

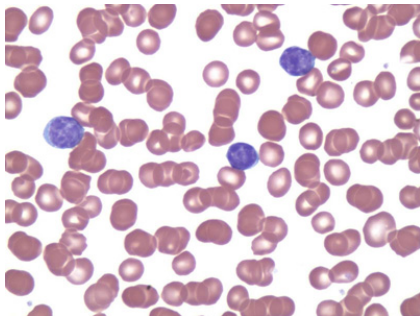
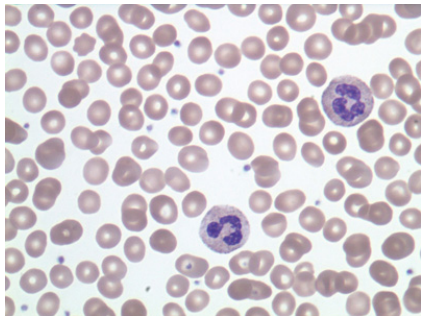
The group fused Lasso for multiple change-point detection

Jean-Philippe Vert



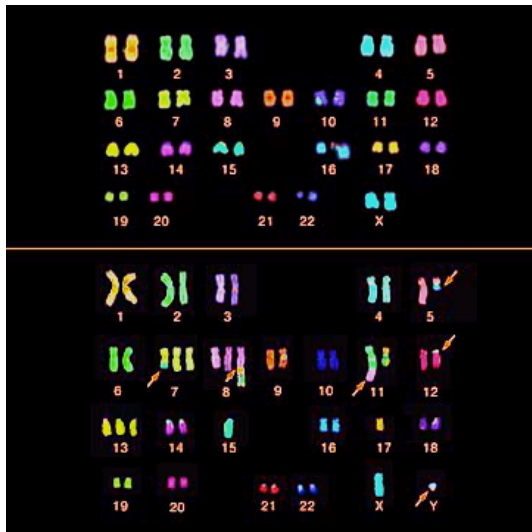
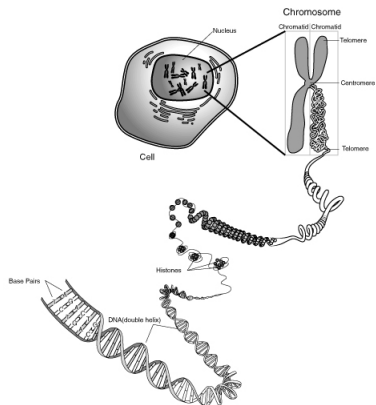
Inference for Change-Point and Related Processes workshop
Isaac Newton Institute for Mathematical Sciences
Cambridge, UK, January 14, 2014

Normal vs cancer cells



What goes wrong?
How to treat?

