

Lab 1: Intro to NMR

March 10, 2014

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1 Preliminaries

- Never bring anything metal into the room with an MRI (i.e. keys, metallic jewelry, chairs)
- Do not enter if you have a pacemaker or metal implant.
- You might also want to leave your wallet outside the room so that credit and access cards are not demagnetized.
- Do not unplug coils while system is running.
- The  icon indicates an action item.

2 Introduction

In this lab, we will acquire spectra using a high field (7T) animal scanner. This lab will cover basic NMR concepts such as acquiring free induction decays (FID), transmitter strength & flip angle calibration, B_0 strength and homogeneity, and basic NMR experiments such as pulse / acquire, spin echoes, and relaxation parameter measurements.

2.1 Hardware

The NMR system is a high field actively shielded 7.054T MRI and MRS animal scanner with a bore size of 16cm.



The gradient coil has a gradient strength of 29 G/cm and a slew rate of 116 G/cm/ms. In contrast, clinical systems have 5G/cm and 20G/cm/ms.

- What is the Larmor frequency of water on this scanner?

$f_0 =$

- How does this compare to a clinical human scanner?

➔ Turn on the gradients.

2.2 RF Coils

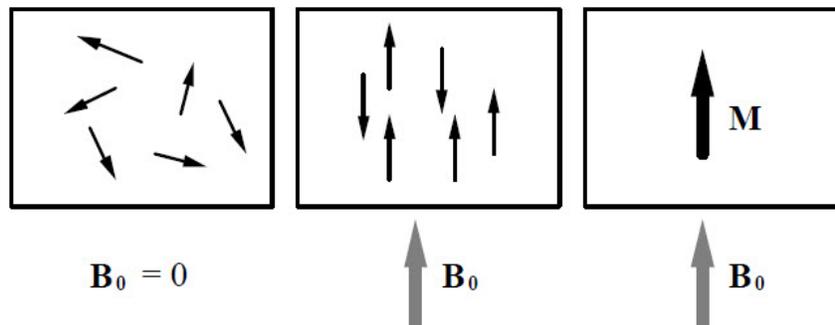
When we drive an RF field through the coil, we generate a field along x that also oscillates at the driving frequency. In this case, we have a quadrature coil, which means we have two coils which are orthogonal to one another. What is $B_1(t)$ in the laboratory frame? In the rotating frame?

Lab Frame: $\vec{B}_1 =$ Rotating Frame: $\vec{B}_1 =$

➔ Set up the transmit/receive RF coils.

2.3 Polarization

Write an equation that describes the total magnetization. (*Hint:* See figure below).



Total Magnetization =

The equilibrium magnetization induced by a field with strength B_0 is just the following:

$$M_o = \frac{N\mu(I_z + 1)B_0}{3kT} \quad (1)$$

Thus the magnetization is proportional to the applied B_0 . μ is the magnetic moment of a single nucleus ($\mu = \gamma\hbar I_z$) and N is the number of nuclear spins per unit volume.

A quantum mechanical description can be used to understand polarization. The potential energy E of a magnetic moment μ in the presence of a B field is

$$E = -\boldsymbol{\mu} \times \mathbf{B} = -\mu_z B_0 = -\gamma\hbar I_z B_0$$

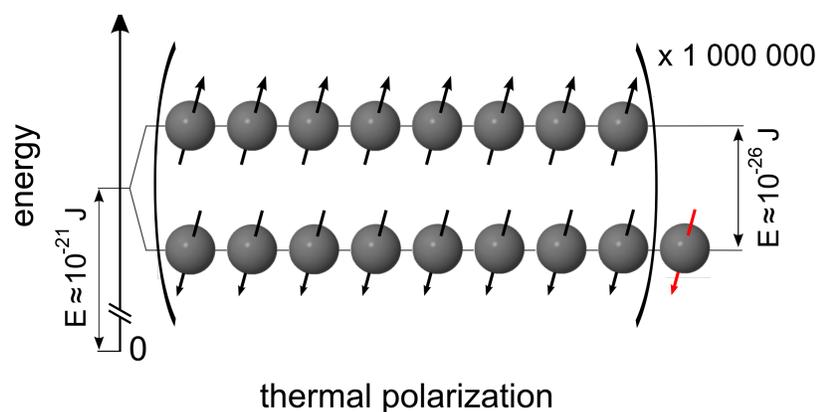
\hbar is Planck's constant over 2π ($\hbar = 6.62606957 \times 10^{-34}$ m² kg / s). For $S = 1/2$ particles, such as hydrogen (protons), the difference between the two energy states can be written as

