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# Convex optimization for learning Gene Regulatory Network

Magali Champion

Sébastien Gadat, Christine Cierco-Ayrolles et Matthieu Vignes

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# Introduction (biological)



Objective : Recover the unknown gene network  $\mathcal{G}$  for which :

- a node of  $\mathcal{G}$  is one of the *p* genes,
- an edge of G represents an interaction between two genes.

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# Introduction (statistical)

*p* studied genes, for which we know the expression data
sample of size *n*



Objective : Recover the unknown gene network  $\ensuremath{\mathcal{G}}$  for which :

- a node of  $\mathcal{G}$  is one of the *p* genes,
- an edge of *G* represents an interaction between two genes.

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# The first idea consists in considering gene $G^{i}$ as an observation and the others genes as explanatory variables.

Model I

$$orall 1 \leq j \leq 
ho, \ \ G^j = \sum_{1 \leq i 
eq j \leq 
ho} G^i + arepsilon.$$



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# The first idea consists in considering gene $G^{i}$ as an observation and the others genes as explanatory variables.

$$\forall 1 \leq j \leq p, \ G^{j} = \sum_{1 \leq i \neq j \leq p} \frac{\theta_{j}^{j}G^{j}}{\epsilon}$$



 $\Theta = (\theta^1, ..., \theta^p)$  is the adjacency matrix associated to the graph  $\mathcal{G}$ , which support is denoted  $\mathcal{S}$ .

Model I

$$\Theta = egin{pmatrix} 0 & 0 & -1 & 0 \ 0.8 & 0 & 2 & 0.8 \ 0 & 0 & 0 & 0 \ 0 & 0 & -1 & 0 \end{pmatrix}$$

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### We can first rewrite the model as the following way :

$$Y = X\theta + \varepsilon.$$



Use of

Linear regression

- Lasso,
- Boosting...

 $\rightarrow$  Main disadvantage : we don't exploit the structure of the graph.

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### Consider the set of gaussian Directed Acyclic Graphs.

### Proposition

Any adjacency matrix  $\Theta$  associated to a DAG  ${\mathcal G}$  satisfies :

$$\Theta = PT^t P,$$

where P and T are permutation and lower-triangular matrices.



$$T = \begin{pmatrix} 0 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 \\ -1 & 0 & 0 & 0 \\ 2 & 0.8 & 0.8 & 0 \end{pmatrix}$$

Model II

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### Consider the set of gaussian Directed Acyclic Graphs.

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Any adjacency matrix  $\Theta$  associated to a DAG  ${\mathcal G}$  satisfies :

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where P and T are permutation and lower-triangular matrices.



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

Model II

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# Optimization problem

We aim at minimizing the negative penalized log-likelihood :

$$(\hat{P}, \hat{T}) = \operatorname*{argmin}_{P \in \mathbb{P}_{p}(\mathbb{R}), T \in \mathbb{T}_{p}(\mathbb{R})} \left\{ \frac{1}{n} \| G - GPT^{t}P \|_{F}^{2} + \lambda \| T \|_{1} \right\},$$

### where

- $\mathbb{P}_{\rho}(\mathbb{R})$  is the set of permutation matrices,
- $\mathbb{T}_{\rho}(\mathbb{R})$  is the set of strict lower-triangular matrices,
- $\|M\|_F = \operatorname{Trace}({}^tMM) = \sum_{i,j} (M_i^j)^2$ ,
- $\|\boldsymbol{M}\|_1 = \sum_{i,j} |\boldsymbol{M}_i^j|.$

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# Oracle inequality

Let  $\hat{\Theta}$  an estimator of the parameter  $\Theta^*$  and R(.) a risk function. Oracle inequalities aim at comparing the risk of the proposed estimator with the risk of the "oracle", defined as the unknown parameter which minimizes the risk.

