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Poster presentation

Using the protein interaction network to predict protein folds without homology

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Genome sequencing projects have increased exponentially our knowledge of protein sequences. A full understanding of the biological roles of these proteins can only be achieved by investigating their function and structure.

Despite the structural genomic initiatives, computational inference using an experimentally studied homolog is still the fastest way to gain information about a proteins structure. In the absence of structurally known homologs prediction becomes difficult as de novo based methods cannot as yet compete with homolog based comparative modeling methods.

In the realm of function prediction when a protein has no homologous neighbours with known function, the proteins interaction partners can be used to decipher its function as interacting proteins will tend to share similar functions. Unfortunately such a method does not naturally extend into structure prediction. Instead we propose a novel method that uses the protein protein interaction network to identify the structure of the protein. We upcast the protein network into a SCOP based domain-domain network, and predict the fold of a query protein to be a fold in the fold network that shows a similar interaction pattern. The algorithm is able to use interaction data from multiple species and makes predictions to the SUPERFAMILY level of SCOP.