Influential Observations in a Graphical Model

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Joint work with Jean-Michel Poggi (LMO, Paris Sud, Orsay & Paris Descartes) Let $X = (X_1, \ldots, X_p) \sim \mathcal{N}_p(\mu, \Sigma)$ be a *p*-dimensional multivariate normal distributed random variable supposed to be such that Σ is invertible

- \triangleright Graphical models encode random variables and their conditional dependencies
- **Directed acyclic graph in which nodes** $\Gamma = \{1, \ldots, p\}$ **represent random** variables and edges represent conditional probabilistic dependencies among them
- A pair (a, b) is in the set of edges if and only if X_a is dependent on X_b conditionally to the remaining variables $\{X_k, k \in \Gamma \setminus \{a, b\}\}\$
- ► cor $(X_a, X_b | \{X_k, k \in \Gamma \setminus \{a, b\}\}) = 0$ corresponds to a zero entry in $\Theta = \Sigma^{-1}$

The L_1 -penalized log-likelihood is

$$
\ell_{\lambda}^{\mathcal{S}}(\Theta) = \log \det \Theta - \text{tr}(\Theta \mathcal{S}) - \lambda ||\Theta||_1
$$

 $\lambda \geq 0$ being the tuning parameter.

$$
\triangleright S = \frac{1}{n} \sum_{i=1}^{n} (X_i - \bar{X})(X_i - \bar{X})'
$$
 is the empirical covariance matrix

 $\hat{\Theta} = \arg \max \ell_{\lambda}^{\mathcal{S}}(\Theta)$ is the ML estimate of the inverse of the concentration matrix Σ^{-1}

The non-null entries of $\hat{\Theta}$ define the edges of the estimated graphical model.

Example

- ≥ 133 patients with stage I-III breast cancer (Hess et al., 2006) treated with chemotherapy prior to surgery
- \blacktriangleright Hess et al. (2006), Natowicz et al. (2008) developed and tested a multigene predictor for treatment response on this data set. They focused on a set of 26 genes having a high predictive value
- \blacktriangleright Patient response to the treatment is classified as either a pathologic complete response (pCR) 34 individuals or a residual disease (not-pCR) 99 individuals
- \triangleright Data: 26 columns and 133 rows. The nth row gives the expression levels of the 26 identified genes for the nth patient. The p columns are named according to the genes
- ► Data already considered by Ambroise et al. (2009) and Giraud et al. (2012) : Gaussian Graphical Model to obtain genes interaction graph (*L*1−penalized likelihood criterion).

Example: network (R package huge)

Example: PCA

Example: PCA

Influence of the observations

What about graph stability?

- \triangleright Classically robustness deals with model stability (and considered globally)
- \triangleright Focus on individual observations diagnosis issues rather than model properties or variable selection problems
- \triangleright We use here Graphical Models to perform diagnosis on observations
- \triangleright We use influence function, a classical diagnostic method to measure the perturbation induced by a single observation: stability issue through **jackknife**

Influence function

- ► X_1, \ldots, X_n r.v. of common distribution function (df) *F* on \mathbb{R}^p ($p \ge 1$)
- **Figure 1** The influence of an infinitesimal perturbation along δ_x on statistic $T(F)$

$$
IC_{T,F}(x) = \lim_{\epsilon \to 0} \frac{T((1-\epsilon)F + \epsilon \delta_x) - T(F)}{\epsilon}
$$

- \triangleright Statistic *T*(*F*) naturally estimated by *T*(*F_n*) where $\mathit{F_{n}}=\frac{1}{n}\sum_{i=1}^{n}\delta_{\mathit{X_{i}}}$ is the empirical df
- ► $IC_{T,F_n}(x_i)$ is used to evaluate the importance of an observation $x_i \in \mathbb{R}^p$
- \triangleright Connection between influence function and jackknife (Miller, 1974): let $F_{n-1}^{(i)} = \frac{1}{n-1} \sum_{j \neq i} \delta_{x_j}$, then $F_n = \frac{n-1}{n} F_{n-1}^{(i)} + \frac{1}{n} \delta_{x_i}$. If $\epsilon = -\frac{1}{n-1}$, we have: $IC_{T,F_n}(x_i) \approx \frac{T((1-\epsilon)F_n+\epsilon \delta x_i)-T(F_n)}{2}$ ϵ ≈ $(n-1)(T(F_n) - T(F_{n-1}^{(i)}))$

A first remark about jackknifed covariance matrix

$$
\triangleright S = \frac{1}{n} \sum_{i}^{n} (X_i - \bar{X})(X_i - \bar{X})'
$$
 covariance matrix

$$
\blacktriangleright S_{-j} = \frac{1}{n-1} \sum_{i \neq j} (X_i - \bar{X}_{-j})(X_i - \bar{X}_{-j})'
$$
 jackknifed covariance matrix

It can be shown that

$$
S_{-j}=\frac{n}{n-1}S-\frac{2}{n}(X_j-\overline{X}_{-j})(X_j-\overline{X}_{-j})'
$$

which quantifies the size of the perturbation

$$
\ell_{\lambda}^{S}(\Theta) = \log \det \Theta - \text{tr}(\Theta S) - \lambda ||\Theta||_{1} ; \lambda \geq 0
$$