### Theorem (Oracle inequality)

 $R(\hat{\Theta}) \leq \inf_{\Theta} \{R(\Theta) + \text{residual term}\}.$ 

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# Oracle inequality

11 3 2 8 4 11

Assumption  $Re(s, c_0)$ : for some integer  $s \in \{1, ..., p\}$ , and  $c_0 \ge 0$ , the following condition holds :

$$\kappa(s, c_0) := \min_{\substack{J \subset \{1, \dots, p\} \\ |J| \le s}} \min_{\substack{M \neq 0 \\ \|M_{J^c}\|_1 \le c_0 \|M_J\|_1}} \frac{\|XM\|_F}{\sqrt{n} \|M_J\|_F} > 0.$$

### Theorem (Oracle inequality)

Let  $\eta > 0$  and  $s \le p$ . Consider the estimate  $\hat{\Theta} = \hat{P}\hat{T}^t\hat{P}$  with  $\lambda = A\sigma\sqrt{\frac{\log p}{n}}$ , where  $A > 4\sqrt{2}$ . Then, with probability at least  $1 - p^{2-A^2/16}$ , there exists  $C(\eta)$  such that :

$$\frac{1}{n} \|G\hat{\Theta} - G\Theta^*\|_F^2 \le (1+\eta) \inf_{\Theta, |\mathcal{S}_{\Theta}| \le s} \left\{ \frac{1}{n} \|G\Theta - G\Theta^*\|_F^2 + \frac{C(\eta)A^2\sigma^2}{\kappa^2(s, 3+4/\eta)} \frac{\log p}{n} \right\}$$

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# For *P* fixed

We aim at minimizing the negative penalized log-likelihood :

$$\hat{T} = \operatorname*{argmin}_{T \in \mathbb{T}_{P}(\mathbb{R})} \left\{ \frac{1}{n} \| G - GPT^{t}P \|_{F}^{2} + \lambda \| T \|_{1} \right\}.$$

 minimization of a convex, differentiable and quadratic function + penalization

$$T_{k+1} = \underset{T}{\operatorname{argmin}} \left\{ \frac{L}{2} \| T - \left( T_k - \frac{\nabla f(T_k)}{L} \right) \|_F^2 + \lambda \| T \|_1 \right\}.$$

• projection on the space of constraints  $\mathbb{T}_{\rho}(\mathbb{R})$ .

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# We aim at minimizing $\hat{P} = \underset{P \in \mathbb{P}_{\rho}(\mathbb{R})}{\operatorname{argmin}} \left\{ \frac{1}{n} \| G - GPT^{t}P \|_{F}^{2} \right\}.$

For T fixed

Since the space of constraints is not convex, we propose a convex relaxation of the criterion to minimize.

### Definition

A bistochastic matrix  $A = (a_{ij})_{1 \le i,j \le p}$  is a matrix such that :

• 
$$\sum_i a_{ij} = \sum_j a_{ij} = 1$$

# Proposition (Birkhoff)

The set of bistochastic matrices  $\mathbb{B}_p(\mathbb{R})$  is a convex set, which permutation matrices are extreme points.

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# Alternate projection

We can write  $\mathbb{B}_p(\mathbb{R})=\Lambda^+\cap\mathcal{LC}_1$  as the intersection of the two sets :

the convex cone  $\Lambda^+ = \Big\{ M = (M_i^j)_{i,j} \in \mathcal{M}_p, \ \forall i, j, \ M_i^j \ge 0 \Big\},$ 

### 2 the affine subspace

$$\mathcal{LC}_1 = \Big\{ \boldsymbol{M} = (\boldsymbol{M}_i^j)_{i,j} \in \mathcal{M}_p, \ \sum_{i=1}^p \boldsymbol{M}_i^j = \sum_{j=1}^p \boldsymbol{M}_i^j = 1 \Big\}.$$

We use alternate projection algorithms (algorithm of Von Neumann or Boyle-Dykstra) to find the expression of the projected bistochastic matrix.

