

Pics, ligne de base, bruit : séparation ternaire de sources assistée (BEADS : positivité, parcimonie), spectres chimiques & miscellanées

L. DUVAL, A. PIRAYRE

IFP Energies nouvelles

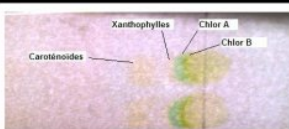
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23 mars 2018

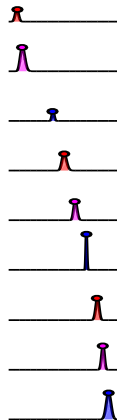


Old peaks cast long shadows



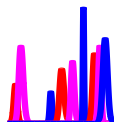
Chromatography: the traditional 2D way.

Old peaks cast long shadows



Chromatography: individual 1D peaks for single compounds

Old peaks cast long shadows



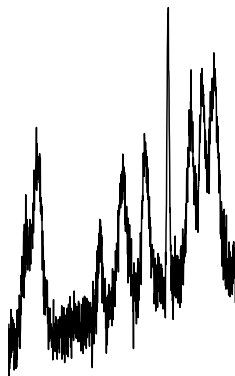
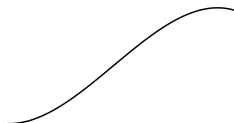
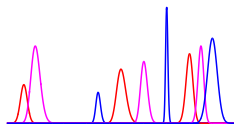
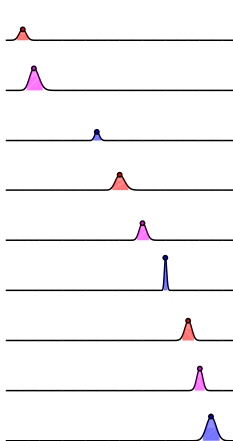
Chromatography: ternary sources separated

Old peaks cast long shadows



Chromatography: observed signal

Old peaks cast long shadows



Chromatography: wrapping it up

The quick version

- ▶ *Issue*: how to accurately & repeatably quantize peaks?
 - ▶ avoiding separate baseline and noise removal
- ▶ *Question*: where is the string behind the bead?
 - ▶ without too accurate models for: peak, noise, baseline



- ▶ *Answer*: use main measurement properties + optimization
 - ▶ sparsity+symmetry, stationarity, smoothness
- ▶ **BEADS: Baseline Estimation And Denoising w/ Sparsity**
 - ▶ other properties + optimization for further processing (BARCHAN)

Outline

INTRODUCTION

FOREWORD

OUTLINE*

BACKGROUND

BEADS MODEL AND ALGORITHM

NOTATIONS

COMPOUND SPARSE DERIVATIVE MODELING

MAJORIZE-MINIMIZE TYPE OPTIMIZATION

EVALUATION AND RESULTS

GC: SIMULATED BASELINE AND GAUSSIAN NOISE

GC: SIMULATED POISSON NOISE

GC: REAL DATA

GC×GC: REAL DATA

ONGOING, EXTENSIONS, CONCLUSION

Background on background

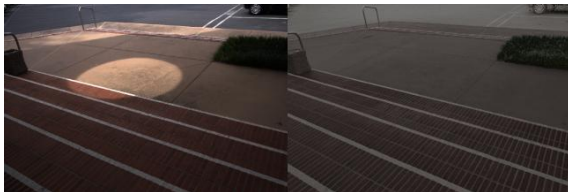


Image processing: varying illumination

- ▶ Background affects quantitative evaluation/comparison
- ▶ In other domains: (instrumental) bias, (seasonal) trend
- ▶ In analytical chemistry: drift, continuum, wander, *baseline*
- ▶ Very rare cases of parametric modeling (piecewise linear, polynomial, spline)

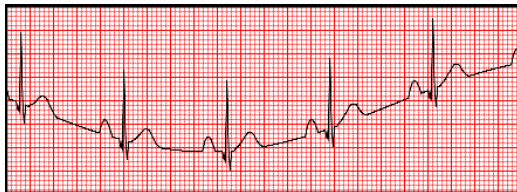
Background on background



Econometrics: trends and seasonality

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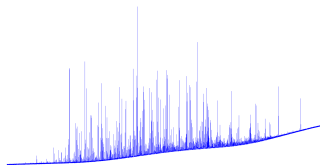
Background on background



Biomedical: ECG isoelectric line or baseline wander

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Background on background



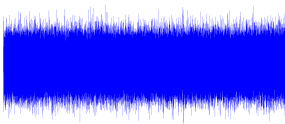
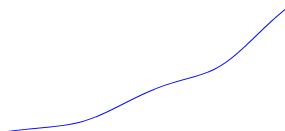
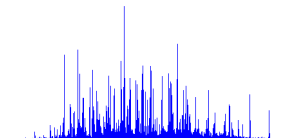
Gas chromatography: baseline

- ▶ Background affects quantitative evaluation/comparison
- ▶ In other domains: (instrumental) bias, (seasonal) trend
- ▶ In analytical chemistry: drift, continuum, wander, *baseline*
- ▶ Very rare cases of parametric modeling (piecewise linear, polynomial, spline)

