effectively a probability distribution on the environmental state space. In most cases, the corresponding evolution equation is hardly solvable analytically, and entropic matching is a way to find approximations within a parameterized family of probability distributions. Depending on the model network, we study for instance families of compound distributions, analytically and numerically. Questions regarding the influence of different molecular structures from environment species on the subnet behavior could be studied.

Good background in applied mathematics is recommended, especially in probability theory. Matlab skills are of advantage.

For further information, please contact Maleen Hanst.

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[1] Leo Bronstein and Heinz Koepl. “Marginal process framework: A model reduction tool for Markov jump processes”. *Physical Review E*, 97(6):062147, 2018