

## Title

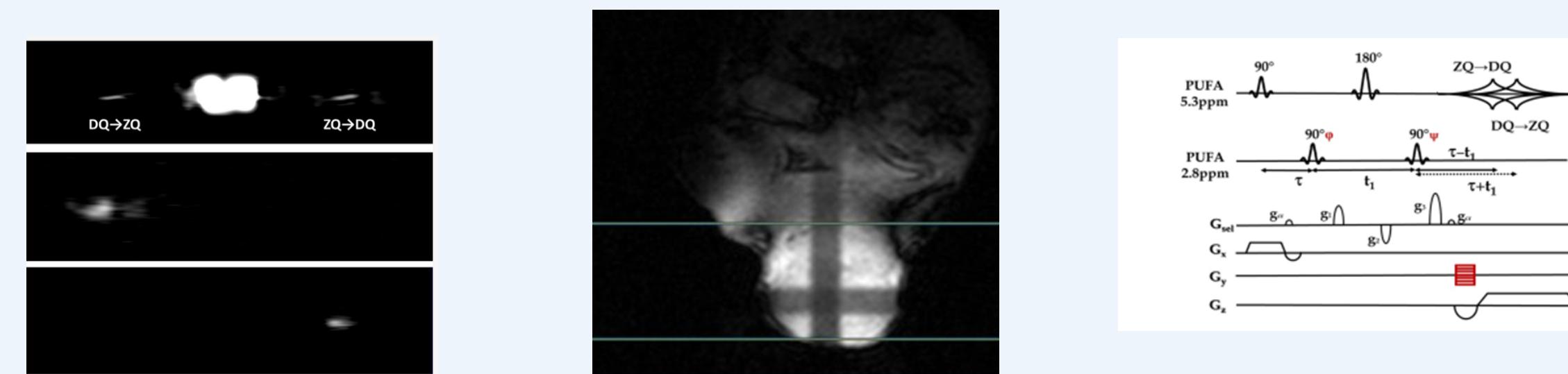
# Visualization and Algorithm for In Vivo pi-SSelMQC Signal Processing in Chemical Shift Imaging Experiments: Recovering Multi-Quantum Coherence Transfer Pathways

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## Introduction

We present a method to process one chemical shift imaging data by removing unwanted lipid and water noise and enhancing the desired signal from lactate as a tumor marker on both sides.

Murine 344SQ lung cancer mouse model; Tumor size:  $10.73 \times 10.72 \times 8.63 \text{ mm}^3$ ; 9.4T Bruker at UNC



