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Blind Source Separation of MALDI spectra from noise by sparse representation in a composite of linear bases

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Overview

- **We apply a Blind Source Separation technique to differentiate between signal and noise on MALDI spectra.**
- We look for efficient representations in a redundant composite of two transforms with different statistical properties, one adapted to represent the signal, the other the noise.
- Results show a clean separation between signal and noise with joint perfect reconstruction of the original signal

Sparse approximation in a composite of bases

- MALDI spectra are typically affected by several sources of noise: chemical background, electrical noise, peak broadening, contaminants...
- The signal of interest usually has statistical properties that differ from those of most of the sources of noise.
- The sparse approximation problem is defined as minimising the error of approximating the data as a linear combination of a limited number of functions taken from an overcomplete base (one with more coefficients than elements in the original signal)
- **We use a blind-source separation approach to differentiate between signal and noise by looking for sparse representations in a composite domain constructed from several bases, each one adapted to represent efficiently one of those sources.**
- We implement the solution to the associated sparse approximation problem by using an iterated algorithm based on **Iterative Shrinkage Methods**, which iterates between
  - · A thresholding operation in the transformed domain to enforce sparseness
  - · A projection to the subspace of the transformed domain of perfect reconstruction of the original signal
- By doing so, we expect to **capture each feature of the raw signal with the corresponding base** that is more adapted to its statistical properties.

Experimental Methods

Sample preparation

The proposed algorithm has been tested on MALDI-MSI datasets of mouse brain tissue sections. Serial mouse brain sections at 12 μm thickness were mounted on ITO glass slides for MALDI.
Tissue sections were sprayed using the SunCollect (Sunchrom) for trypsin and matrices deposition.
α-Cyano-4-hydroxycinnamic acid matrix was used for in-situ digested protein imaging respectively.
MALDI images were acquired using a MALDI TOF-TOF instrument (MALDI-7090, Shimadzu, UK) in linear or reflectron mode for protein imaging and in-situ digest imaging samples, respectively at 30 μm resolution.

Data processing

Raw data were loaded in IonView software (Shimadzu, UK) and TIC and Basepeak spectra were exported to ASCII format for further processing in Matlab.

Results and discussion

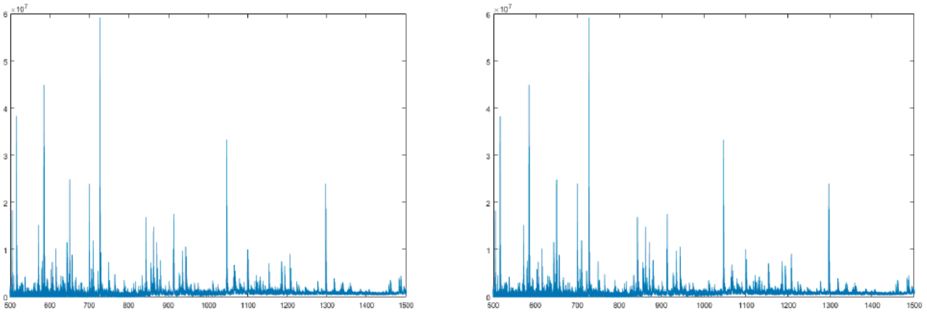
Representation used

- 1D Dual-Tree Complex Wavelet transform.
  - Represented by matrix **W**.
  - **Efficiently represents signal.**
- 1D Discrete Fourier transform.
  - Represented by matrix **F**.
  - **Efficiently represents noise.**

Algorithm

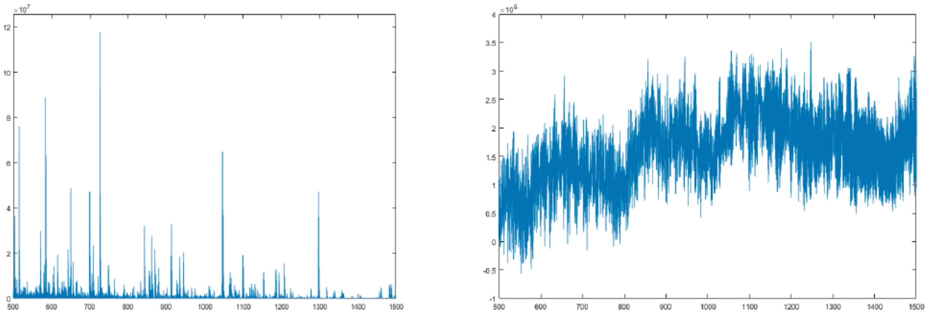
- **x**; input raw spectrum
- **A**: composite orthogonal transform
- Column-wise concatenation of α**W** and β**F**, with α, β two scalars
- $\mathbf{a}^{(0)} = \mathbf{A}\mathbf{x}$, $i = 0$, $\theta(0) = \max(\mathrm{abs}(\mathbf{a}^{(0)}))$, γ in $(0,1)$
- Until convergence repeat:
  - Form $\mathbf{b}^{(i)}$ by thresholding $\mathbf{a}^{(i)}$ with threshold θ
  - Form $\mathbf{x}_s^{(i+1)}$ and $\mathbf{x}_n^{(i+1)}$ by transforming $\mathbf{b}^{(i)}$ to the original signal domain of **W** and **F**
  - Form $\mathbf{a}^{(i+1)}$ by projecting $\mathbf{b}^{(i)}$ to the subspace of perfect reconstruction of **x**
  - $\theta^{(i+1)} = \gamma\theta^{(i)}$
- Use $\mathbf{x}_s^{(end)}$ as estimate of noise-free signal

