

Theoretical Issues in the Analysis of Biological Interaction Networks

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Interaction networks are fundamental to many biological processes. At a bio-molecular level, they arise in the study of gene transcriptional regulation, protein-protein interactions and metabolic reactions. Recent advances in biological measurement techniques have made it possible to study the bio-molecular networks behind cellular processes in a more comprehensive way than was previously possible. These developments have led to a considerable growth of interest in the analysis of bio-molecular interaction networks in recent years and a number of core problems have now emerged. In this talk, we shall discuss several mathematical questions that arise in the context of bio-molecular network analysis. In particular:

- (i) A number of algorithms have been proposed for the determination of protein function from network topology in recent years. While these appear to work reasonably well when applied to specific networks, several fundamental questions relating to their convergence and uniqueness properties have yet to be answered. We shall point out where such problems may arise for two recently published algorithms and present some preliminary results.
- (ii) Much of the recent work on biological networks has focussed on the identification of global network properties, such as the degree distribution, from studying sampled subnetworks. This naturally gives rise to the question of how reliably such global properties can be inferred from the properties of sampled subnetworks. Attention has only recently been directed towards this issue, and, while some initial results have been published, a formal treatment is still lacking. We shall outline and discuss some open questions relating to the sampling properties of complex networks.

Joint work with Dr. Mark Verwoerd of the Hamilton Institute