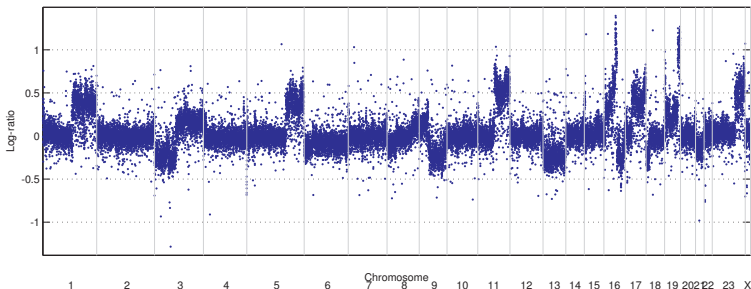
Chromosomal aberrations in cancer



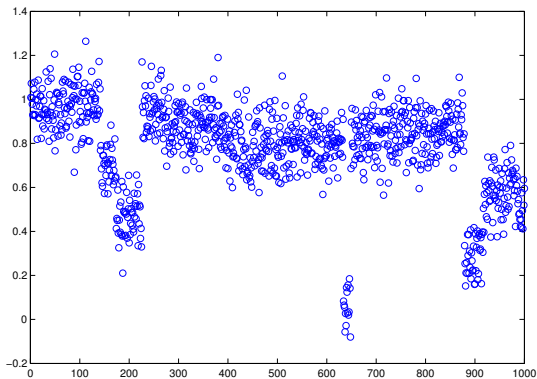
Measuring DNA copy number

Motivation

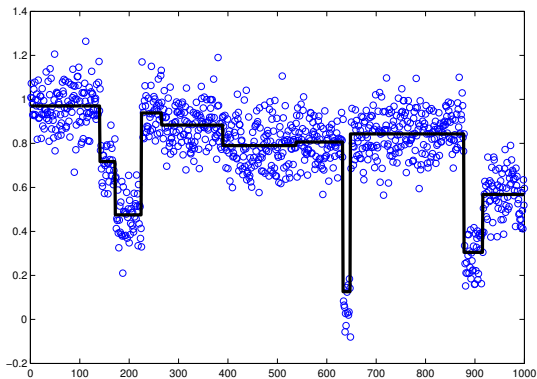
- Comparative genomic hybridization (CGH) data measure the **DNA copy number** along the genome
- Very useful, in particular in cancer research to observe systematically variants in DNA content
- Progressively replaced by high throughput sequencing techniques



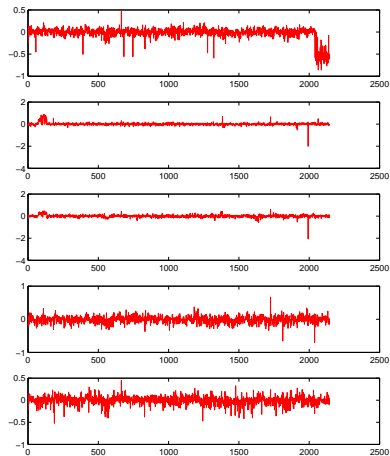
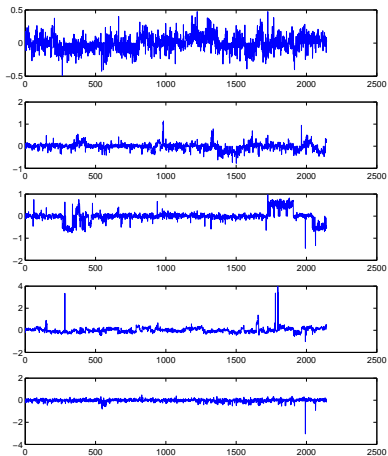
Problem 1: find change-points in one (long) profile



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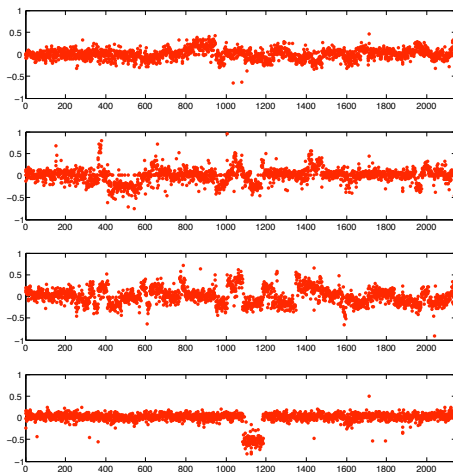


Problem 2: learn to discriminate profiles



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

Problem 3: Find frequent breakpoints

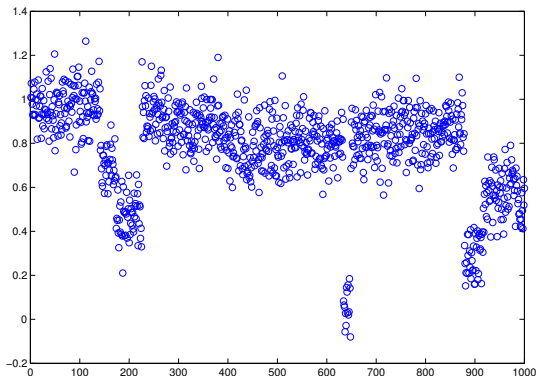


A collection of bladder tumour copy number profiles.

- 1 Fast fused lasso for change-point detection
- 2 Fused SVM for discrimination of profiles
- 3 Group fused lasso for multiple frequent change-point detection

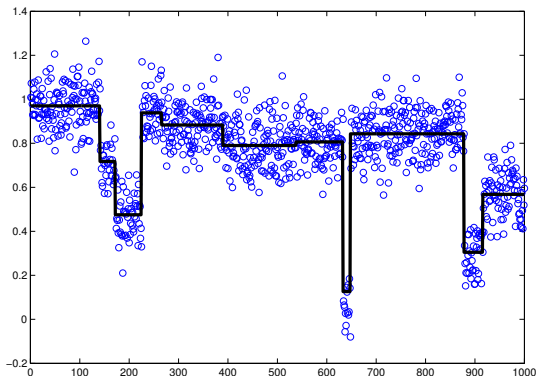
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Can we identify breakpoints and "smooth" each profile?



