

Title

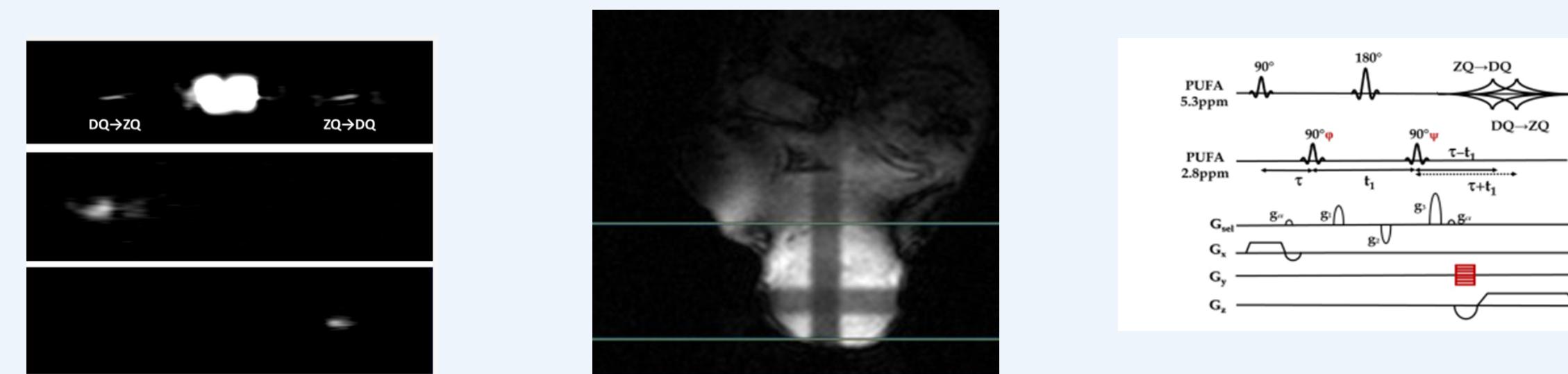
Visualization and Algorithm for In Vivo pi-SSelMQC Signal Processing in Chemical Shift Imaging Experiments: Recovering Multi-Quantum Coherence Transfer Pathways

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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