Background on background

Analytical chemistry, biological data

- Signal separation into three main morphological components



Notations and assumptions

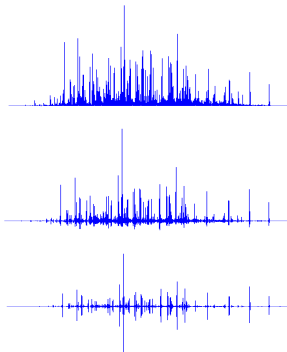
Morphological decomposition: $\mathbf{y} = \mathbf{x} + \mathbf{f} + \mathbf{w}$, signals in \mathbb{R}^N

- ▶ \mathbf{y} : observation (spectrum, analytical data)
- ▶ \mathbf{x} : clean series of peaks (no baseline, no noise)
- ▶ \mathbf{f} : baseline
- ▶ \mathbf{w} : noise

Assumption: without peaks, the baseline can be (approx.) recovered from noise-corrupted data by low-pass filtering

- ▶ $\hat{\mathbf{f}} = \mathbf{L}(\mathbf{y} - \hat{\mathbf{x}})$: \mathbf{L} : low-pass filter; $\mathbf{H} = \mathbf{I} - \mathbf{L}$: high-pass filter
- ▶ formulated as $\|\mathbf{y} - \hat{\mathbf{x}} - \hat{\mathbf{f}}\|_2^2 = \|\mathbf{H}(\mathbf{y} - \hat{\mathbf{x}})\|_2^2$
- ▶ Going further with \mathbf{D}_i : differentiation operators

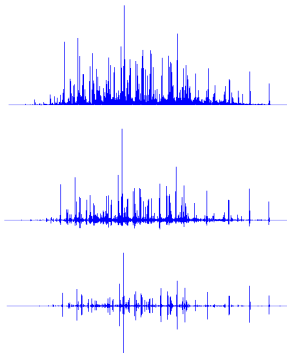
Compound sparse derivative modeling



An estimate $\hat{\mathbf{x}}$ can be obtained via:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x}} \left\{ F(\mathbf{x}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \sum_{i=0}^M \lambda_i R_i(\mathbf{D}_i \mathbf{x}) \right\}.$$

Compound sparse derivative modeling



Examples of (smooth) sparsity promoting functions for R_i

- ▶ $\phi_i^A = |x|$
- ▶ $\phi_i^B = \sqrt{|x|^2 + \epsilon}$
- ▶ $\phi_i^C = |x| - \epsilon \log(|x| + \epsilon)$

Compound sparse derivative modeling

Take the positivity of chromatogram peaks into account:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x}} \left\{ F(\mathbf{x}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \sum_{n=0}^{N-1} \theta_{\epsilon}(x_n; r) + \sum_{i=1}^M \lambda_i \sum_{n=0}^{N_i-1} \phi([\mathbf{D}_i \mathbf{x}]_n) \right\}.$$

Start from:

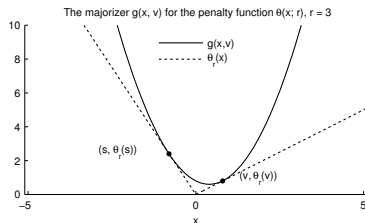
$$\theta(x; r) = \begin{cases} x, & x \geq 0 \\ -rx, & x < 0 \end{cases}$$

Compound sparse derivative modeling

Take the positivity of chromatogram peaks into account:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x}} \left\{ F(\mathbf{x}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \sum_{n=0}^{N-1} \theta_{\epsilon}(x_n; r) + \sum_{i=1}^M \lambda_i \sum_{n=0}^{N_i-1} \phi([\mathbf{D}_i \mathbf{x}]_n) \right\}.$$

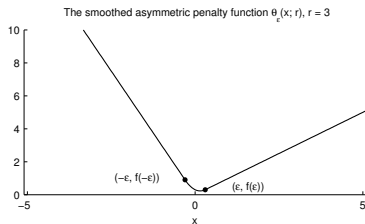
and majorize it



Take the positivity of chromatogram peaks into account:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x}} \left\{ F(\mathbf{x}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \sum_{n=0}^{N-1} \theta_{\epsilon}(x_n; r) + \sum_{i=1}^M \lambda_i \sum_{n=0}^{N_i-1} \phi([\mathbf{D}_i \mathbf{x}]_n) \right\}.$$

then smooth it:



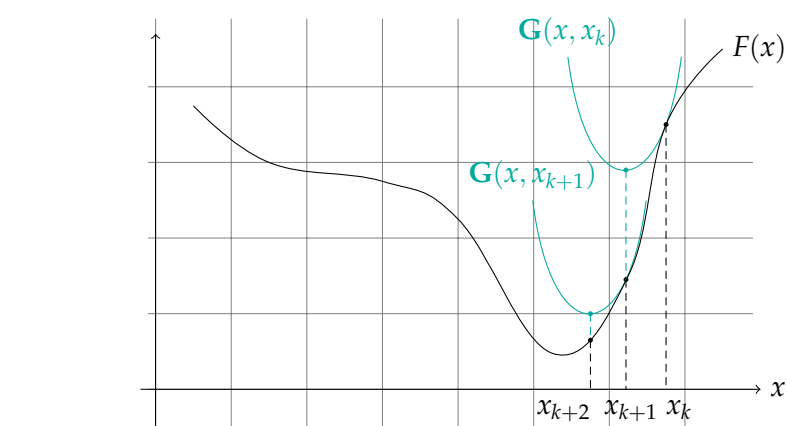
Compound sparse derivative modeling

Take the positivity of chromatogram peaks into account:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x}} \left\{ F(\mathbf{x}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \sum_{n=0}^{N-1} \theta_{\epsilon}(x_n; r) + \sum_{i=1}^M \lambda_i \sum_{n=0}^{N_i-1} \phi([\mathbf{D}_i \mathbf{x}]_n) \right\}.$$

