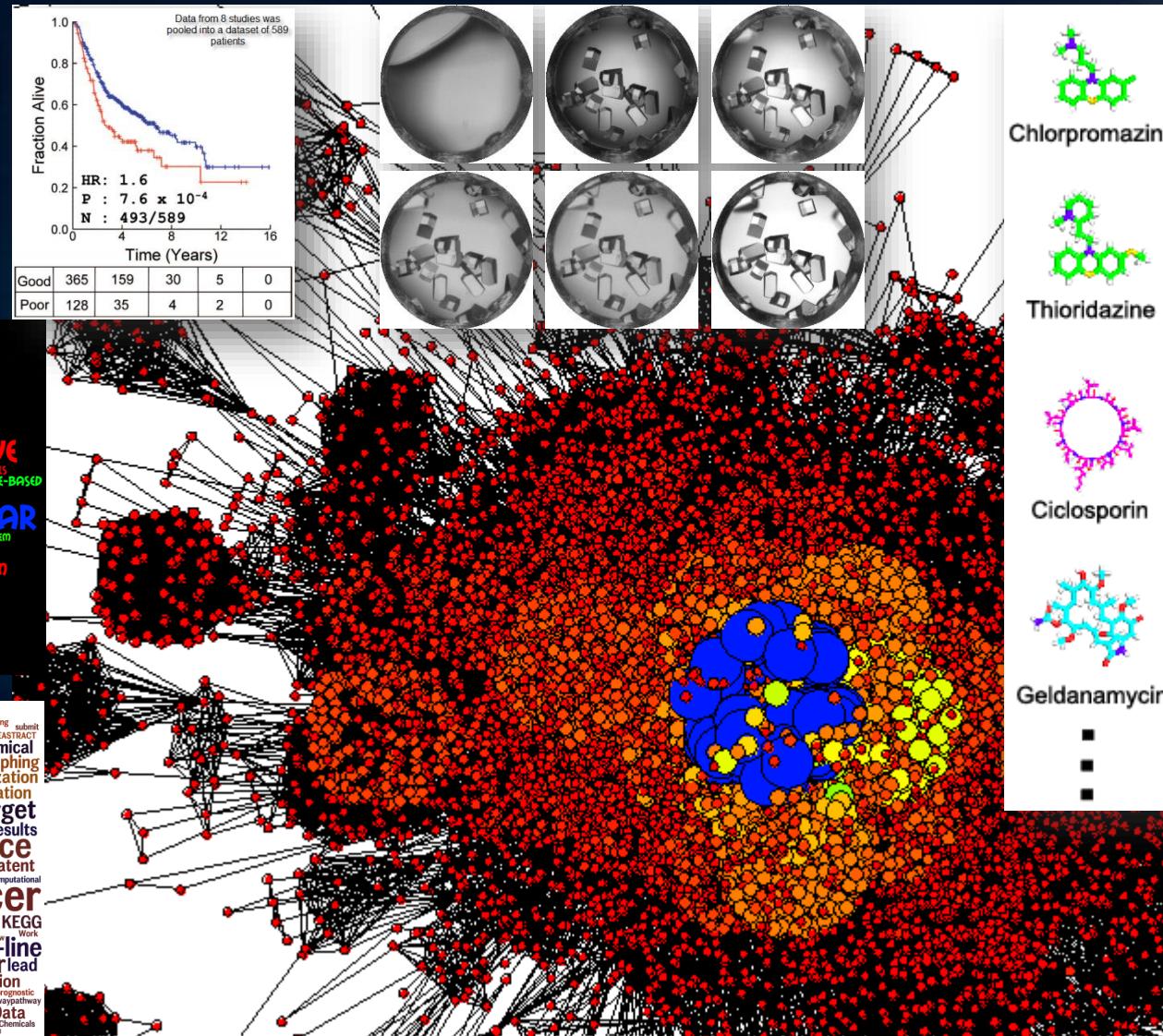
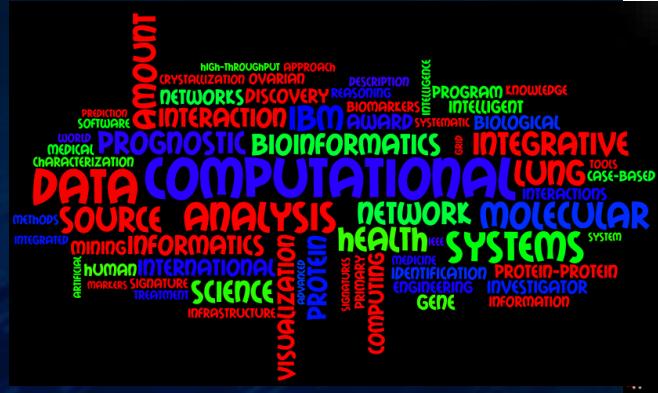


