

# Graph Kernels and Support Vector Machines for Pattern Recognition

**Léo Andéol<sup>1</sup>**

Supervised by: Prof. Hichem Sahbi

Master DAC - Sorbonne Université

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<sup>1</sup>leo.andéol@gmail.com

# Summary

## 1 Motivation and Objectives

## 2 Methodology

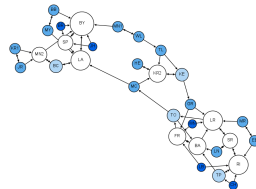
## 3 Experiments

## 4 Conclusion

- References

# Motivation and Objectives I

- Data as graphs : proteins, social networks, ..
- Comparing them would be useful : classification, clustering
- Big Data : many, large graphs



*Moreno's sociogram (Source : Wikipedia)*



*Fragment of a protein transformed into a graph (Vishwanathan et al., 2010)*

# Motivation and Objectives II : Current methods

## Support Vector Machine (Cortes and Vapnik, 1995)

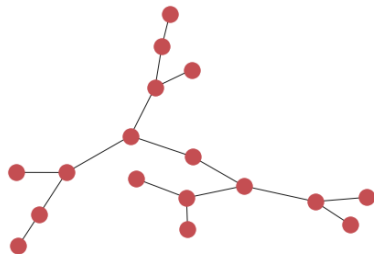
- Operates on vectorial
- Great accuracy
- Great capacity of generalization
- Allows the use of kernels in its dual form

## Kernels

- Maps data to higher dimensions
- Allows functions to replace the dot product
- Improves the accuracy of SVMs

# Motivation and Objectives III

- These methods are adapted to **vectorial data**
- Graphs are not
- Vectorizing adjacency matrices does not solve the problem (isomorphism)
- New types of kernels were discovered
- They are very **complex** to compute



$$\begin{pmatrix} 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}$$

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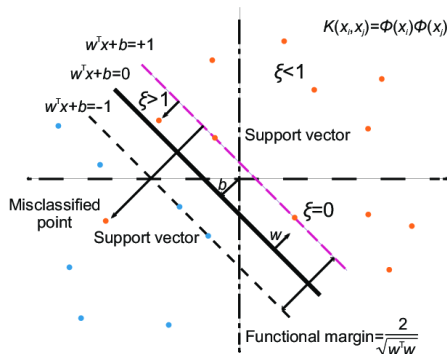
# Support Vector Machines

- We have a set of pairs  $\{(\mathbf{x}_i, y_i)\}$  of size  $N$  where  $y_i \in \{-1, +1\}$
- We want to maximize the margin, and to minimize the generalization error
- We thus minimize

$$\min_{\mathbf{w}} \quad \frac{1}{2} \|\mathbf{w}\|^2$$

$$\text{s.t.} \quad y_i(\mathbf{x}_i \cdot \mathbf{w} + w_0) \geq 1$$

$$1 \leq i \leq N$$

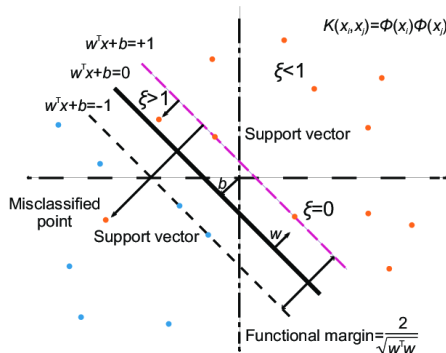


*Soft-margin SVM (Ma et al., 2017)*

# Support Vector Machines

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- We thus minimize

$$\begin{aligned} \min_{\mathbf{w}} \quad & \frac{1}{2} \|\mathbf{w}\|^2 + C \sum_{i=1}^N \xi_i \\ \text{s.t.} \quad & y_i(\mathbf{x}_i \cdot \mathbf{w} + w_0) \geq 1 - \xi_i \\ & 1 \leq i \leq N \quad \xi_i \geq 0 \end{aligned}$$



*Soft-margin SVM (Ma et al., 2017)*



# Kernels

- Dual version of the SVM

$$\max_{\mathbf{w}} \sum_{i=1}^n \alpha_i - \frac{1}{2} \sum_{j=1}^n \sum_{i=1}^n \alpha_i \alpha_j y_i y_j \mathbf{x}_i^\top \mathbf{x}_j$$

