Deep Unfolding RPCA for High Resolution Flow Estimation

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Outline

1. Introduction
2. Model-based Methods
3. Proposed Unfolded Algorithm
4. Numerical Results

Introduction

Introduction

Clinical Context: open brain surgery

- Precise identification of tumor contours in brain surgery.
- Tumor areas are highly vascularized.

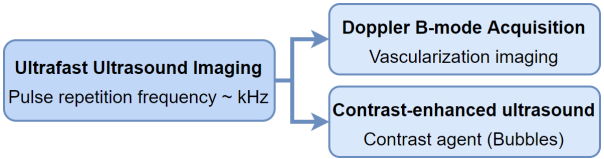
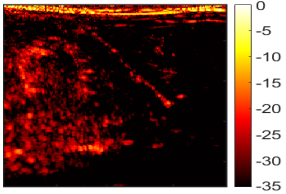


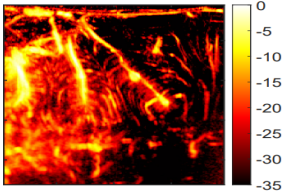
Figure 1: Surgery room ©Chloé Barthélémy

Goal

- Retrieval of blood flow from US images

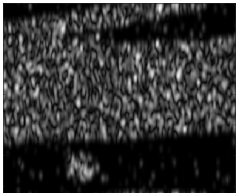


(a) *Observation*

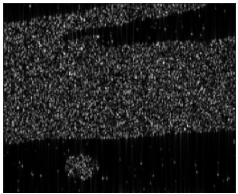


(b) *Desired blood structure*

- US image deconvolution



(a) *Blurred observation*



(b) *Desired TRF*

Model-based Methods

RPCA Model

- Let $\boldsymbol{S}$ be the matrix of the ultrasound acquisition, the model is:

$$\boldsymbol{S} = \boldsymbol{T} + \boldsymbol{H}\boldsymbol{x} + \boldsymbol{N}, \tag{1}$$

  where $\boldsymbol{T}$, $\boldsymbol{H}\boldsymbol{x}$ and $\boldsymbol{N}$ are the **tissue**, **blood** and **noise** matrices.
- Embedding a deconvolution step in RPCA [She+19]: $\boldsymbol{H}\boldsymbol{x} = H_m \circledast \boldsymbol{x}$. H_m is the PSF kernel, $\circledast$ is the convolution operator and $\boldsymbol{x}$ is the high-resolution blood component. $\boldsymbol{H}$ is the BCCB matrix obtained from H_m.
- The blood matrix $\boldsymbol{x}$ is assumed **sparse**. The tissue slowly changes over time and so, $\boldsymbol{T}$ can be described as a **low-rank** matrix.
- $\boldsymbol{x}$ and $\boldsymbol{T}$ are obtained by solving Eq. (2) using e.g., ADMM [Boy+10]:

$$[\hat{\boldsymbol{x}}, \hat{\boldsymbol{T}}] = \arg\min_{\boldsymbol{x},\boldsymbol{T}} \left\{ ||\boldsymbol{S} - \boldsymbol{H}\boldsymbol{x} - \boldsymbol{T}||_F^2 + \lambda||\boldsymbol{x}||_1 + \mu||\boldsymbol{T}||_* \right\}. \tag{2}$$

ADMM Framework

General ADMM problem form [Boy+10]:

$$\begin{aligned} &\textbf{minimize} && f(\hat{x}) + g(\hat{z}) \\ &\textbf{subject to} && A\hat{x} + B\hat{z} = c, \end{aligned} \tag{3}$$

Minimize the augmented Lagrangian:

$$L(\hat{x}, \hat{z}, \gamma) = f(\hat{x}) + g(\hat{z}) + (\rho/2) \left\| A\hat{x} + B\hat{z} - c + \gamma/\rho \right\|_2^2 + cst\,, \tag{4}$$