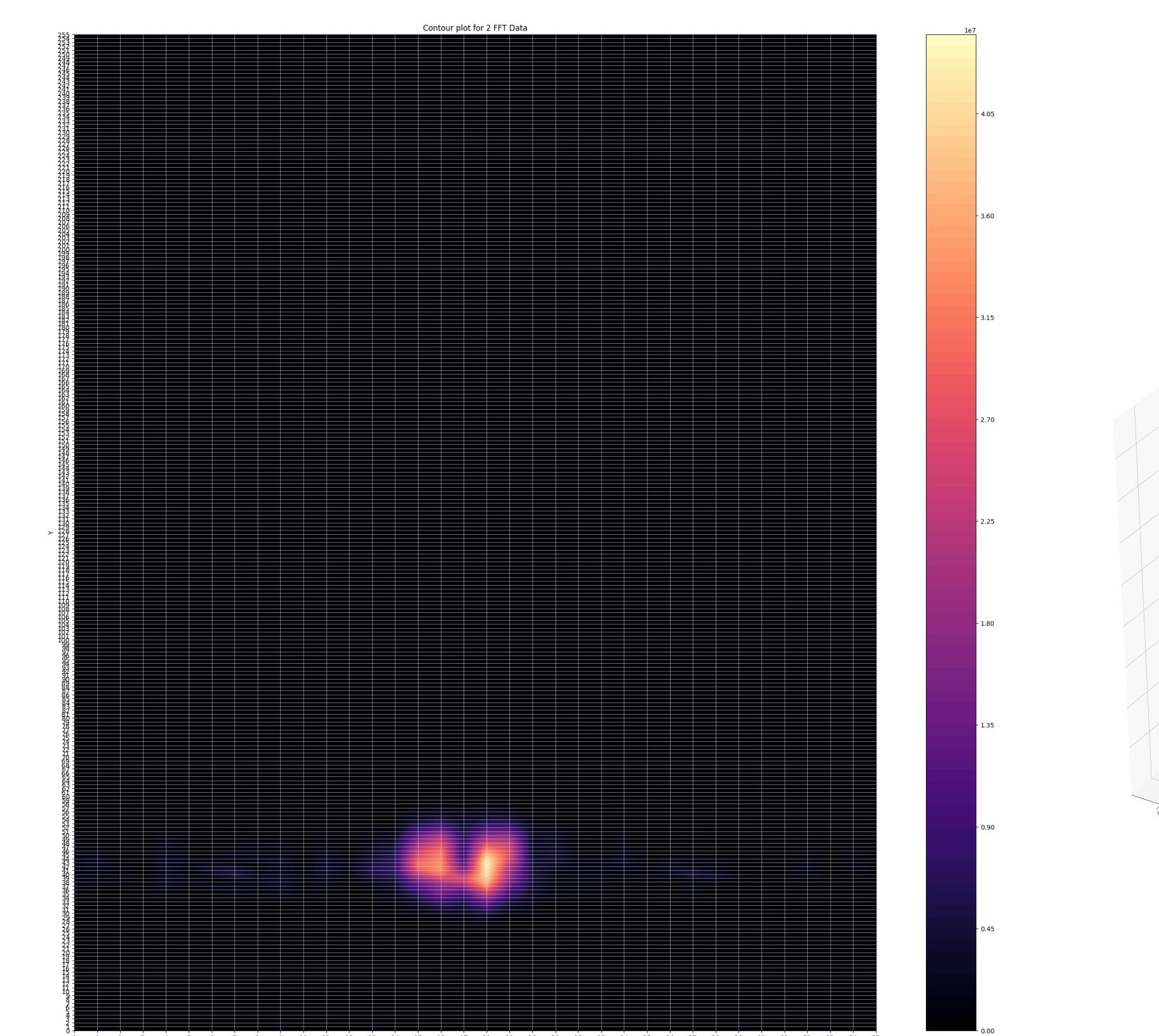
METHODS

1. A 256×36 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.

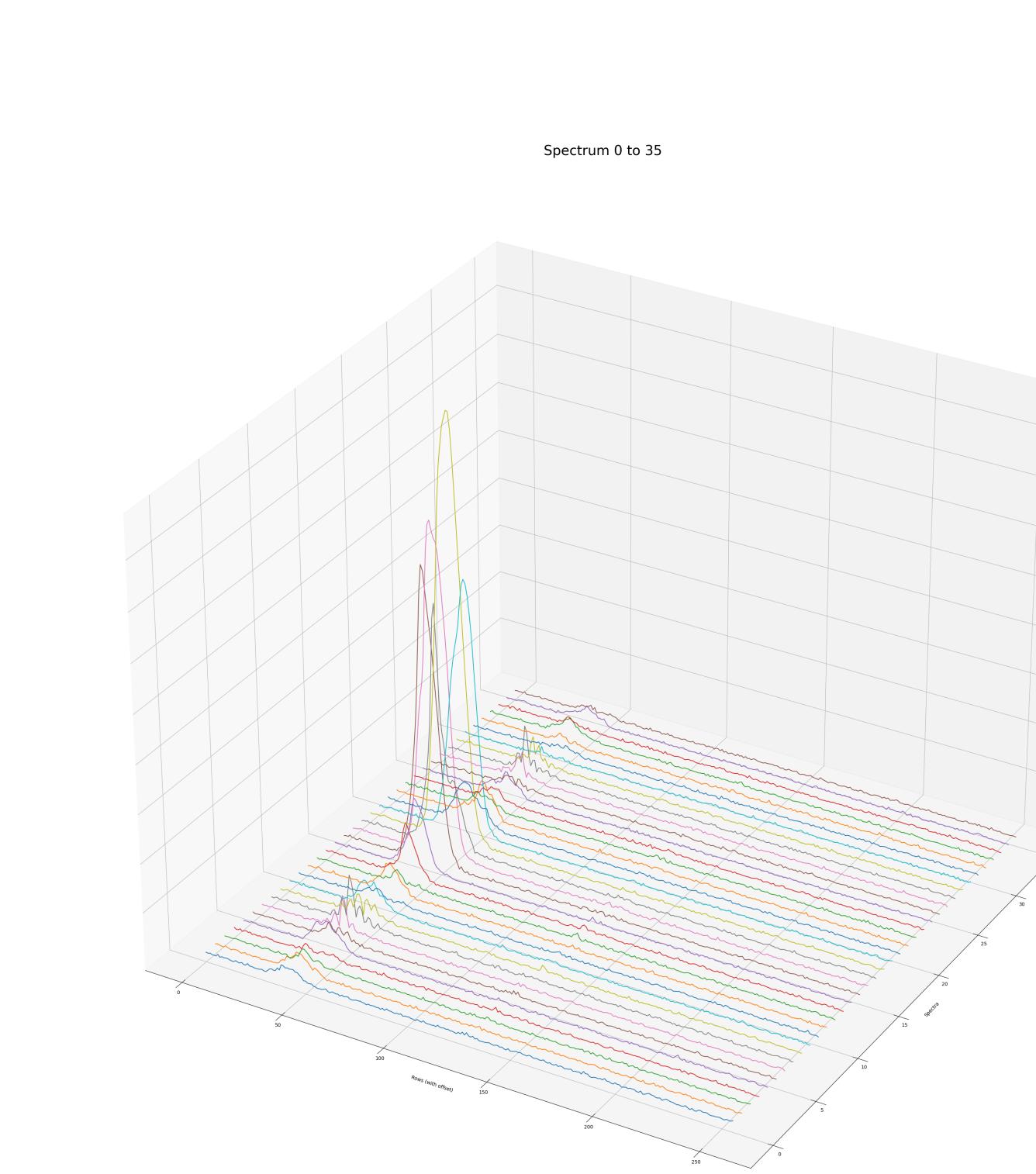
References:
QiuHong He, Hong Yuan, and Yen-Yu Ian Shih, "Double-echo phase-incrementing SSel-MQC (pi-SSelMQC) in biomarker imaging with full signal recovery and excellent lipid and water suppression." Proc. Intl. Soc. Mag. Reson. Med. (2023)

