Some contributions of machine learning to bioinformatics

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Where I come from

- A joint lab about “Cancer computational genomics, bioinformatics, biostatistics and epidemiology”
- Located in th Institut Curie, a major hospital and cancer research institute in Europe
- Hosted in a brand new building in the center of Paris (near Notre-Dame, Saint-Germain, Pantheon...)

Our research

Main topics

- Epidemiology of cancer (eg, studies on etiology of breast cancer)
- General biostatistics (eg, clinical trials, risk modelling...)
- Biostatistics and machine learning for bioinformatics (high-throughput data processing, modeling, predictive models...)
- Systems biology: analysis, modeling, inference of important regulatory and signaling systems
- IT: software developments, DB, web

Main topics in machine learning / statistics

- Processing high-throughput data (normalization, analysis): transcriptome, genome (CGH/SNP), proteomics, kinome. High-throughput sequencing is coming soon.
- Making predictive models, in particular diagnosis / prognosis
- Data mining / integration of heterogeneous data
- Structural bioinformatics, protein-protein interactions, virtual screening, chemogenomics

Outline

1. Including prior knowledge in classification and regression
2. Virtual screening and chemogenomics
3. Inference on biological networks
4. Conclusion

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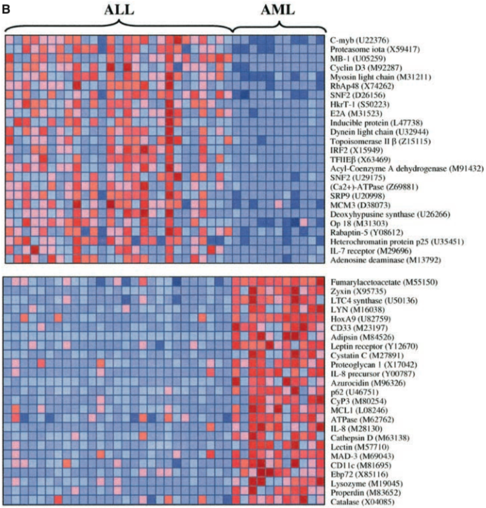
Motivation



Goal

- Design a classifier to automatically assign a class to future samples from their expression profile
- Interpret biologically the differences between the classes

Difficulty

- Large dimension
- Few samples

Linear classifiers

The model

- Each sample is represented by a vector $x = (x_1, \ldots, x_p)$
- Goal: estimate a linear function:

$$f_\beta(x) = \sum_{i=1}^{p} \beta_i x_i + \beta_0 \; .$$

- Interpretability: the weight β_i quantifies the influence of feature i (but...)

Training the model

$$f_\beta(x) = \sum_{i=1}^{p} \beta_i x_i + \beta_0 \ .$$

- Minimize an empirical risk on the training samples:

$$\min_{\beta \in \mathbb{R}^{p+1}} R_{emp}(\beta) = \frac{1}{n} \sum_{i=1}^{n} l(f_\beta(x_i), y_i) \, ,$$

- ... subject to some constraint on β, e.g.:

$$\Omega(\beta) \leq C \, .$$

Example : Norm Constraints

The approach

A common method in statistics to learn with few samples in high dimension is to constrain the Euclidean norm of β

$$\Omega_{ridge}(\beta) = \| \beta \|_2^2 = \sum_{i=1}^{p} \beta_i^2 ,$$

(ridge regression, support vector machines...)

Pros

- Good performance in classification

Cons

- Limited interpretation (small weights)
- No prior biological knowledge

Example : Feature Selection

The approach

Constrain most weights to be 0, i.e., select a few genes (< 100) whose expression are sufficient for classification.

- Greedy feature selection (T-tests, ...)
- Contrain the norm of β: LASSO penalty ($\| \beta \|_1 = \sum_{i=1}^{p} | \beta_i |$), elastic net penalty ($\| \beta \|_1 + \| \beta \|_2$), ...)

Pros

- Good performance in classification
- Biomarker selection
- Interpretability

Cons

- The gene selection process is usually not robust
- No use of prior biological knowledge

Incorporating prior knowledge

The idea

- If we have a specific prior knowledge about the "correct" weights, it can be included in Ω in the contraint:

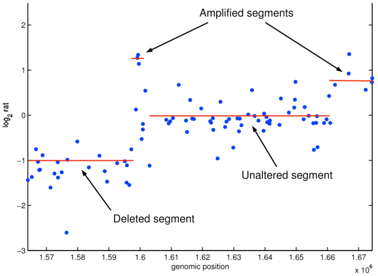
$$\text{Minimize } R_{emp}(\beta) \text{ subject to } \Omega(\beta) \leq C \,.$$

- If we design a convex function Ω, then the algorithm boils down to a convex optimization problem (usually easy to solve).
- Similar to priors in Bayesian statistics

Example: CGH array classification

The problem

- Comparative genomic hybridization (CGH) data measure the DNA copy number along the genome
- Very useful, in particular in cancer research
- Can we classify CGH arrays for diagnosis or prognosis purpose?
- Prior knowledge: we expect β to be sparse, and piecewise constant along the genome

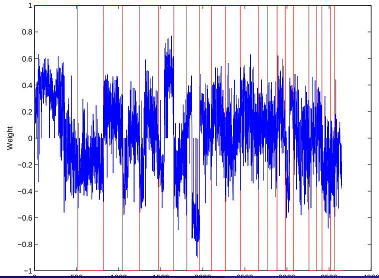


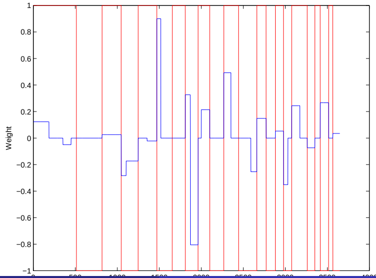
Example: CGH array classification

A solution (Rapaport et al., 2008)

$$\Omega_{fusedlasso}(\beta) = \sum_i |\beta_i| + \sum_{i \sim j} |\beta_i - \beta_j| \,.$$

- Good performance on diagnosis for bladder cancer, and prognosis for melanoma.
- More interpretable classifiers





Example: finding discriminant modules in gene networks

The problem

- Classification of gene expression: too many genes
- A gene network is given (PPI, metabolic, regulatory, signaling, co-expression...)
- We expect that “clusters of genes” (modules) in the network contribute similarly to the classification

