Lecture 1: Segmentation and classification of genomic profiles

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"Optimization, machine learning and bioinformatics" summer school, Erice, Sep 9-16, 2010.

Motivation

Pinding multiple change-points in a single profile

8 Finding multiple change-points shared by many signals

Supervised classification of genomic profiles

5 Conclusion

Motivation

- 2 Finding multiple change-points in a single profile
- Finding multiple change-points shared by many signals
- 4 Supervised classification of genomic profiles
- 5 Conclusion

Chromosomic aberrations in cancer



Comparative Genomic Hybridization (CGH)



Problem 1: Finding multiple change-points in 1 profile



Problem 1: Finding multiple change-points in 1 profile



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Problem 2: Finding multiple shared change-points in many profiles



2010 7/47

Problem 2: Finding multiple shared change-points in many profiles



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Application: find frequent breakpoints



A collection of bladder tumour copy number profiles.

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Other applications

• Low-dimensional summary and visualization of the set of profiles



Detection of frequently altered regions



Problem 3: discrimination of genomic profiles



Aggressive (left) vs non-aggressive (right) melanoma.

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1. Genomic profiles



A general framework to solve Problems 1, 2 and 3 by rephrasing them as constrainted optimization problems of the form

 $\min_{w} R(w) \quad \text{s.t.} \quad \Omega(w) \leq C.$

Fast algorithms that scale in time and memory to

- Profiles length: $p = 10^6 \sim 10^9$
- Number of profiles (dimension): $n = 10^2 \sim 10^3$
- Number of change-points: $k = 10^2 \sim 10^3$
- Analysis of their statistical properties in some situations.



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Reminder: Problem 1



- Let $Y \in \mathbb{R}^{p}$ the signal
- We want to find a piecewise constant approximation Û ∈ ℝ^p with at most k change-points.

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• We can define an "optimal" piecewise constant approximation $\hat{U} \in \mathbb{R}^p$ as the solution of

$$\min_{U\in\mathbb{R}^p} \parallel Y-U\parallel^2 \hspace{1.5cm} ext{ such that } \hspace{1.5cm} \sum_{i=1}^{p-1} \mathbf{1} \left(U_{i+1}
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ight) \leq k$$

- This is an optimization problem over the (^P_k) partitions...
 Dynamic programming finds the solution in O(p²k) in time and O(p²) in memory
- But: does not scale to $p=10^6\sim 10^9.1$



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Promoting sparsity with the ℓ_1 penalty

The ℓ_1 penalty (Tibshirani, 1996; Chen et al., 1998)

If $R(\beta)$ is convex and "smooth", the solution of

$$\min_{\beta \in \mathbb{R}^p} \boldsymbol{R}(\beta) + \lambda \sum_{i=1}^p |\beta_i|$$



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Efficienty computation of the regularization path

$$\min_{\beta \in \mathbb{R}^{p}} \|Y - X\beta\|^{2} + \lambda \sum_{i=1}^{p} |\beta_{i}|$$
(1)

- No explicit solution, but this is just a quadratic program.
- LARS (Efron et al., 2004) provides a fast algorithm to compute the solution for all λ's simultaneously (regularization path)



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Promoting piecewise constant profiles penalty

The total variation / variable fusion penalty

If $R(\beta)$ is convex and "smooth", the solution of

$$\min_{\beta \in \mathbb{R}^p} R(\beta) + \lambda \sum_{i=1}^{p-1} |\beta_{i+1} - \beta_i|$$

is usually piecewise constant (Rudin et al., 1992; Land and Friedman, 1996).

Proof:

- Change of variable $u_i = \beta_{i+1} \beta_i$, $u_0 = \beta_1$
- We obtain a Lasso problem in $u \in \mathbb{R}^{p-1}$
- u sparse means β piecewise constant

TV signal approximator

$$\min_{\beta \in \mathbb{R}^p} \| Y - \beta \|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} |\beta_{i+1} - \beta_i| \le \mu$$

Adding additional constraints does not change the change-points:

• $\sum_{i=1}^{p} |\beta_i| \le \nu$ (Tibshirani et al., 2005; Tibshirani and Wang, 2008) • $\sum_{i=1}^{p} \beta_i^2 \le \nu$ (Mairal et al. 2010)



$$\min_{\beta \in \mathbb{R}^p} \| Y - \beta \|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} |\beta_{i+1} - \beta_i| \le \mu$$