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

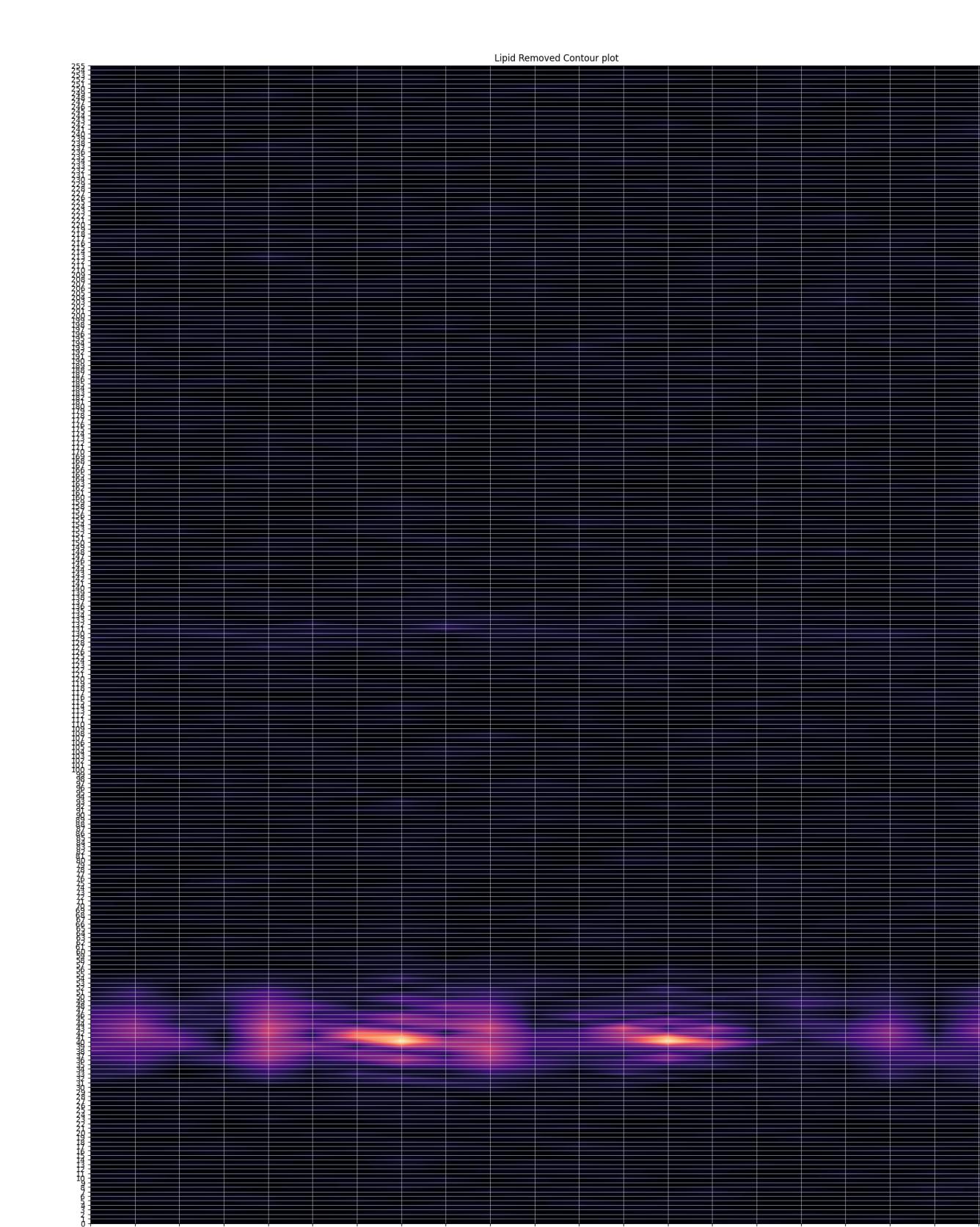
Acknowledgement:
We thank the funding support for the small animal MRI core at UNC (P30 CA016086), Bowles Center for Alcohol Studies (P60 AA011605), and Carolina Institute for Developmental Disabilities (U54 HD079124).