- A map  $\phi$  can be used

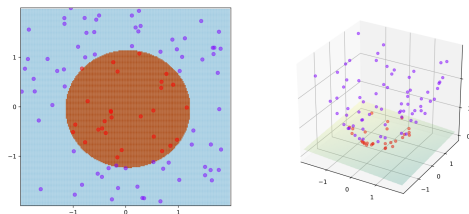


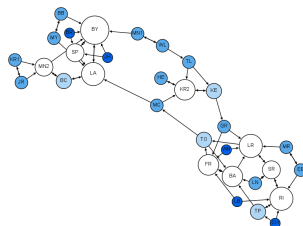
Figure 1: Kernel Trick (Source : Wikipedia)

- The dot product can be replaced by a p.s.d function

# Graph Kernels

We want to classify non **vectorial data**. There are two types of methods available :

- Kernels on graphs
- Kernels on graph nodes



*Moreno's sociogram (Source : Wikipedia)*



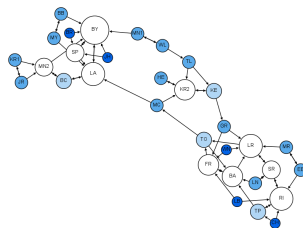
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Some graph kernel families :

- Graphlets (Shervashidze et al., 2009)
- Shortest paths (Borgwardt and Kriegel, 2005)



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# Graph Kernels

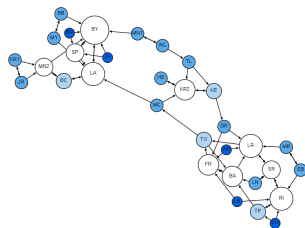
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Some graph kernel families :

- Graphlets (Shervashidze et al., 2009)
- Shortest paths (Borgwardt and Kriegel, 2005)
- **Random walks** (Vishwanathan et al., 2010)

⇒ The complexity is too large.

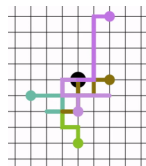


*Moreno's sociogram (Source : Wikipedia)*

# Random Walks I

Random walks on undirected, connected graphs

- Starts at a vertex
- Randomly picks an edge and moves to the next vertex
- Repeats it for a finite (or not) number of steps



2D Random walk (Source : Wikipedia)



A graph  $G_1$



A graph  $G_2$



$G_x = G_1 \otimes G_2$

- Computing a random walk on a product graph is equivalent to computing a random walk on each graph (Imrich and Klavzar, 2000)
- The product graph is computed using the Kronecker product  $\otimes$

# Random Walks II

- Unlabeled product graph :  $W_{\times} = A_1 \otimes A_2$
- Labeled product graph :  $W_{\times} = \sum_{l=1}^d A_1^{(l)} \otimes A_2^{(l)}$

$$\kappa(G_1, G_2) = \sum_{k=0}^{\infty} \mu(k) q_{\times}^{\top} W_{\times}^k p_{\times}$$

- $p_{\times}$  and  $q_{\times}$  resp. start and end probabilities : priors  $\implies$  uniform probabilities
- $\mu(k)$  accentuates walks of certain lengths

# Acceleration methods

## Inverse Kernel

A special case where  $\mu(k) = \lambda^k$  leads to the following kernel

$$\kappa(G_1, G_2) = q_{\times}^{\top} (I - \lambda W_{\times})^{-1} p_{\times}$$

- $O(n^6)$  complexity
- Some methods will try to accelerate it



# Sylvester Equation

- Currently applicable only to unlabeled graphs
- Restricted to  $\mu(k) = \lambda^k \implies$  inverse kernel

## Method

The Sylvester equation we solve is the following

$$A_i X A_j + C = X$$

by multiplying  $X$  to  $q_x$  we get

$$q_x^\top \text{vec}(M) = q_x^\top (I - \lambda W_x)^{-1} p_x$$

- The complexity is  $O(n^3)$

# Conjugate Gradient

- Applicable to unlabeled and labeled graphs
- Restricted to  $\mu(k) = \lambda^k \implies$  inverse kernel
- The matrix should be symmetrized.