then majorize it:

$$g_0(x, v) = \begin{cases} \frac{1+r}{4|v|} x^2 + \frac{1-r}{2} x + |v| \frac{1+r}{4}, & |v| > \epsilon \\ \frac{1+r}{4\epsilon} x^2 + \frac{1-r}{2} x + \epsilon \frac{1+r}{4}, & |v| \leq \epsilon. \end{cases}$$



MM principles.

BEADS Algorithm (short)

Input: \mathbf{y} , \mathbf{A} , \mathbf{B} , λ_i , $i = 0, \dots, M$

1. $\mathbf{b} = \mathbf{B}^\top \mathbf{B} \mathbf{A}^{-1} \mathbf{y}$

2. $\mathbf{x} = \mathbf{y}$ (Initialization)

Repeat

3. $[\Lambda_i]_{n,n} = \frac{\phi'([\mathbf{D}_i \mathbf{x}]_n)}{[\mathbf{D}_i \mathbf{x}]_n}, \quad i = 0, \dots, M,$

4. $\mathbf{M} = \sum_{i=0}^M \lambda_i \mathbf{D}_i^\top \Lambda_i \mathbf{D}_i$

5. $\mathbf{Q} = \mathbf{B}^\top \mathbf{B} + \mathbf{A}^\top \mathbf{M} \mathbf{A}$

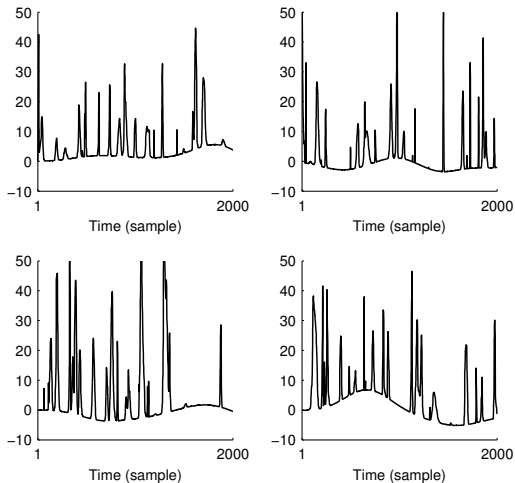
6. $\mathbf{x} = \mathbf{A} \mathbf{Q}^{-1} \mathbf{b}$

Until converged

8. $\mathbf{f} = \mathbf{y} - \mathbf{x} - \mathbf{B} \mathbf{A}^{-1} (\mathbf{y} - \mathbf{x})$

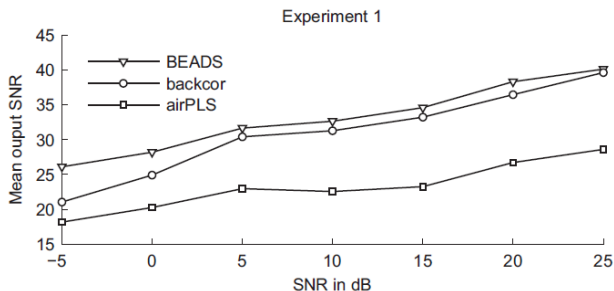
Output: \mathbf{x} , \mathbf{f}

Evaluation 1



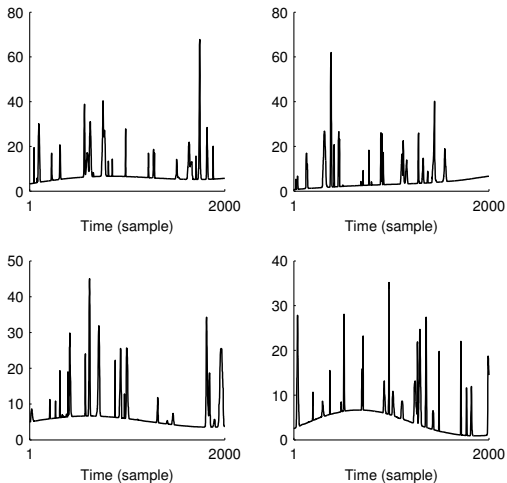
Simulated chromatograms w/ polynomial+sine baseline

Evaluation 1 with Gaussian noise



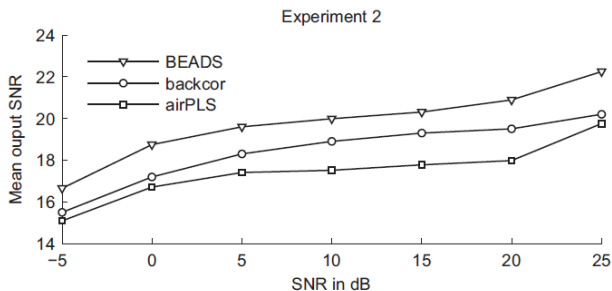
	0 dB		10 dB		20 dB	
	Mean	Std	Mean	Std	Mean	Std
BEADS	28.1	8.52	32.64	8.02	38.33	6.74
backcor	24.91	9.75	31.27	8.33	36.47	6.53
airPLS	20.26	9.65	22.54	10.15	26.71	7.76