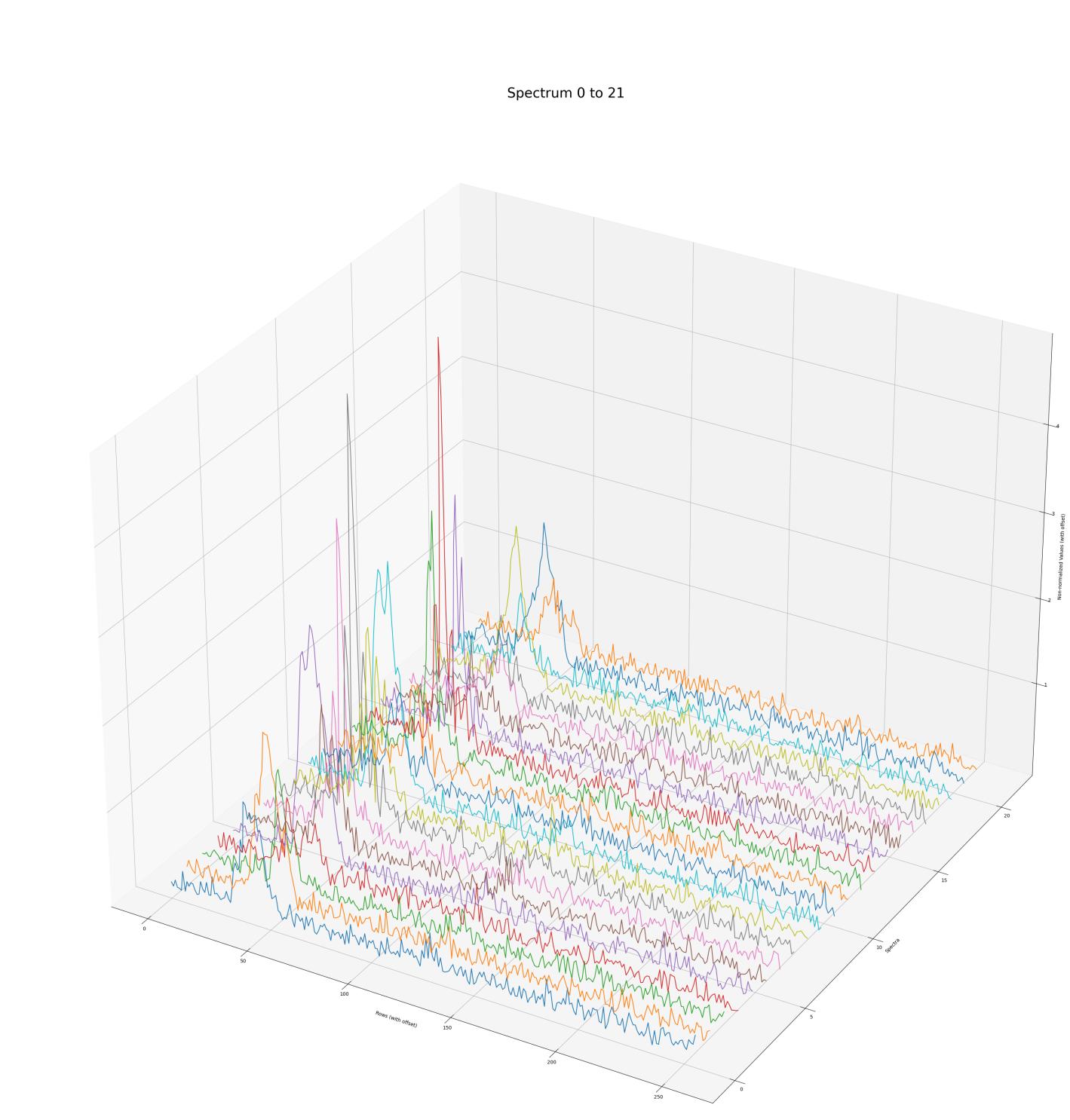
FIG_A.1: visualized original data with 2 Fast Fourier Transforms (FFT)



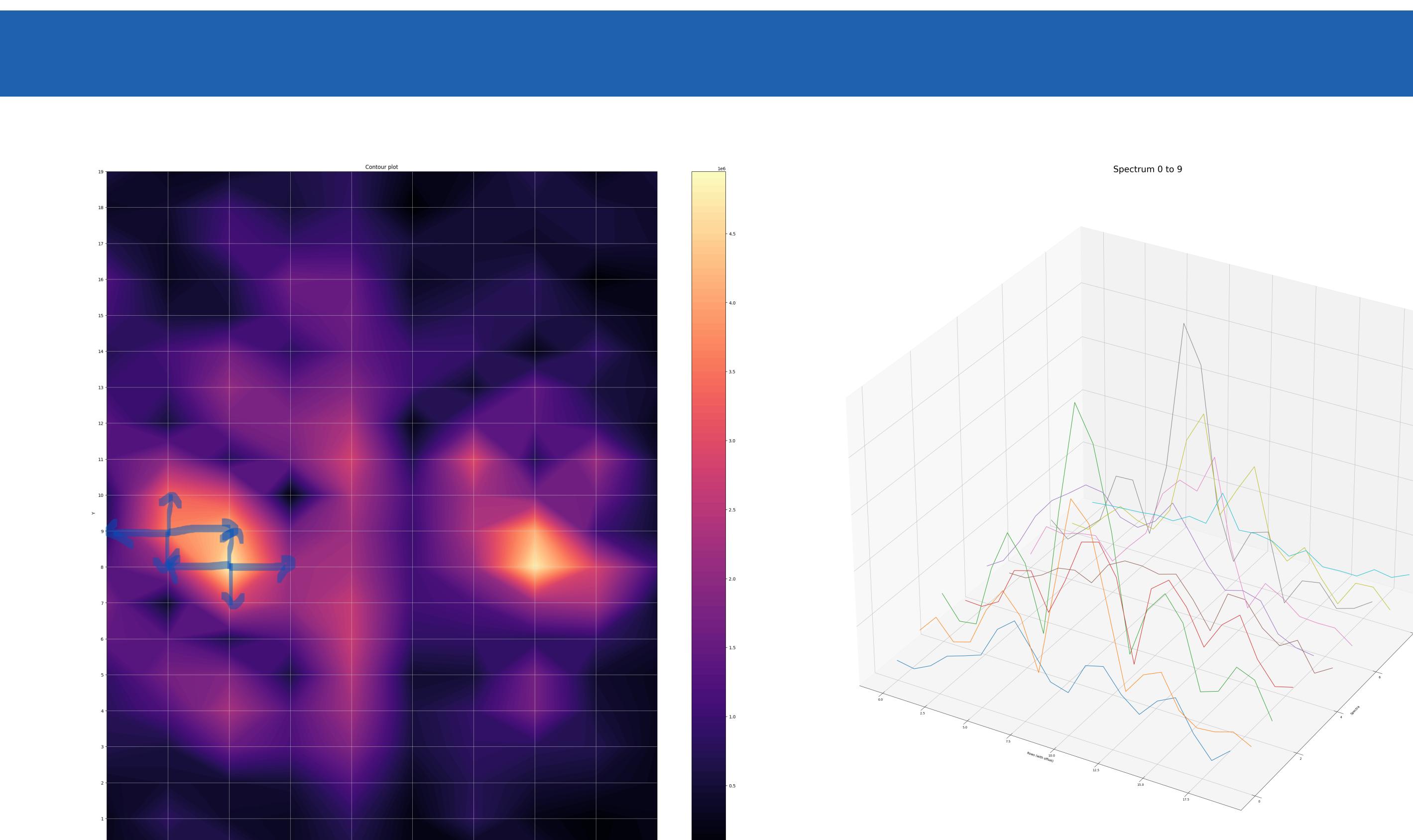
FIG_A.2: original data in 3D line stacked plot, with the intention of removing data in columns



