Designing a Computational System to Predict Protein-Protein Interactions in Arabidopsis Thaliana

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Overview

- Introduction and Background
- Purpose
- Methods
- Results
- Conclusions
- Acknowledgements
Introduction

- Predicting protein-protein interactions is one of the most challenging problems of the post-genomic era.
- High-throughput methods can be used but are noisy and often yield false-positive/negative results.
- Computational techniques can be employed to identify interactions between proteins.
Purpose

To build a computational protein-protein interaction prediction system for *Arabidopsis thaliana*
High-throughput methods
- Mass spectrometry and Yeast 2-Hybrid (Y2H), for example
- Advantages and disadvantages

Computational methods
- Machine learning
- Example
Methods

- Computational projects are based on experimental data available to the public
- Organism-specific databases provide downloadable files
  - The Arabidopsis Information Resource (TAIR)
  - InParanoid, NCBI, Gene Ontology (GO)
Methods

- TAIR is the database of choice for all *A. thaliana* information
  - Leader of *A. thaliana* research and funding
  - “Gold Standard” dataset
- ftp provides downloadable files
  - Files collected from sources like GO, NCBI, private research, etc.
  - Our project…
Methods

- These datasets could be used to make predictions about protein interactions
  - Machine learning
- Positive set—pairs of interacting proteins determined using experimental methods
- Negative set—randomly generated from the master list of all *A. thaliana* genes
Methods

- Feature sets
  - Used to generate arrays of “scores” that will eventually be combined to make a prediction based on some threshold value
  - For example: orthologs, microarray data
Results

- Results are determined from the score values assigned to each feature set
- Results are not facts!
Results

The three categories of data (from left to right):

• Label (positive or negative)
  • shows that the sample contained about 3000 protein pairs, approximately 800 of which were known interactions (positive)

• Two feature sets—the ortholog and microarray data
Results

- Visualization of the microarray data
  - Blue “x”s represent the positive dataset
  - Red represent the negative.
- The x-axis is the absolute difference in average intensities (where gene expression data was available) of each protein in the given pair.
Conclusions

- The results at this stage are insufficient to make generalizations about classification methods.
  - For example:
    - Distinctions will be possible when there are more feature sets (ie: microarray data).
- With the addition of feature sets, conclusions will be possible regarding the classification methods as well as regarding protein interaction predictions.
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