Evaluation 2



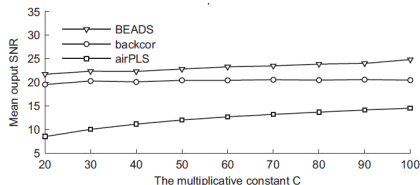
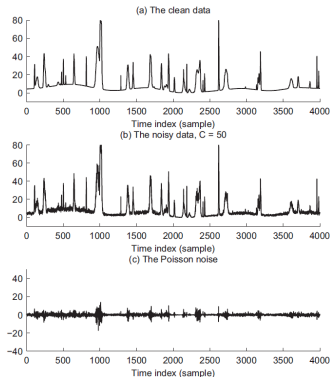
Simulated chromatograms w/ limited power spectrum noise

Evaluation 2 with Gaussian noise



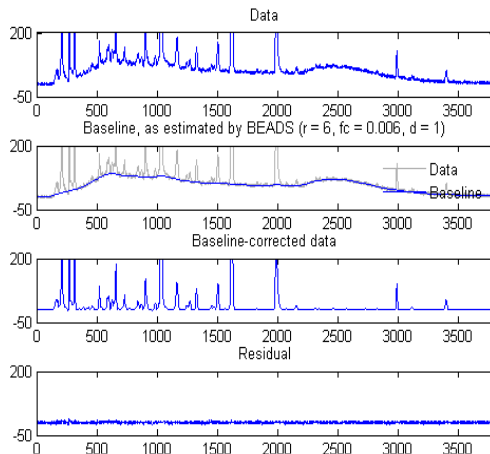
	0 dB		10 dB		20 dB	
	Mean	Std	Mean	Std	Mean	Std
BEADS	18.75	3.71	19.99	3.17	20.89	3.32
backcor	17.20	4.57	18.93	3.74	19.54	3.18
airPLS	16.71	4.80	17.52	5.54	17.98	4.82

Evaluation 3 with Poisson noise



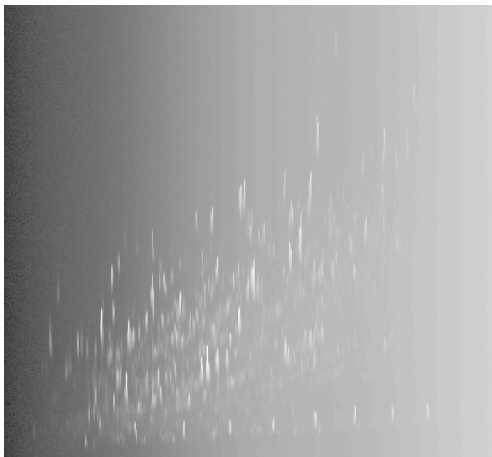
Simulated chromatograms w/ Poisson noise

Results: mono-dimensional chromatography (data 1)



Original, superimposed, clean, noise

Results: two-dimensional chromatography (data 2)



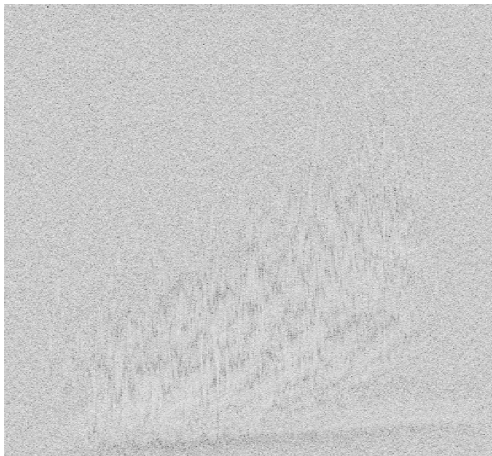
Original data

Results: two-dimensional chromatography (data 2)



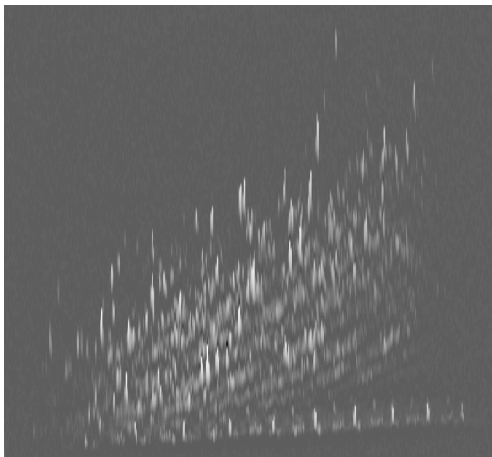
2D background (estimated)

Results: two-dimensional chromatography (data 2)



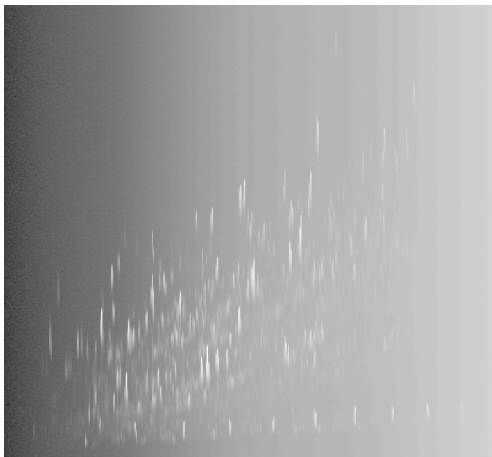
Noise (estimated)

Results: two-dimensional chromatography (data 2)



BEADS corrected data

Results: two-dimensional chromatography (data 2)



Original data (again!)