$$\Delta E = \gamma\hbar B_0 = h\frac{\gamma}{2\pi} B_0$$

Our signal comes from the the difference between our two populations (red spin shown in the figure below), one parallel (n_+) and the other anti-parallel (n_-). The n_+ population is of lower energy and the tendency is to occupy the minimum energy state. Thermal energy is sufficient to exceed the energy separation such that they occupy both energy states. Where the ratio of the two populations is dependent on the Boltzmann distribution:

$$\frac{n_-}{n_+} = e^{-\Delta E/kT}$$

where k is the Boltzmann constant ($1.3806488 \times 10^{-23}$ m² kg s⁻² K⁻¹), and T is the temperature in Kelvin. Typically, this ratio is about 0.999993 per Telsa, implying an excess of only 7 out of 10^6 in the parallel state. Macroscopically however, this excess accounts for the polarization that we observe with NMR and MRI, albeit a weak one.



The polarization, P , just describes the fraction of the spins aligned with the B_0 vector. Here we have a main magnetic field strength of $B_0 \cong 7$ T. Approximately, what would the polarization of water protons be in a patient (*Hint: Body temperature is 37 °C*)?

$$P =$$

For comparison the Earth's field $B_e = 50\mu\text{T}$, and $P = 3.3 \times 10^{-10}$. A standard clinical scanner operating a 1.5 T will give $P = 9 \times 10^{-6}$, a big gain but it is still 6 orders of magnitude shy of 100% polarization. At $B_0 = 7$ T what fold change do we get in polarization over the earth's field for polarization? From 1.5 T to 7T?

$$\Delta M_{7TvsEarth} =$$

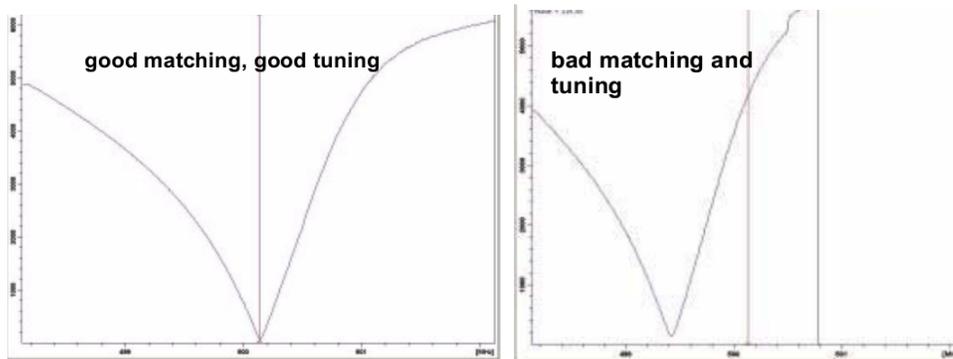
2.4 Coil Capacitance Calibration

We can use some linear circuit analysis to optimize the efficiency of the transmitter (B_1 coil). The coil is itself a resonant circuit, and can be loosely approximated as a series LRC circuit. L is the inductor, which is just the coil itself. The circuit has a resonance with some width (proportional to Q), and a resonant frequency centered at