Solution:

$$\hat{x}^{k+1} = \arg\min_{\hat{x}} f(\hat{x}^k) + (\rho/2) \left\| A\hat{x}^k + B\hat{z}^k - c + \gamma^k/\rho \right\|_2^2\,, \tag{5}$$

$$\hat{z}^{k+1} = \arg\min_{\hat{z}} g(\hat{z}^k) + (\rho/2) \left\| A\hat{x}^k + B\hat{z}^k - c + \gamma^k/\rho \right\|_2^2\,, \tag{6}$$

$$\gamma^{k+1} = \gamma^k + (A\hat{x}^{k+1} + B\hat{z}^{k+1} - c)\,, \tag{7}$$

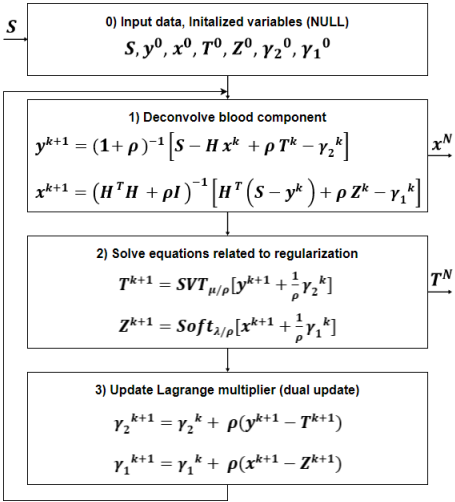
Thus, by defining :

$$M_1 = \begin{bmatrix} H & I \end{bmatrix}\ ;\ M_2 = \begin{bmatrix} I & 0 \end{bmatrix}\ ;\ M_3 = \begin{bmatrix} 0 & I \end{bmatrix}\ ;$$

$$\hat{x} = \begin{bmatrix} x \\ y \end{bmatrix}\ ;\ \hat{z} = \begin{bmatrix} Z \\ T \end{bmatrix}\ ;\ \gamma = \begin{bmatrix} \gamma_1 \\ \gamma_2 \end{bmatrix}\ ;$$

$$f(\hat{x}) = \tfrac{1}{2} \left\| S - M_1\hat{x} \right\|_F^2\,; \quad g(\hat{z}) = \lambda \left\| M_2\hat{z} \right\|_1 + \mu \left\| M_3\hat{z} \right\|_*\,;$$

DRPCA Algorithm



DRPCA Algorithm

S

0) Input data, Initalized variables (NULL)

$$S, y^0, x^0, T^0, Z^0, \gamma_2{}^0, \gamma_1{}^0$$

1) Deconvolve blood component

$$y^{k+1} = (\mathbf{1} + \rho)^{-1}\left[S - H x^k + \rho T^k - \gamma_2{}^k\right]$$

$$x^{k+1} = \left(H^T H + \rho I\right)^{-1}\left[H^T\left(S - y^k\right) + \rho Z^k - \gamma_1{}^k\right]$$

x^N

2) Solve equations related to regularization

$$T^{k+1} = SVT_{\mu/\rho}[y^{k+1} + \frac{1}{\rho}\gamma_2{}^k]$$

$$Z^{k+1} = Soft_{\lambda/\rho}[x^{k+1} + \frac{1}{\rho}\gamma_1{}^k]$$

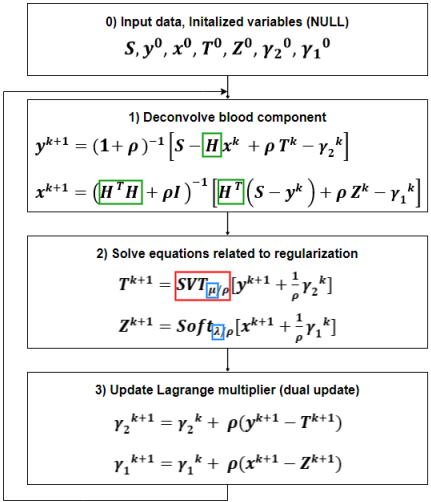
T^N

3) Update Lagrange multiplier (dual update)

$$\gamma_2{}^{k+1} = \gamma_2{}^k + \rho(y^{k+1} - T^{k+1})$$

$$\gamma_1{}^{k+1} = \gamma_1{}^k + \rho(x^{k+1} - Z^{k+1})$$

DRPCA Algorithm Limitations



H has to be measured by an independent procedure: inconvenient and often infeasible

The Singular Value Thresholding operation (SVT) is computationally expensive.

