

COSNet: a Cost Sensitive Neural Network for Semi-supervised Learning in Graphs



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Outline



- The Gene Function Prediction (GFP) problem
- Related approach for GFP
- Our proposal for GFP
- Results in yeast
- Conclusions

Gene Function Prediction



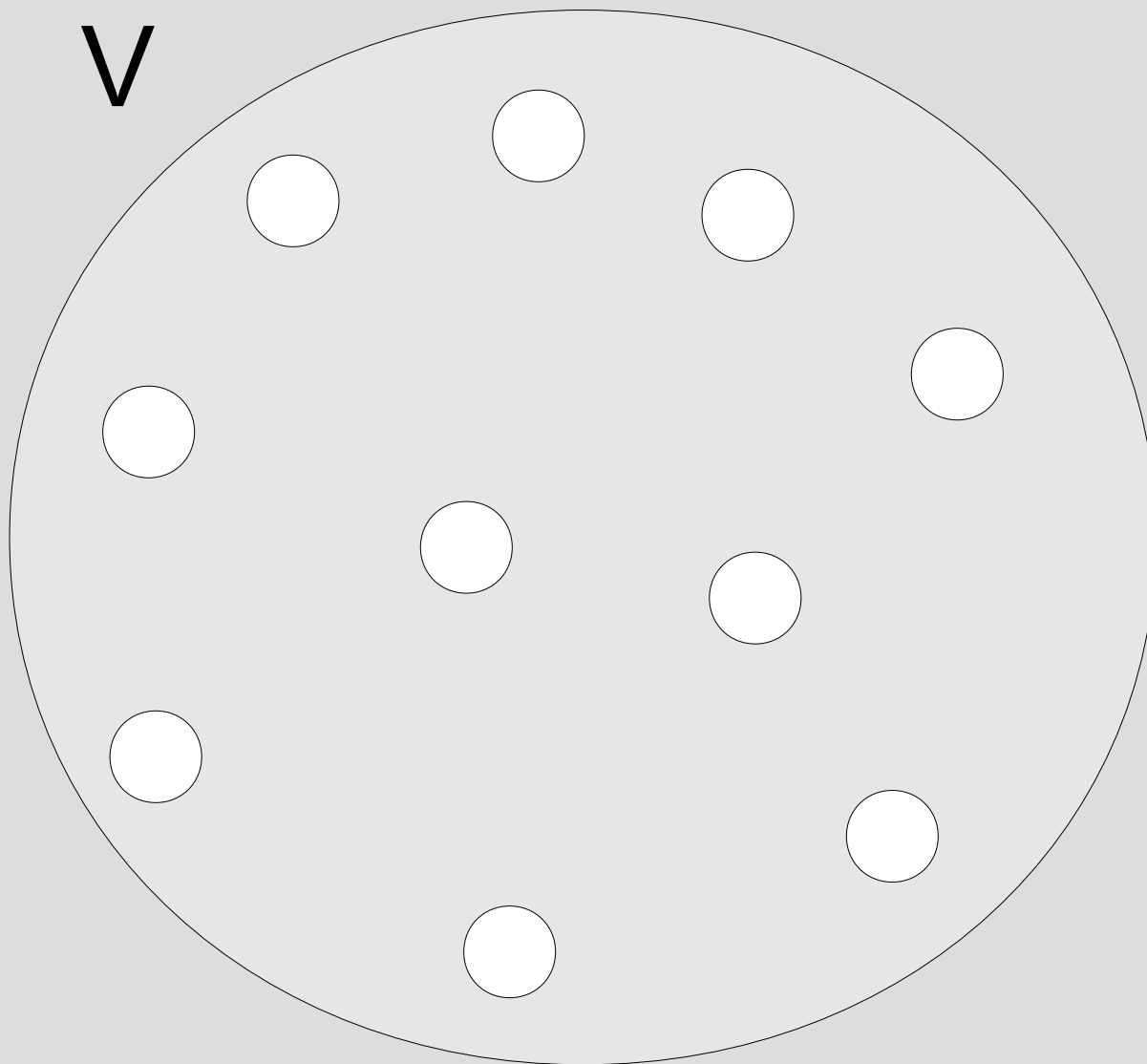
Genome sequencing

- **Main problem:** understanding biological functions of new genes
- **Taxonomy:** hierarchical definition of gene properties
 - Gene Ontology(GO), FunCat
- **Annotation:** established involvement of a gene in the biological mechanism represented by a functional class (term)

