

Gene Regulatory Network Inference by Evolutionary Computation

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Time series measurements generated by high throughput techniques such as NMR and mass spectroscopic methods carry topological and kinetic information regarding the underlying system that produced them. There is an urgent need for computational tools that allow efficient extraction of these information from time series data.

In this talk we discuss evolutionary computation approaches to the challenging problem of inferring the structural and kinetic order parameters of gene regulatory networks modeled as a set of ordinary differential equations in which the component processes are represented as power-laws in the dependent variables. Our methods are validated on several gene regulatory network inference benchmarks.