# Visual Data Mining in Integrative Cancer Informatics

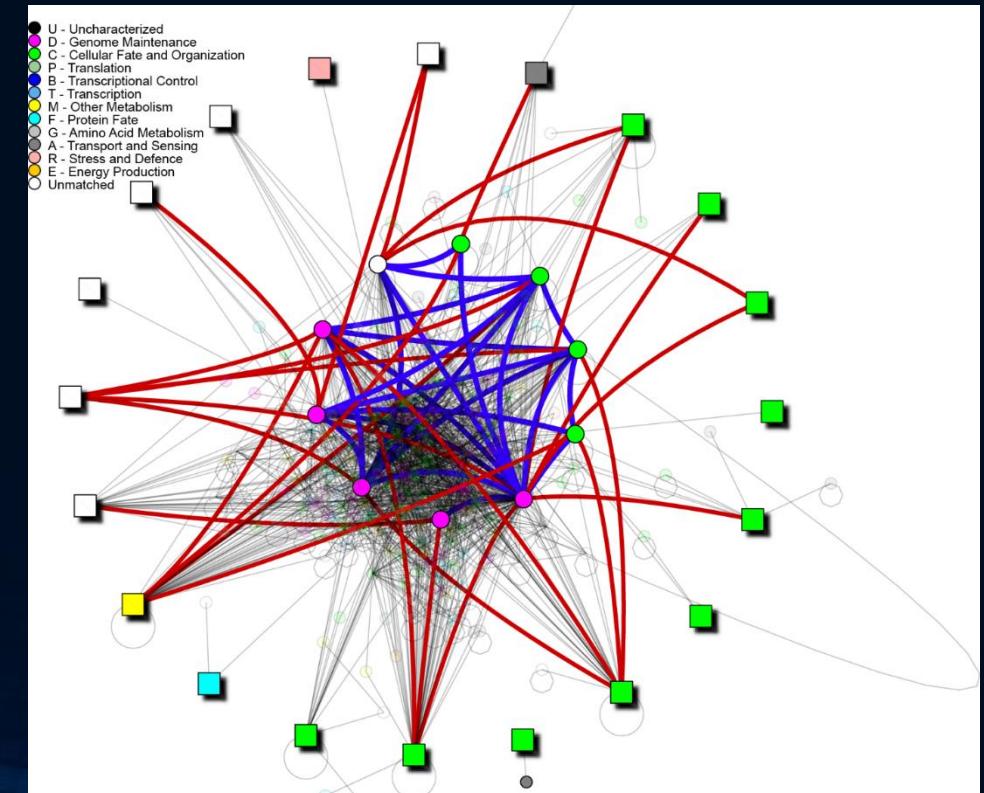
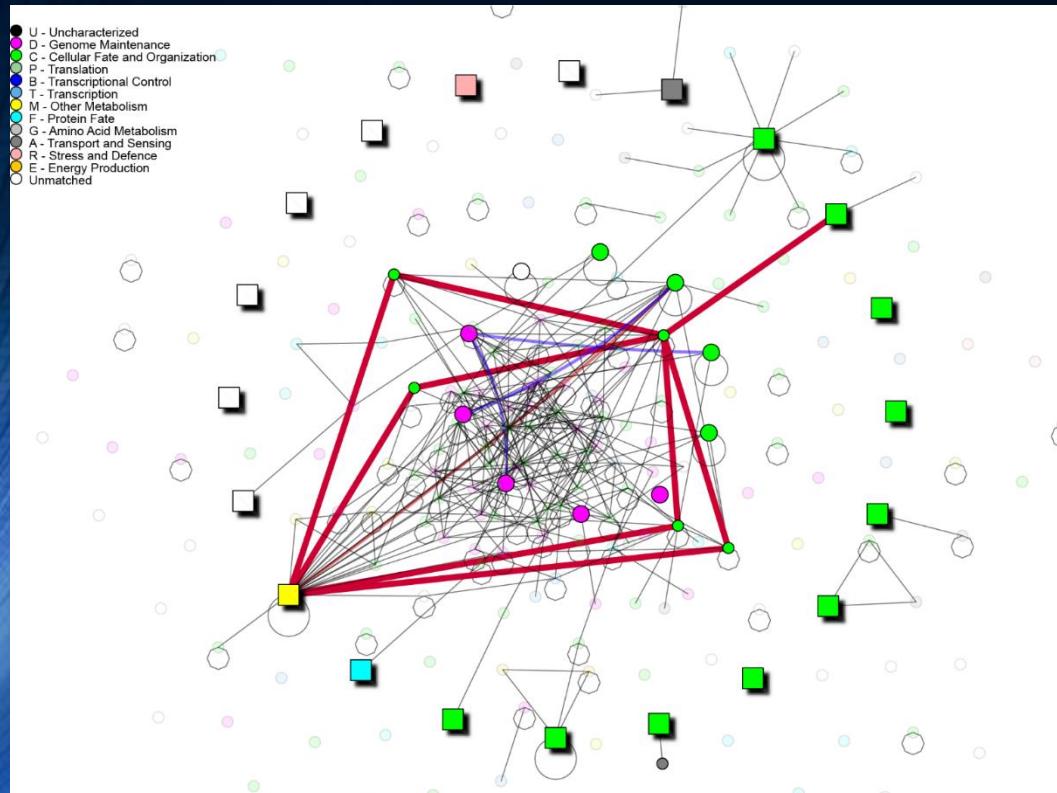
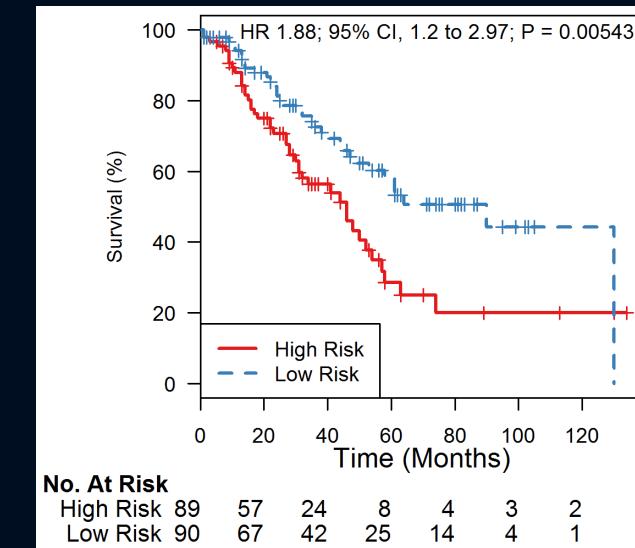
Igor Jurisica