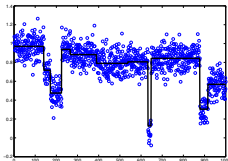
- A classical multiple change-point detection problem
- Should scale to lengths of order $10^6 \sim 10^8$

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- A classical multiple change-point detection problem
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An optimal solution

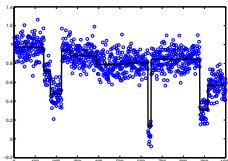


- For a signal $Y \in \mathbb{R}^p$, define an optimal approximation $\beta \in \mathbb{R}^p$ with k breakpoints as the solution of

$$\min_{\beta \in \mathbb{R}^p} \|Y - \beta\|^2 \quad \text{such that} \quad \sum_{i=1}^{p-1} \mathbf{1}(\beta_{i+1} \neq \beta_i) \leq k$$

- This is an optimization problem over the $\binom{p}{k}$ partitions...
- Dynamic programming finds the solution in $O(p^2 k)$ in time and $O(p^2)$ in memory
- But: does not scale to $p = 10^6 \sim 10^8$...

An optimal solution

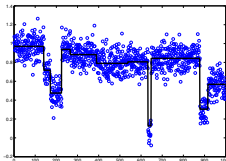


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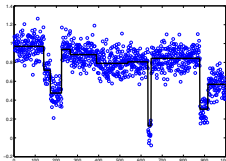


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Promoting sparsity with the ℓ_1 penalty

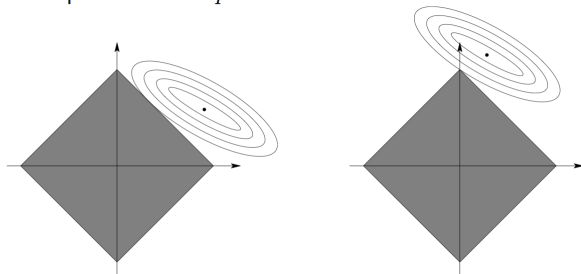
The ℓ_1 penalty (Tibshirani, 1996; Chen et al., 1998)

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

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

is usually **sparse**.

Geometric interpretation with $p = 2$



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:

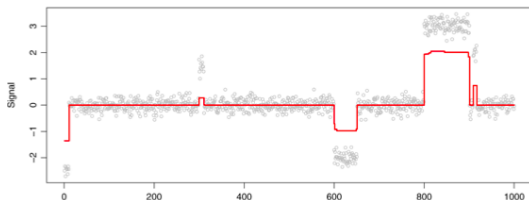
- Change of variable $u_i = \beta_{i+1} - \beta_i$, $u_0 = \beta_1$
- We obtain a Lasso problem in $u \in \mathbb{R}^{p-1}$
- u sparse means β piecewise constant

TV signal approximator

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

Adding additional constraints does not change the change-points:

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



Solving TV signal approximator

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

- QP with sparse linear constraints in $O(p^2)$ -> 135 min for $p = 10^5$ (Tibshirani and Wang, 2008)
- Coordinate descent-like method $O(p)$? -> 3s for $p = 10^5$ (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)

Solving TV signal approximator in $O(p \ln K)$

Theorem (V. and Bleakley, 2010; see also Hoefling, 2009)

TV signal approximator is a **binary segmentation** algorithm

Algorithm 1 Greedy dichotomic segmentation

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 $[1, n]$
 - 2: $\mathcal{P} = \{I_0\}$
 - 3: **for** $i = 1$ to k **do**
 - 4: $I^* \leftarrow \arg \max_{I \in \mathcal{P}} \gamma(I^*)$
 - 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}
-

Apparently greedy algorithm finds the global optimum!

Solving TV signal approximator in $O(p \ln K)$

Theorem (V. and Bleakley, 2010; see also Hoefling, 2009)

TV signal approximator is a **binary segmentation** algorithm

Consequences:

- Good news: very fast methods to find the global optimum of TV approximator
- Good news: we can analyze this greedy method by expressing the solution as the global minimum of an objective function
- Bad news: TV approximator is no more than a binary segmentation method...

