Magnetic Resonance Spectroscopy: The Basics

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Highlights:

- Magnetic resonance spectroscopy provides a 'virtual biopsy' of chemicals throughout the body.
- Choice of nuclei, field strength, pulse sequence, pulse sequence parameters, and localization will change which chemicals can be detected
- Optimization of shimming, suppression, voxel location, and post-processing will provide high quality spectra free of artifacts necessary for accurate spectral interpretation and diagnosis.

Target audience: Clinicians, technologists, and scientists who want to learn more about the basic physics and methods utilized for *in vivo* magnetic resonance spectroscopy (MRS) for research and clinical use.

Objectives: By gaining an understanding the fundamental principles of MRS data acquisition and post-processing, attendees will recognize how different parameters can change the spectrum. This will allow them to select the optimal methods to obtain the best results and prevent mistakes that could lead to the wrong conclusion or misdiagnosis.

Purpose: MRS is a non-invasive, objective, and quantitative method of measuring the concentration of chemicals, or metabolites, in the tissues of the brain and body, providing a "virtual biopsy". These measures can then be used in research to elucidate underlying mechanisms of disease or in the clinic for diagnosis or treatment monitoring.

Methods: Several factors dictate which chemicals can be measured: Unlike MRI, which primarily measures proton water signal, MRS has a choice of nuclei (proton, phosphorus, carbon, sodium or fluorine) which yields different metabolites. Field strength not only provides greater signal to noise ratio which can help detect metabolites of low concentration but also increases spectral dispersion which also can allow for detection of additional chemicals. Different pulse sequences can also provide SNR gains and spectral specificity but an also add other dimensions both spectrally and spatially. Changes to parameters in these sequences can alter which molecules are detected such as echo time which is influenced by the T2 relaxation rate of the molecule. Spectral editing methods such as JPRESS and MEGAPRESS can utilize j-coupling properties of molecules to provide further spectral specificity. Using these same principles, correlated spectroscopy adds a second spectral dimension for disambiguation of metabolites. Localization using single voxel methods (STEAM, PRESS) and chemical shift imaging provides concentrations of chemicals in specific regions of the brain or body which will differ depending upon where the data is acquired.

Results: In its most basic form, data analysis of spectra is done by applying a Fourier transform across the free induction decay acquired on the MRI scanner. Peaks of each metabolite are identified by their chemical shift and the height or area of the peak is measured. These measurements are then normalized to a constant measure such as water or creatine although with the major assumption that concentrations of these factors do not change with disease. Basic post-processing packages allow for the reconstruction of the spectra on the scanner itself and can be output for clinical diagnosis. For research studies, the raw data is often extracted for more sophisticated off-line post-processing.

Discussion: In addition to data acquisition and post-processing methods, there are additional considerations during the exam to ensure optimal data collection and interpretation. For example, shimming to improve magnetic field homogeneity can have a major impact on spectral quality and quantitation accuracy. As the utility of MRS is reliant on differentiating healthy tissue from disease, reproducibility is important to both research and clinical applications of MRS.

Conclusion: The data acquisition, post-processing, and quality assurance methods described in this talk will provide the basis for the important scientific and clinical applications to be described in the following presentations in this session.