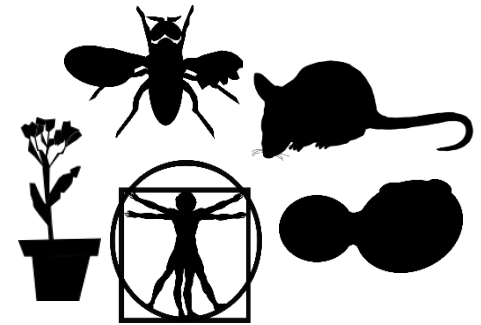


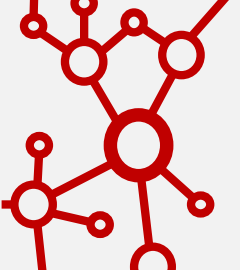
What is the Problem?

- **High throughput experiments** can test many combinations of proteins, but **threaten to introduce noise**
- There are numerous definitions of **what constitutes a “positive interaction”** and **many different experimental tests** to elucidate these
- **Compendiums of PPIs need to be filtered** to a researcher’s specific needs
- For each new organism, we **specify a new parameter set** to obtain a **high quality dataset of PPIs**
- **Garbage In; Garbage Out:** A PPI predictor trained on noisy data threatens to generate noisy results



Hypothesis: PPI predictors trained on a smaller dataset of higher quality PPIs will outperform larger datasets of lesser or unknown quality





POSITOME

A Method for Improving Protein-Protein Interaction Quality and Prediction Accuracy

Kevin Dick, Frank Dehne, Ashkan Golshani, James R. Green

What is the Positome?

A data curation tool for generating datasets of higher/known quality

POSITOME
A web service to produce a list of high quality protein interaction data.

Name
First: Last:

Email

Enter Organisms of Interest
Select either the same (intra-species) or differing (inter-species) organisms to obtain a high quality list of positive interactions. Both Taxonomy Id and species names are listed.

Intra-Species
Inter-Species

Organism
9606 | Homo sapiens

Interaction Filters
Select the detection methods you wish to keep in the resulting interactions. Applying the "Recommended Settings" will consider those methods used in the publication.

Apply Recommended Settings?
Conservative
Permissive

Detection Method Filters

- Two-hybrid
- Phenotypic Suppression
- Phenotypic Enhancement
- Affinity Capture-MS
- Affinity Capture-Western
- Dosage Rescue

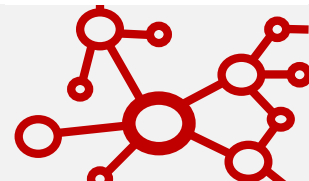
Advantages and Features

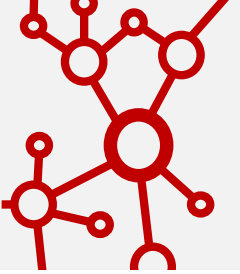
- Addresses “Garbage In, Garbage Out” challenges
- Researchers rapidly generate positive datasets
- Flexible to the need of the user (definition of “interaction”)
- Works with any type of PPI predictor
- Can be used for Intra- and Inter-species predictions
- Automatically updates every month; value as a tool expected to improve in time
- Computationally efficient for timely return of results
- Several precomputed datasets available
- Job completion notification

User-Friendly Web Form



RESTful Web Service





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How well Does it Work?

A. thaliana



M. musculus



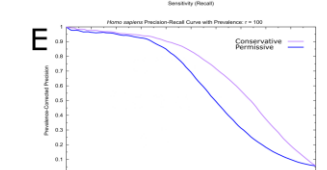
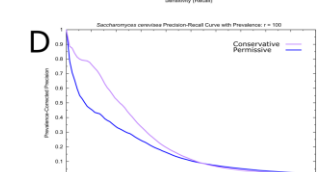
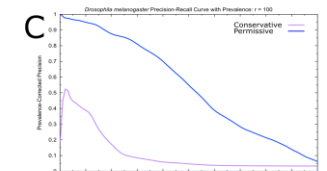
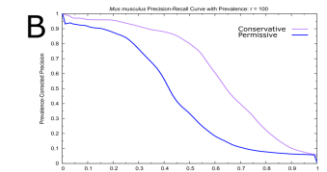
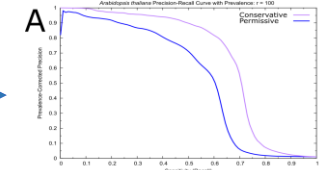
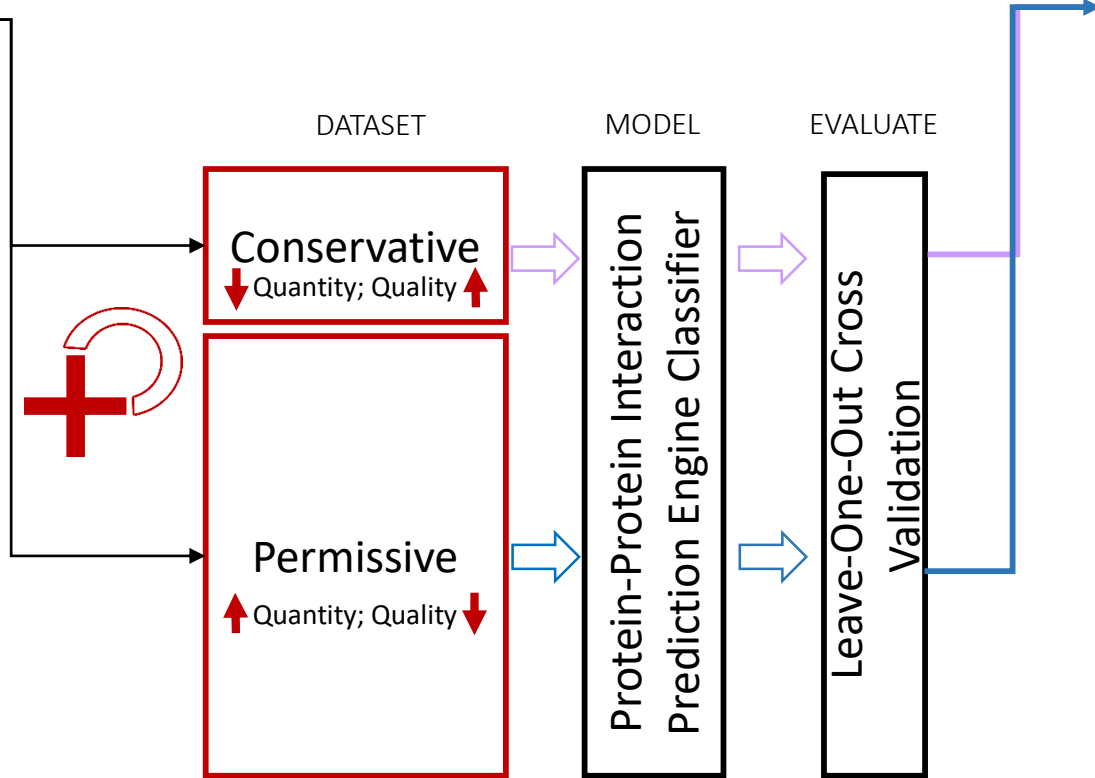
D. melanogaster



S. cerevisiae



H. sapiens



Historical Growth in Quality, Organism Taxonomy: 7227

Web Interface and REST Web Service Available at:

<http://bioinf.sce.carleton.ca/POSITOME/>