## Method

- Computes  $A = (I - \lambda W_{\times})$  and symmetrizes it
- Optimizes  $Ax = p_{\times}$
- The complexity is  $O(rdn^3)$  for  $r$  iterations and  $d$  labels
- Efficient if the matrix has a small effective rank

# Fixed Point Iterations

- Applicable to labeled and unlabeled graphs
- Restricted to  $\mu(k) = \lambda^k \implies$  inverse kernel

## Method

The algorithm iterates on the following function

$$x_{t+1} = p_{\times} + \lambda W_{\times} x_t$$

Either until  $\|x_{t+1} - x_t\| < \epsilon$  or a maximum number of iterations is reached.

- The complexity is  $O(kdn^3)$  for  $k$  iterations and  $d$  labels
- Convergence requires  $\lambda \leq \frac{1}{\xi_1}$

# Spectral Decomposition I

- Currently applicable only to unlabeled graphs
- No restrictions on  $\mu(k)$

## Method

- Eigendecomposition of the adjacency matrix
- Inverse becomes trivial to compute on diagonal matrix

$$\kappa(G_1, G_2) = \sum_{k=0}^{\infty} \mu(k) q_{\times}^{\top} (V_{\times} D_{\times} V_{\times}^{-1})^k p_{\times}$$

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# Spectral Decomposition II

- The complexity is  $O(pn^3)$  for  $p$  the complexity of the power series
- It is even lower since the eigendecomposition of each graph is computed only once
- Currently our most efficient method on unlabeled graphs

# Nearest Kronecker Product Approximation

- Labeled-graph kernel computation can be turned into an unlabeled one with some loss in accuracy, but gain in computation time
- The idea is to approximate two matrices  $S$  and  $T$  such that  $\|W_{\times} - A \otimes B\|_F$  is minimized
- Computed in  $O(dn^2)$  time
- All methods such as Spectral Decomposition can then be applied



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# Databases and metrics

## Synthetic Database

A database of toy data was required to verify claims made in the studied article. A generator was written that can make graphs of "star", "tree" and "ring" types, of different sizes with different labels.

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## Real Databases

- Proteins : 1113 proteins, 2 classes
- Enzymes : 600 enzymes, 6 classes

# Databases and metrics

## Synthetic Database

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## Real Databases

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## Metrics

$$L(X, \mathbf{y}) = \frac{1}{|X|} \sum_{i=1}^{|X|} \begin{cases} 1 & \text{if } f(\mathbf{x}_i) \neq y_i \\ 0 & \text{otherwise} \end{cases}$$

# Implementation

- Sylvester Equation  
 $A_1 X A_2 + C = X$

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$$(I - \lambda W_{\times})x = p_{\times}$$

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- Fixed point

$$x_{t+1} = \lambda W_{\times} x_t + p_{\times}$$

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- Conjugate Gradient

$$(I - \lambda W_{\times})x = p_{\times}$$

- Spectral Decomposition

$$q_{\times}^{\top} P_{\times} (I - \lambda D_{\times})^{-1} P_{\times}^{-1} p_{\times}$$

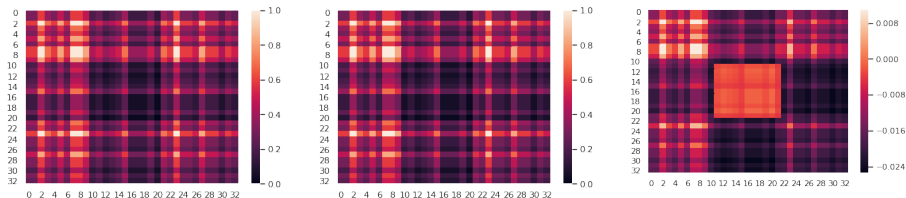


# Performance : Gram matrices

	Raw kernel	Inverse Kernel	Sylvester Equation	Conjugate Gradients	Fixed points	Spectral Decomp.
Raw.	0	1.1e-4	9.8e-5	8.9e-5	1.0e-4	1.0e-04
Inv.	-	0	2.1e-5	7.9e-5	4.0e-6	6.8e-6
Syl.	-	-	0	8.0e-5	1.7e-5	1.4e-5
Con.	-	-	-	0	7.9e-5	7.9e-5
Fix.	-	-	-	-	0	2.8e-6
Spe.	-	-	-	-	-	0