Extension to *hierarchical clustering*: `ClusterPath` (Hocking et al., ICML 2011)

- 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 $u < k < v$, $\sigma \in \{-1, 1\}$

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

where

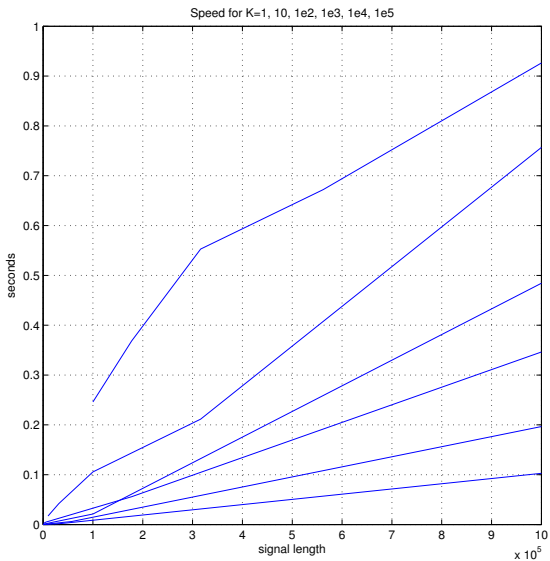
$$A_k = -F_k + \frac{(v - k) F_u + (k - u) F_v}{v - u},$$
$$B_k = \frac{(v - k) \sigma_u + (k - u) \sigma_v}{v - u}.$$

Then the functions $\gamma(l)$, $l_L(l)$ and $l_R(l)$ are respectively given by:

$$\begin{aligned}\gamma(l) &= \max_{k \in [u+1, v-1], \sigma \in \{-1, 1\}} f_l(k, \sigma), \\ (k^*, \sigma^*) &= \operatorname{argmax}_{k \in [u+1, v-1], \sigma \in \{-1, 1\}} f_l(k, \sigma), \\ l_L(l) &= (u, k^*, \sigma_u, \sigma^*), \\ l_R(l) &= (k^*, v, \sigma^*, \sigma_v).\end{aligned}$$

- 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 $K = 100$, $p = 10^7$



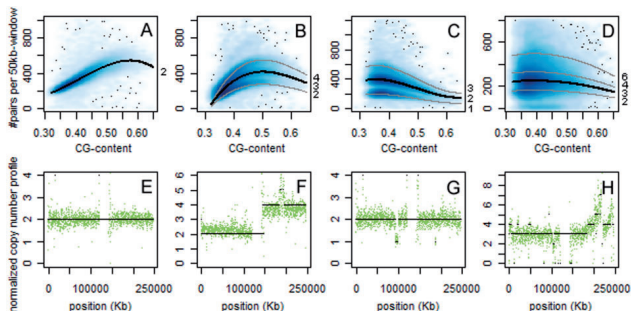
Genome analysis

Advance Access publication November 15, 2010

Control-free calling of copy number alterations in deep-sequencing data using GC-content normalization

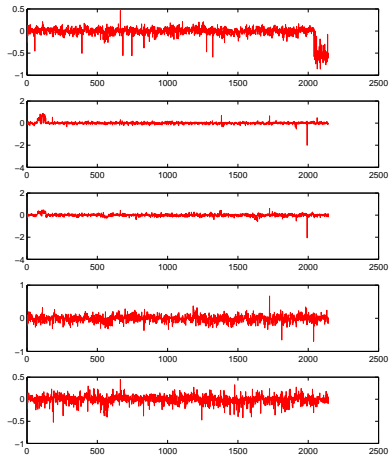
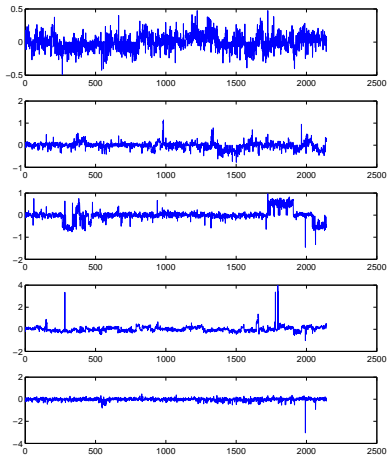
Valentina Boeva^{1,2,3,4,*}, Andrei Zinovyev^{1,2,3}, Kevin Bleakley^{1,2,3}, Jean-Philippe Vert^{1,2,3}, Isabelle Janoueix-Lerosey^{1,4}, Olivier Delattre^{1,4} and Emmanuel Barillot^{1,2,3}