Gene Function Prediction Problem



V



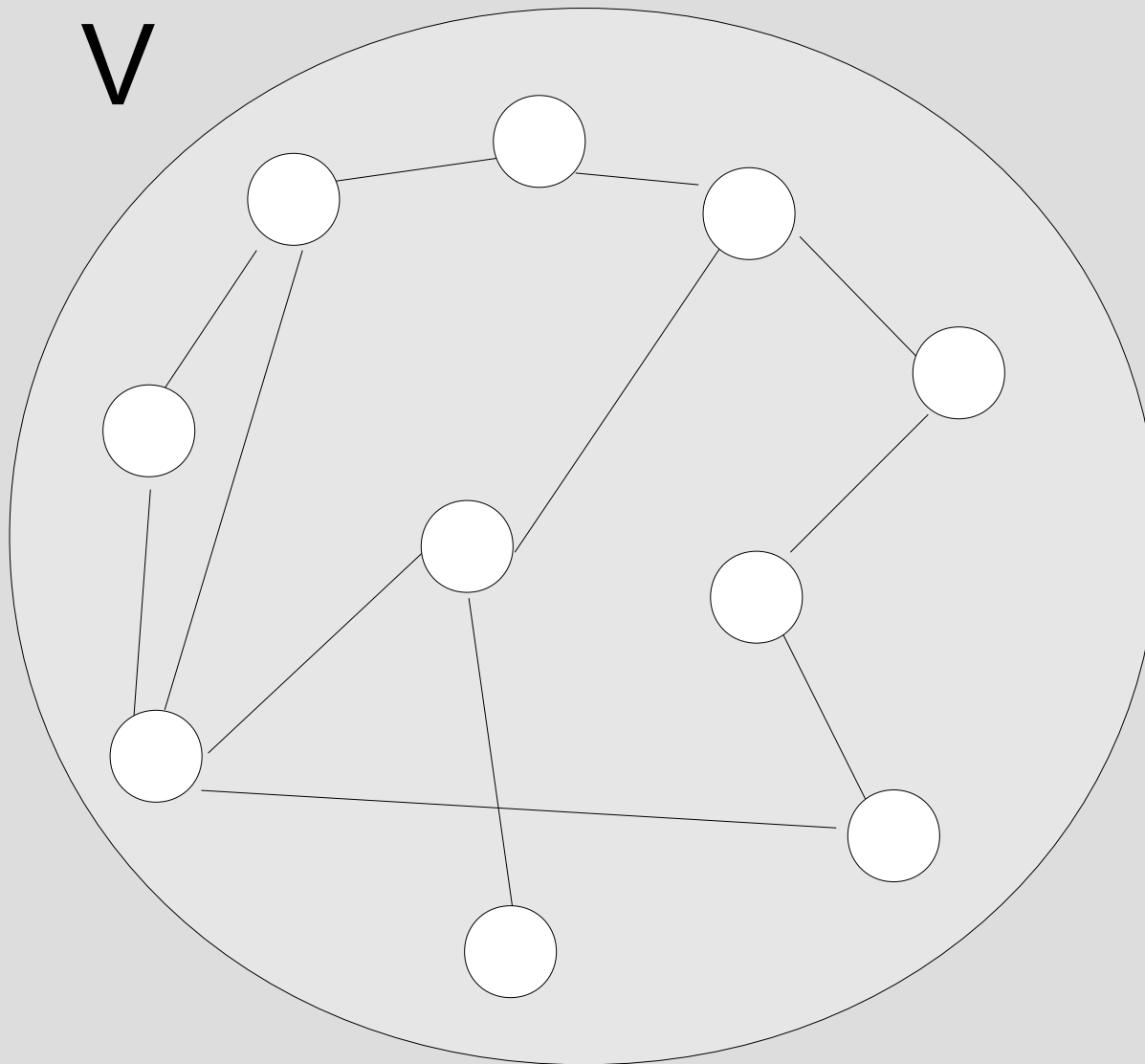
Input:

- V genes

Gene Function Prediction Problem



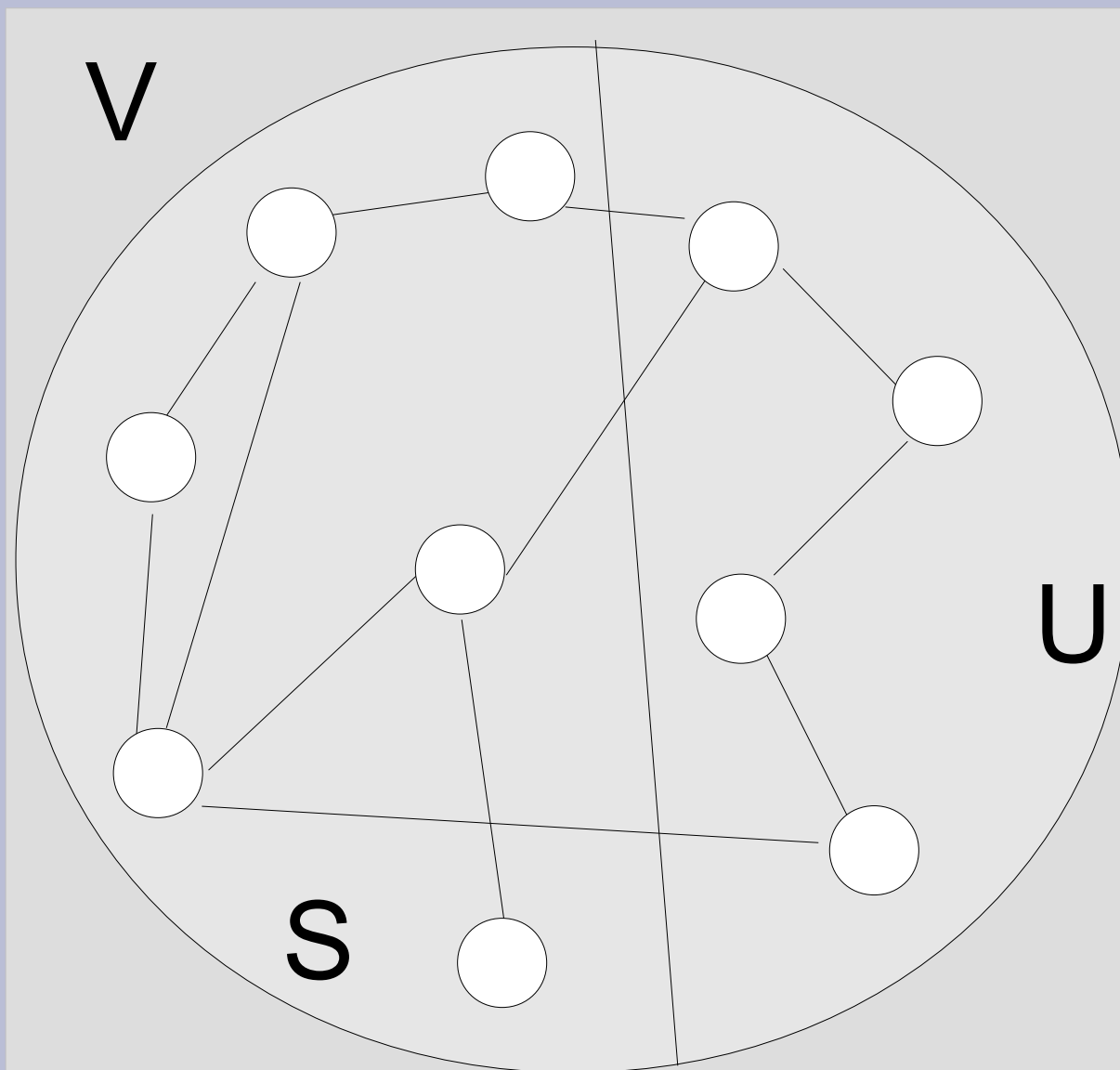
V



Input:

- V genes
- W symmetric matrix

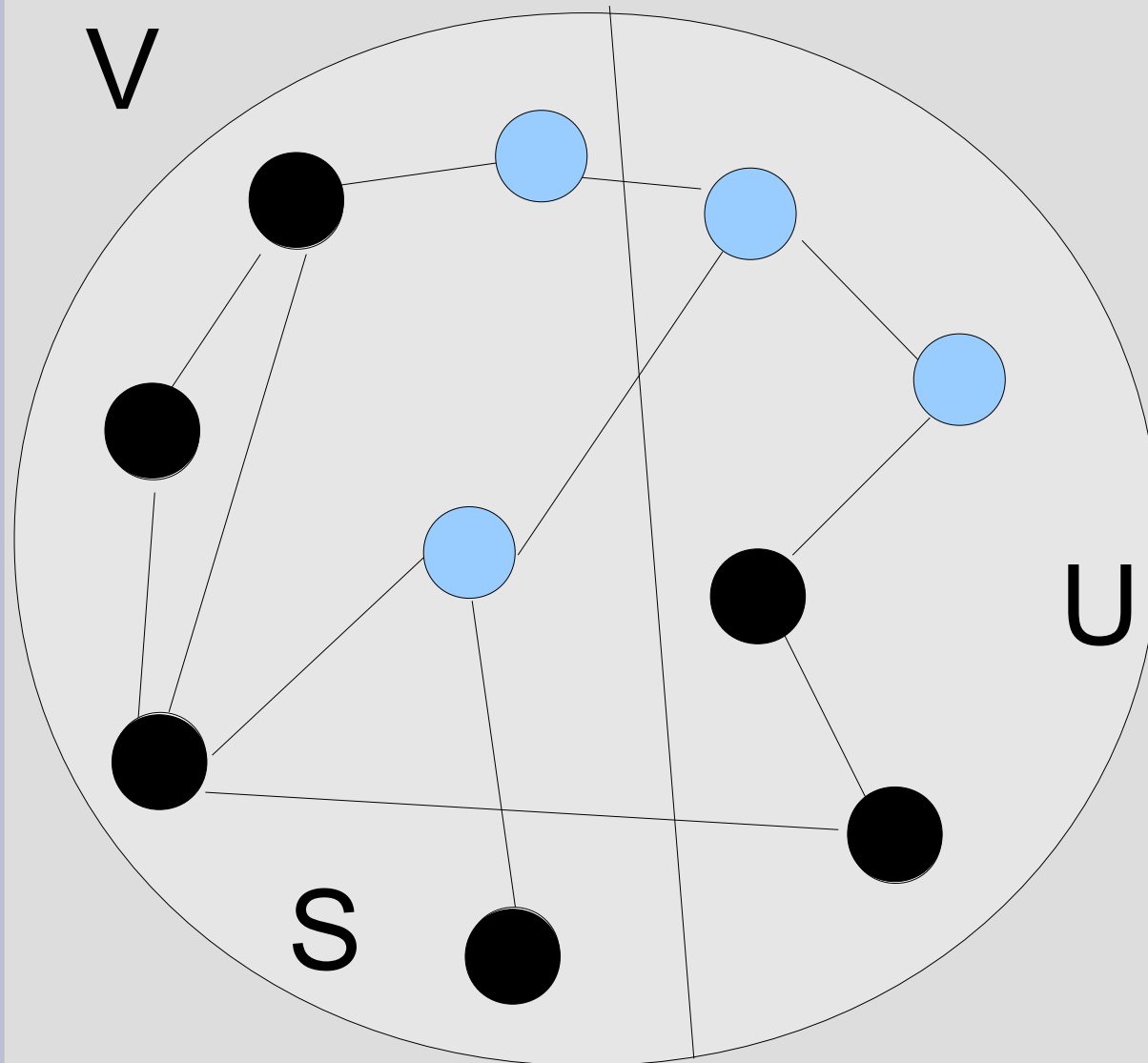
Gene Function Prediction Problem



Input:

- V genes
- W symmetric matrix
- S, U bipartition of V
 - S labeled genes
 - U unlabeled genes

Gene Function Prediction Problem



Input:

- V genes
- W symmetric matrix
- S, U bipartition of V
 - S labeled genes
 - U unlabeled genes
- S^p, S^n bipartition of S

Output:

- U^p, U^n bipartition of U

Machine learning methods for GFP

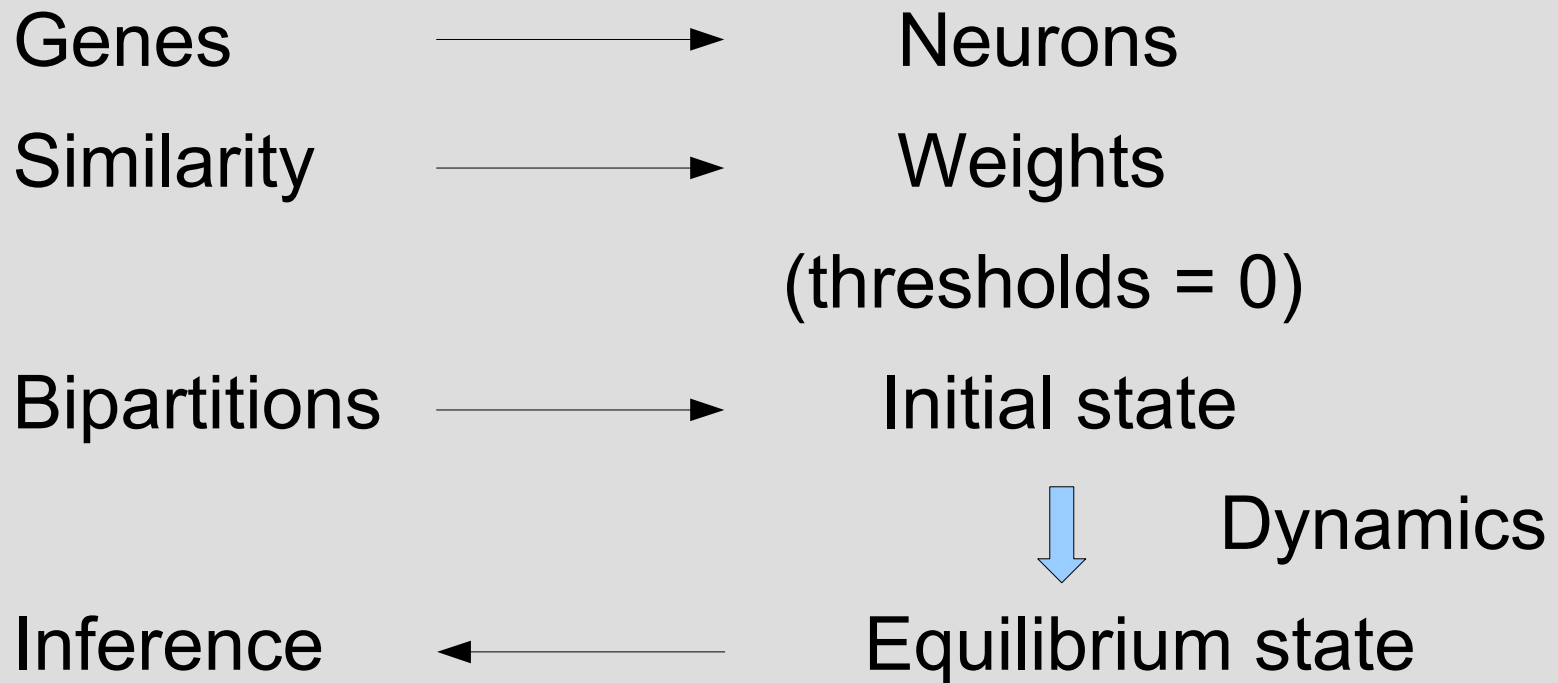


- Inductive methods
 - Learn a model to infer functions for all genes
 - Support Vector Machines [Lanckriet et al 2004]
- Transductive methods
 - Infer functional predictions only for genes in test set
 - MRF [Deng et al 2002],
 - Neural networks [Karaoz et al 2003],
 - Functional Linkage Networks [Marcotte 1999]
 - Label propagation [Zhu et al 2003, Mostafavi 2008-2010].

Gene Annotation using Integrated Networks (GAIN)



- Karaoz et al. (2003)
- Discrete Hopfield network

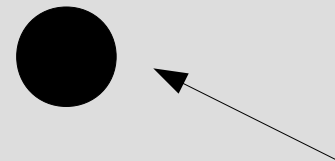
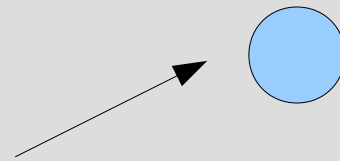


GAIN



- Initial state for each neuron i :

$$x_i(0) = 1, \quad -1, \quad 0 \quad \leftarrow \quad ?, \text{ Unlabeled}$$



positive label

negative label

$$x_i(t+1) = \text{Sgn} \left(\sum_{j=1}^{i-1} w_{ij} x_j(t+1) + \sum_{k=i+1}^n w_{ik} x_k(t) \right)$$

GAIN



- Energy function

$$E(x) = -\frac{1}{2} \cdot \sum_{i=1}^n x_i \left(\sum_{j \in 1}^n x_j w_{ij} \right)$$

- E is a **monotonic decreasing** function:

$$E(x(0)) \geq E(x(1)) \geq E(x(2)) \geq \dots \geq E(x(t)) \geq \dots$$

- The **equilibrium state** $\tilde{x} = (\tilde{s}, \tilde{u})$ characterizes the bipartition of U

$$U^p = \{i \in U \mid u_i = 1\}$$

$$U^n = \{i \in U \mid u_i = -1\}$$

Drawbacks of GAIN



- All nodes may be updated
 - prior knowledge might not be preserved
- "Same relevance" for positive and negative examples
 - Data imbalance not managed

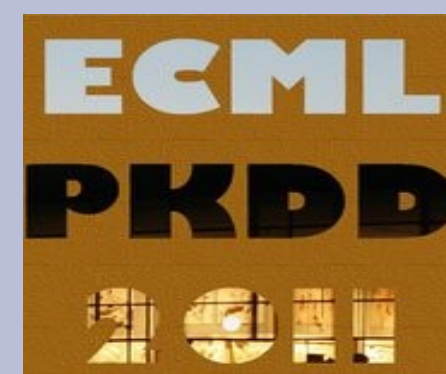
Drawbacks of GAIN

- GAIN tries to find a global minimum \tilde{x} of E assuming that the initial state \bar{s} of labeled nodes is a part of \tilde{x} , i.e.

$$\tilde{x} = (\bar{s}, \tilde{u})$$

- In many cases \bar{s} is not a part of a minimum
 - No coherence with the prior knowledge

Parametrized Hopfield network



GAIN:

- *Positive labels* $:= 1$
- *Negative labels* $:= -1$
- *Thresholds* $:= \underline{0}$

Our approach:

- *Positive labels* $:= \sin\alpha$
 - *Negative labels* $:= -\cos\alpha$
 - *Thresholds* $:= \underline{\gamma}$
- ← parameters to be learned!