 \triangleright $\hat{\Theta}$ = arg max $\ell_λ^S(\Theta)$: MLE of $Σ^{-1}$, the inverse of the concentration matrix, based on X_i , $i = 1, \ldots, n$

$$
\quad \bullet \quad \widehat{\Theta_{-j}} = \arg \max \ell_{\lambda}^{S_{-j}}(\Theta) \colon \text{MLE of } \Sigma^{-1} \text{ based on } X_i, i \neq j
$$

Let <u>Θ</u> = $\left(1_{\theta_{ij}\neq 0}\right)_{1\leqslant i,j\leqslant n}$ a matrix of 0's and 1's: adjacency matrix

Let $I_1(i)$ be the number of edges affected by the removing observation *i*

$$
I_1(j)=\frac{1}{2}||\widehat{\underline{\Theta}}-\widehat{\underline{\Theta}_{-j}}||_0
$$

A first influence index: example

Let $\underline{\Theta}=\bigl(1_{\theta_{ij}\neq 0}\bigr)_{1\leqslant i,j\leqslant n}$ a matrix of 0's and 1's

Let $I_1(j)$ be the number of edges affected by the removing observation *j* $(j = 1, \ldots, 133)$

$$
I_1(j)=\frac{1}{2}||\hat{\underline{\Theta}}-\widehat{\underline{\Theta}_{-j}}||_0
$$

Histogram of I, for cancer dataset

Link between influence and likelihood

- \triangleright Strong links between jackknife and likelihood (influence function as derivative of the statistic)
- ^I the *L*¹ penalized log-likelihood of *S*[−]*^j* can be expressed in terms of *S*:

$$
\ell_{\lambda}^{S_{-j}}(\Theta) = \log \det \Theta - \frac{n}{n-1} \text{tr}(\Theta S) - \frac{1}{n} (x_j - \overline{x}_{-j})' \Theta(x_j - \overline{x}_{-j}) + \lambda ||\Theta||_1
$$

$$
\ell_{\lambda}^{S_{-j}}(\Theta) = \ell_{\lambda}^{S}(\Theta) - \frac{1}{n} (x_j - \overline{x}_{-j})' \Theta(x_j - \overline{x}_{-j})
$$

- In The effect is to add a L_2 term that taking into account the contribution of *x^j* to the penalized likelihood
- **Example 3** A natural definition of influence could be given by $(x_j \overline{x}_{-j})' \hat{\Theta}(x_j \overline{x}_{-j})$

A second influence index

Let $I_2(.)$ be the difference of the likelihoods induced by the removing of one observation

$$
h_2(j) = \ell_{\lambda}^{S}(\hat{\Theta}) - \ell_{\lambda}^{S-j}(\widehat{\Theta_{-j}})
$$

=
$$
\frac{1}{n}(x_j - \overline{x}_{-j})' \hat{\Theta}(x_j - \overline{x}_{-j})
$$

Link between the two influence indices on the example

$$
\triangleright \ \ I_1(j) = \frac{1}{2} ||\hat{\Theta} - \widehat{\Theta_{-j}}||_0 \ \text{versus} \ \ I_2(j) = \ell_{\lambda}^S(\hat{\Theta}) - \ell_{\lambda}^{S_{-j}}(\hat{\Theta_{-j}})
$$

for the 133 observations of cancer dataset

Fluctuations of maximum likelihood of concentration matrix $(I_2(j))$ is not enough to infer stability of adjacency matrix $(I_1(j))$

Remark: Influence measuring stability of the links through jackknife

Reference graph is generated from the whole dataset and influence of a perturbation induced by the deletion of an observation can be measured by any distance between Θ and Θ[−]*ⁱ*

Let $J_1(a, b)$ be the number of times that status of edge (a, b) is changed by the removing of one observation

$$
J_1(a,b)=\sum_{i=1}^n\mathbb{1}_{\left|\frac{\widehat{\Theta}(a,b)-\widehat{\Theta_{-i}(a,b)}}{2}\right|\neq 0}
$$

 $25*26/2=325$ possible edges and for each edge the theoretical range of J_1 is between 0 and 133.

$$
\begin{array}{c|cccc}\n\hline\n0 & 1 & 2 & 3 & 4 & 5 & 8 & 9 \\
\hline\n325 & 5 & 1 & 3 & 1 & 1 & 1 & 1\n\end{array}
$$

The two groups of cancer data set

Patient response to the treatment is classified as either a pathologic complete response (pCR) 34 individuals or a residual disease (not-pCR) 99 individuals

Above influence functions

Which class is the less affected by removing or adding observation *i*?