<http://www.cs.utoronto.ca/~juris>



# Why Should we Care ?

- Need to interpret results
- Need to plan experiments
- Most of the research done on <20% of proteome



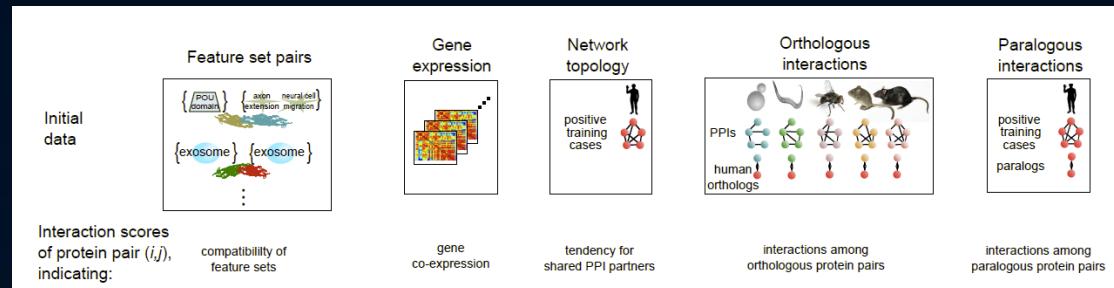


# Predicting PPIs

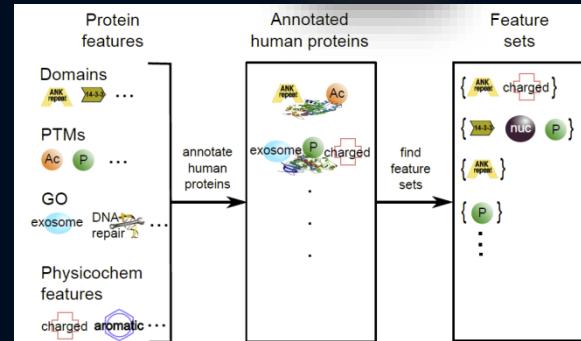
## 1. Establish training set

Positive cases: high-conf human PPIs  
Negative cases: random human protein pairs