- QP with sparse linear constraints in O(p²) -> 135 min for p = 10⁵ (Tibshirani and Wang, 2008)
- Coordinate descent-like method O(p)? -> 3s s for p = 10⁵ (Friedman et al., 2007)
- For all μ with the LARS in O(pK) (Harchaoui and Levy-Leduc, 2008)
- For all μ in $O(p \ln p)$ (Hoefling, 2009)
- For the first K change-points in $O(p \ln K)$ (Bleakley and V., 2010)

Require: *k* number of intervals, $\gamma(I)$ gain function to split an interval *I* into $I_L(I)$, $I_R(I)$

- 1: I_0 represents the interval [1, p]
- 2: $\mathcal{P} = \{I_0\}$
- 3: for *i* = 1 to *k* do
- 4: $I^* \leftarrow \underset{I \in \mathcal{P}}{\operatorname{arg\,max}} \gamma(I^*)$

5:
$$\mathcal{P} \leftarrow \mathcal{P} \setminus \{I^*\}$$

6:
$$\mathcal{P} \leftarrow \mathcal{P} \cup \{I_L(I^*), I_R(I^*)\}$$

- 7: end for
- 8: return \mathcal{P}

From greedy segmentation to TV approximator

Theorem

TV approximator is a greedy dichotomic segmentation.

Consequences:

- Fast methods for TV approximator
- Theoretical results for (apparently) greedy segmentation

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Technical details

• Represent an interval [u + 1, v] by a quadruplet $I = (u, v, \sigma_u, \sigma_v)$ where $\sigma_u, \sigma_v \in \{-1, 0, 1\}$

• Let $F_u = \sum_{i=1}^{u} Y_u$, and for u < k < v, $\sigma \in \{-1, 1\}$

$$f_l(k,\sigma) = \begin{cases} \sigma A_k/2 & \text{if } \sigma_u = \sigma_v \neq 0, \\ A_k/(\sigma - B_k) & \text{otherwise }, \end{cases}$$

where

$$A_{k} = -F_{k} + \frac{(v-k) F_{u} + (k-u) F_{v}}{v-u},$$
$$B_{k} = \frac{(v-k) \sigma_{u} + (k-u) \sigma_{v}}{v-u}.$$

Then the functions $\gamma(I)$, $I_L(I)$ and $I_R(I)$ are respectively given by:

$$\gamma(I) = \max_{k \in [u+1, v-1], \sigma \in \{-1, 1\}} f_l(k, \sigma),$$

$$(k^*, \sigma^*) = \arg_{k \in [u+1, v-1], \sigma \in \{-1, 1\}} f_l(k, \sigma),$$

$$I_L(I) = (u, k^*, \sigma_u, \sigma^*),$$

$$I_R(I) = (k^*, v, \sigma^*, \sigma_v).$$

- Homotopy method (LARS)
- Similar to Harchaoui and Levy-Leduc (2008), removing superfluous computations
- The next breakpoint in a segment, and the μ where it appears, is independent of events in other segments

Speed trial : 2 s. for $K = 100, p = 10^7$



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Reminder: Problem 2



- Let $\mathbf{Y} \in \mathbb{R}^{p \times n}$ the *n* signals of length *p*
- We want to find a piecewise constant approximation Û ∈ ℝ^{p×n} with at most k change-points.

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1. Genomic profiles

"Optimal" segmentation by dynamic programming



• Define the "optimal" piecewise constant approximation $\hat{U} \in \mathbb{R}^{p \times n}$ of *Y* as the solution of

$$\min_{U \in \mathbb{R}^{p \times n}} \|Y - U\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} \mathbf{1} \left(U_{i+1, \bullet} \neq U_{i, \bullet} \right) \le k$$

- DP finds the solution in $O(p^2 kn)$ in time and $O(p^2)$ in memory
- But: does not scale to $p = 10^6 \sim 10^9$...

