

# BioGraphNet: a distributed forum for heterogeneous biological networks.

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Presented at BOSC, Glasgow 2004

# Protein Interaction Databases

(July 2004, figures rounded)

	DIP	BIND	IntAct	MINT	GRID
<b># proteins (x1000)</b>	17		27	18	56
<b># interactions (x1000)</b>	45	96	30	43	57
<b># organisms</b>	100	870		18	3
<b># experiments</b>	50000		570		
<b># articles (x1000)</b>	3	10			

<http://biographnet.sourceforge.net>

<http://llama.med.harvard.edu/Software.html>

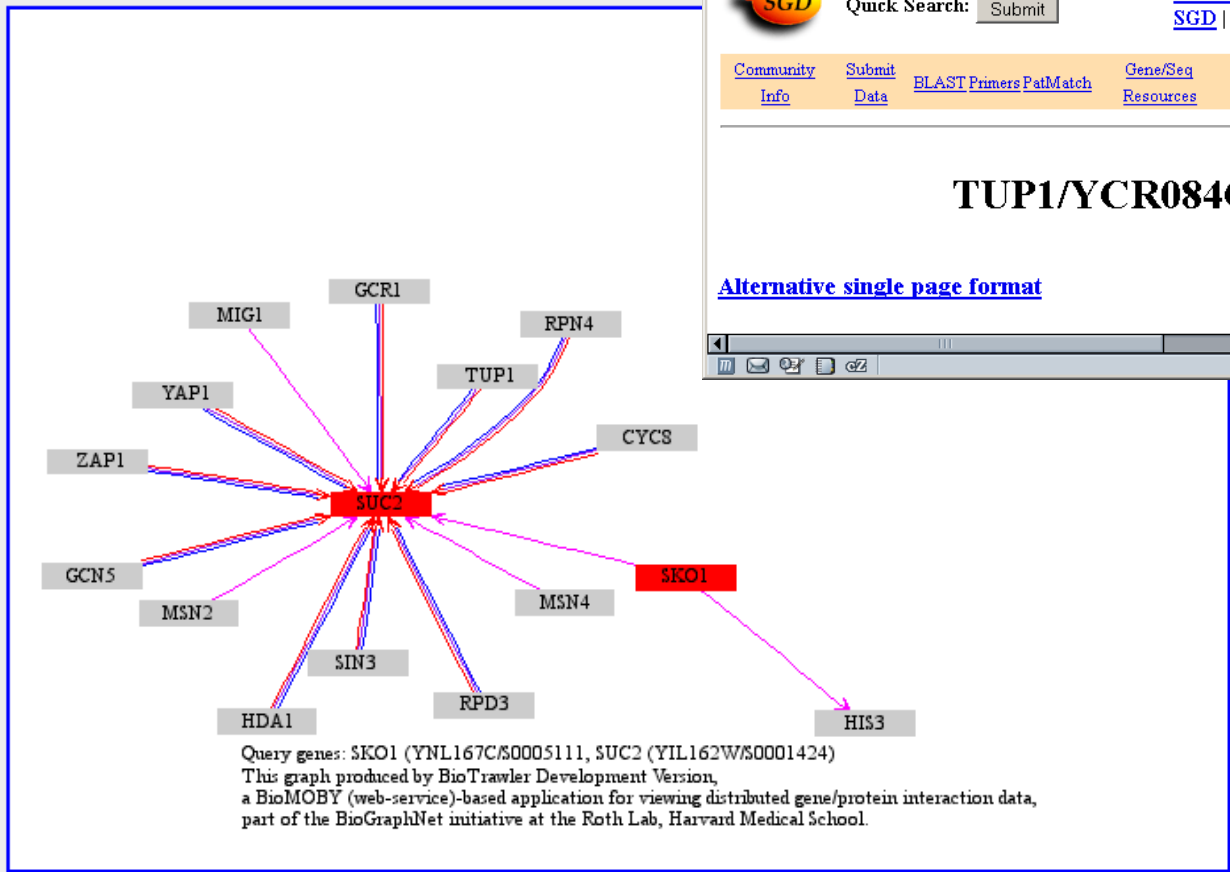
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### How to use the figure

Depending on the number of interaction partners your query genes (shown in red) have, it may not be possible to read the names. Mouse over a gene to see alternative names. Click on a gene open a new browser window containing its SGD page. If you click on a blank part of the figure, you'll get the entire image loaded in a page.