Two solutions (Rapaport et al., 2007, 2008)

$$\Omega_{spectral}(\beta) = \sum_{i \sim j} (\beta_i - \beta_j)^2 ,$$

$$\Omega_{graphfusion}(\beta) = \sum_{i \sim j} |\beta_i - \beta_j| + \sum_i |\beta_i| .$$

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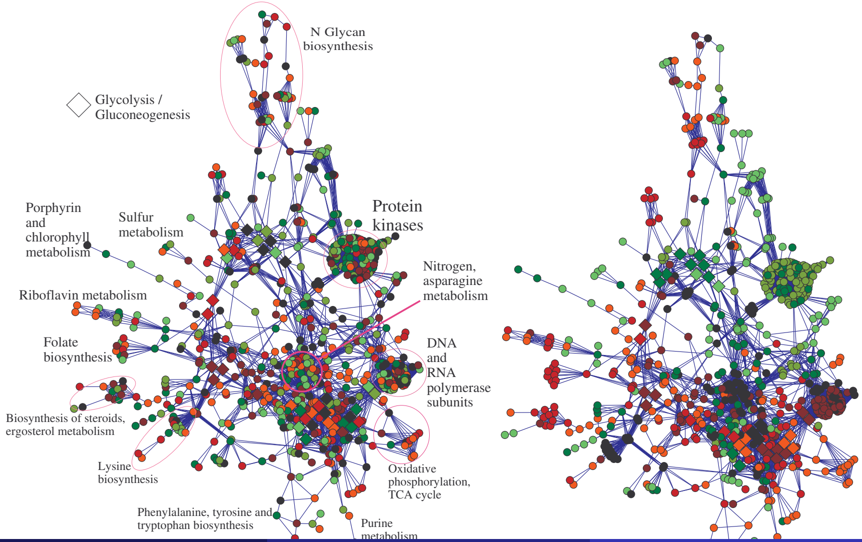
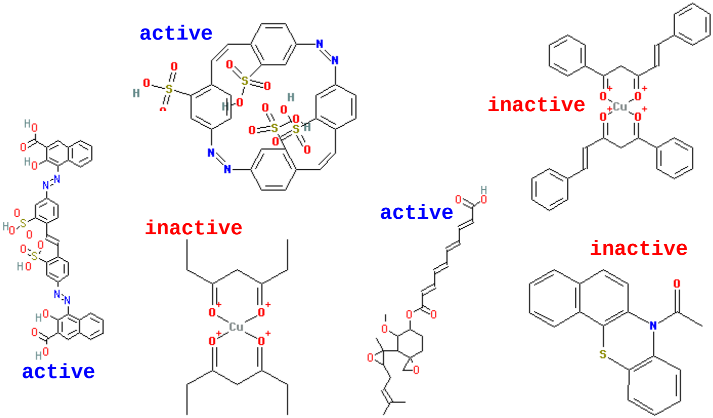


Outline

Ligand-Based Virtual Screening and QSAR



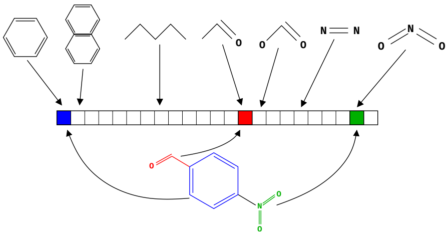
NCI AIDS screen results (from http://cactus.nci.nih.gov).

Classical approaches

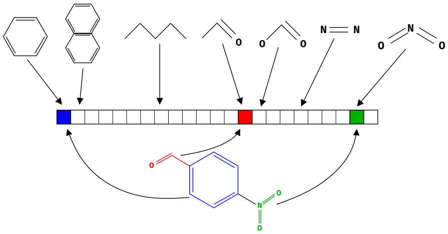
Two steps

1. Map each molecule to a vector of fixed dimension using molecular descriptors
   - Global properties of the molecules (mass, logP...)
   - 2D and 3D descriptors (substructures, fragments, ...)
2. Apply an algorithm for regression or pattern recognition.
   - PLS, ANN, ...

Example: 2D structural keys



Which descriptors?



Difficulties

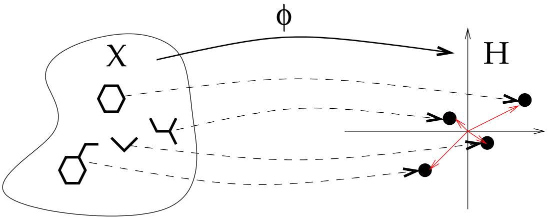
- Many descriptors are needed to characterize various features (in particular for 2D and 3D descriptors)
- But too many descriptors are harmful for memory storage, computation speed, statistical estimation

Kernels

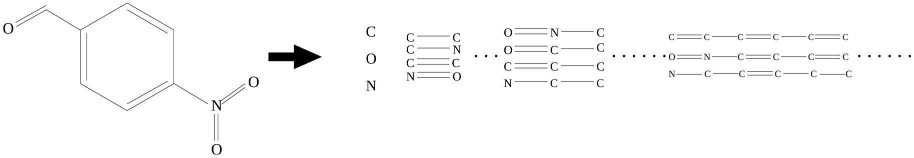
Definition

- Let $\Phi(x) = (\Phi_1(x), \ldots, \Phi_p(x))$ be a vector representation of the molecule x
- The kernel between two molecules is defined by:

$$K(x, x') = \Phi(x)^\top \Phi(x') = \sum_{i=1}^{p} \Phi_i(x)\Phi_i(x') \,.$$



Example: 2D fragment kernel



- $\phi_d(x)$ is the vector of counts of all fragments of length d:

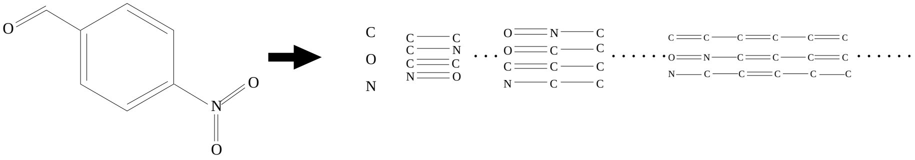
$$\phi_1(x) = (\quad \texttt{\#(C),\#(O),\#(N),} \quad \ldots)^\top$$

$$\phi_2(x) = (\quad \texttt{\#(C-C),\#(C=O),\#(C-N),} \quad \ldots)^\top \quad \text{etc...}$$

