Statistical Inference of biological networks

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Biological networks Gaussian graphical models Towards system biology Inferring gene regulation networks

From genomics to postgenomics

Genomics: genome sequencing of various organisms (human genome \sim 04)

Postgenomics: try to understand how it works!

- Massive "omics" data sets
- Involves biology, physics, computer sciences, maths...





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Size of genomes

Genome of a bacteria:

- 1 to 5 millions of base pairs
- 1 to 5 thousands genes
- a few millions of possible gene-gene interactions

Human genome:

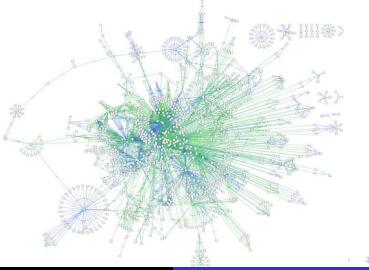
- around 3.4 billions of base pairs
- around 25 000 genes
- more than 100 millions of possible gene-gene interactions

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Gene - gene regulation network of E. coli



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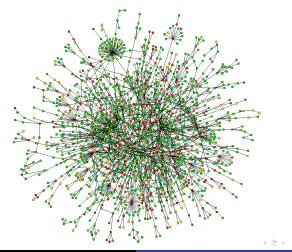
Statistical Inference in Gaussian Graphical Models

Biological networks Gaussian graphical models Gaussian graphical models



Protein - protein network of S. cerevisiae

1458 proteins (vertices) and their 1948 known interactions (edges)

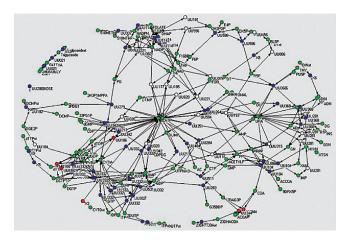


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Metabolic pathway of U. urealyticum



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Why focusing on regulation networks?

• **Traditional biology** studies the specific functions of individual genes, proteins or cells.

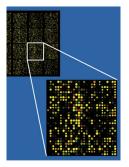
• **System biology** tries to understand how the whole system works by investigating the interaction network between genes, proteins, metabolites, etc.

 \longrightarrow emergent properties

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Inferring gene regulation networks

Data: massive transcriptomic data sets produced by microarrays.



- **Differential analysis** of data obtained in different conditions: with or without deletion of a gene, with or without stress, etc.
- Analysis of the conditional dependences in the data (exploits the whole data set).

Towards system biology Inferring gene regulation networks

A few statistical tools

Descriptive tools:

• Kernel methods (supervised learning)

Model based tools:

- Bayesian Networks
- Gaussian Graphical Models

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Gaussian Graphical Models

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Gaussian graphs Penalized empirical risk

Gaussian Graphical Models

Statistical model: The transcription levels $(X^{(1)}, \ldots, X^{(p)})$ of the *p* genes are modeled by a Gaussian law in \mathbb{R}^{p} .

Graph of the conditional dependences: graph g with

an edge
$$i \stackrel{g}{\sim} j$$
 between the genes i and j

$$\frac{iff}{X^{(i)}}$$
 and $X^{(j)}$ are not independent given $\{X^{(k)}, k \neq i, j\}$

$\mathsf{regulation} \ \mathsf{network} \ \longleftrightarrow \ \mathsf{graph} \ \mathbf{g}$

Biological networks Gaussian graphical models Gaussian graphs Penalized empirical risk

The task of the statistician

Goal: estimate **g** from a sample X_1, \ldots, X_n .

Main difficulty: $n \ll p$

- $p \approx$ a few 100 to a few 1000 genes
- $n \approx$ a few tens

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Gaussian graphs Penalized empirical risk

Some new algorithms

New algorithms: based on thresholding or regularization

Multiple testing	Convex minimization
- Drton & Perlman (2004)	- Meinshausen & Bühlmann (2006)
- Schäfer & Strimmer (2005)	- Huang <i>et al.</i> (2006)
- Wille & Bühlmann (2006)	- Yuan & Lin (2007)
- Verzelen & Villers (2007)	- Banerjee <i>et al.</i> (2007)
- Bühlmann & Kalisch (2008)	- Friedman <i>et al.</i> (2007)

- → quite disappointing numerical performances (Villers *et al.* 2008)
- → no theoretical results or in an asymptotic framework (with strong hypotheses on the covariance)

Penalized empirical risk estimation

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Partial correlations

Hypothesis: $(X^{(1)}, \ldots, X^{(p)}) \sim \mathcal{N}(0, C)$ in \mathbb{R}^p , with C positive definite.

