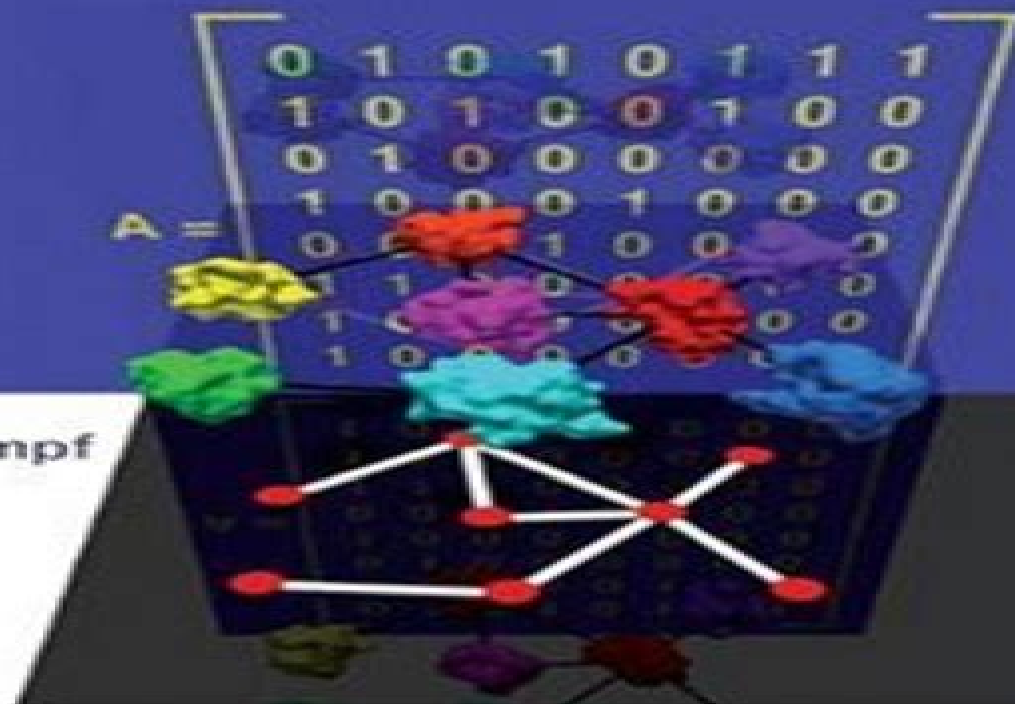


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Statistical and Evolutionary Analysis of **Biological Networks**

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particular scale free structures which have no characteristic spatial and or time scale For such systems the use of standard mathematical methods relying on the average behavior of the whole system is often incorrect or useless while a detailed many body description is almost hopeless because of the combinatorial complexity of the problem Here we focus on two problems The first part addresses to statistical analysis of random biopolymers Apart from the evolutionary context our studies cover more general problems of planar topology appeared in description of various systems ranging from gauge theory to biophysics We investigate analytically and numerically a phase transition of a generic planar matching problem from the regime where almost all the vertices are paired to the situation where a finite fraction of them remains unmatched The second part of this work focus on statistical properties of networks We demonstrate the possibility to define co expression gene clusters within a network context from their specific motif distribution signatures We also show how a method based on the shortest path function SPF can be applied to gene interactions sub networks of co expression gene clusters to efficiently predict novel regulatory transcription factors TFs The biological significance of this method by applying it on groups of genes with a shared regulatory locus found by genetic genomics is presented Finally we discuss formation of stable patters of motifs in networks under selective evolution in context of creation of islands of superfamilies

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