- The 2D fragment kernel is defined, for $\lambda < 1$, by

$$K_{fragment}(x, x') = \sum_{d=1}^{\infty} r(\lambda)\phi_d(x)^\top \phi_d(x') \, .$$

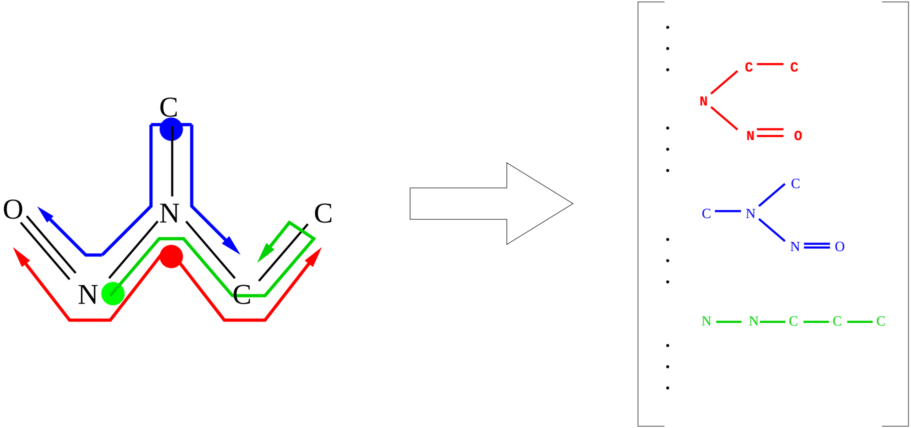
Example: 2D fragment kernel



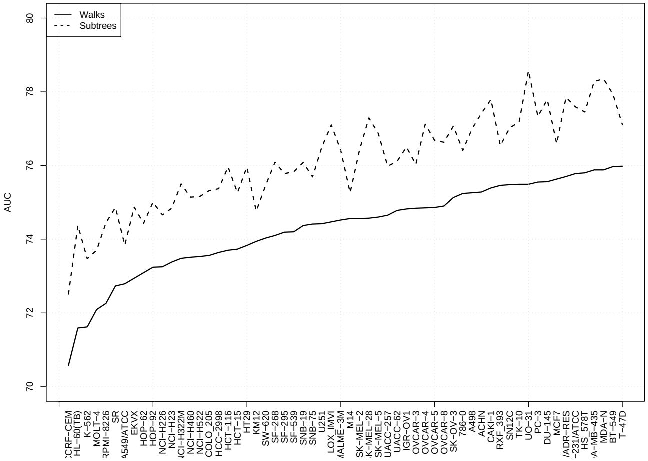
In practice

- $K_{fragment}$ can be computed efficiently (geometric kernel, random walk kernel...) although the feature space has infinite dimension.
- Increasing the specificity of atom labels improves performance
- Selecting only “non-tottering” fragments can be done efficiently and improves performance.

Example: 2D subtree kernel

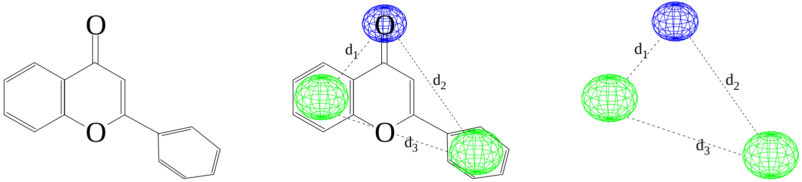


2D Subtree vs fragment kernels (Mahé and V, 2007)



Screening of inhibitors for 60 cancer cell lines (from Mahé and V., 2008)

Example: 3D pharmacophore kernel (Mahé et al., 2005)



$$K(x,y) = \sum_{p_x \in \mathcal{P}(x)} \sum_{p_y \in \mathcal{P}(y)} \exp\left(-\gamma d\left(p_x, p_y\right)\right) .$$

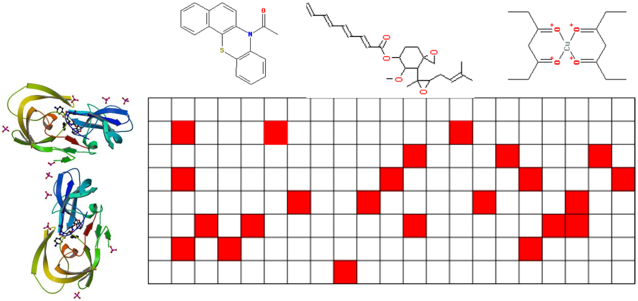
Results (accuracy)

Kernel	BZR	COX	DHFR	ER
2D (Tanimoto)	71.2	63.0	76.9	77.1
3D fingerprint	75.4	67.0	76.9	78.6
3D not discretized	**76.4**	**69.8**	**81.9**	**79.8**

Chemogenomics

The problem

- Similar targets bind similar ligands
- Instead of focusing on each target individually, can we screen the biological space (target families) vs the chemical space (ligands)?
- Mathematically, learn $f(target, ligand) \in \{bind, notbind\}$



Chemogenomics with SVM

Tensor product SVM

- Take the kernel:

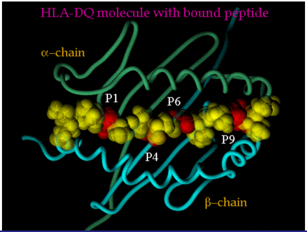
$$K\left((t,l),(t',l')\right) = K_t(t,t')K_l(l,l')\,.$$

- Equivalently, represent a pair (t,l) by the vector $\phi_t(t) \otimes \phi_l(l)$
- Allows to use any kernel for proteins K_t with any kernel for small molecules K_l
- When K_t is the Dirac kernel, we recover the classical paradigm: each target is treated independently from the others.
- Otherwise, information is shared across targets. The more similar the targets, the more they share information.