Notation: We write $\theta = (\theta_k^{(j)})$ for the $p \times p$ matrix such that $\theta_j^{(j)} = 0$ and $\mathbb{E}(X^{(j)} | X^{(k)}, k \neq j) = \sum_{k \neq j} \theta_k^{(j)} X^{(k)}.$

Skeleton of
$$\theta$$
: we have $\theta_i^{(j)} = \frac{\mathsf{Cov}\left(X^{(i)}, X^{(j)} | X^{(k)}, \ k \neq i, j\right)}{\mathsf{Var}\left(X^{(j)} | X^{(k)}, \ k \neq j\right)}$ so

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Goal: Estimate θ from a sample X_1, \ldots, X_n with quality criterion

$$\mathrm{MSEP}(\hat{\theta}) = \mathbb{E}\left[\|C^{1/2}(\hat{\theta} - \theta)\|_{p \times p}^{2}\right] = \mathbb{E}\left[\|X_{new}^{T}(\hat{\theta} - \theta)\|_{1 \times p}^{2}\right]$$

Estimation strategy:

- **(**) Choose a collection \mathcal{G} of candidate graphs.
- (2) Associate to each graph $g \in \mathcal{G}$ an estimator $\hat{ heta}_g$ of heta.
- Select one of them by minimizing a penalized empirical risk.

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1- Collection of candidate graphs

Choice of a collection ${\mathcal{G}}$ of candidate graphs

Examples

- Set of all the graphs with p vertices and degree $\leq D$,
- Set of all the graph with p vertices and degree ≤ D containing a known subgraph g_o.

Model associated to $g \in \mathcal{G}$ to estimate θ : $g \curvearrowright \Theta_g = \left\{ \theta \in \mathbb{R}^{p \times p} : i \stackrel{g}{\approx} j \Rightarrow \theta_i^{(j)} = 0 \right\}$

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2- Estimator $\hat{\theta}_g$ associated to g

Characterization: $\theta = \operatorname{argmin}_{A \in \Theta} \|C^{1/2}(I - A)\|_{p \times p}^2$ where Θ = set of matrices with null diagonal.

Biological networks Gaussian graphical models

Empirical version:
$$C^{1/2} \leftrightarrow X = \begin{bmatrix} X_1^T \\ \vdots \\ X_n^T \end{bmatrix} = [X^{(1)}, \dots, X^{(p)}]$$

$$\hat{\theta}_g = \operatorname*{argmin}_{A \in \Theta_g} \|X(I - A)\|_{n \times p}^2$$

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Penalized empirical risk

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Penalized empirical risk

Biological networks Gaussian graphical models Penalized empirical risk

3- Which estimator should be chosen among $\{\hat{\theta}_g, g \in \mathcal{G}\}$?

Ideal: choose $\hat{\theta}_{g_*}$ minimizing

$$\mathrm{MSEP}(\hat{\theta}_g) = \mathbb{E}\left(\|C^{1/2}(\theta - \hat{\theta}_g)\|^2\right) \approx \|C^{1/2}(\theta - \theta_g)\|^2 + \sum_{j=1}^{p} \frac{\mathrm{deg}(j)}{nC_{jj}^{-1}}$$

Selection criterion: set $\hat{ heta}=\hat{ heta}_{\hat{m{g}}}$ where $\hat{m{g}}$ minimizes over ${\mathcal{G}}$

$$\operatorname{crit}(g) = \underbrace{\|X(I - \hat{\theta}_g)\|^2}_{H_{\mathcal{F}}}$$

empirical MSEP

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Gaussian graphical models Penalized empirical risk 3- Which estimator should be chosen among $\{\hat{ heta}_g, \ g \in \mathcal{G}\}$?

Biological networks

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Gaussian graphical models Penalized empirical risk 3- Which estimator should be chosen among $\{\hat{\theta}_g, g \in \mathcal{G}\}$?

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Biological networks Gaussian graphical models

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which penalty pen?