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### Query genes Interactions

Specify the genes/proteins you're interested in, either by typing them into the area below, or uploading a file containing them. (For a demo, just click 'Display graph'.) You can use any common convention for naming them: SGD standard name, "yname" (ORF name), alias, or even SGD ID. All that is required is that the names be separated by whitespace. Upper and lower case are considered the same.

sko1 suc2

Choose file:

# Motivation

- Heterogeneous biological networks
  - protein interaction
  - genetic interaction (*sensu* synthetic lethality)
  - transcriptional regulation
  - sequence homology
  - correlated expression
- Unlikely to belong in same database
- Experiments/predictions by distributed groups, best able to maintain.
- Value lies in integration, visualization of multiple data sets

# Web services

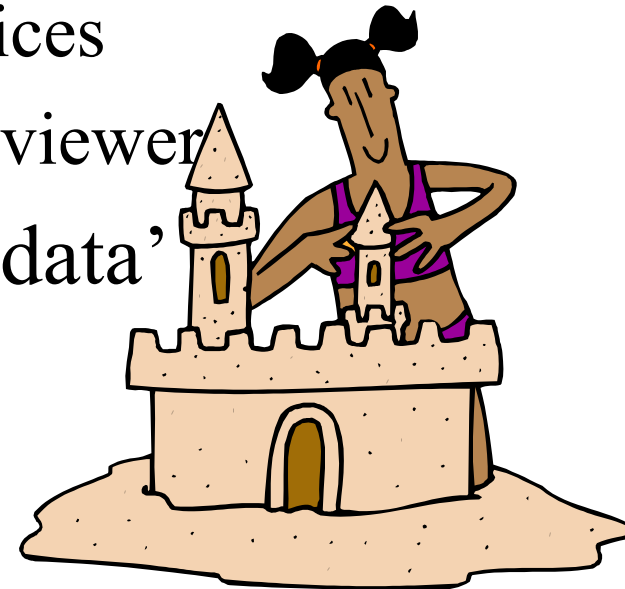
- Platform-independent standard format
- Standard discovery mechanism to find services
- XML allows semantic tagging of data
  - addition of new data does not break old code
  - aesthetic changes do not break understanding
- Service/data ontologies
  - allow computer-computer negotiation of services

# BioMOBY is the ‘playground’

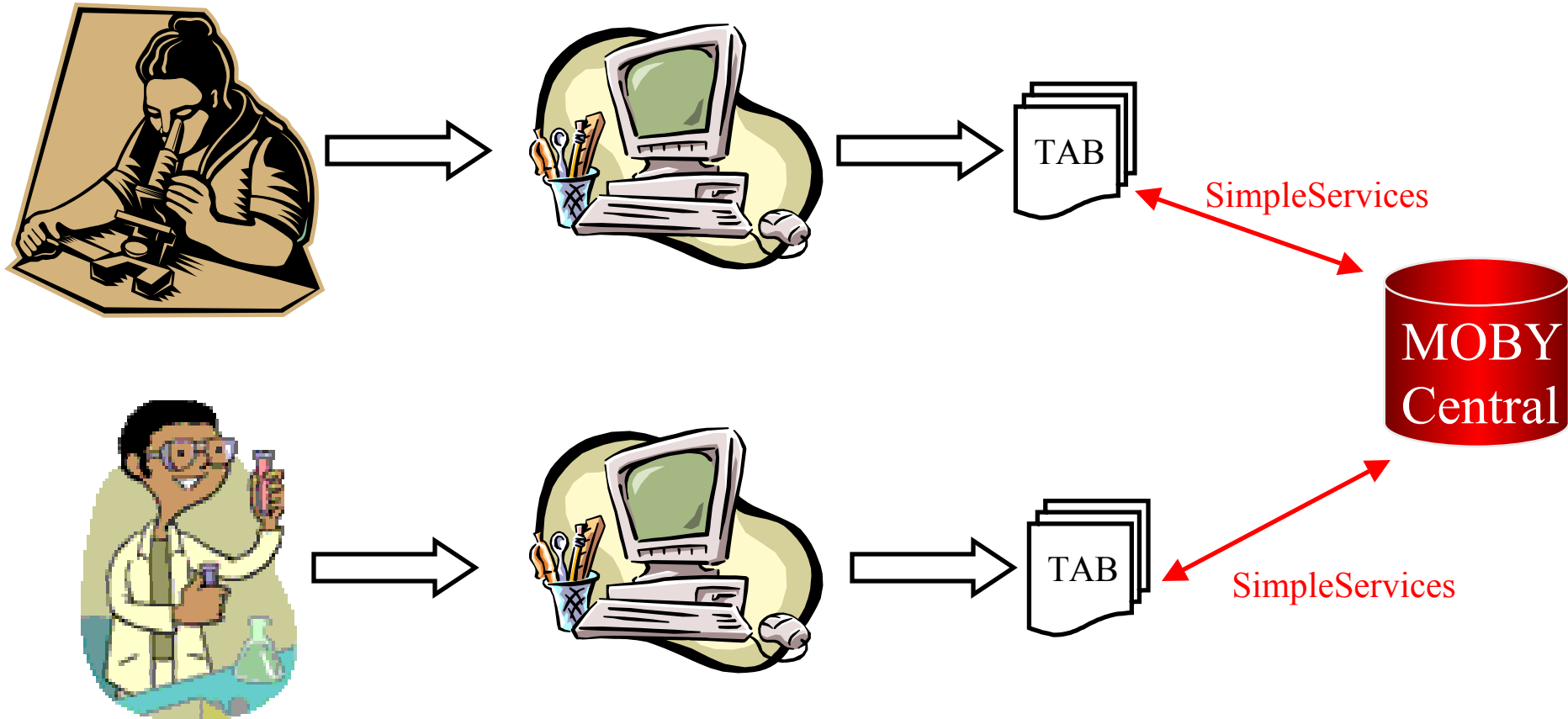
- Web services for bioinformatics
- Services register at MOBY Central with ‘signature’ triple: input/service/output
- MOBY Central knows about all service & object types
- Service discovery through signature
- Open: anyone can register any service, create new objects