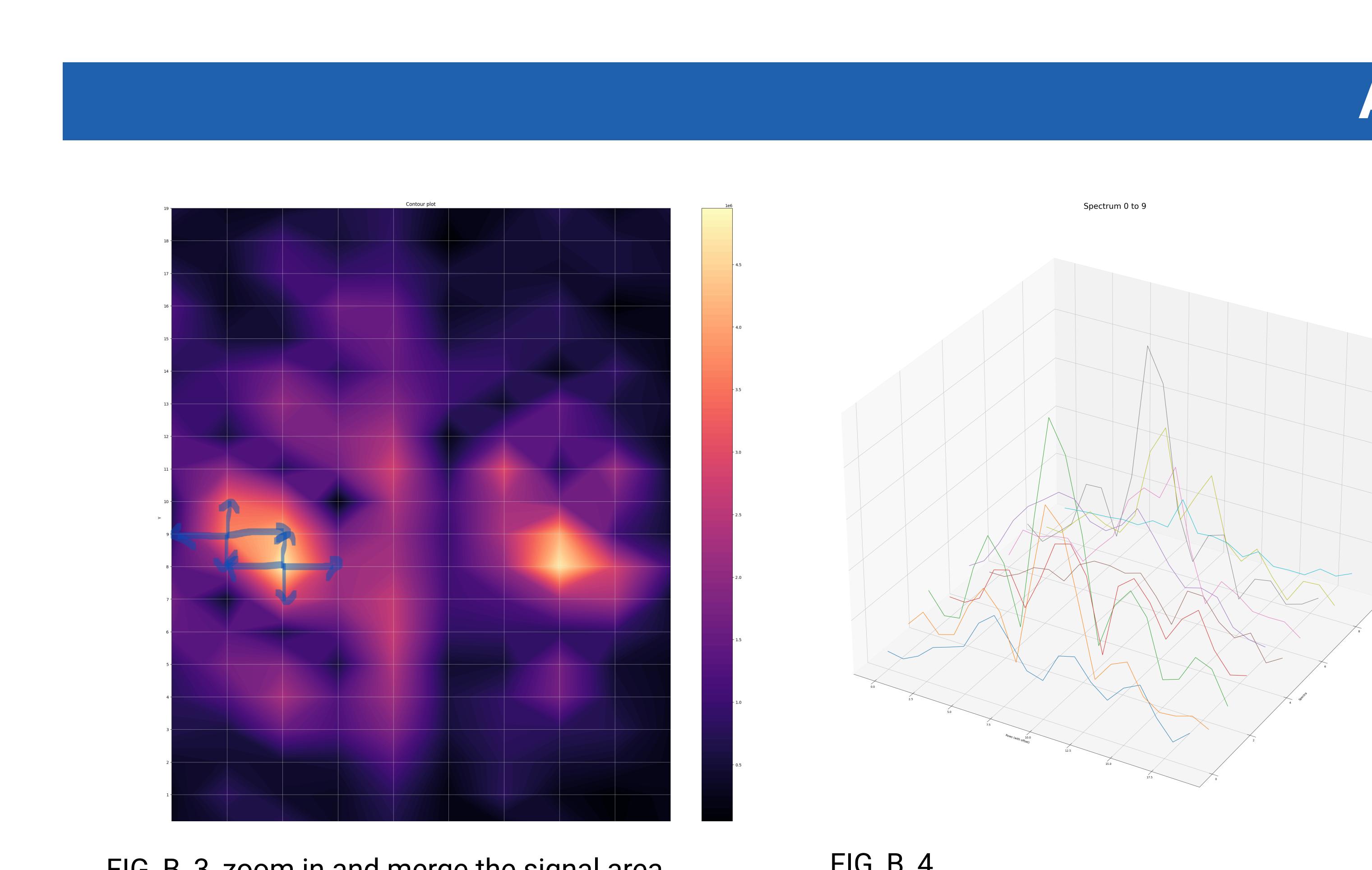
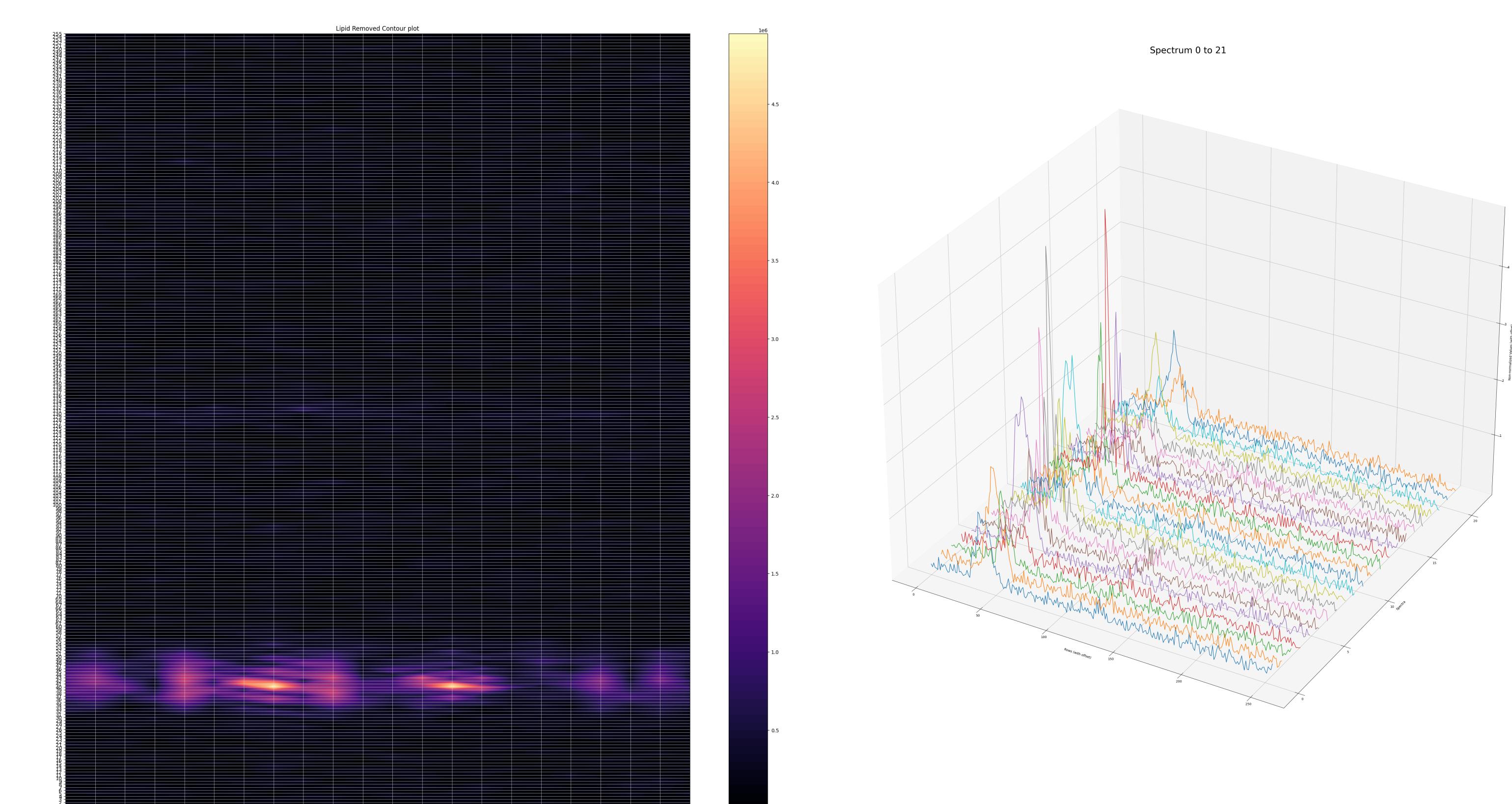
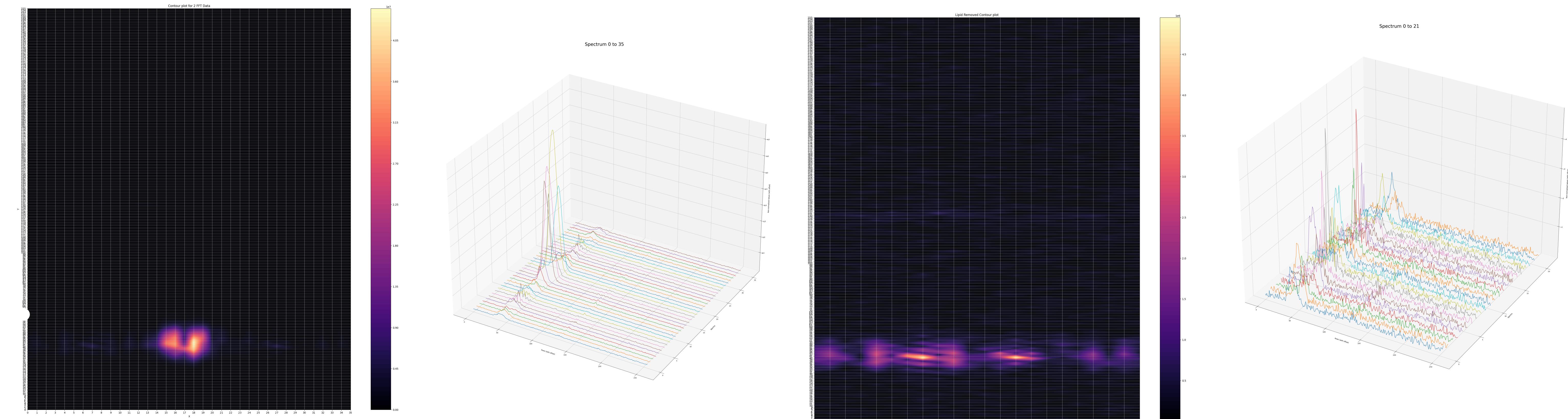
## METHODS