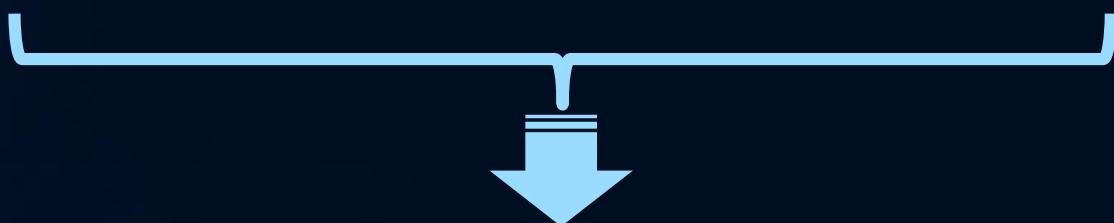
## 3. Compute interaction scores of protein pairs



## 2. Identify feature sets characterizing single proteins



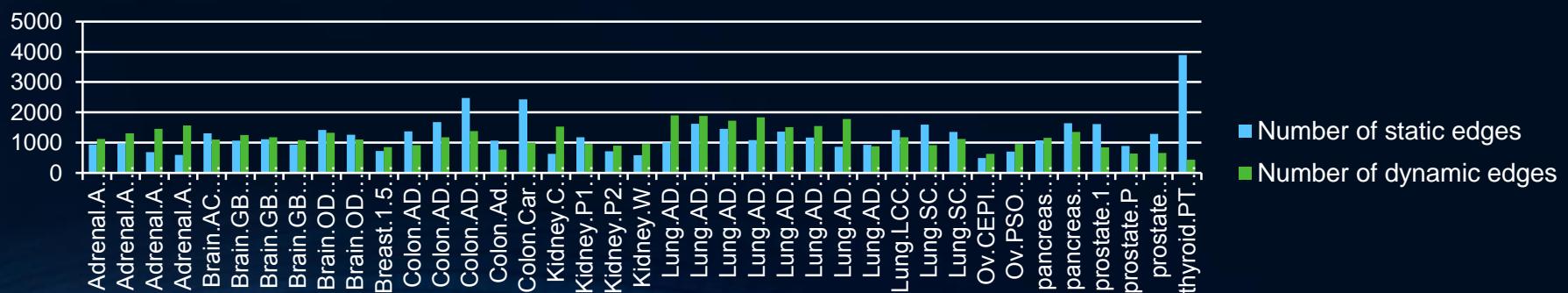
## 4. Calculate probability of interaction