Results: two-dimensional chromatography (data 3)



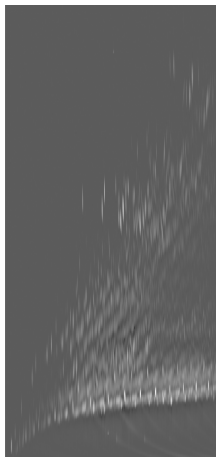
2D background (estimated)

Results: two-dimensional chromatography (data 3)



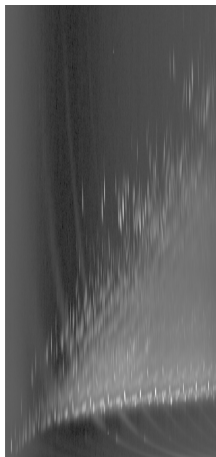
Noise (estimated)

Results: two-dimensional chromatography (data 3)



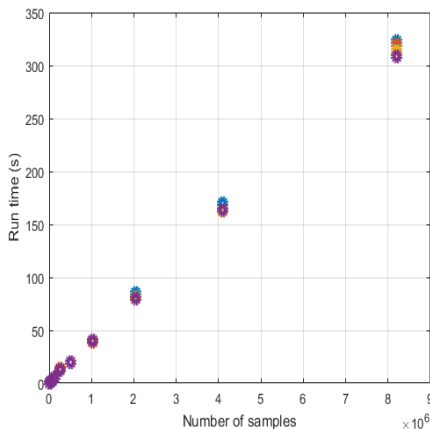
BEADS corrected data

Results: two-dimensional chromatography (data 3)



Original data (again!)

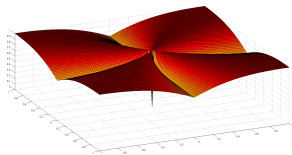
Results: computing scalability



Linear cost per sample (almost)

Ongoing work

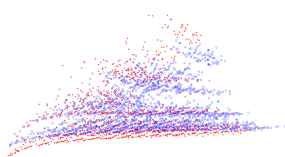
- ▶ Tests on analytical chemistry data: NIR, NMR, XPS
- ▶ Novel filtering: improved Savitzky-Golay filters
- ▶ Novel deconvolution: sparse & positive with norm ratios



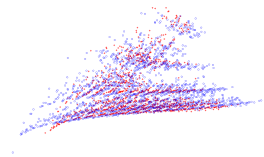
SOOT: Non-convex ℓ_0 count index approximation

- ▶ Novel metrics: errors related to peak quantities
- ▶ Baseline and noise use: uncertainty, trace products
- ▶ **2D chromatography comparisons: BARCHAN warping**
- ▶ **Improved usability: parameter estimation**

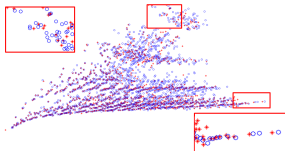
BARCHAN: 2D chromatography warping



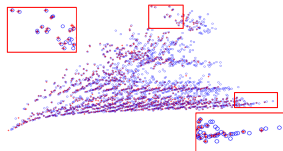
No transformation



Rigid



Non-rigid



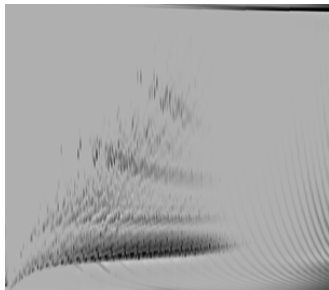
BARCHAN

Semi-rigid morphing of two different 2D chromatograms.

BARCHAN: 2D chromatography warping

Ingredients of a GMM plus EM optimization:

- ▶ Point sets $X = \{X_1, \dots, X_N\}$ and $Y = \{Y_1, \dots, Y_M\}$
- ▶ $p(X_n) = \frac{w}{N} + \sum_{m=1}^M \frac{1-w}{2M\pi\sigma^2} \exp\left(-\frac{\|X_n - T(Y_m)\|^2}{2\sigma^2}\right)$
- ▶ $\min_{\sigma, W, s, t} E = E_1(\sigma, W, s, t) + \frac{\lambda}{2} \text{Tr}(W^\top G W)$

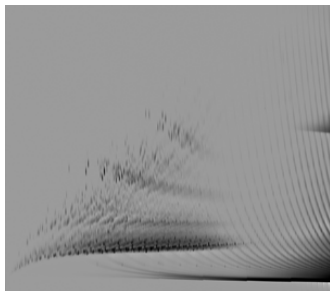


Calculated deformation of a 2D chromatogram with BARCHAN.