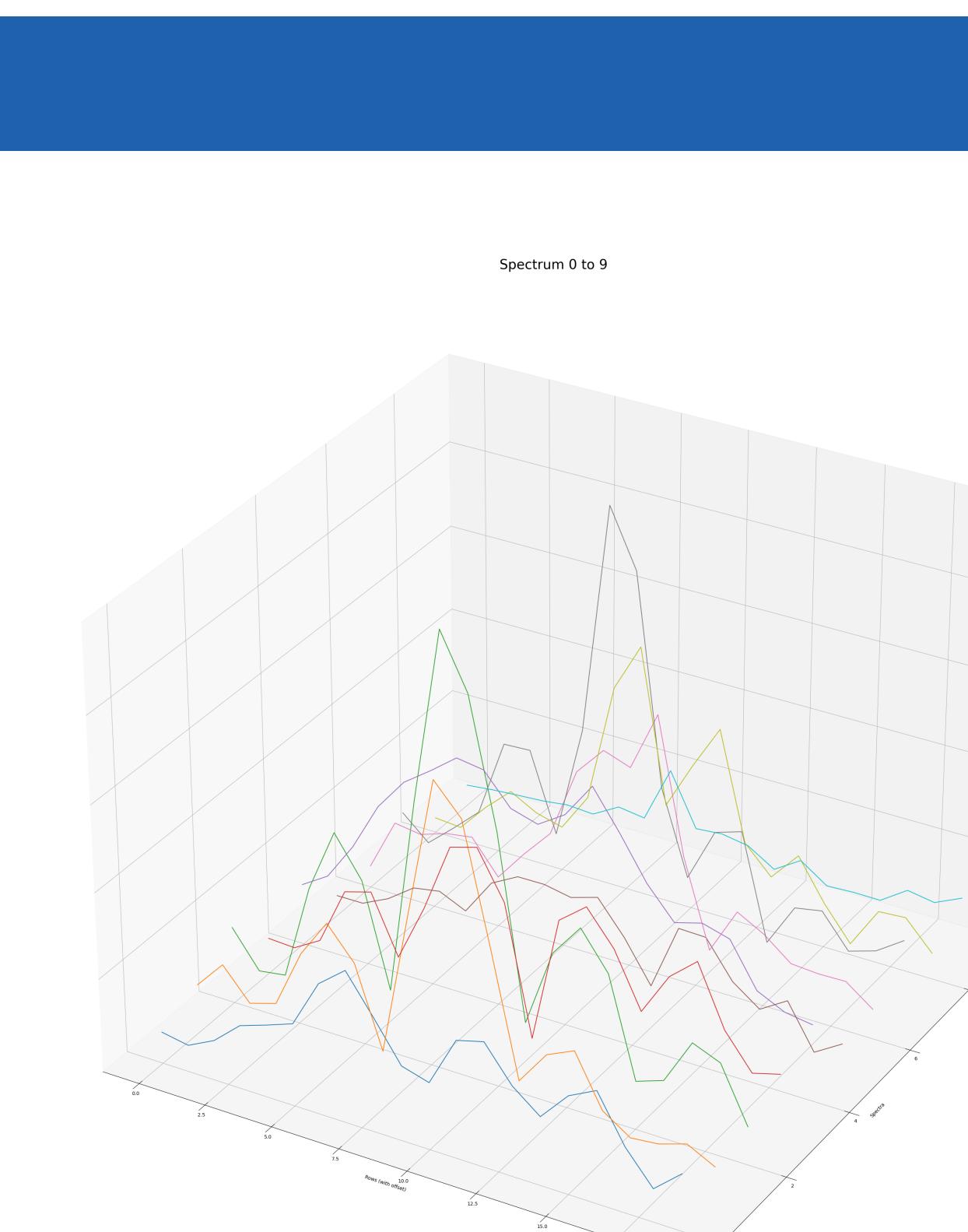
FIG_B_1, data after central lipid removed



