

# Spectral denoising for MR Spectroscopic Imaging using Non-Local Means

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## Purpose

Magnetic resonance spectroscopic imaging (MRSI) is an imaging modality used for studying tissues in-vivo in order to assess and quantify metabolites for diagnostic purposes. However, long scanning times, low spatial resolution, poor signal-to-noise ratio (SNR) and the subsequent noise-sensitive non-linear model fitting are major roadblocks in accurately quantifying the metabolite concentration. In this work, we propose a spectrally adaptive method for denoising of MRSI spectra based on the concept of Non-Local Means (NLM)<sup>1,2</sup> which relies on spectral redundancy in the given data-set. Due to lack of phase information in the acquired data, we perform a 'spectral dephasing' step to consider a wide range of phase variations to improve the NLM-based pattern analysis. We evaluated our method on human in-vivo data and assessed the improvement in SNR for NAA.

## Methods

**Non-Local Means:** For the spectra to be denoised, the NLM filter<sup>1,2</sup> searches for other similar spectra patches in the frequency-phase space in the given data-set. A weighted average is performed using these patches with a higher weight being assigned to highly similar spectra. This is represented as:

$$\hat{S}_{ij}(\omega) = \sum_{x_{kl} \in \Omega^3} w(x_{ij}, x_{kl}) S_{kl}(\omega)$$

**Spectral dephasing:** For each voxel  $x_{ij}$ , the signal is shifted by a set of phase angles  $\Theta$ :

$$S_{ij}^{\Theta}(t) = S_{ij}(t) \cdot e^{-i\Theta}, \text{ where } \Theta \in [-n_1\pi, (n_2 + 2)\pi], \{n_1, n_2 \in \mathbb{R} \mid n_1, n_2 \geq 0\}$$

The real component of these dephased signals are then combined to generate a 2D frequency-phase matrix.

**Spectral Rephasing:** Post-NLM, the spectra in the frequency-phase space for each voxel undergo an inverse phase shift to remove the dephasing effect. The rephased spectra are averaged over all  $\Theta$  to generate a single complex denoised spectra. The SNR is then calculated by dividing the maximum value of the metabolite peak with the standard deviation of the spectral region having pure noise.

**Data acquisition:** We acquired 2D-brain MRSI data of a healthy human volunteer on a GE 3T scanner using a PRESS sequence with TE/TR = 35/2000 msec, spectral bandwidth = 1kHz. The data was zero-filled and reconstructed to generate a grid of 32x32 voxels and 256 spectral points. We acquired data with 6 (ground truth), 3 and 1 averages with a total scan duration of 33 minutes.

## Results and Discussion

The experimental results are summarized in the table below. The Full-Width Half Maximum (FWHM) of the water peak either remained the same or reduced post-NLM which indicated that the spatial resolution was preserved. The images for NAA are shown in Fig. 1. The corresponding SNR and FWHM are shown in Table 1.

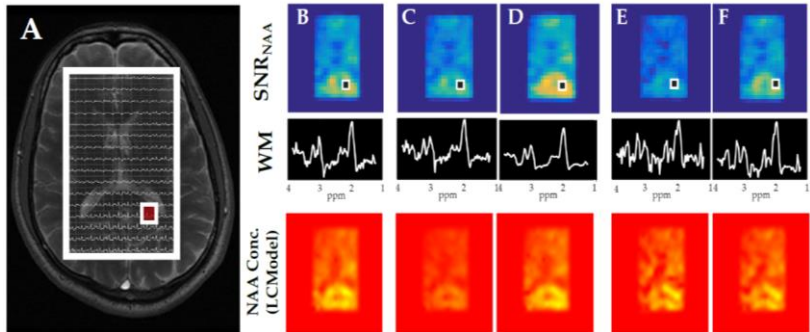


Table 1: SNR values (NAA) pre- and post-NLM with the corresponding FWHM values. \* indicates ground-truth data.

Averages	NAA		Water
	Mean SNR	Improvement	FWHM
1	5.7	N.A.	0.125
3	8.82	N.A.	0.135
6*	11.44	N.A.	0.135
1 (NLM)	<b>11.38</b>	1.98	<b>0.13</b>
3 (NLM)	<b>23.29</b>	2.63	<b>0.134</b>

Fig. 1: (A) Original human in-vivo brain MRSI data with the excitation region shown (white grid). (From Top) Row 1 & 2: SNR of NAA and the corresponding WM voxel spectra in: (B) 6-averages data, (C) 3-averages data (original) and (D) denoised, (E) single-scan data (original) and (F) denoised with corresponding spectra. Row 3: LCMModel based absolute concentration estimate of NAA in: 6-averages data, 3-averages data (original) and denoised, 1-average data (original) and denoised. The NAA concentration estimate and spectral SNR improve considerably as seen in columns D (SNR = 23.29) and F (SNR = 11.38) against the ground-truth (SNR = 11.44).

## Conclusion

Our proposed denoising method using a spatially adaptive NLM was evaluated on in-vivo MRSI data and showed a significant improvement in SNR. The 3-averages data had an SNR improvement by a factor of over 2 as compared to the ground-truth data. This would potentially accelerate acquisition by taking fewer scan averages. Future work would involve assessing our method for lower concentration metabolites such as Glu and improving computational efficiency.

## References

- [1] Buades et al., Computer Vision and Pattern 2005; 2(0):60-65.
- [2] Coupe et al., IEEE Trans Medical Imaging 2008; 27(4):425-441.