BARCHAN: 2D chromatography warping

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- ▶ $\min_{\sigma, W, s, t} E = E_1(\sigma, W, s, t) + \frac{\lambda}{2} \text{Tr}(W^\top GW)$

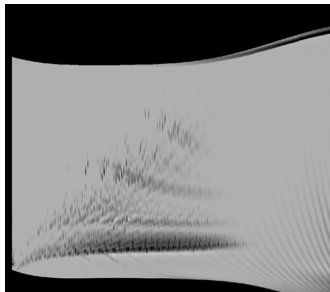


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BARCHAN: 2D chromatography warping

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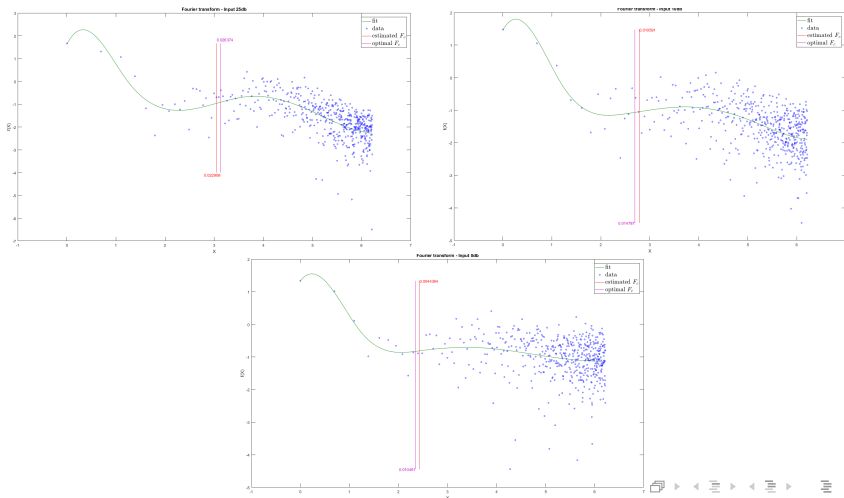
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- ▶ $\min_{\sigma, W, s, t} E = E_1(\sigma, W, s, t) + \frac{\lambda}{2} \text{Tr}(W^\top GW)$



Calculated deformation of a 2D chromatogram with BARCHAN.

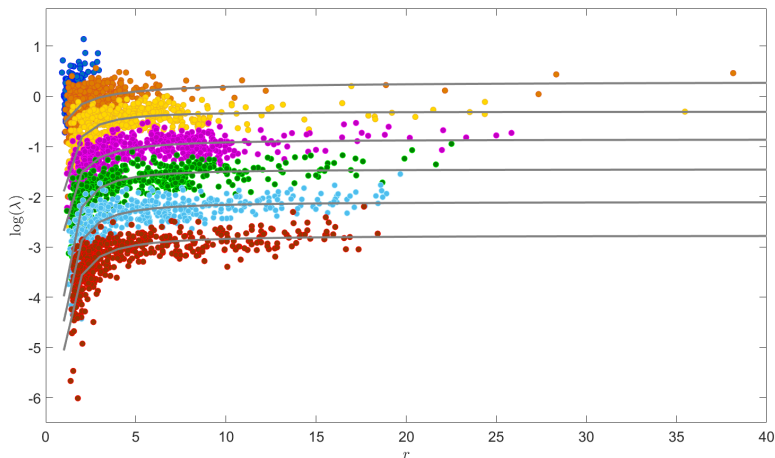
Improved usability: parameter estimation

► Cut-off frequency estimation



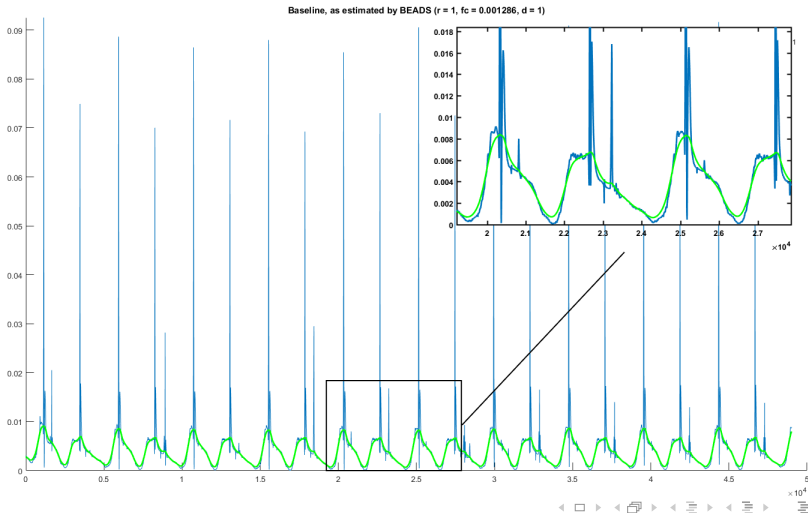
Improved usability: parameter estimation

- Noise, asymmetry (r) and regularization (λ)



