PathBLAST : Mining For Conserved Pathways In Genome-Scale Molecular Interaction Networks

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1 Introduction.

Genome scale protein interaction networks are being mapped and identified at an ever-increasing speed. In order to make sense of this deluge of new data, new tools are needed in order to assemble a coherent picture of these interaction networks and their functional significance. PathBLAST [1]is one such method for identifying conserved pathways between two molecular interaction networks. Pathways are scored and selected based on sequence homology and topological similarity using a dynamic programming algorithm, as previously described [1]. Since interaction networks are obtained from high-throughput methods, these often include many false positives. To help eliminate the false interactions, here we present a new scoring system to assign a confidence value to each interaction. The model considers the co-expression of interactors [2], the number of times an interaction was observed and its topological clustering coefficient [3]. Using the revised PathBLAST, we report new biological findings illustrating conserved pathways between yeast and a variety of other model species for which interaction data is already available (Fig.1). The ability to mine conserved pathways across multiple species provides insight into how these pathways have evolved and can delineate roles for previously uncharacterized proteins through analysis at the level of both sequence and function.

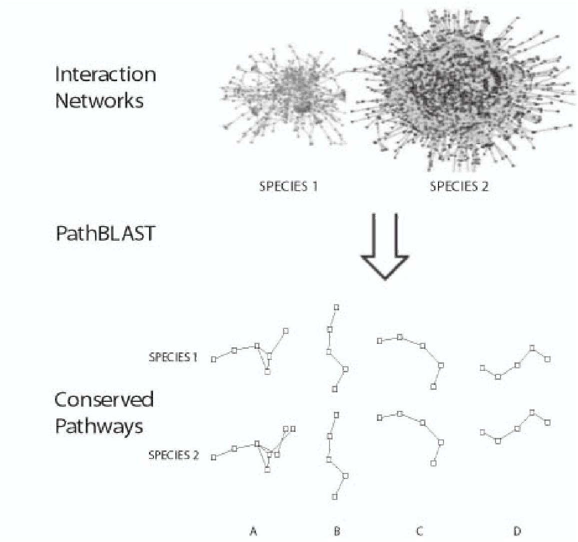

Figure 1: Mining conserved pathways using PathBLAST[1].

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2 References and bibliography.

References

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