# BioGraphNet is a ‘sandbox’

- Serves up biological graphs from a network of distributed computers.
  - Common standard for sharing distributed network information (‘SimpleServices’)
  - Small ‘starter’ collection of services
  - Sample application: BioTrawler viewer
- Tools to ‘play with interaction data’

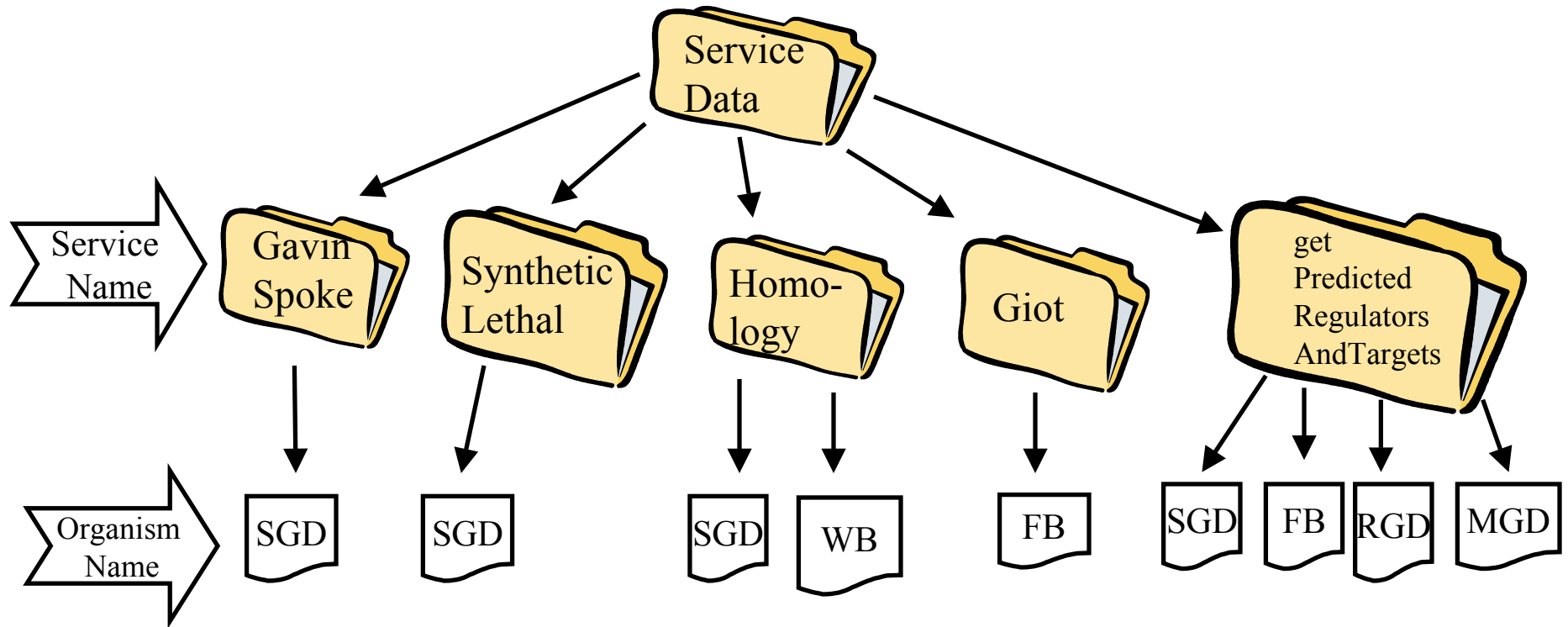


# SimpleServices.pm

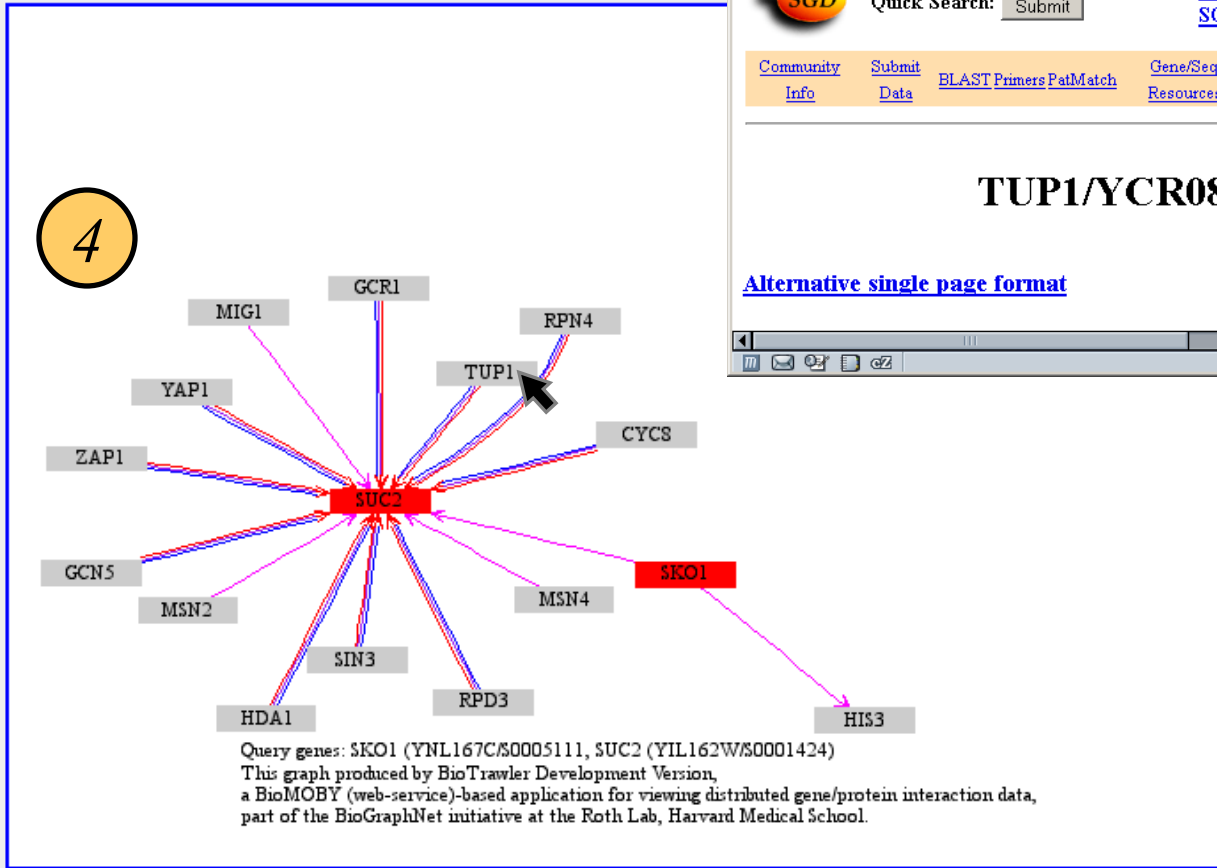