Parametrized DHN: $\langle W, \underline{\gamma}, \alpha \rangle$

Parametrized Hopfield network



- $H = \langle W, \underline{\gamma}, \alpha \rangle$ DHN on nodes in V
 - W connection matrix
 - $\underline{\gamma} = (\gamma_1, \gamma_2, \dots, \gamma_n)$ vector of activation thresholds
 - $\alpha \in] 0, \pi/2 [$, neuron values are $\sin\alpha, -\cos\alpha$
- In GAIN
 - $\underline{\gamma} = \underline{0}$
 - $\alpha = \pi/4$

Sub Network



Labeled

S

Unlabeled

U

Two Subnetworks: $H|_{S,U^p}$

and

$H|_{U,S^p}$

Deal with Data Imbalance and prior knowledge "coherence"

Preserve prior knowledge

Sub-network property



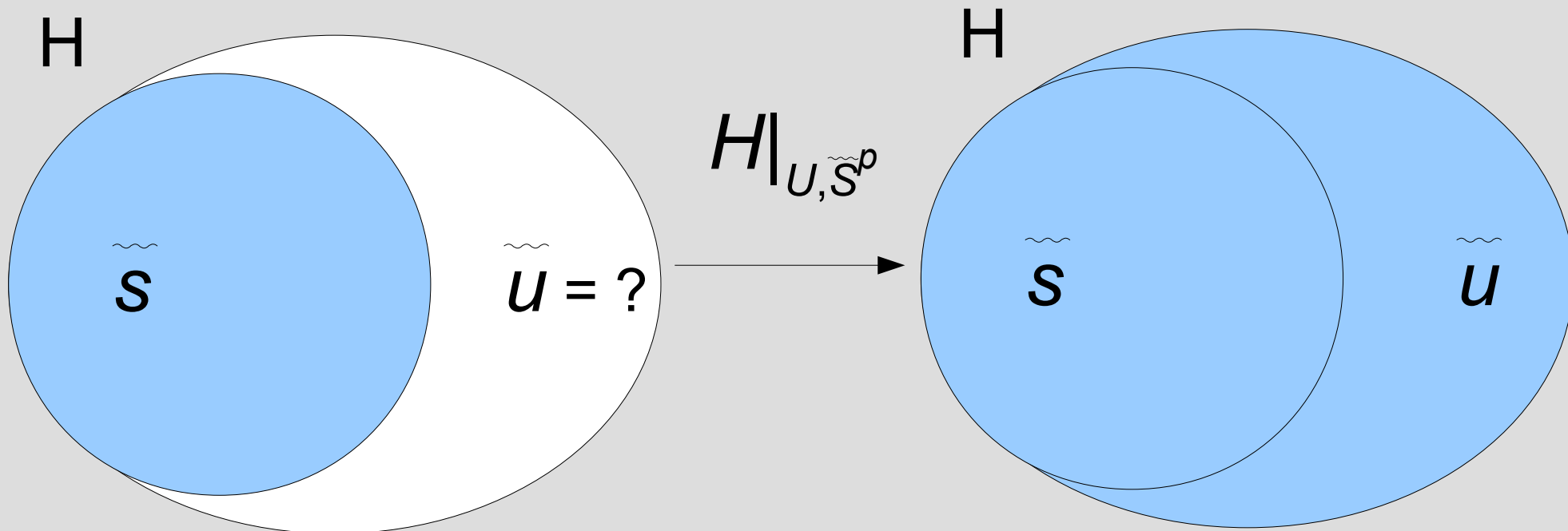
- Given
 - DHN $H < W, \underline{\gamma}, \alpha >$ with neurons V
 - S, U bipartition of V
 - S^p, S^n bipartition of S
 - U^p, U^n bipartition of U

It holds: if $\tilde{x} = (\tilde{s}, \tilde{u})$ is an energy global minimum H ,
then \tilde{u} is an energy global minimum of $H|_{U, S^p}$

Sub-network property



- Having a part \tilde{s} of a minimum of energy of H , it's possible to discover the hidden part \tilde{u} by minimizing the energy of $H|_{U, \tilde{s}^p}$

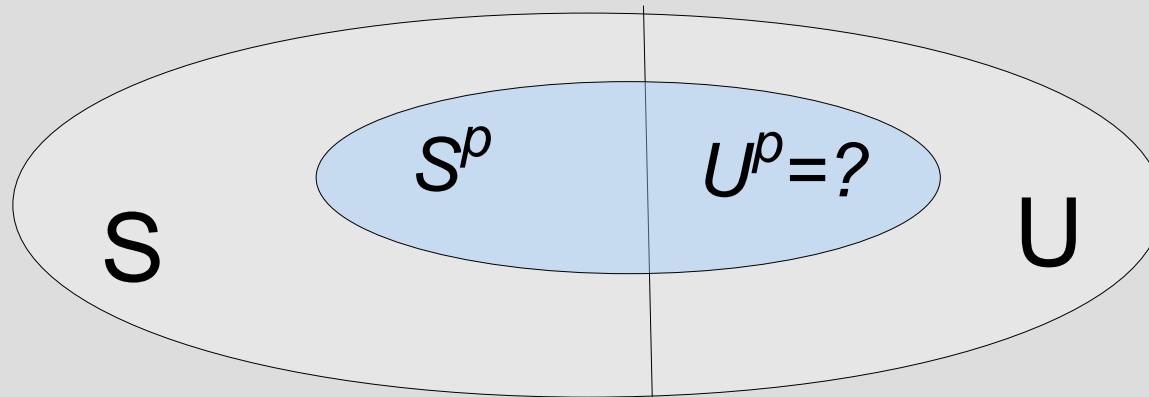


Sketch of COSNet



- INPUT: W similarity matrix; S, U bipartition of V ; S^p, S^n bipartition of S
- OUTPUT: U^p, U^n bipartition of U
 1. Generate a temporary solution U^p, U^n
 2. Find the couple (α, γ) such that the initial state of the network $H|_{S, U^p}$ is as close as possible to an equilibrium state
 3. Extend the parameters (α, γ) to the network $H|_{U, S^p}$
 4. Run the network $H|_{U, S^p}$