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# Algorithm of Boyle-Dykstra



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# Alternate minimization

$$\begin{split} (\hat{P}, \hat{T}) &= \underset{P \in \mathbb{B}_{p}(\mathbb{R}), T \in \mathbb{T}_{p}(\mathbb{R})}{\operatorname{argmin}} \frac{1}{n} \|G - GPT^{t}P\|_{F}^{2} + \lambda \|T\|_{1}. \\ P_{0} \in \mathbb{P}_{p}(\mathbb{R}) \xrightarrow{\operatorname{optimization}} T_{0} \xrightarrow{\operatorname{proj}} T_{0}' \in \mathbb{T}_{p}(\mathbb{R}) \\ & \text{projected gradient descent} \\ P_{1} \in \mathbb{B}_{p}(\mathbb{R}) \xrightarrow{\operatorname{optimization}} T_{1} \xrightarrow{\operatorname{proj}} T_{1}' \in \mathbb{T}_{p}(\mathbb{R}) \\ & \text{projected gradient descent} \\ P_{2} \in \mathbb{B}_{p}(\mathbb{R}) \xrightarrow{\cdots} \underbrace{\operatorname{Projection over}} \mathbb{P}_{p}(\mathbb{R}) \end{split}$$

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# Permutation matrices

We rewrite the problem of finding the projection of any bistochastic matrix  $B \in \mathbb{B}_{\rho}(\mathbb{R})$  on  $\mathbb{P}_{\rho}(\mathbb{R})$  as :

Remark that the new function  $-2\langle B, P \rangle_F$  to minimize is linear, whereas the space of constraints  $\mathbb{P}_p(\mathbb{R})$  is the set of all extreme points of the convex polytope.

There exists thus an extreme point solution of the relaxed problem

$$P = \operatorname*{argmin}_{P \in \mathbb{B}_{p}(\mathbb{R})} - 2\langle B, P 
angle_{F}.$$

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# Another issue

Joint work with Victor

Instead of relaxing the condition  $P \in \mathbb{P}_p(\mathbb{R})$ , we propose to use genetic algorithms, which are heuristic searchs that mimic the process of natural evolution.



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# In few words (initialization)

We take N permutation matrices. Each of them will be represented by a sequence of "genes", called "chromosome".

$$P = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}$$
chromosome  $\longrightarrow 2 \ 3 \ 6 \ 1 \ 4 \ 5$ 

We search the strict lower-triangular matrix T associated to each chromosome.

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# In few words (crossover)

Selection for the crossover : roulette wheel selection
 Method of crossover

1	2	3	4	5	6			1	3	2	
6	5	1	3	2	4	~		3	4	5	

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# In few words (crossover)

Selection for the crossover : roulette wheel selection
 Method of crossover

1	2	3	4	5	6	 4	5	1	3	2	6
6	5	1	3	2	4	 6	1	3	4	5	2

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### Confusion matrix :

		Prediction			
		edge	no edge		
Reality	edge	true positives	false negatives		
	no edge	false positives	true negatives		

### We then define :

• the recall

 $R = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}.$ 

### • the precision

$$Pr = rac{\text{True Positives}}{\text{True Positives} + \text{False Positives}}$$

# Performances

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# Experimental results

### We also compute :

- the MSE :  $\|\hat{\Theta} \Theta^*\|_F^2$
- the MSEP :  $\frac{1}{n} \|G G\hat{\Theta}\|_F^2$ .

For n = 100 and p = 5

	Optimization	G-A	Boosting	Lasso
R	0.86	0.91	0.91	0.83
Pr	0.63	0.69	0.42	0.46
MSE	2.62	0.29	2.33	
MSEP	8.02	4.88	5.26	

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# Experimental results

### We also compute :

- the MSE :  $\|\hat{\Theta} \Theta^*\|_F^2$
- the MSEP :  $\frac{1}{n} \|G G\hat{\Theta}\|_F^2$ .

For n = 100 and p = 5

	Optimization	G-A	Boosting	Lasso	Random
R	0.86	0.91	0.91	0.83	094
Pr	0.63	0.69	0.42	0.46	0.71
MSE	2.62	0.29	2.33		0.29
MSEP	8.02	4.88	5.26		4.88