1. A  $256 \times 36$  matrix acquired by pulse sequence method, after 2 Fast Fourier Transforms, was visualized for different frequencies in a contour plot and a 3D line stacked plot FIG\_A.
2. The central lipid and water signals were removed (see Figure B).
3. An algorithm was applied to indicate if the sum of the neighborhood values was above the threshold. If it was, the algorithm scaled the value by 10, while keeping the other data unchanged.

References:  
QiuHong He, Hong Yuan, and Yen-Yu Ian Shih, "Double-echo phase-incrementing SSelMQC (pi-SSelMQC) in biomarker imaging with full signal recovery and excellent lipid and water suppression." Proc. Intl. Soc. Mag. Reson. Med. (2023)

Development of phase-incrementing Magnetic Resonance Spectroscopic Imaging (pi-MRSI) Methods (U.S. Patent 11,604,242 B2 issued on Mar. 14, 2023)

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## Algorithm

Our algorithm checked each point in the grid by adding its value to the value of each neighboring point. We iterated over the neighboring points one at a time, including the points above, below, to the left, and to the right.

If the sum of the current point and any one of these neighboring points was greater than the threshold we had set, the algorithm scaled the number at that spot by 10 times. Otherwise, if the sum was not greater than the threshold, the algorithm considered the spot as noise and kept the number unchanged.

The threshold was defined as 300,000 because the sum of the signal values had to be greater than the central and largest single value in column 2 and row 8, as observed in the contour plot.

$$N[i][j] = M[i][j] \text{ if } \text{any}(M[ni][nj] > T \text{ for } ni, nj \in [(i-1, j), (i+1, j), (i, j-1), (i, j+1)]) \\ \text{else } 0$$