Notation: let EDkhi(d, N, x) be the inverse of

$$x \mapsto \mathbb{P}\left(F_{d+2,N} \geq \frac{x}{d+2}\right) - \frac{x}{d} \mathbb{P}\left(F_{d,N+2} \geq \frac{N+2}{Nd} x\right)$$

where $F_{d,N}$ is a Fisher(d,N).

The penalty

Penality: For K > 1 we set

$$pen(d) = K \frac{n-d}{n-d-1} EDkhi \left[d+1, n-d-1, \left(C_{p-1}^d (d+1)^2 \right)^{-1} \right]$$
$$\lesssim K \left(1 + e^{\rho} \sqrt{2\log \rho} \right)^2 (d+1) \quad \text{when} \quad d \le \rho \frac{n}{2\log \rho}.$$

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When $\deg(\mathcal{G}) = \max \{\deg(g), g \in \mathcal{G}\}$ fulfills

$$\mathsf{deg}(\mathcal{G}) \leq \rho \; \frac{n}{2 \left(1.1 + \sqrt{\log \rho}\right)^2}, \quad \text{for some} \; \; \rho < 1,$$

then the MSEP of $\hat{\theta}$ is bounded by

$$\mathrm{MSEP}(\hat{\theta}) \leq c_{K,\rho} \log(p) \inf_{g \in \mathcal{G}} \left\{ \mathrm{MSEP}(\hat{\theta}_g) \vee \frac{\|C^{1/2}(I-\theta)\|^2}{n} \right\} + R_n$$

where $R_n = O(\mathrm{Tr}(C)e^{-\kappa_p n}).$

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() Where does the condition on the degree come from?

2 Can we choose a smaller penalty?

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Theory

Condition on the degree

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Which size of graph can we hope to estimate?

Prediction error: $MSEP(\hat{\theta}) = \mathbb{E}(\|C^{1/2}(\theta - \hat{\theta})\|^2) = \mathbb{E}(\|C^{1/2}(I - \hat{\theta})\|^2) - \|C^{1/2}(I - \theta)\|^2$

To control the MSEP, we would like to have with large probability

$$(1-\delta)\|C^{1/2}(I-\hat{\theta})\|_{p\times p} \le \frac{1}{\sqrt{n}}\|X(I-\hat{\theta})\|_{n\times p} \le (1+\delta)\|C^{1/2}(I-\hat{\theta})\|_{p\times p}$$

for all matrices $\hat{\theta} \in \bigcup_{g \in \mathcal{G}} \Theta_g$.

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Which size of graph can we hope to estimate?

Prediction error: $MSEP(\hat{\theta}) = \mathbb{E}(\|C^{1/2}(\theta - \hat{\theta})\|^2) = \mathbb{E}(\|C^{1/2}(I - \hat{\theta})\|^2) - \|C^{1/2}(I - \theta)\|^2$

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Proposition: From empirical to population MSEP

When $\deg(\mathcal{G}) = \max \{\deg(g), g \in \mathcal{G}\}$ fulfills

$$\deg(\mathcal{G}) \leq
ho \; rac{n}{2\left(1.1 + \sqrt{\log
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ight)^2}, \quad ext{for some} \; \;
ho < 1,$$

then for $\delta > \sqrt{\rho}$,

we have with probability $\geq 1-2\exp\left(-\textit{n}(\delta-\sqrt{
ho})^2/2
ight)$

$$(1-\delta)\|C^{1/2}(I-A)\| \le \frac{1}{\sqrt{n}}\|X(I-A)\| \le (1+\delta)\|C^{1/2}(I-A)\|$$

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Lemma: Restricted Infimum of Random Matrices

Consider a $n \times p$ matrix Z with $n \leq p$ and i.i.d. $Z_{i,j} \sim \mathcal{N}(0,1)$. Consider also a collection V_1, \ldots, V_N of subspaces of \mathbb{R}^p with dimension d < n.

Then for any
$$x > 0$$

$$\mathbb{P}\left[\inf_{v \in V_1 \cup \ldots \cup V_N} \frac{\frac{1}{\sqrt{n}} \|Zv\|}{\|v\|} \le 1 - \frac{\sqrt{d} + \sqrt{2\log N} + \delta_N + x}{\sqrt{n}}\right] \le e^{-x^2/2}$$
where $\delta_N = \frac{1}{N\sqrt{8\log N}}$.