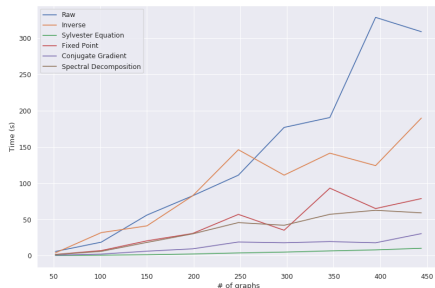
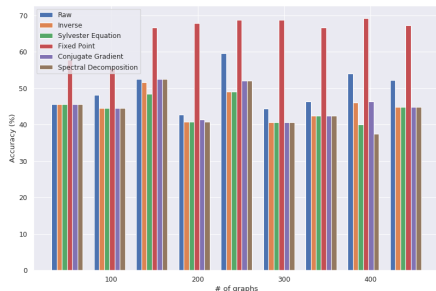
Table 1: Mean standard deviation of matrix entries

# Performance : Gram matrices



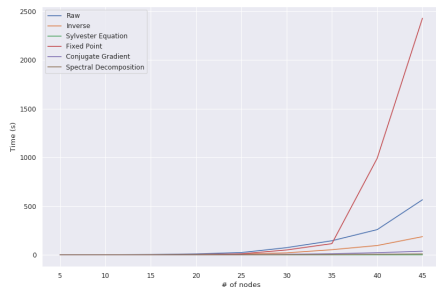
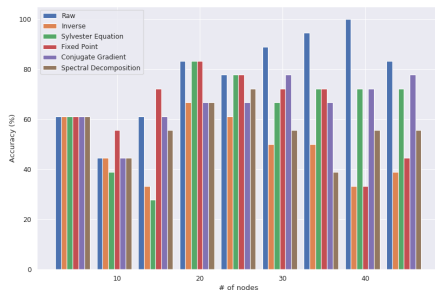
**Figure 2:** *A gram matrix computed with the raw method, another with the fixed point method, and the difference between the two*

# Performance : Complexity I



**Figure 3:** Accuracy and Computation time of different methods depending on the number of graphs

# Performance : Complexity II



**Figure 4:** Accuracy and Computation time of different methods depending on the size of graphs

# Protein and Enzymes

# Conclusion

## Conclusion

- Random walks : decent accuracy
- Several acceleration methods were introduced
- Performances are greatly improved
- conclusion on real data : todo

## Future work

- Generalized Sylvester Equation : algorithm and complexity
- Generalizing the Spectral Decomposition to labeled graphs

# References

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# Appendix : Graphs

## Definition

A graph Bondy et al. (1976) is a type of mathematical structure that represents connections between objects. It is more precisely an ordered pair  $G = (V, E)$  of two sets: vertices  $V$  (or nodes) and edges  $E$  that connect two vertices together.

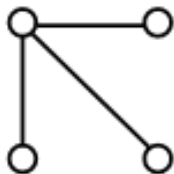
$$E \subseteq \{(u, v) : (u, v) \in V^2\}$$

## Properties

- Undirected
- Labeled or not
- Degree
- Path and Cycle
- Connected
- Tree
- Subgraph
- Line Graph



# Appendix : Graphlets



I



II



III



IV

Some graphlets of size 4 and 5 (Shervashidze et al., 2009)

## Definition

Let  $G$  and  $G_2$  be two graphs,  $\mathbf{f}_G$  and  $\mathbf{f}_{G_2}$  the frequency vectors of respectively  $G$  and  $G_2$ , then the kernel  $\kappa$  is defined as

$$\kappa(G, G_2) = \mathbf{f}_G^\top \mathbf{f}_{G_2}$$

## Appendix : P.S.D

### Definition

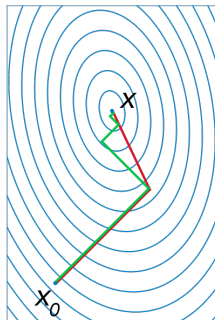
A kernel  $K$  is positive semi definite if and only if

$$\sum_{i=1}^n \sum_{j=1}^n \kappa(\mathbf{x}_i, \mathbf{x}_j) c_i c_j \geq 0 \quad \forall i \in \{1..n\} \quad c_i \in \mathbb{R} \quad (1)$$

It is also p.s.d if its gram matrix have non-negative eigenvalues.

## Appendix : Conjugate Gradient

- The idea is to make the new gradient orthogonal to the former
- Convergence guaranteed in  $n$  steps to solve  $Ax = b$  where  $A \in \mathbb{R}^{n \times n}$



*Conjugate gradient (red) compared to Gradient Descent (green)*