# Service directory structure



# Results from BioTrawler Deve



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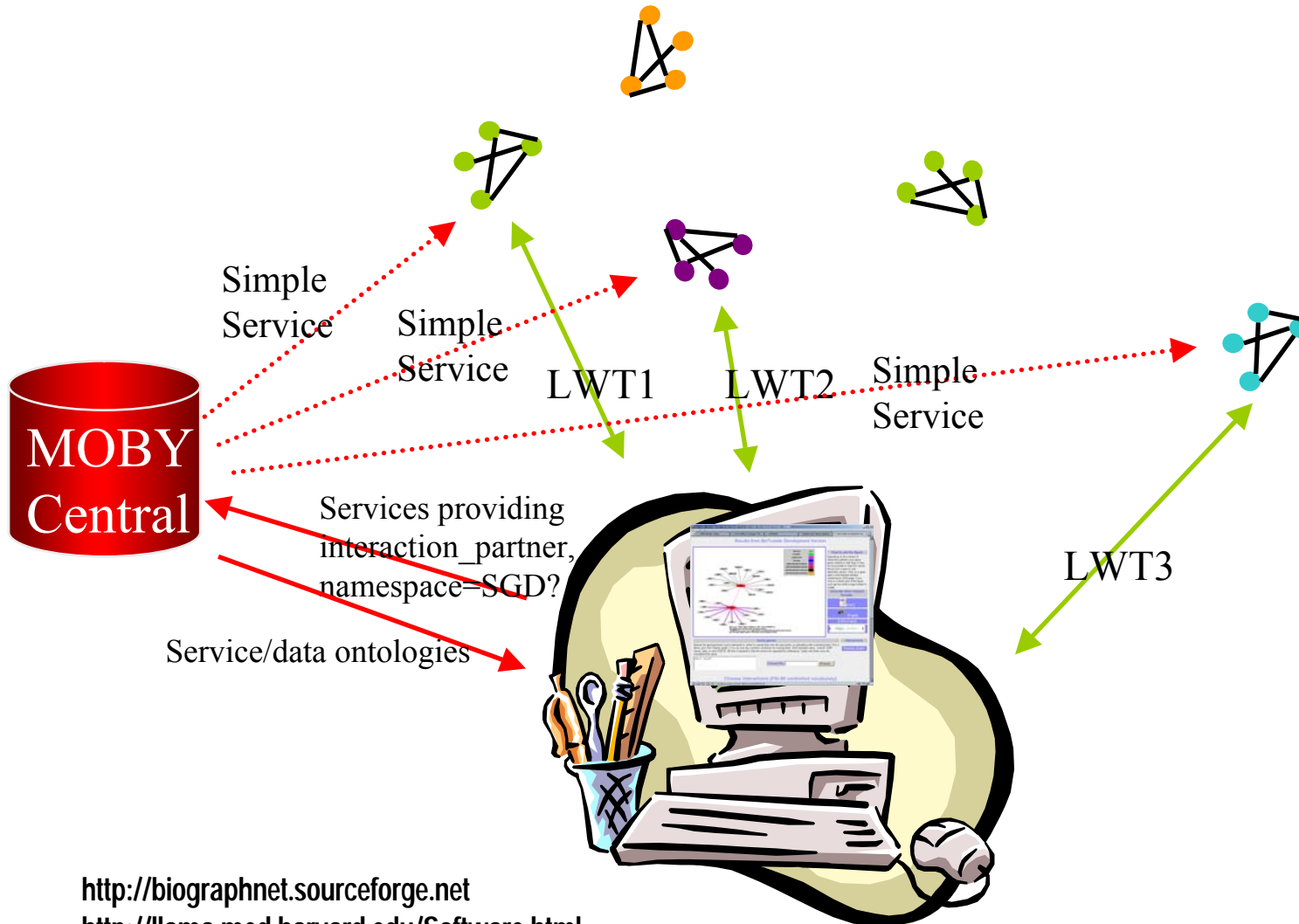
[Display graph](#)

sko1 suc2

1

Choose file:  Browse...

# How BioTrawler works



# The future

- Solicit community needs
- Find volunteers with data/algorithms (GRID/Tyers' group already signed on)
- Encourage established interaction browsers to support this web-service-style input
- Extend interaction ontology to deeper levels of PSI-MI?
- Introduce 'evidence types'

# Powered By

## Acknowledgments

- Gabriel Berriz, Fritz Roth (Roth Lab, Harvard)
- BioMOBY crew (M Wilkinson, L. Stein, et al.)
- BioPAX consortium (J Zucker, J Luciano, et al.)
- Proteomics Standards Initiative-Molecular Interactions (PSI-MI)
- GRID (BJ Breitkreuz, Tyers' Lab, U. Toronto)

## MOBY Services

BioGraphNet online:

- <http://biographnet.sourceforge.net>
- <http://llama.med.harvard.edu/Software.html>