¹Institut Curie, ²INSERM, U900, Paris, F-75248, ³Mines ParisTech, Fontainebleau, F-77300 and ⁴INSERM, U830, Paris, F-75248 France



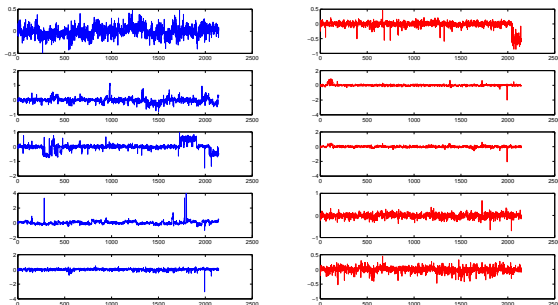
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Extension: cancer prognosis



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

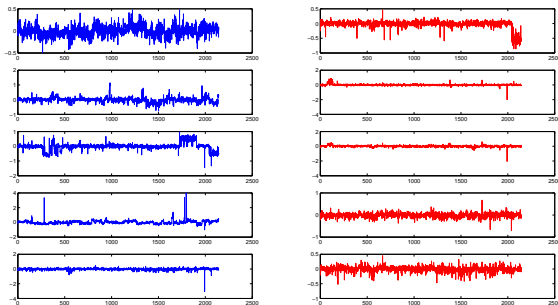
The problem



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

Prior knowledge

- **Sparsity** : 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 for supervised classification (Rapaport et al., 2008)

Find a linear predictor $f(Y) = \beta^T Y$ that best discriminates the aggressive vs non-aggressive samples, subject to the constraints that it should be sparse and piecewise constant:

$$\min_{\beta \in \mathbb{R}^p} \sum_{i=1}^n \ell(y_i, \beta^T x_i) + \lambda_1 \|\beta\|_1 + \lambda_2 \|\beta\|_{TV}$$

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 $p = 10^8 \sim 10^9$

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

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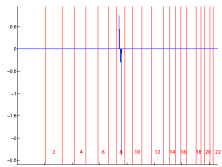
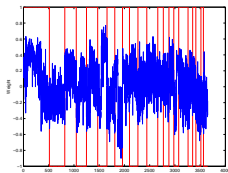
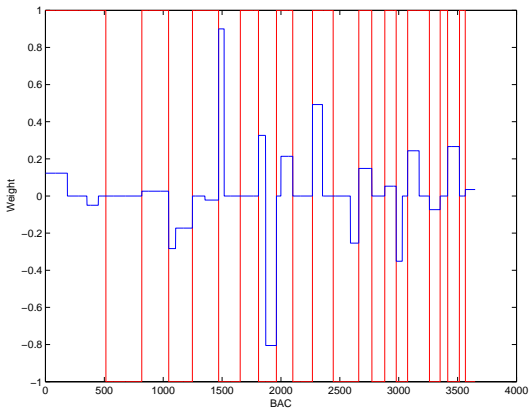
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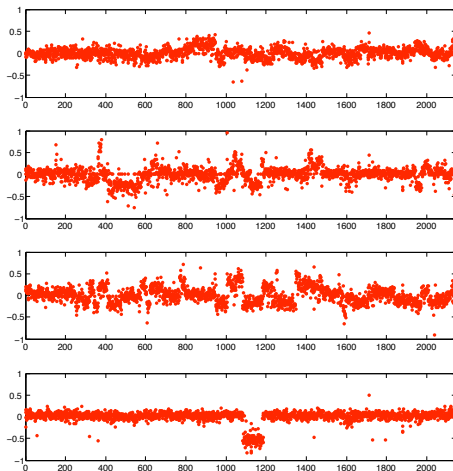
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Example: prognosis in melanoma



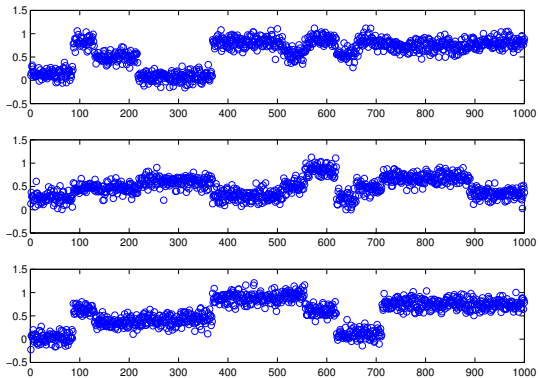
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Can we detect frequent breakpoints?