FIG_B_2, data after central lipid removed



FIG_B_3, zoom in and merge the signal area



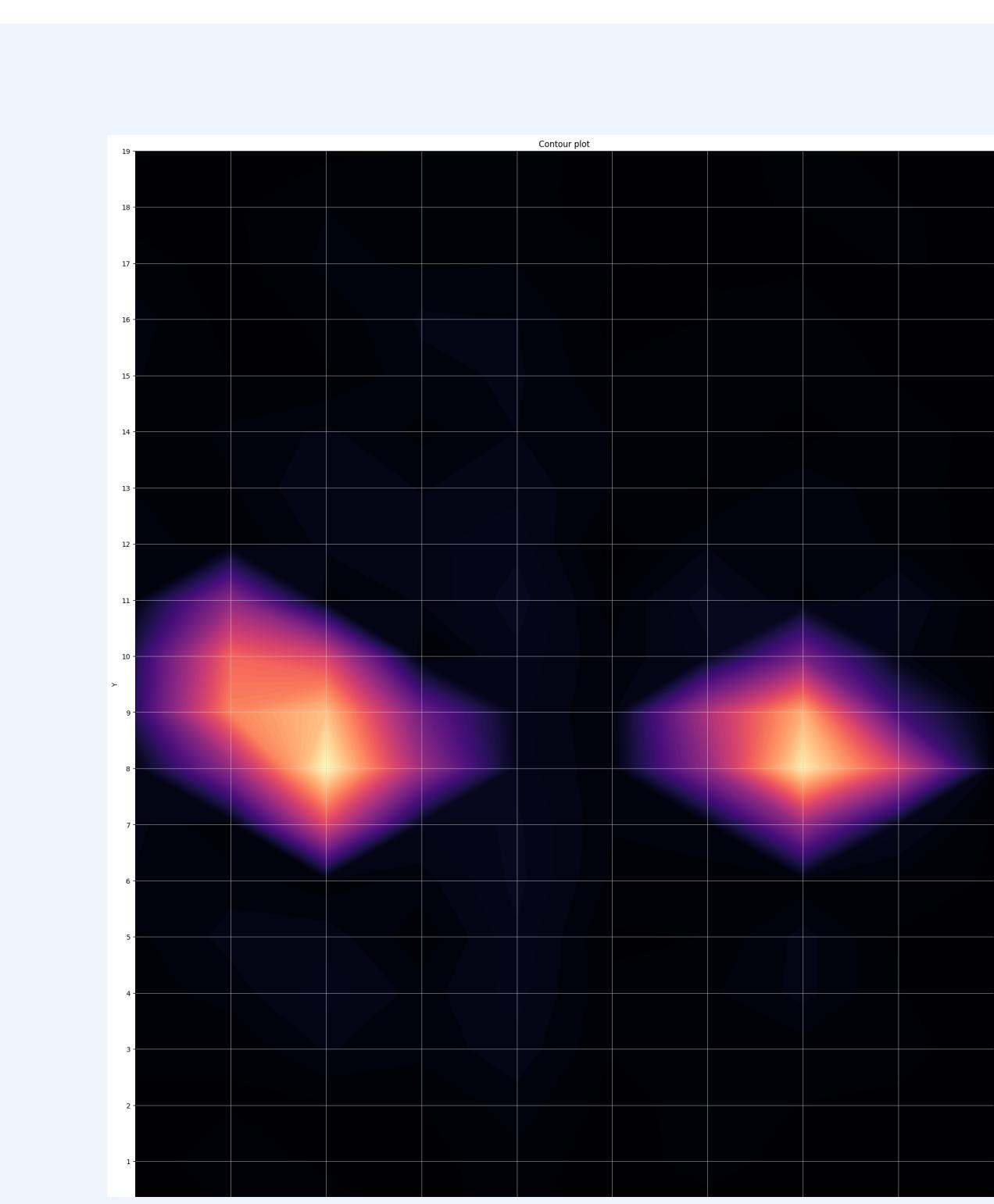
FIG_B_4

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.