Example: MHC-I epitope prediction across different alleles

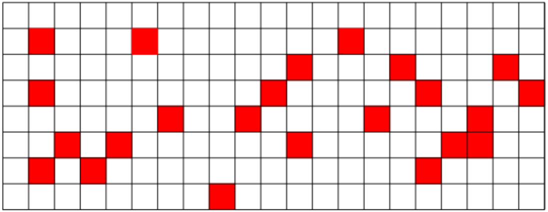
The approach (Jacob and V., 2007)

- take a kernel to compare different MHC-I alleles (e.g., based on the amino-acids in the paptide recognition pocket)
- take a kernel to compare different epitopes (9-mer peptides)
- Combine them to learn the $f(allele, epitope)$ function
- State-of-the-art performance
- Available at http://cbio.ensmp.fr/kiss



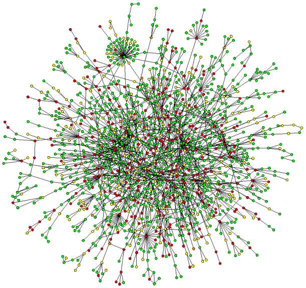
Generalization: collaborative filtering with attributes

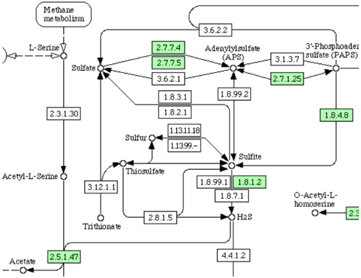
- General problem: learn $f(x, y)$ with a kernel K_x for x and a kernel K_y for y.
- SVM with a tensor product kernel $K_x \otimes K_y$ is a particular case of something more general: estimating an operator with a spectral regularization.
- Other spectral regularization are possible (e.g., trace norm) and lead to efficient algorithms
- More details in Abernethy et al. (2008).

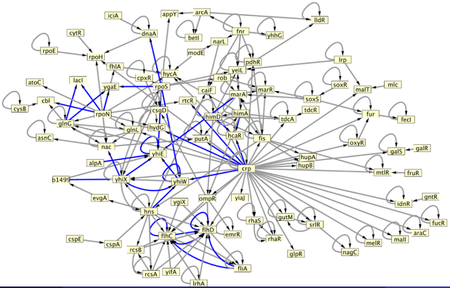


Outline

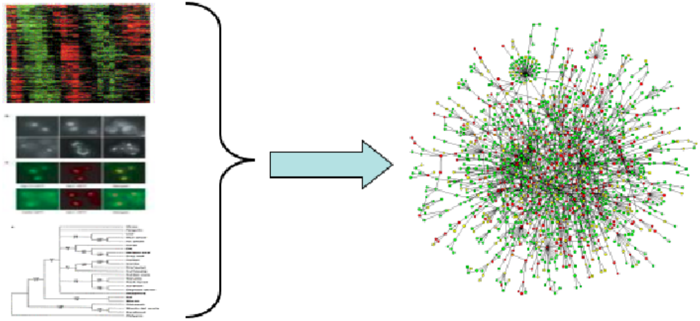
Biological networks







Our goal



Data

- Gene expression,
- Gene sequence,
- Protein localization, ...

Graph

- Protein-protein interactions,
- Metabolic pathways,
- Signaling pathways, ...

More precisely

“De novo” inference

- Given data about individual genes and proteins
- Infer the edges between genes and proteins

“Supervised” inference

- Given data about individual genes and proteins
- and given some known interactions
- infer unknown interactions

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Main messages

1. Most methods developed so far are "de novo" (e.g., co-expression, Bayesian networks, mutual information nets, dynamical systems...)
2. However most real-world application fit the "supervised" framework
3. Solving the "supervised" problem is much easier (and more efficient) than the "de novo" problem. It requires less hypothesis.

De novo methods

Typical strategies

- Fit a dynamical system to time series (e.g., PDE, boolean networks, state-space models)
- Detect statistical conditional indenpence or dependency (Bayesian netwok, mutual information networks, co-expression)

Pros

- Excellent approach if the model is correct and enough data are available
- Interpretability of the model
- Inclusion of prior knowledge

Cons

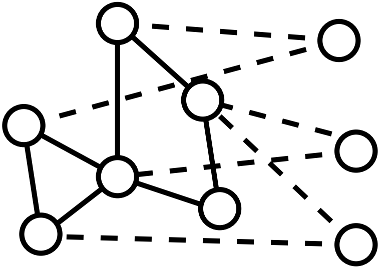
- Specific to particular data and networks
- Needs a correct model!
- Difficult integration of heterogeneous data
- Often needs a lot of data and long computation time

Supervised methods

Motivation

In actual applications,

- we know in advance parts of the network to be inferred
- the problem is to add/remove nodes and edges using genomic data as side information



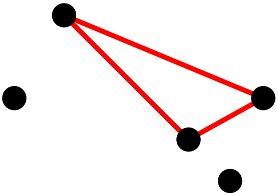
Supervised method

- Given genomic data and the currently known network...
- Infer missing edges between current nodes and additional nodes.

Supervised approach by Metric learning

Idea

- The direct similarity-based method fails because the distance metric used might not be adapted to the inference of the targeted protein network.
- Solution: use the known subnetwork to refine the distance measure, before applying the similarity-based method
- Examples: kernels CCA (Yamanishi et al. 2004), kernel metric learning (V and Yamanishi, 2005)



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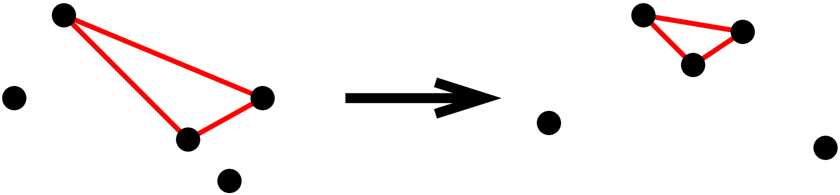

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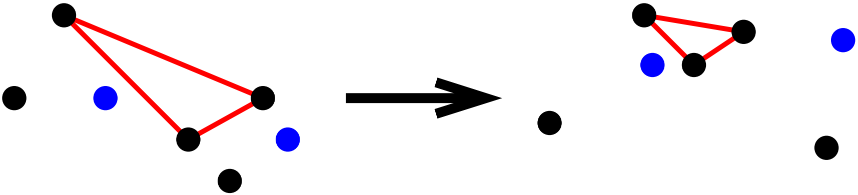

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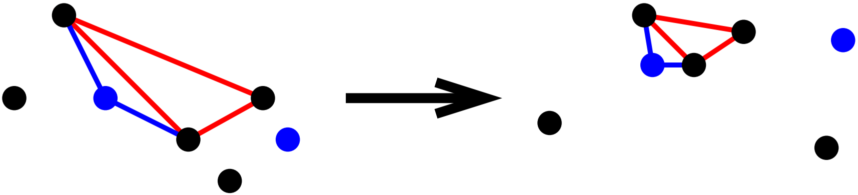
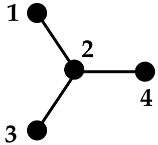


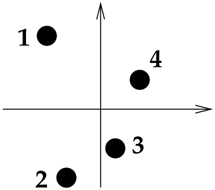
Supervised inference by pattern recognition

Formulation and basic issue

- A pair can be connected (1) or not connected (-1)
- From the known subgraph we can extract examples of connected and non-connected pairs
- However the genomic data characterize individual proteins; we need to work with pairs of proteins instead!