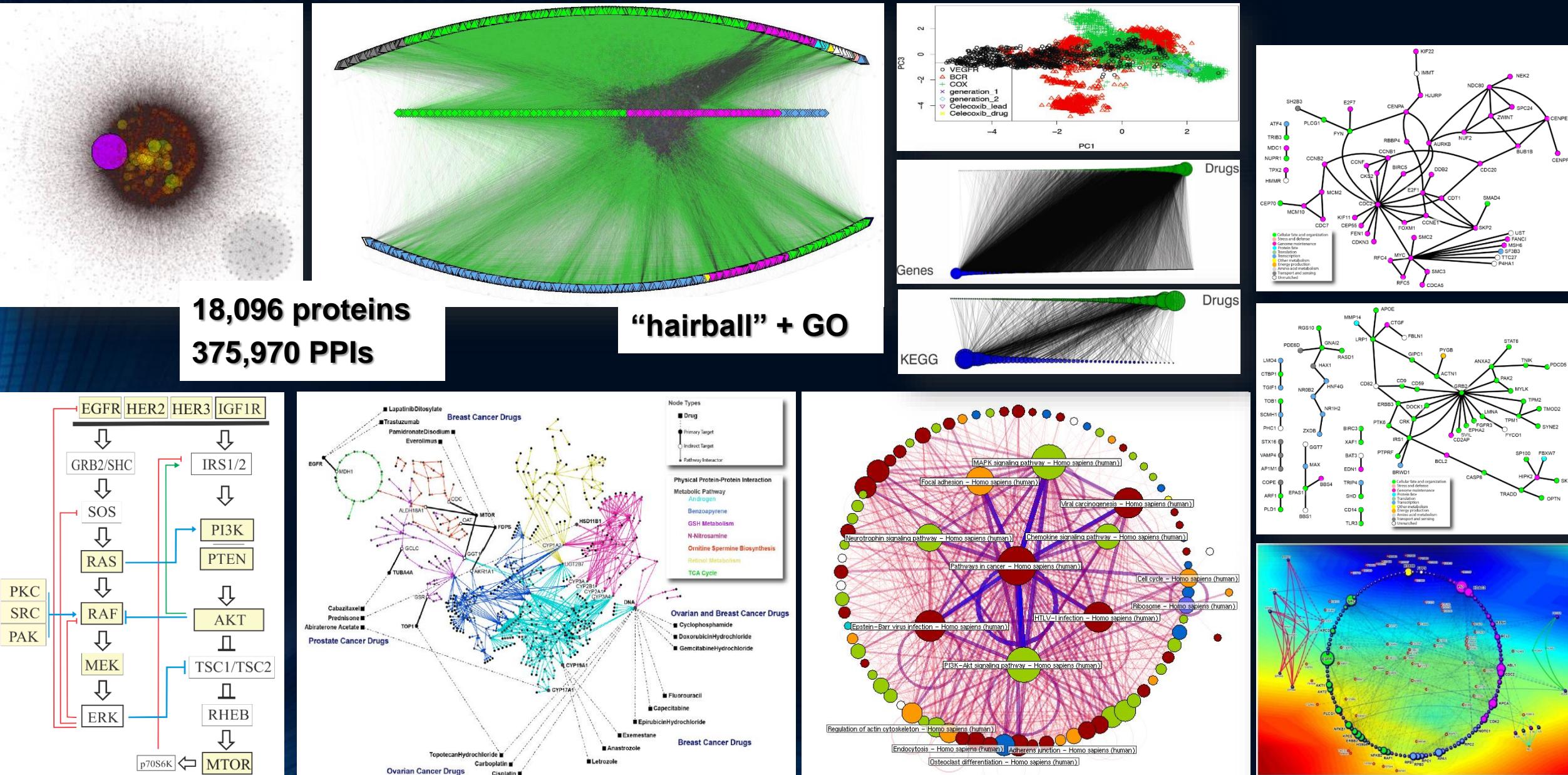
Protein\_1, Protein\_2, Probability, Evidence

Validation rates: 40-83%  
Sensitivity: 79%

## 5. Identify condition-specific interactions



# Integrative Modeling



# Signature-function-treatment



CDIP

[ophid.utoronto.ca/cdip](http://ophid.utoronto.ca/cdip)



XgDB

[ophid.utoronto.ca/OCI/xg/](http://ophid.utoronto.ca/OCI/xg/)



I2D

[ophid.utoronto.ca/i2d](http://ophid.utoronto.ca/i2d)



mirDIP

[ophid.utoronto.ca/mirDIP](http://ophid.utoronto.ca/mirDIP)



GAP

[ophid.utoronto.ca/gap](http://ophid.utoronto.ca/gap)



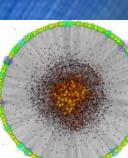
NetwoRx

[ophid.utoronto.ca/networx/](http://ophid.utoronto.ca/networx/)



SCRIPDB

[dcv.uhnres.utoronto.ca/SCRIPDB/](http://dcv.uhnres.utoronto.ca/SCRIPDB/)



NAViGaTOR

[ophid.utoronto.ca/navigator](http://ophid.utoronto.ca/navigator)



GeneCards

[ophid.utoronto.ca/genecards](http://ophid.utoronto.ca/genecards)

Members: 662,029  
Devices: 2,786,318

## HELP CONQUER CANCER

Powered by **IBM**.

**world community grid**  
technology solving problems

Member name: Testname Points: 4242 Progress: 65%

**Mapping Cancer Markers**

//Progressing//

Your computer is looking at some combination of genes...

Chromosome Map

Run Time Per Calendar Day  
311y:108d:23h:37m:59s

Powered by **IBM**.