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Lemma: Restricted Supremum of Random Matrices

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A geometrical constraint

When C = I, there exists some constant $c(\delta) > 0$ such that for any n, p, \mathcal{G} fulfilling

$$\mathsf{deg}(\mathcal{G}) \geq c(\delta) \, rac{n}{1 + \log{(p/n)}},$$

there exists no $n \times p$ matrix X fulfilling

$$(1-\delta) \| C^{1/2}(I-A) \| \le \frac{1}{\sqrt{n}} \| X(I-A) \| \le (1+\delta) \| C^{1/2}(I-A) \|$$

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Theory

Minimal penalty

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Minimal size of pen(d)?

In the simple case where $\mathbf{g} = \emptyset$ we would like to select a "small" \hat{g}

Minimal penalty

$$\implies$$
 "pen(d) $\ge 2d \log(p)$ "

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Proposition: Over-fitting

For some D < n < p and $p \ge e^{2/(1-\gamma)} + 1$, assume that:

- $pen(d) = 2(1 \gamma)d \log(p 1)$ with $\gamma \in (0, 1)$,
- {graphs with at most D edges} $\subset \mathcal{G}$,
- $\mathbf{g} = \emptyset$.

Then,

$$\mathbb{P}\left(\deg(\hat{g}) \geq \frac{c(\gamma)\min(n, p^{\gamma/4})}{(\log p)^{3/2}} \wedge \lfloor \gamma D/8 \rfloor\right) \geq 1 - \frac{3}{p-1} - 2e^{-\gamma^2 n/8^3}$$
where $c(\gamma) \geq 0$ is an (explicit) constant depending on γ only.

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In practice

Numerical performance

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Numerical performance

Comparison to Meinshausen & Buhlmann's procedure.

Setting:

- random "Erdos-Reny" graphs & and random covariance matrices
- n = 15 observations

Focus on two settings:

- when the density of the graph increases
- when the number p of covariables increases

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n = 15, p = 10, edges = 10%, 30% & 33%

edges $= 10\%$						
	KGGM	MB				
risk/oracle	2.5	3.3				
Puissance	81%	81%				
FDR	4.4%	3.7%				

edges = 30% $edges = 3$					= 33%	
	KGGM	MB			KGGM	MB
risk/oracle	4.9	6.9	· · ·	risk/oracle	4.9	6.4
Puissance	20%	14%		Puissance	10%	3.5%
FDR	5.4%	2.9%		FDR	4.1%	1.1%

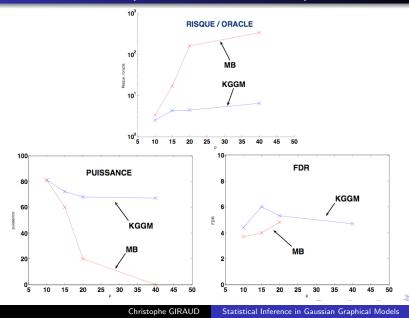
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When *p* increases (n = 15, fixed sparsity)



Conclusion

Some nice features:

- **good theoretical properties:** non-asymptotic control of the MSEP with no condition on the covariance matrix *C*
- good numerical performances: even when $n \ll p$

• very high numerical complexity: typically $n \times p^{\deg(\mathcal{G})+1}$	
\implies cannot be used in practice when $p > 50$	

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Conclusion

Some nice features:

- good theoretical properties: non-asymptotic control of the MSEP with no condition on the covariance matrix *C*
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BUT • very high numerical complexity: typically $n \times p^{\deg(\mathcal{G})+1}$ \implies cannot be used in practice when p > 50...

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Practical implementation

Ongoing work: with S. Huet and N. Verzelen

Reduction of the collection of graphs, with the aim to find a balance between

- computational efficiency
- estimation accuracy

- C. Giraud. Estimation of Gaussian graphs by model selection. Preprint (2007). http://hal.archives-ouvertes.fr/hal-00178275/fr/
- Y. Baraud, C. Giraud, S. Huet. Gaussian model selection with unknown variance. To appear in the Annals of Statistics (2008?).
- N. Verzelen. High-dimensional Gaussian model selection on a Gaussian design. Preprint (2008).

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