Known graph



Genomic data

Supervised inference by pattern recognition

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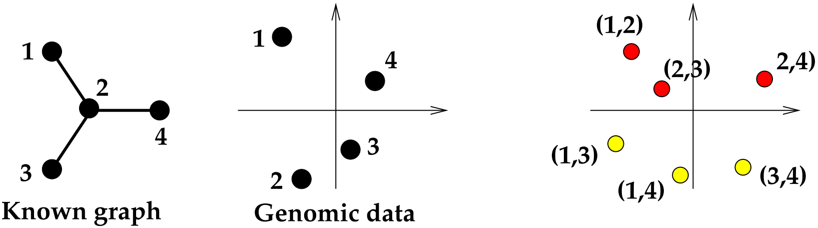

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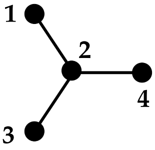

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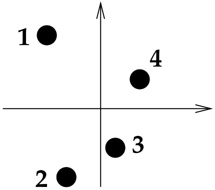
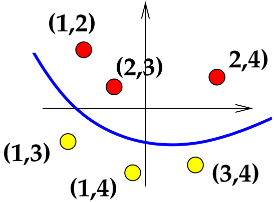


Genomic data



Tensor product SVM (Ben-Hur and Noble, 2006)

- Intuition: a pair (A, B) is similar to a pair (C, D) if:
  - A is similar to C and B is similar to D, or...
  - A is similar to D and B is similar to C
- Formally, define a similarity between pairs from a similarity between individuals by

$$K_{TPPK}((a,b),(c,d)) = K(a,c)K(b,d) + K(a,d)K(b,c) \, .$$

- If K is a positive definite kernel for individuals then K_{TPPK} is a p.d. kernel for pairs which can be used by SVM
- This amounts to representing a pair (a, b) by the symmetrized tensor product:

$$(a,b) \rightarrow (a \otimes b) \oplus (b \otimes a) \, .$$

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- This amounts to representing a pair (a, b) by the symmetrized tensor product:

$$(a, b) \to (a \otimes b) \oplus (b \otimes a) \; .$$

Metric learning pairwise SVM (V. et al, 2007)

- Intuition: a pair (A, B) is similar to a pair (C, D) if:
  - $A - B$ is similar to $C - D$, or...
  - $A - B$ is similar to $D - C$.
- Formally, define a similarity between pairs from a similarity between individuals by

$$K_{MLPK}((a,b),(c,d)) = (K(a,c) + K(b,d) - K(a,c) - K(b,d))^2 \; .$$

- If K is a positive definite kernel for individuals then K_{MLPK} is a p.d. kernel for pairs which can be used by SVM
- This amounts to representing a pair (a, b) by the symmetrized difference:

$$(a,b) \to (a-b)^{\otimes 2} \; .$$

Metric learning pairwise SVM (V. et al, 2007)

- Intuition: a pair (A, B) is similar to a pair (C, D) if:
  - $A - B$ is similar to $C - D$, or...
  - $A - B$ is similar to $D - C$.
- Formally, define a similarity between pairs from a similarity between individuals by

$$K_{MLPK}((a,b),(c,d)) = (K(a,c) + K(b,d) - K(a,c) - K(b,d))^2 .$$

- If K is a positive definite kernel for individuals then K_{MLPK} is a p.d. kernel for pairs which can be used by SVM
- This amounts to representing a pair (a, b) by the symmetrized difference:

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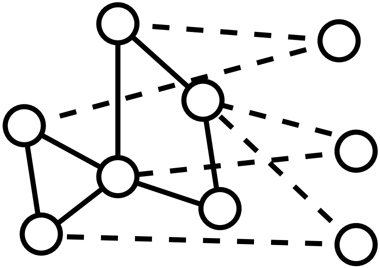
Supervised inference with local models

The idea (Bleakley et al., 2007)

- Motivation: define specific models for each target node to discriminate between its neighbors and the others
- Treat each node independently from the other. Then combine predictions for ranking candidate edges.



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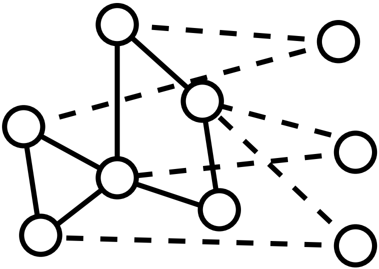
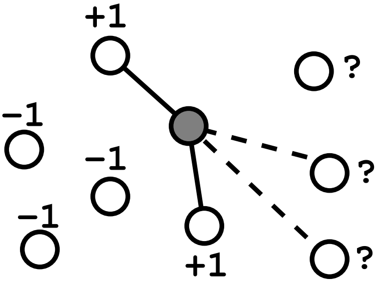
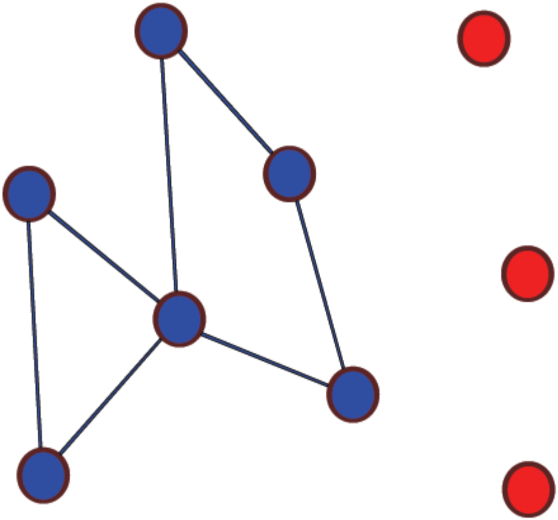