Generating a temporary solution



p_s positive rate in S
 p_u positive rate in U

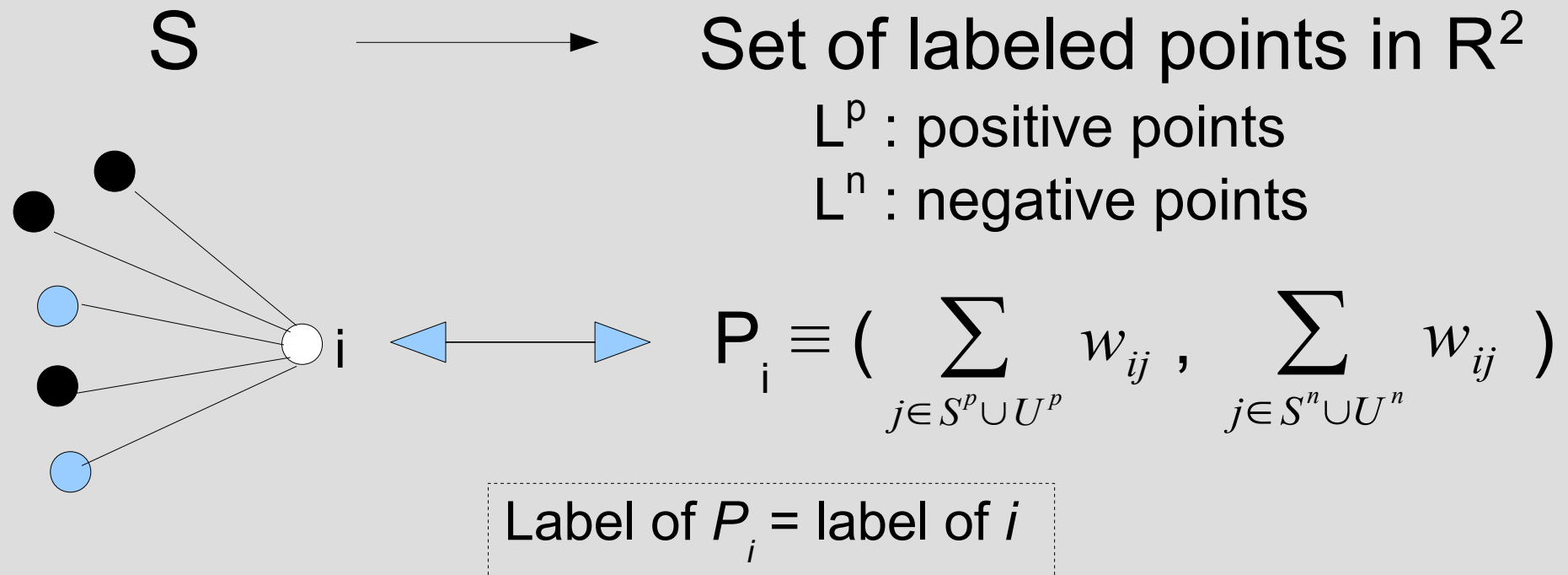
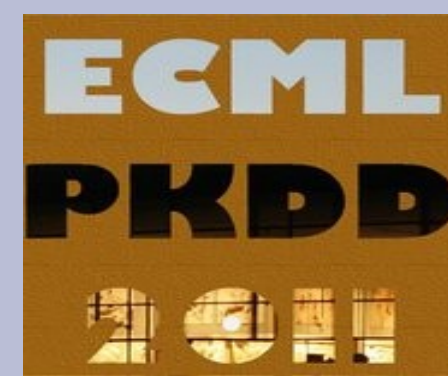
Procedure:

- Generate k according to binomial distribution $B(|U|, \frac{|S^p|}{|S|})$
- $U^p := k$ elements randomly chosen in U
- $U^n := U \setminus U^p$

FACT:

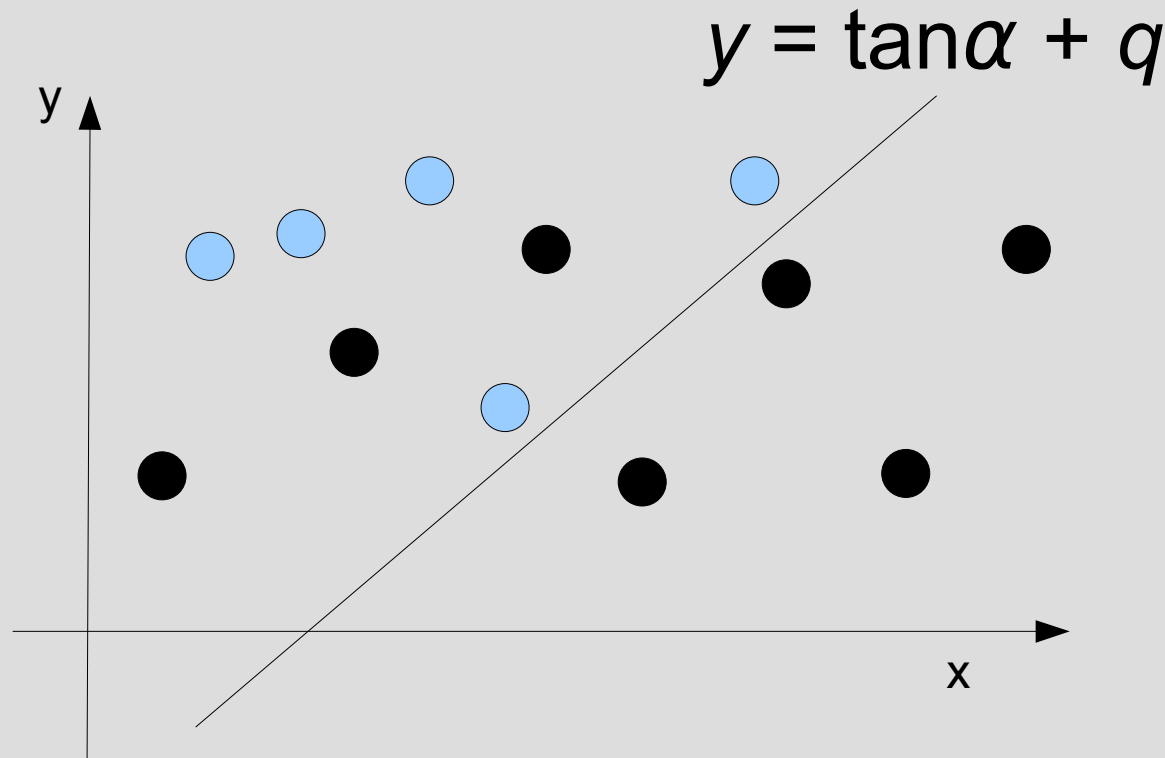
$$\frac{|S^p|}{|S|} = \underset{x}{\operatorname{argmax}} \operatorname{Prob} \left\{ p_u = x \mid p_s = \frac{|S^p|}{|S|} \right\}$$

Finding the optimal parameters



AIM: "optimal" separation of L^p from L^n by a straight line
 $y = \tan\alpha + q$ according to the **Fscore** criterion

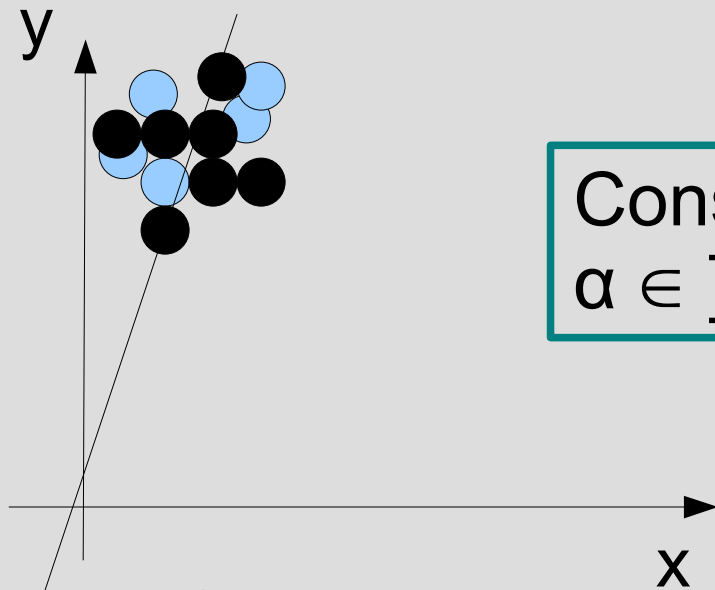
Finding the optimal parameters



$\gamma = -q \cos\alpha$
as first approach
we chose the
same γ for each
neuron

Fact: Fscore (opt) = 1 \iff the corresponding state of $H|_{S,U^p}$ is an *equilibrium point*

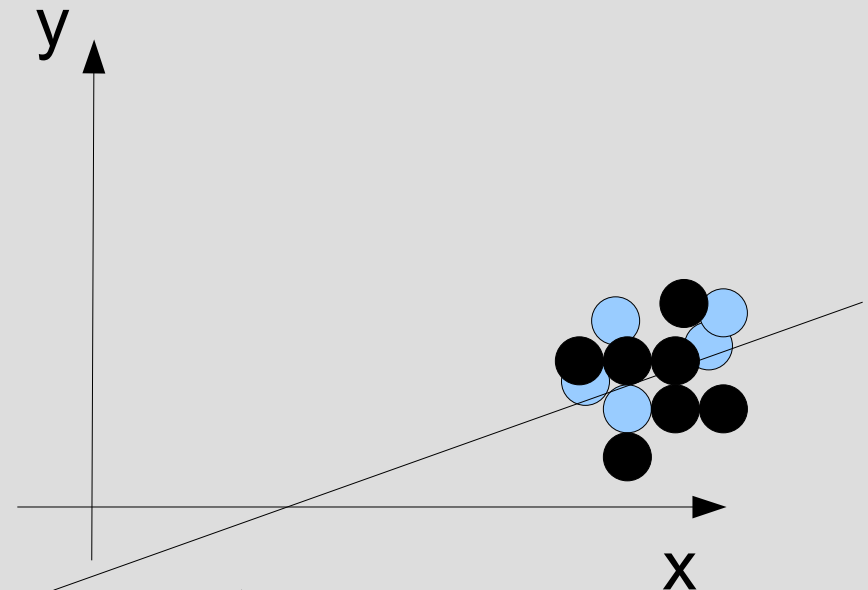
Data imbalance management



Constraint:
 $\alpha \in]0, \pi/2[$

$$|S^p| \ll |S^n|, \quad \alpha > \pi/4$$

$$|\sin \alpha| > |\cos \alpha|$$



$$|S^p| \gg |S^n|, \quad \alpha < \pi/4$$

$$|\sin \alpha| < |\cos \alpha|$$

Finding the final solution



- Dynamics of the sub-network $H|_{U,S^p}$ with the found parameters until fixed point \tilde{u} is reached
- Infer bipartition of U as follows:
 - $U^p = \{i \in U \mid \tilde{u}_i = \sin\alpha\}$
 - $U^n = \{i \in U \mid \tilde{u}_i = -\cos\alpha\}$