Selecting pre-defined groups of variables

Group lasso (Yuan & Lin, 2006)

If groups of covariates are likely to be selected together, the ℓ_1/ℓ_2 -norm induces sparse solutions *at the group level*:

$$\Omega_{group}(w) = \sum_{g} \|w_g\|_2$$



$$\Omega(w_1, w_2, w_3) = \|(w_1, w_2)\|_2 + \|w_3\|_2$$
$$= \sqrt{w_1^2 + w_2^2} + \sqrt{w_3^2}$$

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TV approximator for many signals

Replace

$$\min_{U \in \mathbb{R}^{p \times n}} \|Y - U\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} \mathbf{1} \left(U_{i+1,\bullet} \neq U_{i,\bullet} \right) \le k$$

by

$$\min_{U \in \mathbb{R}^{p \times n}} \|Y - U\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} w_i \|U_{i+1,\bullet} - U_{i,\bullet}\| \le \mu$$

Questions

- Practice: can we solve it efficiently?
- Theory: does it benefit from increasing p (for n fixed)?

• Make the change of variables:

$$\gamma = U_{1,\bullet},$$

$$\beta_{i,\bullet} = w_i \left(U_{i+1,\bullet} - U_{i,\bullet} \right) \quad \text{for } i = 1, \dots, p-1.$$

• TV approximator is then equivalent to the following group Lasso problem (Yuan and Lin, 2006):

$$\min_{\beta \in \mathbb{R}^{(p-1) \times n}} \| \bar{Y} - \bar{X}\beta \|^2 + \lambda \sum_{i=1}^{p-1} \| \beta_{i,\bullet} \|,$$

where \bar{Y} is the centered signal matrix and \bar{X} is a particular $(p-1) \times (p-1)$ design matrix.

TV approximator implementation

$$\min_{\beta \in \mathbb{R}^{(p-1) \times n}} \| \bar{Y} - \bar{X}\beta \|^2 + \lambda \sum_{i=1}^{p-1} \| \beta_{i,\bullet} \|,$$

Theorem

The TV approximator can be solved efficiently:

- approximately with the group LARS in *O*(*npk*) in time and *O*(*np*) in memory
- exactly with a block coordinate descent + active set method in O(np) in memory

Although \bar{X} is $(p-1) \times (p-1)$:

- For any *R* ∈ ℝ^{p×n}, we can compute *C* = X^T*R* in *O*(*np*) operations and memory
- For any two subset of indices $A = (a_1, \dots, a_{|A|})$ and $B = (b_1, \dots, b_{|B|})$ in [1, p-1], we can compute $\bar{X}_{\bullet,A}^{\top} \bar{X}_{\bullet,B}$ in O(|A||B|) in time and memory
- For any $A = (a_1, \ldots, a_{|A|})$, set of distinct indices with $1 \le a_1 < \ldots < a_{|A|} \le p 1$, and for any $|A| \times n$ matrix R, we can compute $C = (\bar{X}_{\bullet,A}^{\top} \bar{X}_{\bullet,A})^{-1} R$ in O(|A|n) in time and memory

Consistency for a single change-point

Suppose a single change-point:

- at position $u = \alpha p$
- with increments $(\beta_i)_{i=1,\dots,n}$ s.t. $\bar{\beta}^2 = \lim_{k \to \infty} \frac{1}{n} \sum_{i=1}^n \beta_i^2$
- corrupted by i.i.d. Gaussian noise of variance σ^2



Does the TV approximator correctly estimate the first change-point as *p* increases?

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Consistency of the unweighted TV approximator

$$\min_{U \in \mathbb{R}^{p \times n}} \|Y - U\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} \|U_{i+1,\bullet} - U_{i,\bullet}\| \le \mu$$

Theorem

The unweighted TV approximator finds the correct change-point with probability tending to 1 (resp. 0) as $n \to +\infty$ if $\sigma^2 < \tilde{\sigma}_{\alpha}^2$ (resp. $\sigma^2 > \tilde{\sigma}_{\alpha}^2$), where

$$\tilde{\sigma}_{\alpha}^{2} = \boldsymbol{p}\bar{\beta}^{2} \frac{(1-\alpha)^{2}(\alpha-\frac{1}{2p})}{\alpha-\frac{1}{2}-\frac{1}{2p}}$$

• correct estimation on $[p\epsilon, p(1-\epsilon)]$ with $\epsilon = \sqrt{\frac{\sigma^2}{2p\beta^2}} + o(p^{-1/2})$.

wrong estimation near the boundaries

Consistency of the weighted TV approximator

$$\min_{\boldsymbol{U}\in\mathbb{R}^{p\times n}} \|\boldsymbol{Y}-\boldsymbol{U}\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} w_i \|\boldsymbol{U}_{i+1,\bullet}-\boldsymbol{U}_{i,\bullet}\| \leq \mu$$

Theorem

The weighted TV approximator with weights

$$\forall i \in [1, p-1], \quad w_i = \sqrt{rac{i(p-i)}{p}}$$

correctly finds the first change-point with probability tending to 1 as $n \rightarrow +\infty$.