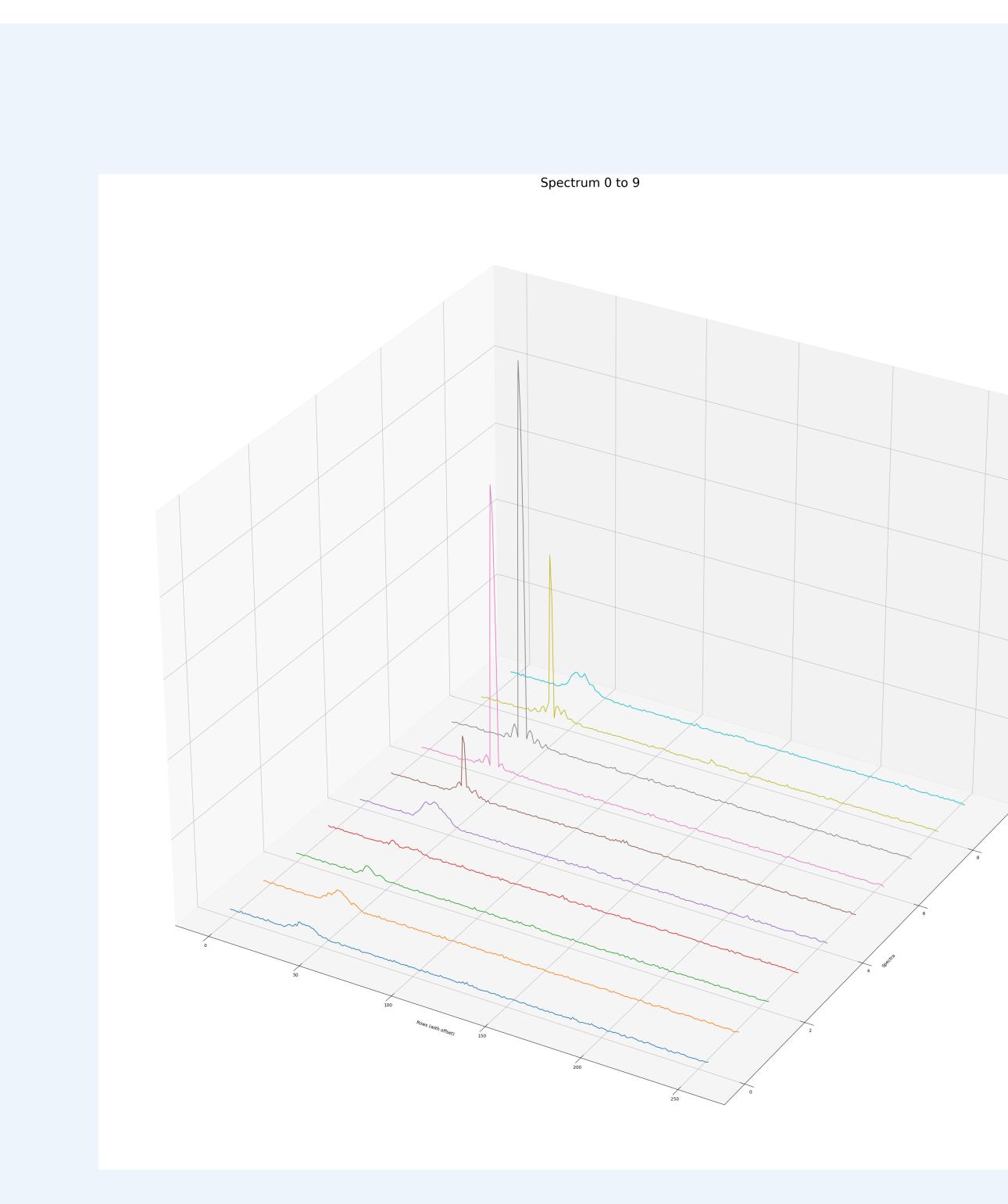
If the sum of the current point and any one of these neighboring points was greater than the threshold we had set, the algorithm scaled the number at that spot by 10 times. Otherwise, if the sum was not greater than the threshold, the algorithm considered the spot as noise and kept the number unchanged.

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.

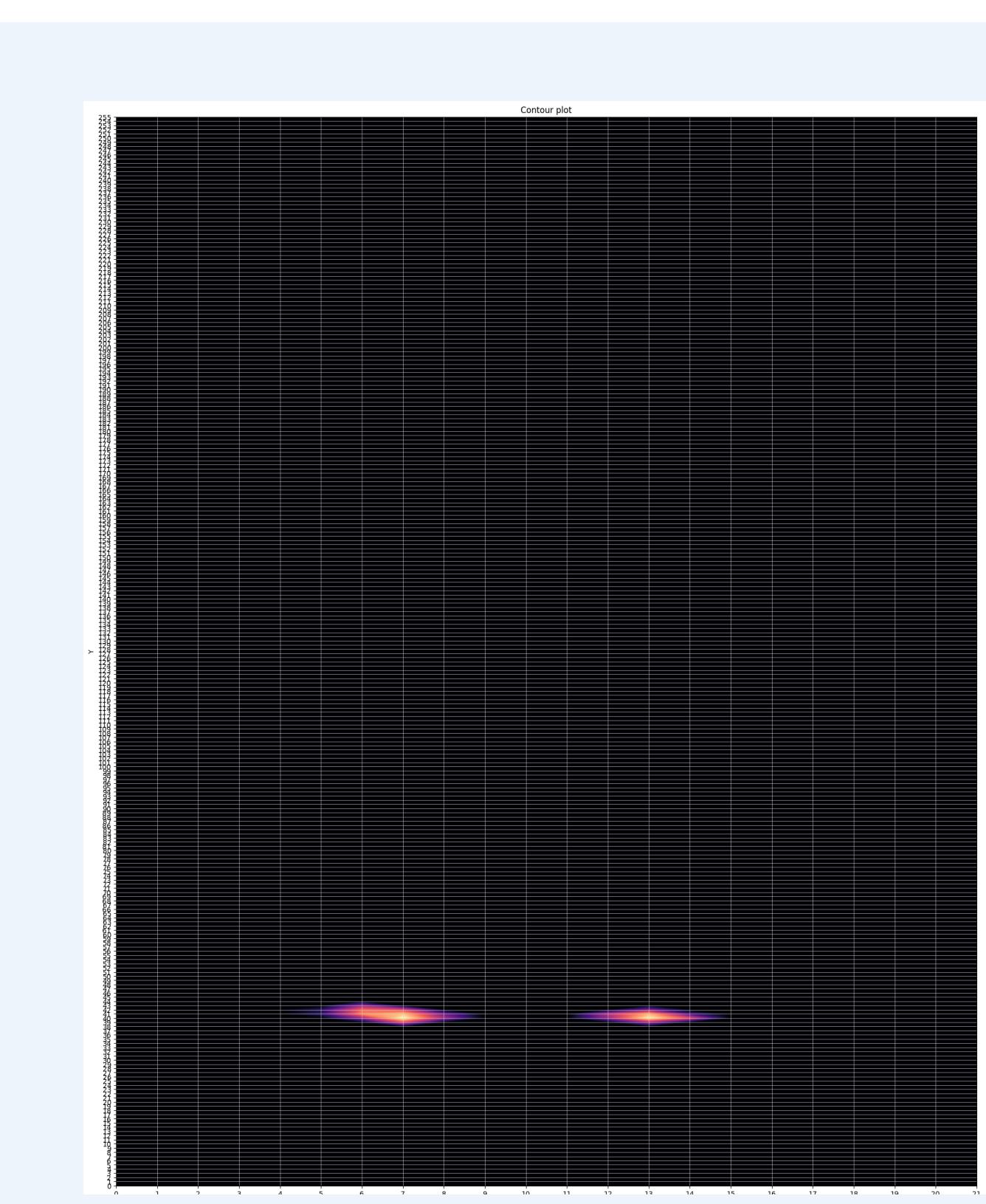
$$N[i][j] = M[i][j] \text{ if } \text{any}(M[ni][nj] > T \text{ for } ni, nj \in [(i-1, j), (i+1, j), (i, j-1), (i, j+1)]) \\ \text{else } 0$$