- ► Two classes: pCR/not-pCR and two adjacency matrices $\Theta^{(1)}$ and $\Theta^{(2)}$
- ► Let $\underline{\Theta}^{(k \vee i)} = \underline{\Theta}^{(k)}$ if the observation *i* is from class *k* and $\underline{\Theta}^{(k \vee i)}$ is the adjacency matrix computed from (individuals of class *k* + individual *i*)
- **►** $I^k_1(i)$ be the number of edges of $\Theta^{(k \vee i)}$ affected by removing of observation i ($k = 1, 2$).

$$
I^k_1(i) = \frac{1}{2} \big| \big| \widehat{\underline{\Theta^{(k \vee i)}}} - \widehat{\underline{\Theta^{(k \vee i)}}} \big| \big|_0
$$

For each *i* we can compute arg min_k $I^k_1(i)$.

Which class is the less affected by removing or adding observation *i*?

Which class is the less affected by removing or adding observation *i*?

- \triangleright What about iterate But ... one group becomes empty (small group have large variability)
- \triangleright Second idea: define a class centroid (open question)
- \triangleright What about stability with respect to starting point (related to centroid definition)

Distributional results for influence index

Two influence indices :

- \blacktriangleright $I_1(j) = \frac{1}{2} ||\underline{\Theta} \underline{\Theta}_{-j}||_0$
- ► $I_2(j) = \ell^S_\lambda(\hat{\Theta}) \ell^{S-j}_\lambda(\widehat{\Theta-j})$

$$
\sqrt{n}\left(l_2(F_n)-l_2(F)\right)\sim\mathcal{N}(0,\sigma^2)
$$

But no known relationship between $I_2(F_n) - I_2(F)$ and distance between the induced graph

 I_1 is not a continuous function of Θ (indicator function): not consistent except if $P(\hat{\Theta} = 0) = 0$ (clique)

Well known problem for median as well as for lasso: bolasso is a possible alternative

A glimpse of Bolasso

Idea: If several datasets (with same distributions) are available, intersecting support sets would lead to the correct pattern with high probability

In practice: Bootstrap the data, intersecting the support of the graph

Adaptation: Jackknife the data, intersecting the support of the graph

Bolasso in practice

Homogeneous dataset

Objective : largest group without influence data

Exhaustive search not possible. Peeling strategy:

- 1. Fit "best" graphical model (glasso+stars) on the dataset
- 2. Remove the observation with the largest influence from the dataset
- 3. Fit "best" graphical model (glasso+stars) on the new dataset
- 4. Back to step 2

Questions:

- \blacktriangleright Is the (penalized) likelihood monotone?
- \blacktriangleright where to stop the peeling?
- \triangleright What about the "stable" network?
- \triangleright What about the "stable" observations?

Peeling in action

References

- ▶ Ambroise, C., Chiquet, J., and Matias, C. (2009). *Inferring sparse Gaussian graphical models with latent structure*. Electron. J. Stat., 3:205–238.
- ► Bach, F.R. (2008). *Bolasso: model consistent Lasso estimation through the bootstrap*. Proceedings of ICML '08. 33–40
- ► Friedman, J., Hastie, T. and Tibshirani R. (2008). *Sparse inverse covariance estimation with the graphical Lasso.* Biostatistics, 9:432–441.
- ▶ Giraud, C., Huet, S. and Verzelen, N. (2012). *Graph selection with GGMselect*. SAGMB, Vol. 11 (3) 1544–6115.
- \blacktriangleright Hess, K.R., Anderson, K., Symmans, W.F., Valero, V., Ibrahim, N., Mejia, J.A., Booser, D., Theriault, R.L., Buzdar, U., Dempsey, P.J., Rouzier, R., Sneige, N., Ross, J.S., Vidaurre, T., Gomez, H.L., Hortobagyi, G.N., and Pustzai, L. (2006). *Pharmacogenomic predictor of sensitivity to preoperative chemotherapy with paclitaxel and fluorouracil, doxorubicin, and cyclophosphamide in breast cancer*. Journal of Clinical Oncology, 24(26):4236-4244.
- ► Meinshausen N., Bühlmann P. (2006). *High-dimensional graphs and variable selection with the Lasso.* Annals of Statistics, 34:1436–1462.
- ▶ Meinshausen N., Bühlmann P. (2010). Stability selection (with discussion). Journal of the Royal Statistical Society: Series B, 72, 417-473.
- ▶ Natowicz, R., Incitti, R., Horta, E.G., Charles, B., Guinot, P., Yan, K., Coutant, C., Andr F., Pusztai, R., and Rouzier, L. (2008). *Prediction of the outcome of a preoperative chemotherapy in breast cancer using dna probes that provide information on both complete and incomplete response*. BMC Bioinformatics, $0(4.40)$

Thank you for your attention (and your questions)

Model-based clustering

Let's try Gaussian mixture model :

$$
f(x) = p f_1(x) + (1-p) f_2(x)
$$

where $f_1 \sim \mathcal{N}_p(\mu_1, \Sigma_1)$ and $f_2 \sim \mathcal{N}_p(\mu_2, \Sigma_2)$.

Model-based clustering

Mclust : best model: diagonal, varying volume and shape (VVI) with 3 components

Model-based clustering

Mclust : best model: diagonal, varying volume and shape (VVI) with 2 components