The LOCAL model



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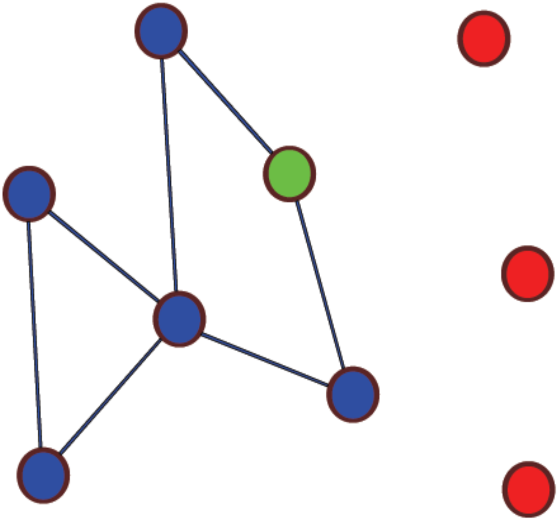

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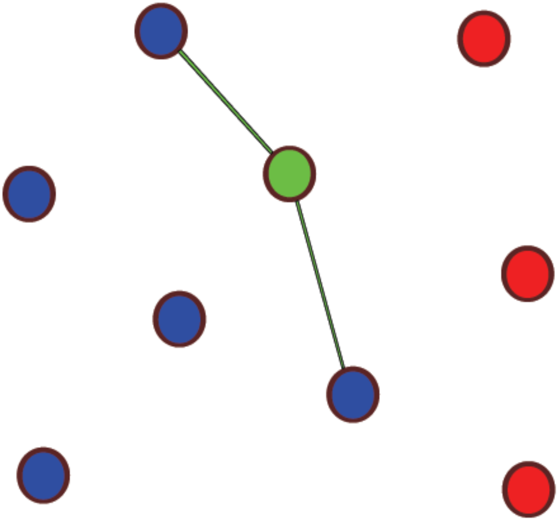

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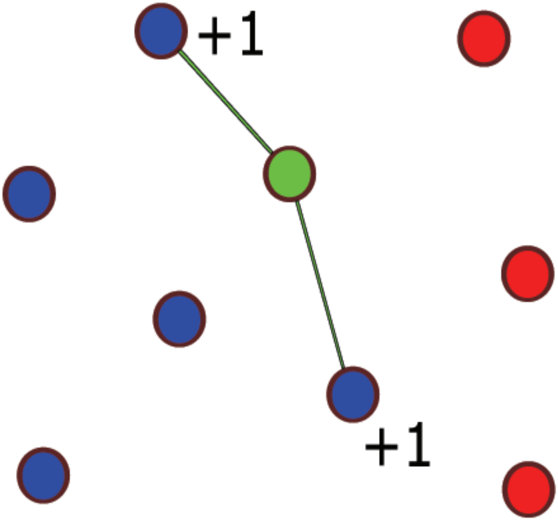

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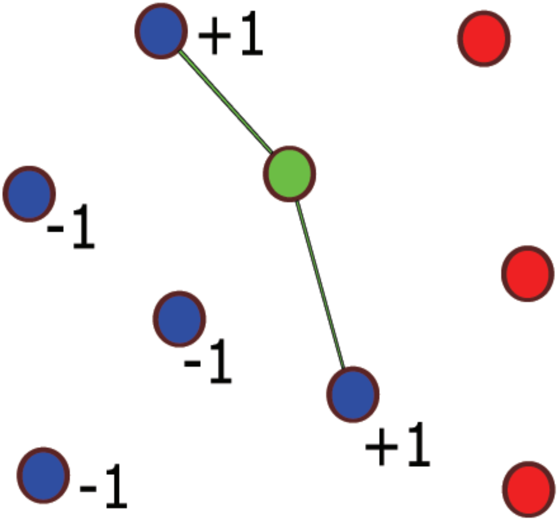

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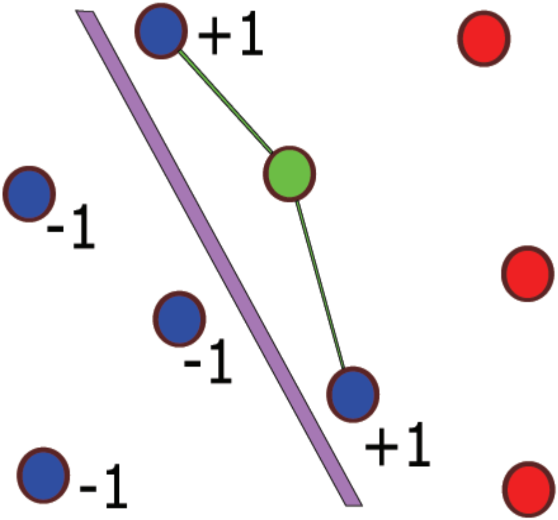

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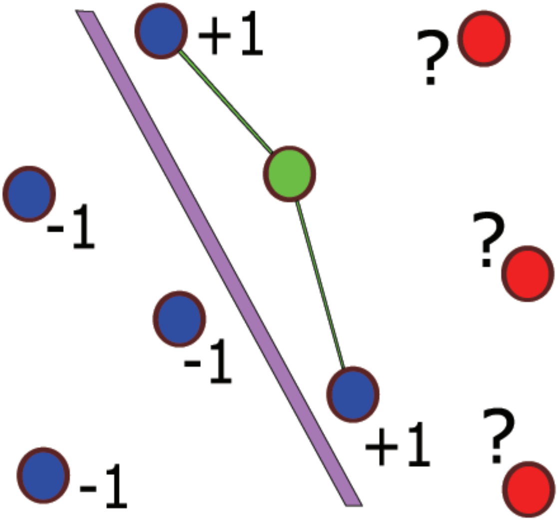

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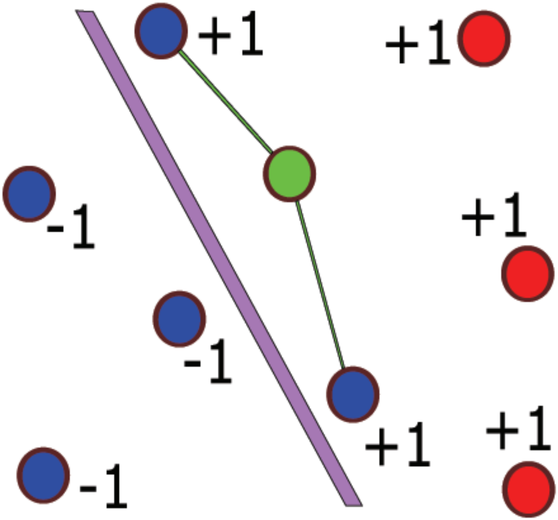