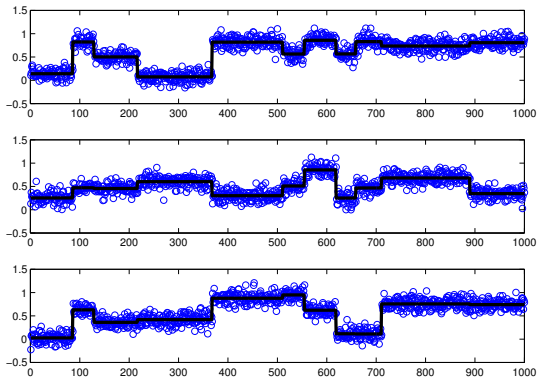


A collection of bladder tumour copy number profiles.

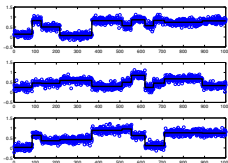
The problem



The problem



"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

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

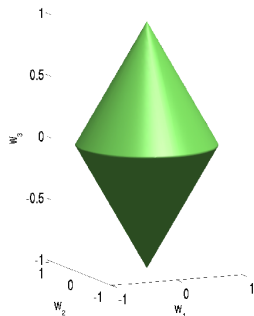
- DP finds the solution in $O(p^2 kn)$ in time and $O(p^2)$ in memory
- But: does not scale to $p = 10^6 \sim 10^8 \dots$

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*:

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



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

Replace

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

by

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

GFLseg = Group Fused Lasso segmentation

Questions

- Practice: can we solve it efficiently?
- Theory: does it recover the correct segmentation?

Replace

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

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GFLseg = Group Fused Lasso segmentation

Questions

- Practice: can we solve it efficiently?
- Theory: does it recover the correct segmentation?

- Make the change of variables:

$$\begin{aligned}\gamma &= U_{1,\bullet}, \\ \beta_{i,\bullet} &= w_i (U_{i+1,\bullet} - U_{i,\bullet}) \quad \text{for } i = 1, \dots, p-1.\end{aligned}$$

- 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.

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

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 $R \in \mathbb{R}^{p \times n}$, we can compute $C = \bar{X}^\top R$ 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 $A = (a_1, \dots, a_{|A|})$, set of distinct indices with $1 \leq a_1 < \dots < a_{|A|} \leq p - 1$, and for any $|A| \times n$ matrix R , we can compute $C = \left(\bar{X}_{\bullet, A}^\top \bar{X}_{\bullet, A} \right)^{-1} R$ in $O(|A|n)$ in time and memory

Speed trial

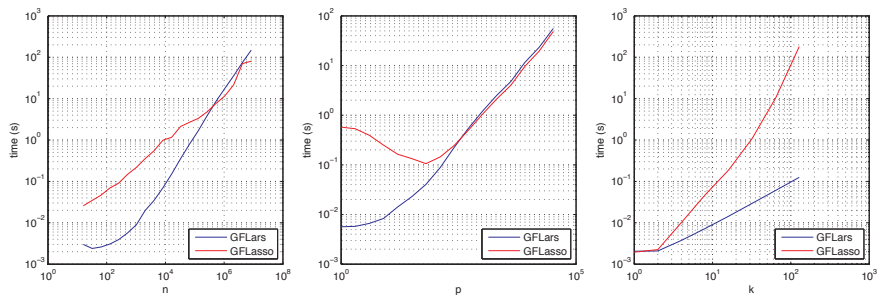
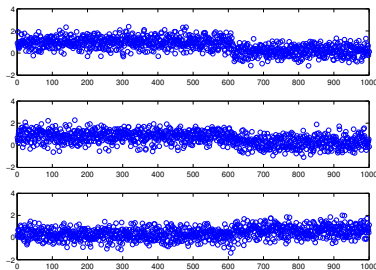


Figure 2: **Speed trials for group fused LARS (top row) and Lasso (bottom row).** *Left column:* varying n , with fixed $p = 10$ and $k = 10$; *center column:* varying p , with fixed $n = 1000$ and $k = 10$; *right column:* varying k , with fixed $n = 1000$ and $p = 10$. Figure axes are log-log. Results are averaged over 100 trials.