Results



- Experimental setup:
 - 5 data yeast data sets
 - **Genome wide**
 - FunCat taxonomy, ontology wide
 - 10-folds Cross Validation
 - **FLAT** approach (no hierarchical information)
 - **F-score** performance measure

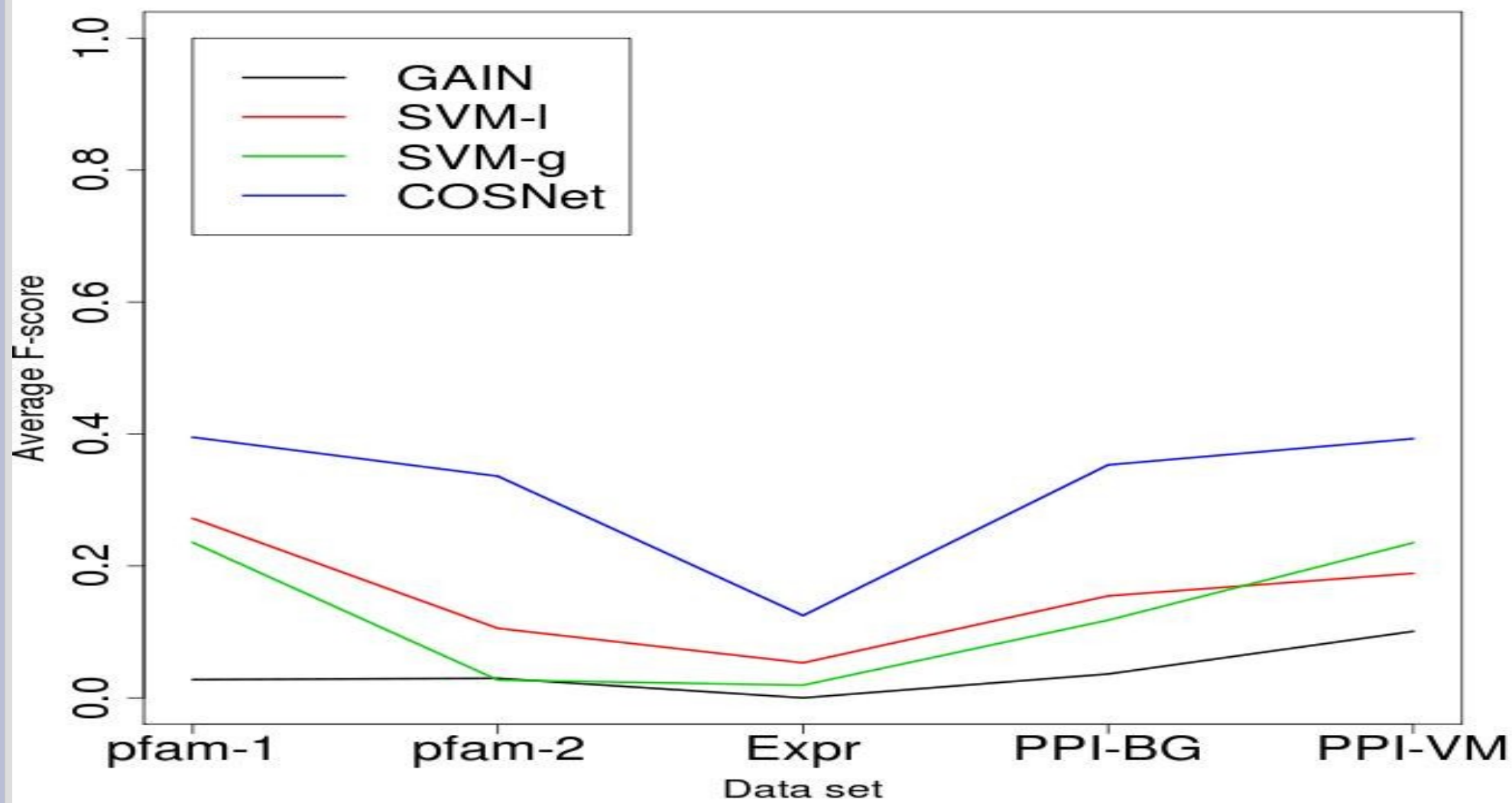
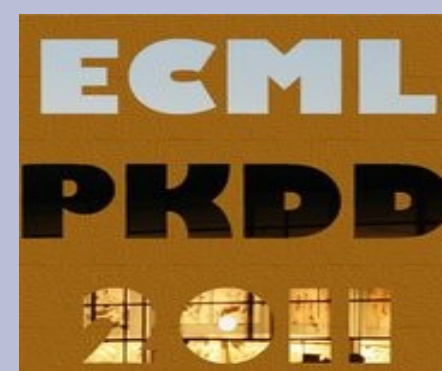
Results



- Average F-score genome wide - ontology wide

<i>Data set</i>	<i>GAIN</i>	<i>SVM - l</i>	<i>SVM - g</i>	<i>COSNet</i>
<i>Pfam-1</i>	0.0277	0.2722	0.2355	0.3892
<i>Pfam-2</i>	0.0296	0.1054	0.0270	0.3233
<i>Expr</i>	0	0.0531	0.0192	0.0957
<i>PPI-BG</i>	0.0362	0.1546	0.1178	0.3486
<i>PPI-VM</i>	0.1009	0.1888	0.2351	0.3844

Results



Conclusions



- We developed a Cost-Sensitive method based on neural network for predicting labels in graph
- Effective in managing high imbalanced data
- Better performance w.r.t. the state-of-the-art methods
- The time complexity $\mathcal{O}(|S| \cdot \log |S| + |W|)$ allows the application to large scale data

Ongoing developments



- Increase the number of parameters
 - Different thresholds for neurons or different slopes
- Multi task extension
 - Use hierarchical relationship between terms
- Data Source integration