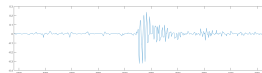
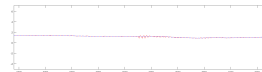
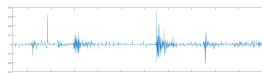
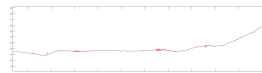
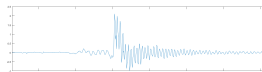
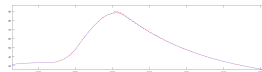
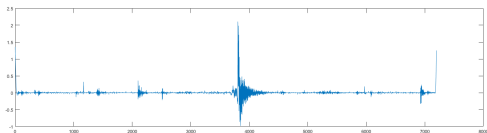
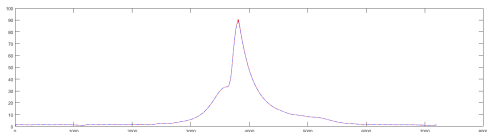
Extended applications

► Lidar application



Extended applications

► Engine knocking application



Other known uses

- ▶ A fairly generic model (sparsity, positivity/negativity), reused by other authors
 - ▶ gas chromatography: mono-dimensional and comprehensive/two-dimensional
 - ▶ Raman spectra: biological and biomedical
 - ▶ MUSE (Multi Unit Spectroscopic Explorer): astronomical hyperspectral galaxy spectrum
 - ▶ X-ray absorption spectroscopy (XAS), X-ray diffraction (XRD), and combined XAS/XRD
 - ▶ high-resolution mass spectrometry
 - ▶ postprandial Plasma Glucose (PPG), multichannel electroencephalogram (EEG) and single-channel electrocardiogram (ECG)
 - ▶ arabic characters

Other known uses

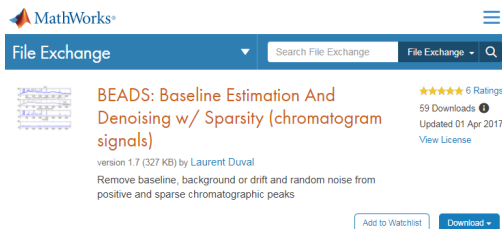
- ▶ A fairly generic model (sparsity, positivity/negativity), reused by other authors
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 - ▶ Raman spectra: biological and biomedical
 - ▶ MUSE (Multi Unit Spectroscopic Explorer): astronomical hyperspectral galaxy spectrum
 - ▶ X-ray absorption spectroscopy (XAS), X-ray diffraction (XRD), and combined XAS/XRD
 - ▶ high-resolution mass spectrometry
 - ▶ postprandial Plasma Glucose (PPG), multichannel electroencephalogram (EEG) and single-channel electrocardiogram (ECG)
 - ▶ arabic characters

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Conclusions

- ▶ Joint baseline/background and noise estimation
 - ▶ Interaction between “separative science” and “source separation”
 - ▶ Little “hard” modeling
 - ▶ Easy to tune, scalable
 - ▶ Codes in Matlab, R and C++¹



The screenshot shows the MathWorks File Exchange interface. At the top is the MathWorks logo and a search bar labeled "Search File Exchange". Below this, the "File Exchange" tab is selected. The main content area displays the "BEADS: Baseline Estimation And Denoising w/ Sparsity (chromatogram signals)" entry. It includes a small thumbnail image of a chromatogram, the title in orange, and a 5-star rating with 6 ratings. Below the title, it says "version 1.7 (327 KB) by Laurent Duval". A description follows: "Remove baseline, background or drift and random noise from positive and sparse chromatographic peaks". On the right, it shows "59 Downloads" and "Updated 01 Apr 2017", with a "View License" link. At the bottom right, there are two buttons: "Add to Watchlist" and "Download".

- ▶ A wide range of applications to unveil

¹<http://www.laurent-duval.eu/>

A little more: additional references



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BEADS Algorithm

We now have a majorizer for F

$$G(\mathbf{x}, \mathbf{v}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \mathbf{x}^\top [\boldsymbol{\Gamma}(\mathbf{v})] \mathbf{x} \\ + \lambda_0 \mathbf{b}^\top \mathbf{x} + \sum_{i=1}^M \left[\frac{\lambda_i}{2} (\mathbf{D}_i \mathbf{x})^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] (\mathbf{D}_i \mathbf{x}) \right] + c(\mathbf{v}).$$

Minimizing $G(\mathbf{x}, \mathbf{v})$ with respect to \mathbf{x} yields

$$\mathbf{x} = \left[\mathbf{H}^\top \mathbf{H} + 2\lambda_0 \boldsymbol{\Gamma}(\mathbf{v}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] \mathbf{D}_i \right]^{-1} \left(\mathbf{H}^\top \mathbf{H} \mathbf{y} - \lambda_0 \mathbf{b} \right).$$

with notations

$$c(\mathbf{v}) = \sum_n \left[\phi(v_n) - \frac{v_n}{2} \phi'(v_n) \right].$$

BEADS Algorithm

We now have a majorizer for F

$$G(\mathbf{x}, \mathbf{v}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \mathbf{x}^\top [\boldsymbol{\Gamma}(\mathbf{v})] \mathbf{x} \\ + \lambda_0 \mathbf{b}^\top \mathbf{x} + \sum_{i=1}^M \left[\frac{\lambda_i}{2} (\mathbf{D}_i \mathbf{x})^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] (\mathbf{D}_i \mathbf{x}) \right] + c(\mathbf{v}).$$