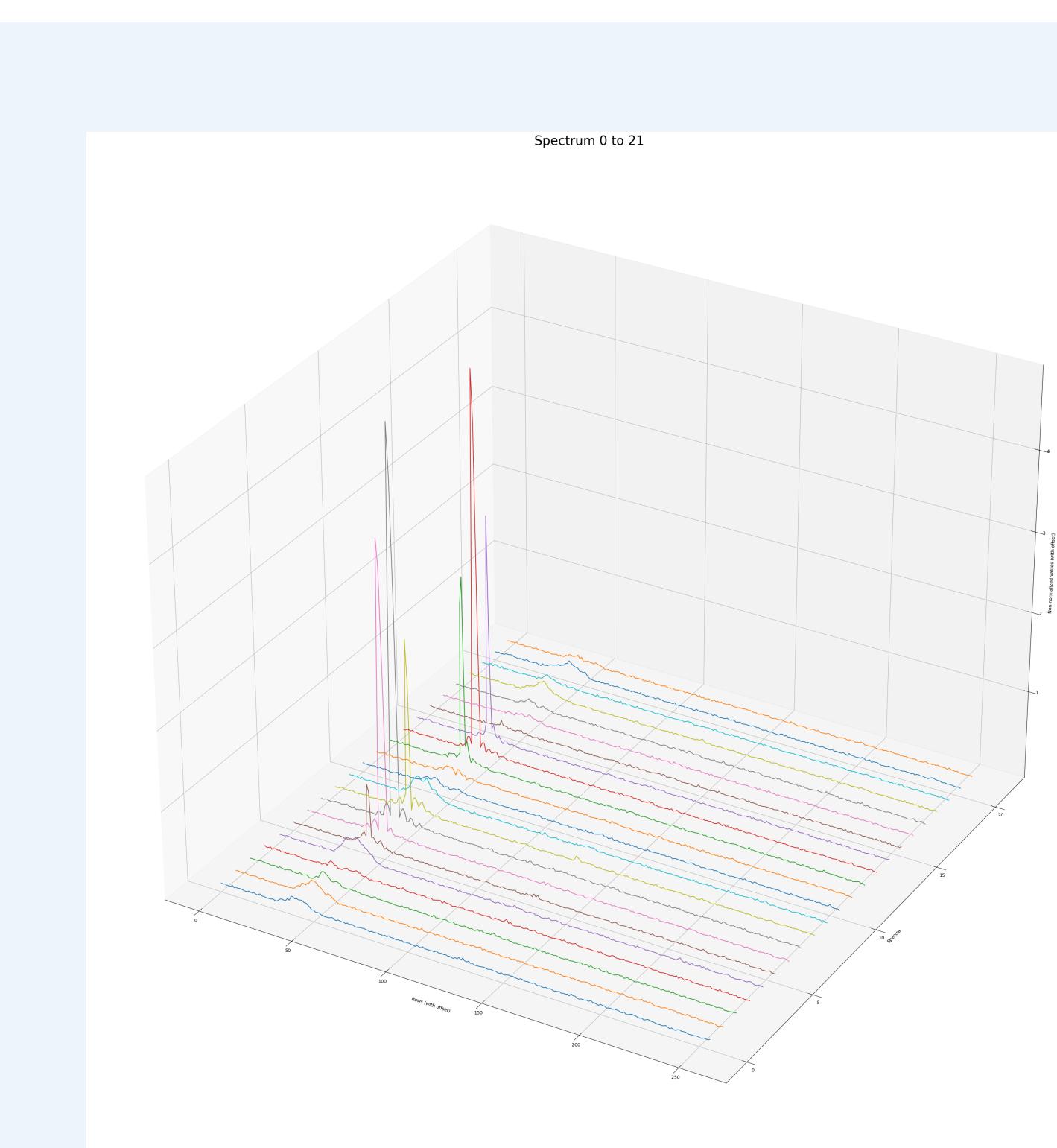
FIG_C_1: after algorithms applied based on the FIG_B_3, showing lactate



FIG_C_2



FIG_C_3: after algorithms applied based on the FIG_B_1.



FIG_C_4