TECHNISCHE UNIVERSITÄT DARMSTADT

Thesis Topic (B.Sc. / M.Sc.)

Learning non-Markovian multi-component temporal processes from biological high-throughput data

Network are of broad interest across almost all sciences (especially physics, biology but also social media) as they pose arguable the most natural way to model interacting systems

We want to study the dynamic interactions of proteins inside cells. We can interpret this so-called proteome as a set of multiple-components interacting through the means of an underlying network.
We can then model the proteome by in Bayesian network with an additional continuous time-dimension to cover the systems dynamics [1], [2].

Markovian processes (memory-less processes) are a common model for temporal processes. However, real data in system biology is always provided only on some coarse-grained level, meaning that only outcomes of aggregated processes can be measured.
In this case, we have to explicitly consider memory effects.

By approximating the temporal distribution function, describing the proteome dynamics, using variational methods (also called mean-field methods) in a quasi-local manner, we are able to aggregate processes by marginalization. The resulting model will then provide a more realistic model, incorporating the systems memory that we can learn.

The student is expected to learn about the mathematical framework of variational methods and statistical models as Bayesian networks. Further basic knowledge about MATLAB is required as one required task is verification of theoretical results using simulation. Real proteomic data-sets might be available.

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Thesis Topic (B.Sc. / M.Sc.)

- Machine Learning
- High-throughput Biology
- Time-course Data
- Variational Methods
- Bayesian Networks
- Network Inference

Deutsch / English

[1] U. Nodelman, C. R. Shelton, and D. Koller, “Continuous Time Bayesian Networks,” *UAI*, pp. 378–387, 2002.

[2] K. Gopalratnam, H. a Kautz, and D. S. Weld, “Extending Continuous Time Bayesian Networks.,” *AAAI*, pp. 981–986, 2005.

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