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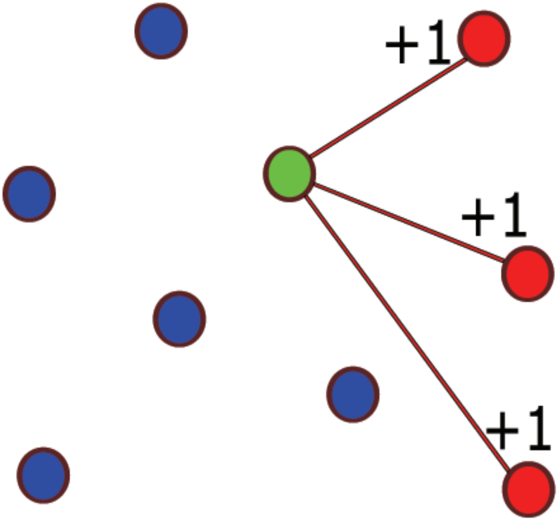

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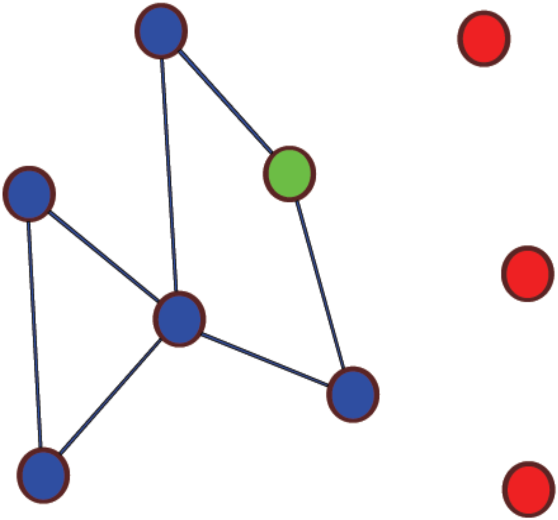

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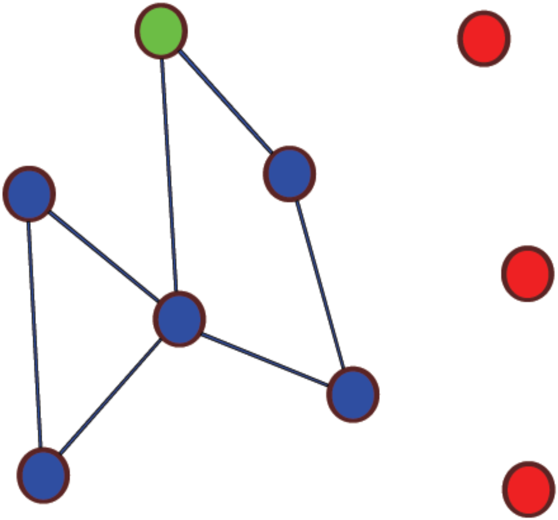

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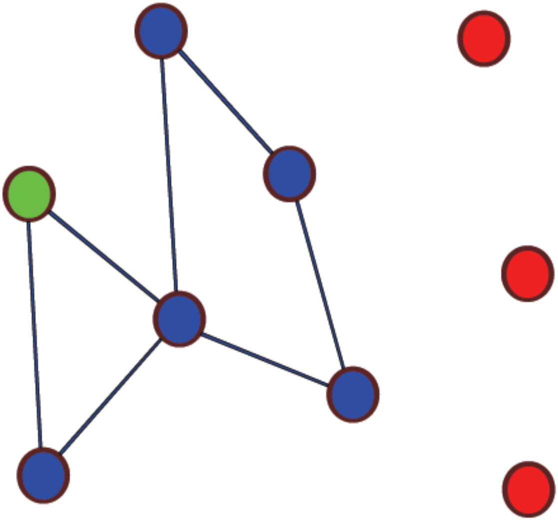

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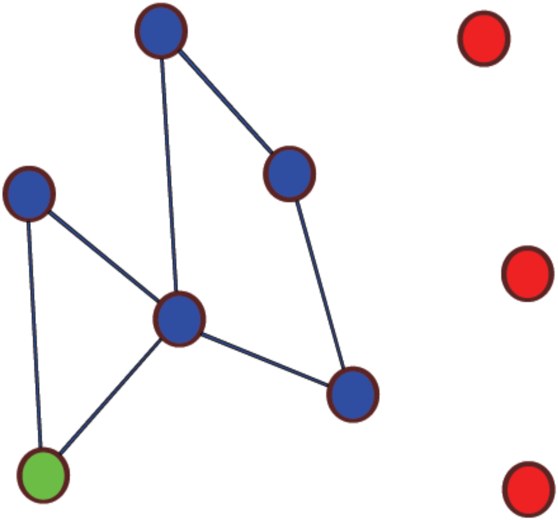

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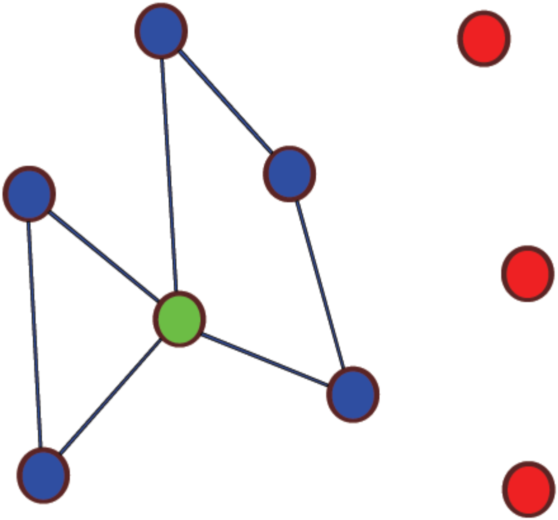