Minimizing $G(\mathbf{x}, \mathbf{v})$ with respect to \mathbf{x} yields

$$\mathbf{x} = \left[\mathbf{H}^\top \mathbf{H} + 2\lambda_0 \boldsymbol{\Gamma}(\mathbf{v}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] \mathbf{D}_i \right]^{-1} \left(\mathbf{H}^\top \mathbf{H} \mathbf{y} - \lambda_0 \mathbf{b} \right).$$

with notations

$$[\boldsymbol{\Gamma}(\mathbf{v})]_{n,n} = \begin{cases} \frac{1+r}{4|v_n|}, & |v_n| \geq \epsilon \\ \frac{1+r}{4\epsilon}, & |v_n| \leq \epsilon \end{cases}$$

BEADS Algorithm

We now have a majorizer for F

$$G(\mathbf{x}, \mathbf{v}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \mathbf{x}^\top [\mathbf{\Gamma}(\mathbf{v})] \mathbf{x} \\ + \lambda_0 \mathbf{b}^\top \mathbf{x} + \sum_{i=1}^M \left[\frac{\lambda_i}{2} (\mathbf{D}_i \mathbf{x})^\top [\mathbf{\Lambda}(\mathbf{D}_i \mathbf{v})] (\mathbf{D}_i \mathbf{x}) \right] + c(\mathbf{v}).$$

Minimizing $G(\mathbf{x}, \mathbf{v})$ with respect to \mathbf{x} yields

$$\mathbf{x} = \left[\mathbf{H}^\top \mathbf{H} + 2\lambda_0 \mathbf{\Gamma}(\mathbf{v}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^\top [\mathbf{\Lambda}(\mathbf{D}_i \mathbf{v})] \mathbf{D}_i \right]^{-1} \left(\mathbf{H}^\top \mathbf{H} \mathbf{y} - \lambda_0 \mathbf{b} \right).$$

with notations

$$[\mathbf{\Lambda}(\mathbf{v})]_{n,n} = \frac{\phi'(v_n)}{v_n}$$

BEADS Algorithm

We now have a majorizer for F

$$G(\mathbf{x}, \mathbf{v}) = \frac{1}{2} \|\mathbf{H}(\mathbf{y} - \mathbf{x})\|_2^2 + \lambda_0 \mathbf{x}^\top [\boldsymbol{\Gamma}(\mathbf{v})] \mathbf{x} \\ + \lambda_0 \mathbf{b}^\top \mathbf{x} + \sum_{i=1}^M \left[\frac{\lambda_i}{2} (\mathbf{D}_i \mathbf{x})^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] (\mathbf{D}_i \mathbf{x}) \right] + c(\mathbf{v}).$$

Minimizing $G(\mathbf{x}, \mathbf{v})$ with respect to \mathbf{x} yields

$$\mathbf{x} = \left[\mathbf{H}^\top \mathbf{H} + 2\lambda_0 \boldsymbol{\Gamma}(\mathbf{v}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^\top [\boldsymbol{\Lambda}(\mathbf{D}_i \mathbf{v})] \mathbf{D}_i \right]^{-1} \left(\mathbf{H}^\top \mathbf{H} \mathbf{y} - \lambda_0 \mathbf{b} \right).$$

with notations

$$[\mathbf{b}]_n = \frac{1-r}{2}$$

BEADS Algorithm

Writing filter $\mathbf{H} = \mathbf{A}^{-1}\mathbf{B} \approx \mathbf{B}\mathbf{A}^{-1}$ (banded matrices) we have

$$\mathbf{x} = \mathbf{A}\mathbf{Q}^{-1} \left(\mathbf{B}^T \mathbf{B} \mathbf{A}^{-1} \mathbf{y} - \lambda_0 \mathbf{A}^T \mathbf{b} \right)$$

where \mathbf{Q} is the banded matrix,

$$\mathbf{Q} = \mathbf{B}^T \mathbf{B} + \mathbf{A}^T \mathbf{M} \mathbf{A},$$

and \mathbf{M} is the banded matrix,

$$\mathbf{M} = 2\lambda_0 \mathbf{\Gamma}(\mathbf{v}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^T [\Lambda(\mathbf{D}_i \mathbf{v})] \mathbf{D}_i.$$

BEADS Algorithm

Using previous equations, the MM iteration takes the form:

$$\mathbf{M}^{(k)} = 2\lambda_0 \mathbf{\Gamma}(\mathbf{x}^{(k)}) + \sum_{i=1}^M \lambda_i \mathbf{D}_i^T [\Lambda(\mathbf{D}_i \mathbf{x}^{(k)})] \mathbf{D}_i.$$

$$\mathbf{Q}^{(k)} = \mathbf{B}^T \mathbf{B} + \mathbf{A}^T \mathbf{M}^{(k)} \mathbf{A}$$

$$\mathbf{x}^{(k+1)} = \mathbf{A}[\mathbf{Q}^{(k)}]^{-1} \left(\mathbf{B}^T \mathbf{B} \mathbf{A}^{-1} \mathbf{y} - \lambda_0 \mathbf{A}^T \mathbf{b} \right)$$