Results



TIC spectrum

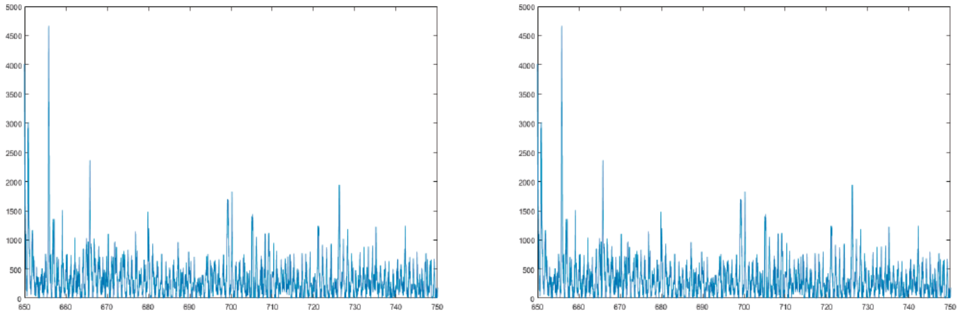
Reconstructed



Estimated signal

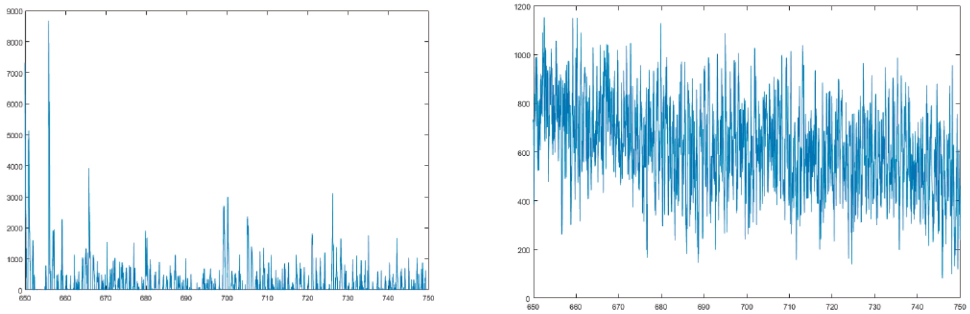
Estimated noise

Figure 1 Noise separation result using a TIC spectrum from a mouse brain protein digest image. Mass range is showed from 500 to 1500 Da for feature visibility. Scalar parameters were set at $\alpha = 0.4$, $\beta = 0.6$, $\gamma = 0.9$. From top to bottom and left to right: original TIC spectrum, reconstructed spectrum from final sparse representation, estimated noise-free signal component, estimated noise component.



Basepeak spectrum

Reconstructed



Estimated signal

Estimated noise

Figure 2 Same settings as in Figure 1 but applied to the Base peak spectrum.
Mass range is showed from 650 to 750 Da for feature visibility.

Additional result: Data reduction

- Additionally, this technique helps to reduce the stored size for spectra
- Because of maximization of sparseness in the transformed domain
- Compression results for the examples shown in this poster:

Example	Original data size	Compressed data size	Estimated signal data size	% of data reduction
TIC spectrum	2.03 MBytes	0.15 MBytes	0.06 MBytes	97.07%
Basepeak spe.	2.03 MBytes	0.70 MBytes	0.17 MBytes	91.53%

Conclusions

- This is a promising approach to separate signal from noise in MALDI spectra. Noise-sources captured include random noise and baseline.
- It is an iterative algorithm but it has the potential to be highly accelerated.
- It provides an estimation of the noise in the same range as the signal, which can be used to estimate noise power, calculate signal to noise ratios, etc.
- As side result, it provides the potential for highly compressing the data.

References

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