The hyper-parameters balancing the regularization terms, λ and μ have to be tuned manually.

Proposed Unfolded Algorithm

Deep Unfolding

- The DRPCA equations are as:

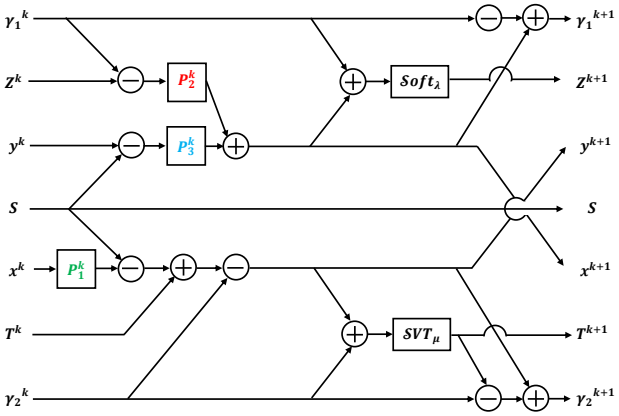
$$
\begin{aligned}
\boldsymbol{y}^{k+1} &= (\mathbf{1}+\boldsymbol{\rho})^{-1}\left[\boldsymbol{S}-\boldsymbol{H}\,\boldsymbol{x}^{k}+\boldsymbol{\rho}\,\boldsymbol{T}^{k}-\boldsymbol{\gamma}_{2}{}^{k}\right]\\
\boldsymbol{x}^{k+1} &= \left(\boldsymbol{H}^{T}\boldsymbol{H}+\boldsymbol{\rho}\boldsymbol{I}\right)^{-1}\left[\boldsymbol{H}^{T}\left(\boldsymbol{S}-\boldsymbol{y}^{k}\right)+\boldsymbol{\rho}\,\boldsymbol{Z}^{k}-\boldsymbol{\gamma}_{1}{}^{k}\right]\\
\boldsymbol{T}^{k+1} &= \boldsymbol{SVT}_{\mu/\rho}[\boldsymbol{y}^{k+1}+\tfrac{1}{\rho}\boldsymbol{\gamma}_{2}{}^{k}]\\
\boldsymbol{Z}^{k+1} &= \boldsymbol{Soft}_{\lambda/\rho}[\boldsymbol{x}^{k+1}+\tfrac{1}{\rho}\boldsymbol{\gamma}_{1}{}^{k}]\\
\boldsymbol{\gamma}_{2}{}^{k+1} &= \boldsymbol{\gamma}_{2}{}^{k}+\boldsymbol{\rho}(\boldsymbol{y}^{k+1}-\boldsymbol{T}^{k+1})\\
\boldsymbol{\gamma}_{1}{}^{k+1} &= \boldsymbol{\gamma}_{1}{}^{k}+\boldsymbol{\rho}(\boldsymbol{x}^{k+1}-\boldsymbol{Z}^{k+1})
\end{aligned}
$$

- Like Corona [Sol+20], replace convolution terms with convolutional layers :

$$P_1 = -H;\;\; P_2 = (H^T H + \rho I)^{-1};\;\; P_3 = (H^T H + \rho I)^{-1} H^T;$$

- Learn hyper-parameters λ and μ.

Single Cell Diagram



$$y^{k+1} = (\mathbf{1} + \rho)^{-1}\left[S - P_1 x^k + \rho\, T^k - {\gamma_2}^k\right]$$

$$x^{k+1} = P_2\left[\rho\, Z^k - {\gamma_1}^k\right] + P_3\left[S - y^k\right]$$