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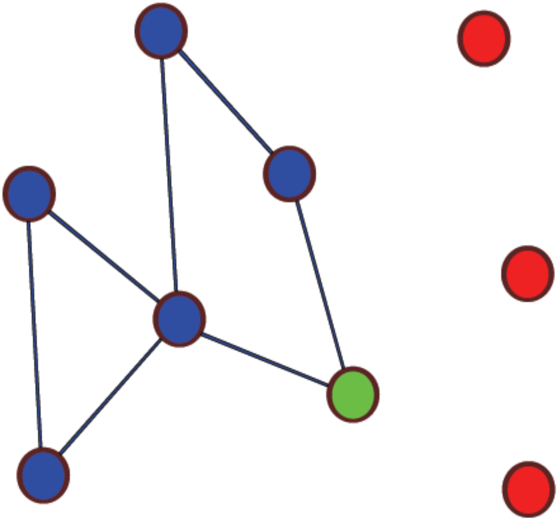
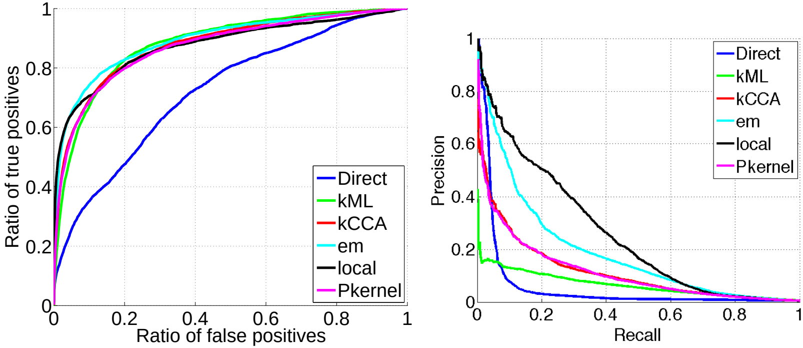
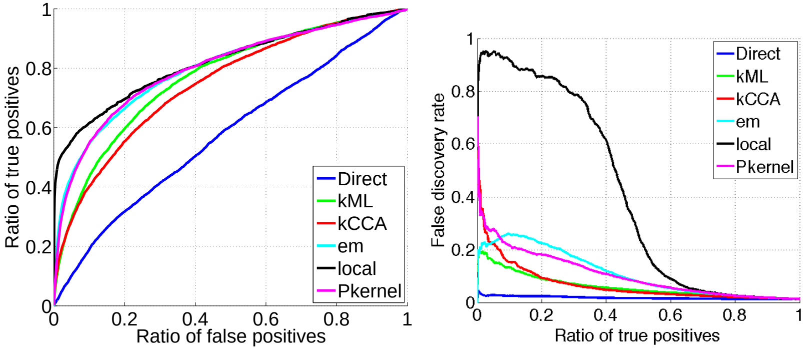


Results: protein-protein interaction (yeast)



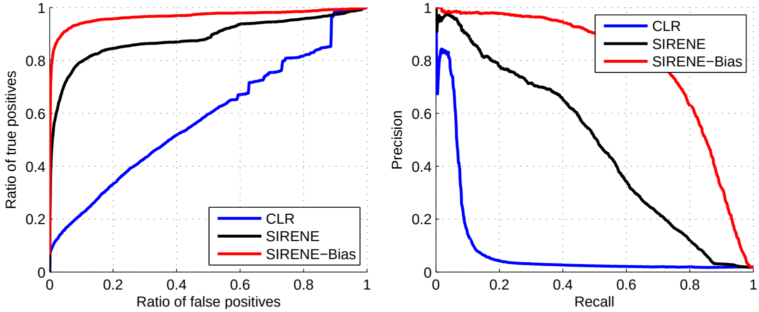
(from Bleakley et al., 2007)

Results: metabolic gene network (yeast)



(from Bleakley et al., 2007)

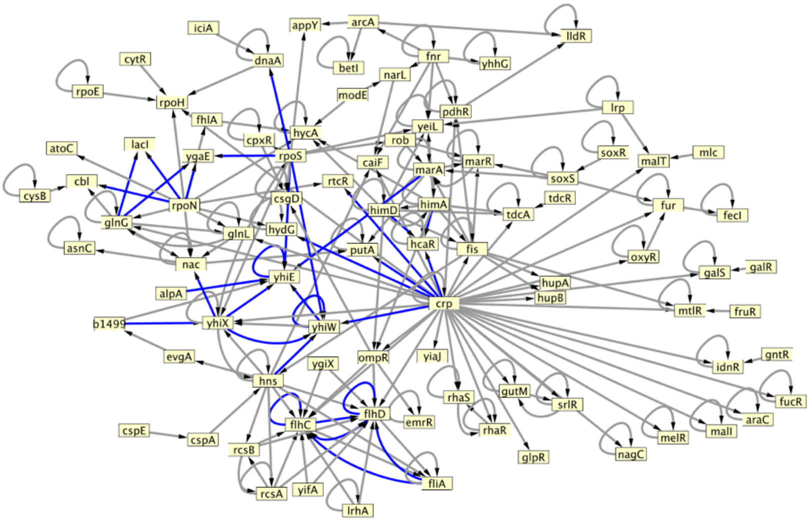
Results: regulatory network (E. coli)



Method	Recall at 60%	Recall at 80%
SIRENE	**44.5%**	**17.6%**
CLR	7.5%	5.5%
Relevance networks	4.7%	3.3%
ARACNe	1%	0%
Bayesian network	1%	0%

SIRENE = Supervised Inference of REgulatory NEtworks (Mordelet and V., 2008)

Results: predicted regulatory network (E. coli)



Prediction at 60% precision, restricted to transcription factors (from Mordelet and V., 2008).

Outline

What we saw

- Modern machine learning methods for regression / classification lend themselves well to the integration of prior knowledge in the penalization / regularization function, in particular for feature selection / grouping. Applications in array CGH classification, siRNA design, microarray classification with gene networks
- Kernel methods (eg SVM) allow to manipulate complex objects (eg molecules, biological sequences) as soon as kernels can be defined and computed. Applications in virtual screening, QSAR, chemogenomics.
- Inference of biological networks can be formulated as a supervised problem if the graph is partly known, and powerful methods can be applied. Application in PPI, metabolic and regulatory networks inference.

People I need to thank

Including prior knowledge in penalization

Franck Rapaport, Emmanuel Barillot, Andrei Zynoviev, Christian Lajaunie, Yves Vandenbrouck, Nicolas Foveau...

Virtual screening, kernels etc..

Pierre Mahé, Laurent Jacob, Liva Ralaivola, Véronique Stoven, Brice Hoffman, Martial Hue, Francis Bach, Jacob Abernethy, Theos Evgeniou...

Network inference

Kevin Bleakley, Fantine Mordelet, Yoshihiro Yamanihi, Gérard Biau, Minoru Kanehisa, William Noble, Jian Qiu...