- we see the benefit of increasing n
- we see the benefit of adding weights to the TV penalty

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1. Genomic profiles

• The first change-point \hat{i} found by TV approximator maximizes $F_i = \|\hat{c}_{i,\bullet}\|^2$, where

$$\hat{\boldsymbol{c}} = ar{\boldsymbol{X}}^{ op} \, ar{\boldsymbol{Y}} = ar{\boldsymbol{X}}^{ op} ar{\boldsymbol{X}} eta^* + ar{\boldsymbol{X}}^{ op} oldsymbol{W} \, .$$

• \hat{c} is Gaussian, and F_i is follows a non-central χ^2 distribution with

$$G_i = \frac{EF_i}{p} = \frac{i(p-i)}{pw_i^2}\sigma^2 + \frac{\bar{\beta}^2}{w_i^2w_u^2p^2} \times \begin{cases} i^2\left(p-u\right)^2 & \text{if } i \leq u \,, \\ u^2\left(p-i\right)^2 & \text{otherwise.} \end{cases}$$

• We then just check when $G_u = \max_i G_i$

Consistent estimation of more change-points?



 $p = 100, k = 10, \bar{\beta}^2 = 1, \sigma^2 \in \{0.05; 0.2; 1\}$

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Erice 2010 38 / 47

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Reminder: Problem 3



- $x_1, \ldots, x_n \in \mathbb{R}^p$ the *n* profiles of length *p*
- $y_1, ..., y_n \in [-1, 1]$ the labels
- We want to learn a function $f : \mathbb{R}^{p} \rightarrow [-1, 1]$

Shrinkage estimators

- Define a large family of "candidate classifiers", e.g., linear predictors f_β(x) = β^Tx for β ∈ ℝ^p
- For any candidate β ∈ ℝ^p, quantify how "good" f_β is on the training set with some empirical risk, e.g.:

$$R(\beta) = \frac{1}{n} \sum_{i=1}^{n} l(f_{\beta}(x_i), y_i).$$

 Choose β that achieves the minimium empirical risk, subject to some constraint:

 $\min_eta R(eta)$ subject to $\Omega(eta) \leq C$.

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Prior knowledge

We expect β to be

- sparse : not all positions should be discriminative, and we want to identify the predictive region (presence of oncogenes or tumor suppressor genes?)
- piecewise constant : within a selected region, all probes should contribute equally



Fused Lasso signal approximator (Tibshirani et al., 2005)

$$\min_{\beta \in \mathbb{R}^p} \sum_{i=1}^p (y_i - \beta_i)^2 + \lambda_1 \sum_{i=1}^p |\beta_i| + \lambda_2 \sum_{i=1}^{p-1} |\beta_{i+1} - \beta_i|.$$

- First term leads to sparse solutions
- Second term leads to piecewise constant solutions



Fused lasso for supervised classification (Rapaport et al., 2008)

$$\min_{\beta \in \mathbb{R}^p} \sum_{i=1}^n \ell\left(y_i, \beta^\top x_i\right) + \lambda_1 \sum_{i=1}^p |\beta_i| + \lambda_2 \sum_{i=1}^{p-1} |\beta_{i+1} - \beta_i|.$$

where ℓ is, e.g., the hinge loss $\ell(y, t) = max(1 - yt, 0).$

Implementation

- When ℓ is the hinge loss (fused SVM), this is a linear program -> up to $p = 10^3 \sim 10^4$
- When ℓ is convex and smooth (logistic, quadratic), efficient implementation with proximal methods -> up to $p = 10^8 \sim 10^9$

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Example: predicting metastasis in melanoma



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$$\min_{w} R(w)$$
 s.t. $\Omega(w) \leq C$.

- The risk R(w) depends on the problem we want to solve
- The penalty Ω(w) depends on the data, here we focused on the total variation and its variants
- Dedicated optimization algorithms lead to fast implementation
- An illustration of a very active and fruitful trend in ML!

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