Consistency

Suppose a single change-point:

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



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

Consistency of the unweighted TV approximator

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

Theorem

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

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

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

Consistency of the weighted TV approximator

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

Theorem

The weighted TV approximator with weights

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

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

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

$$\hat{c} = \bar{X}^\top \bar{Y} = \bar{X}^\top \bar{X} \beta^* + \bar{X}^\top W.$$

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

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

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

Consistency for a single change-point

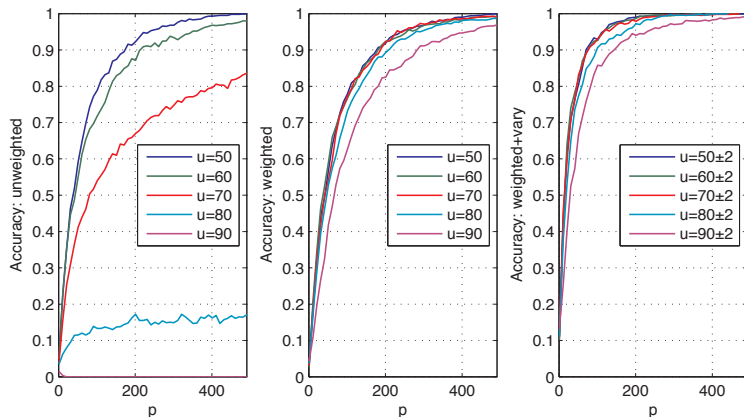


Figure 3: **Single change-point accuracy for the group fused Lasso.** Accuracy as a function of the number of profiles p when the change-point is placed in a variety of positions $u = 50$ to $u = 90$ (left and centre plots, resp. unweighted and weighted group fused Lasso), or: $u = 50 \pm 2$ to $u = 90 \pm 2$ (right plot, weighted with varying change-point location), for a signal of length 100.

Estimation of several change-points

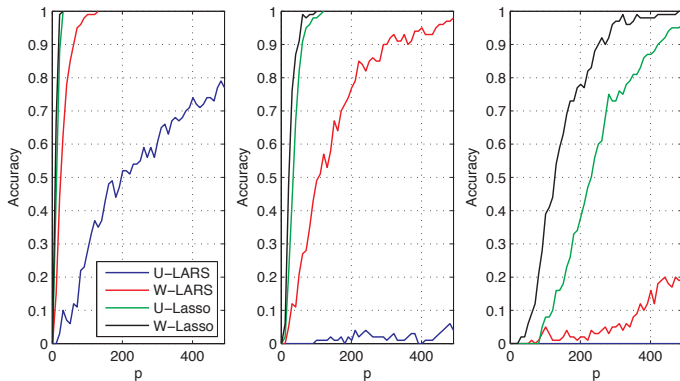
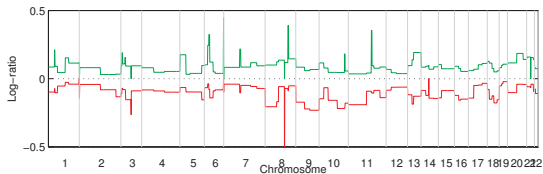
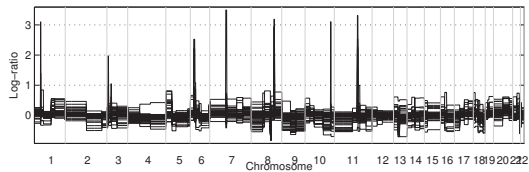
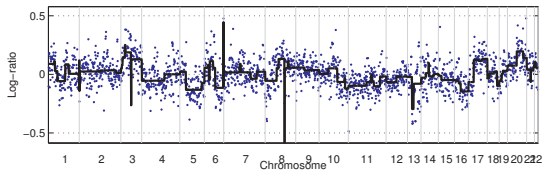


Figure 4: **Multiple change-point accuracy.** Accuracy as a function of the number of profiles p when change-points are placed at the nine positions $\{10, 20, \dots, 90\}$ and the variance σ^2 of the centered Gaussian noise is either 0.05 (left), 0.2 (center) and 1 (right). The profile length is 100.

Application: detection of frequent abnormalities



Conclusion

- Convex norms with singularities at piecewise-constant profiles
- Global optimum of fused lasso found by binary segmentation
- Efficient proximal methods for optimization with general loss functions (supervised classification, regression, ...)
- Benefit of increasing the number of profiles

Some questions

- Theoretical results for K change-points in n profiles of length p
- What if just a few profiles have a change-point?
- What about time series on a network?
- How to choose the number of change-points?

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