

Poster presentation

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Prediction and ranking of human protein-protein interactions within a Bayesian framework

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Background

Protein-protein interactions carry out and regulate many fundamental cellular activities. The comprehensive study of such interactions on a global scale leads to a better understanding of diverse cellular processes and of the molecular mechanisms of diseases when these processes are deregulated. Large scale experimental datasets of the human interactome are becoming available [1] but their coverage is still very low. Bioinformatic predictors can fill this gap and provide high quality interaction datasets.

Methods

We investigate the prediction of direct physical interactions between human proteins, by integrating in a Bayesian framework, several different pieces of evidence including orthology, functional features and local network topology, in an attempt to increase the coverage of the known human interactome. We examine the contribution of different features as well as the use of different datasets.

Results

A semi-naïve Bayes network integrating expression data, orthology, protein localization, domain information and local network topology generates the highest accuracy prediction while maintaining a high coverage. We used this predictor to determine the most likely interacting human protein pairs and rank them according to their likelihood of interaction

Conclusion

Our Bayesian predictor has generated tens of thousands of high likelihood human protein interaction predictions. These are being analyzed and compared to currently known interactions.

References

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