**MRSI Spectral Analyses**

**Lab Assignment A:**

1. Generate a spectrum with peaks (i.e. add a peak to the starter file):
    a. at 3.2 ppm, amp=2, linewidth = 30
    b. at 3.0 ppm, amp=2, linewidth = 20
    c. at 2.0 ppm, amp=4, linewidth = 40

    (it is basically a normal brain tissue spectrum, but with linewidths varied)
    Plot the FID and real, imaginary, and magnitude spectrum from SW/2 to -SW/2. Assuming the water frequency is 0. Water peak is at 4.6ppm.

⇨ What is the sweepwidth of your spectrum? (see definitions in slides)

⇨ What is the effect of the different linewidths for the peaks at 3.0 and 3.2?

2. Explain what happens to your spectra in terms of both SNR (visually assess) and spectral resolution when applying the following filters:
    a) 5Hz decaying exponential filter
    b) 20Hz decaying exponential filter
    → Calculate the SNR of the 3 peaks after (b) applying the 20 Hz decaying exponential filter. Use SNR = peak height / (stdev of the noise).

3. Convert to ppm. Calculate and report the conversion from ppm to frequency of each peak.

➔ For the items above, show any code you modified and figures of FIDs and processed spectra.

**Lab Assignment B – SIVIC**

1. Start sivic
2. Open data:
    a. Click exam (open an exam) (image, spectra, metabolite file (can hit cancel for the metabolite file)
    b. → open 1_images/ _fla.idf and open 1_fids/spectra _fb_1.ddf for the raw FIDs of each channel.
    ⇨ Take a screen shot of the FIDs from channel 4 (coil = 4)
3. Under the “Preprocess tab”:
    a. Change the apodization to 0 Hz
    b. Use Zero Fill - none
    c. click “Apply”.
4. Under the “Recon Tab”:
    a. Click transform (spatial domain and spectral domain)
5. Under the “Phase Tab”:
    a. Select a voxel in the CSF
    b. Adjust frequency and amplitude controls to display the full water peak

c. Take a screen shot of your water peak.

6. Phase the water peak in all voxels in one channel. Take a screen shot.
   - ⇨ Does your water peak exhibit any ringing, suggestive of a sinc artifact?
7. Open the spectra again – spectra → open data file – t521_fb_1.ddf
   a. In the "4D Data" Tab, select the last (most recent) one as "Active"
   b. To see the FID, make this FID the only visible one.
   c. In "Preproc" → Apply a 5 Gauss apodization → Recon → Phase
   d. Make all spectral files visible. Display the water peak. Take a screen shot.
8. Open the spectra again and repeat w/ a 15 Gauss apodization.
   a. Make all spectral files visible. Display the water peak. Take a screen shot.
   - ⇨ Compare the effect on the spectra of the no apodization, 5 and 15 Gauss apodizations.
   - ⇨ Change the x-axis to ppm, to frequency, and to points.
   - ⇨ Record your x-axis range and your y-axis range
9. Close your spectra
10. Open the spectra again and repeat with:
    a. In "Preprocess":
       i. Apply a 15 Gauss apodization and
       ii. Zerofill the spec to "next $y^2$ ". (really means next $2^n$)
    b. Display the water peak, using the same x-axis and y-axis ranges. Take a screen shot.
    c. Change the x-axis to ppm, to frequency, and to points.
    - ⇨ Compare the effect on the spectra of the zerofilling. (Note, you can't overlay these two spectral files).
11. Close all spectra and open image and spectra from 1_combined dataset) (_phased_sum_cp.ddf)
12. Open corrected spectra on top "open spectra -> load spectra" (_sum_cp_cor.ddf)
    a. Change (if needed) your frequency and amplitude to center on metabolites choline, creatine, NAA.
    b. Display the Selected Box, Sat bands, Sat outline, and Grid.
    c. Take a screen shot of the Image and of the 2 overlaid spectra.
    - ⇨ What is the difference between the 2 spectra datasets?
13. Make the _sum_cp_cor the only visible and active dataset.
14. Go to the "Quant" Tab:
    a. Generate metabolite maps from MRS quant tab.
    b. Display overlay of peak heights on the image
    c. Unselect overlay text on the spectra
15. Select a slice that includes tumor and normal brain
    a. Adjust the display for both image and spectra – zoom, window/level image, adjust spectral amplitude, etc.
    b. Take a screenshot of the image + the spectra that includes voxels of tumor and normal brain
    - ⇨ What do you see? (hint: Does the metabolic abnormality follow the anatomic abnormal region?)