$$T^{k+1} = SVT_{\mu/\rho}[y^{k+1} + \tfrac{1}{\rho}{\gamma_2}^k]$$

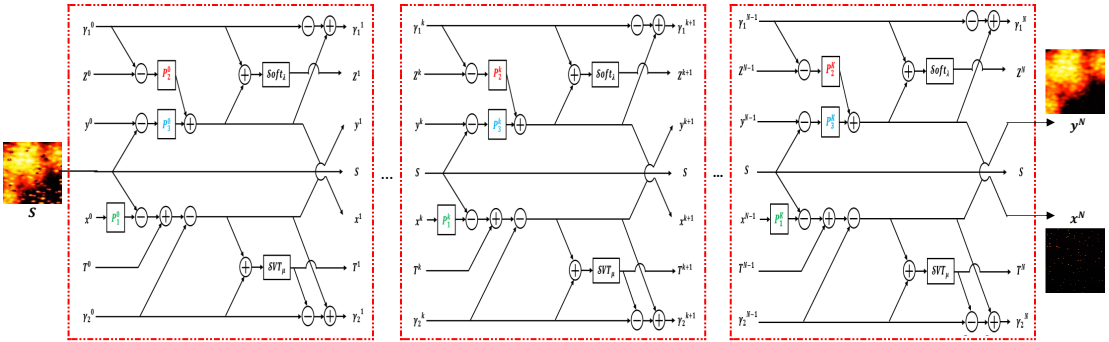
$$Z^{k+1} = Soft_{\lambda/\rho}[x^{k+1} + \tfrac{1}{\rho}{\gamma_1}^k]$$

$${\gamma_2}^{k+1} = {\gamma_2}^k + \rho(y^{k+1} - T^{k+1})$$

$${\gamma_1}^{k+1} = {\gamma_1}^k + \rho(x^{k+1} - Z^{k+1})$$

Neural Network Diagram

Assemble the network by putting successive layers as...



The P^k and hyper-parameters are estimated via supervised deep learning.

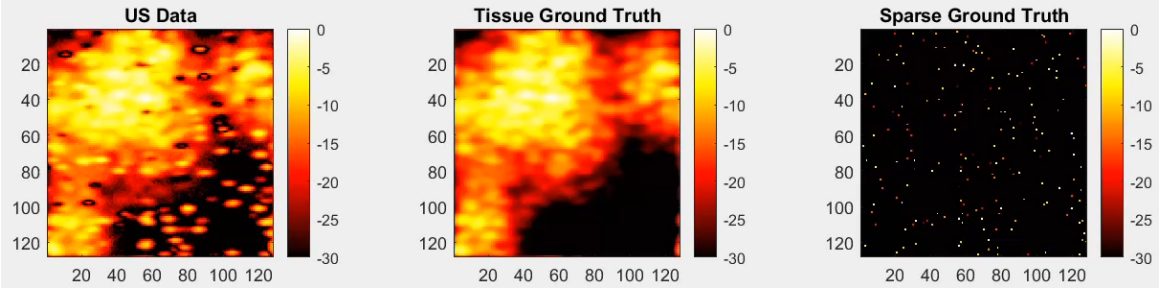
Numerical Results

Simulation Data

Simulation platform adapted from [Sol+20]. The data model is:

$$\boldsymbol{S} = H_{\mathrm{GT}} \circledast (\boldsymbol{y}_{\mathrm{GT}} + \boldsymbol{x}_{\mathrm{GT}}) + \boldsymbol{N}_{\mathrm{GT}}, \tag{8}$$

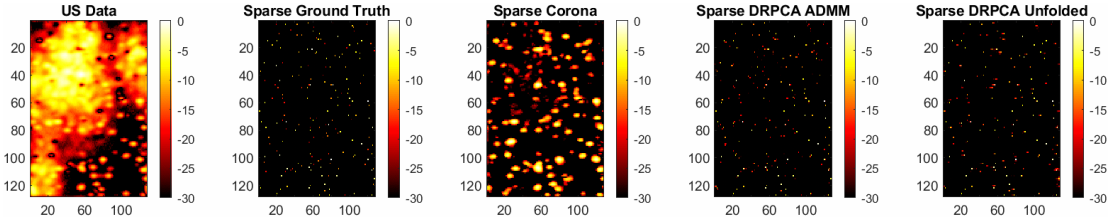
where $\boldsymbol{y}_{\mathrm{GT}}$, $\boldsymbol{x}_{\mathrm{GT}}$ and $\boldsymbol{N}_{\mathrm{GT}}$ are the ground truth of the high-resolution **tissue**, the high-resolution **blood** component (Bubbles) and the additive Gaussian **noise**. H_{GT} is the ground truth convolution kernel.



