Abstract for GR-TR Conference on Statistical Mechanics and Dynamical Systems

Plenary Invited Invited Talk

Combinatorics of linear codes as a realisation of constraint satisfaction in biological networks

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Complex biological structures incorporate self-organization at all levels, from the combinatorics of linear codes to three dimensional chemical scaffolds. It is of interest to try to compare them with the emergent structures predicted by ab initio null models. A special case is the so called content-based network [1, 2], where the rules for the formation of bonds derive from a string-matching condition, and the network can be regarded as a superposition of classical random networks with hidden variables [3]. Given biological input regarding the distribution of the information content of the connections (binding sites), this model has been shown to predict, with a high degree of fidelity, the statistics of the transcriptional gene regulatory network of yeast [4] and, more recently, of *E. coli* [5]. I will discuss the implications and shortcomings of this approach to modeling biological networks. Finally, I will discuss this model as a particular realization of a constraint-satisfaction network [6, 7, 8], with a variable information content or specificity.

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