Tissue: Low-pass filtered modulated mixture of gaussians. Has a weak and spatially regular movement.
Blood: Sparse matrix of a random number of bubbles with Gaussian drawn amplitudes and pseudo-random (parametric) erratic trajectories.

Numerical Results

- Classical vs unfolded methods carried out on a simulated data.



- Training parameters of our network

Layers	Epochs	Learning rate	Kernel sizes
20	100	0.01	9/5

- Quality Metrics

	CORONA [Sol+20]	DRPCA [She+19]	Unfolded DRPCA (Ours)
PSNR (dB)	24.41	30.32	36.17
SSIM3	0.13	0.71	0.94

Numerical Results

- Power Doppler image ($\boldsymbol{I}_{PD}$) in dB is defined for a given position (x, z), as:

$$\boldsymbol{I}_{PD}(x,z) = 10\log 10\left(\frac{1}{N_t}\sum_{k=1}^{N_t}\boldsymbol{I}(x,z,k)^2\right). \tag{9}$$

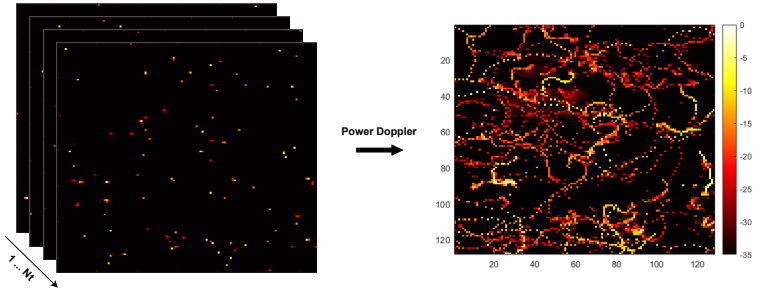
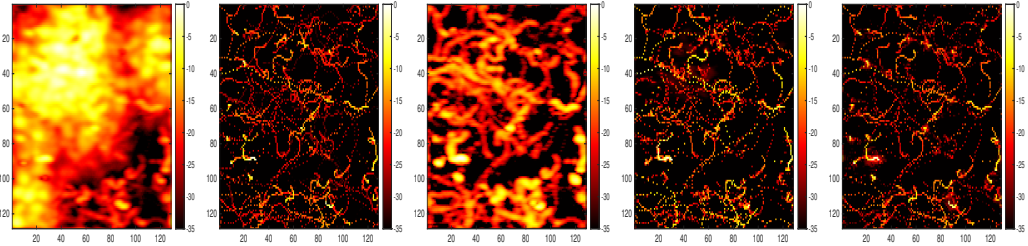


Figure 2: The power Doppler image combines the information from the entire sequence into a single frame

Numerical Results

- **Power Doppler Results**



(a) US Data (b) Ground Truth (c) Corona (d) DRPCA ADMM (e) DRPCA Unfolded

Figure 3: Power Doppler images of the estimated blood component from the simulated data

- A supervised deep unfolding network solving RPCA problem and performing blind deconvolution is proposed.
- It performs better than state of the art Corona and its iterative version. It doesn't require prior knowledge of the PSF and automatically adjusts hyper-parameters.
- Perspective: Develop a non-supervised learning method and challenge the unfolded DRPCA method on real datasets.

Thank you!

Questions ?

Contact :
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References

[She+19] H. Shen et al. "High-resolution and high-sensitivity blood flow estimation using optimization approaches with application to vascularization imaging". In: *Proc. IEEE IUS*. 2019.

[Boy+10] S. Boyd et al. "Distributed optimization and statistical learning via the alternating direction method of multipliers". In: *Found. Trends Mach. Learn.* (2010).

[Sol+20] Oren Solomon et al. "Deep Unfolded Robust PCA With Application to Clutter Suppression in Ultrasound". In: *IEEE Trans. Med. Imag.* (2020).