$$\omega = \frac{1}{\sqrt{LC}}. \quad (2)$$

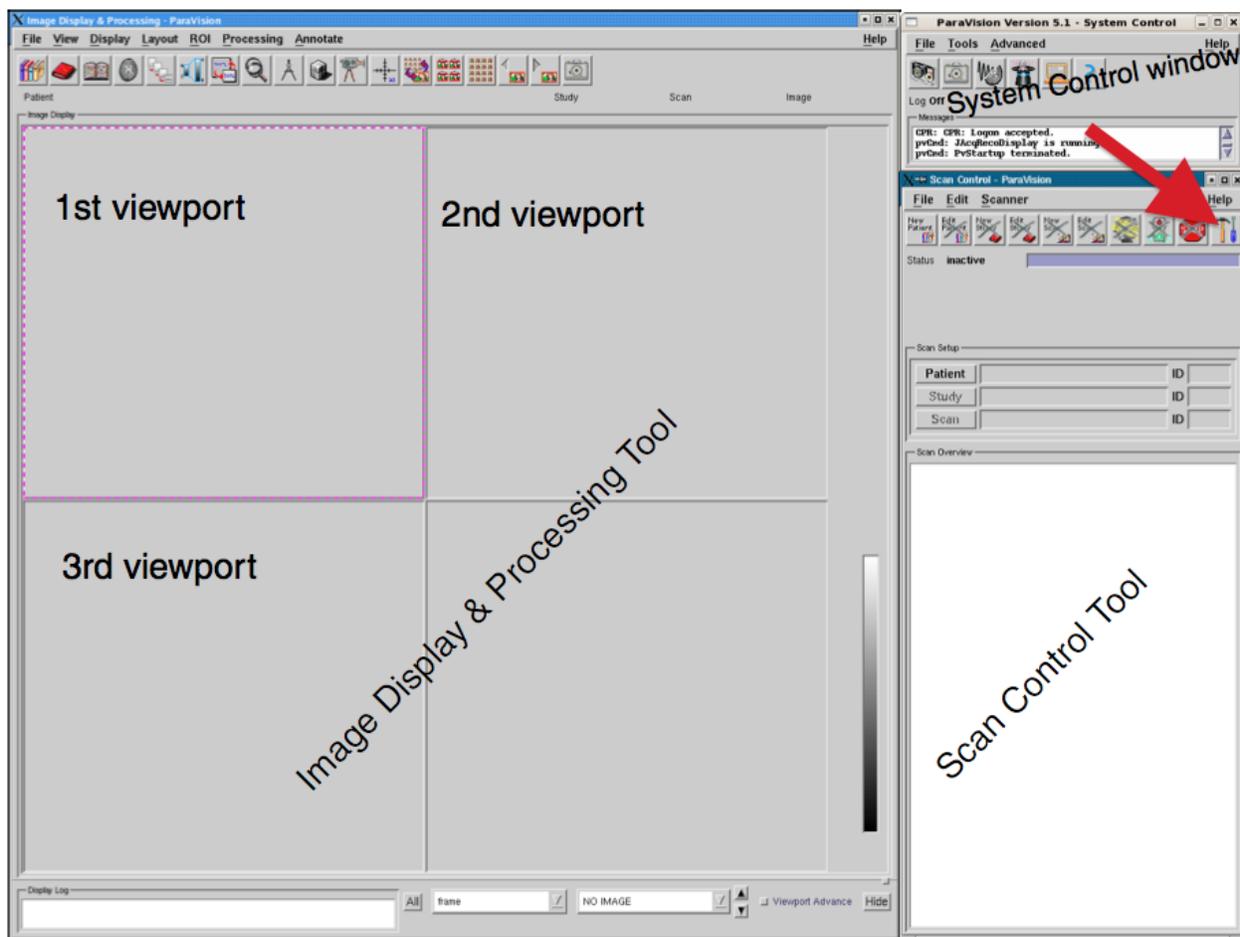
In order to maximize the efficiency of the transmitter, we will want to first measure the resonant frequency. The spectrometer automatically generates an ω versus C curve aka "Wobble Curve". We can manually adjust C_t to the Larmor resonance frequency this is called "Tuning". Tuning simply involves adjusting the probe so that the minimum of the wobble curve is at the base of the display (i.e. touching the horizontal frequency axis). This represents minimum reflection of the transmitted signal. We can also adjust C_m such that the resistance is 50Ω this is called "Matching".

These are tunable parameters on coil which are by necessity since the resonance frequency of the coil can vary significantly due to loading. Matching will generally alter the vertical position of the wobble curve minimum while tuning will alter the horizontal position. However the tune and match adjustments interact with each other and must be adjusted in tandem. When the wobble curve minimum is centered and at the base of the screen the probe has been optimally tuned and matched.



➔ Before we start calibrating the coils, we need to load our coils. Place the sample in the center of the coil (the center is the black line on the coil) and connect the coil to the measurement system via the adaptor/splitter to tune each part of the coil individually (quadrature coils).

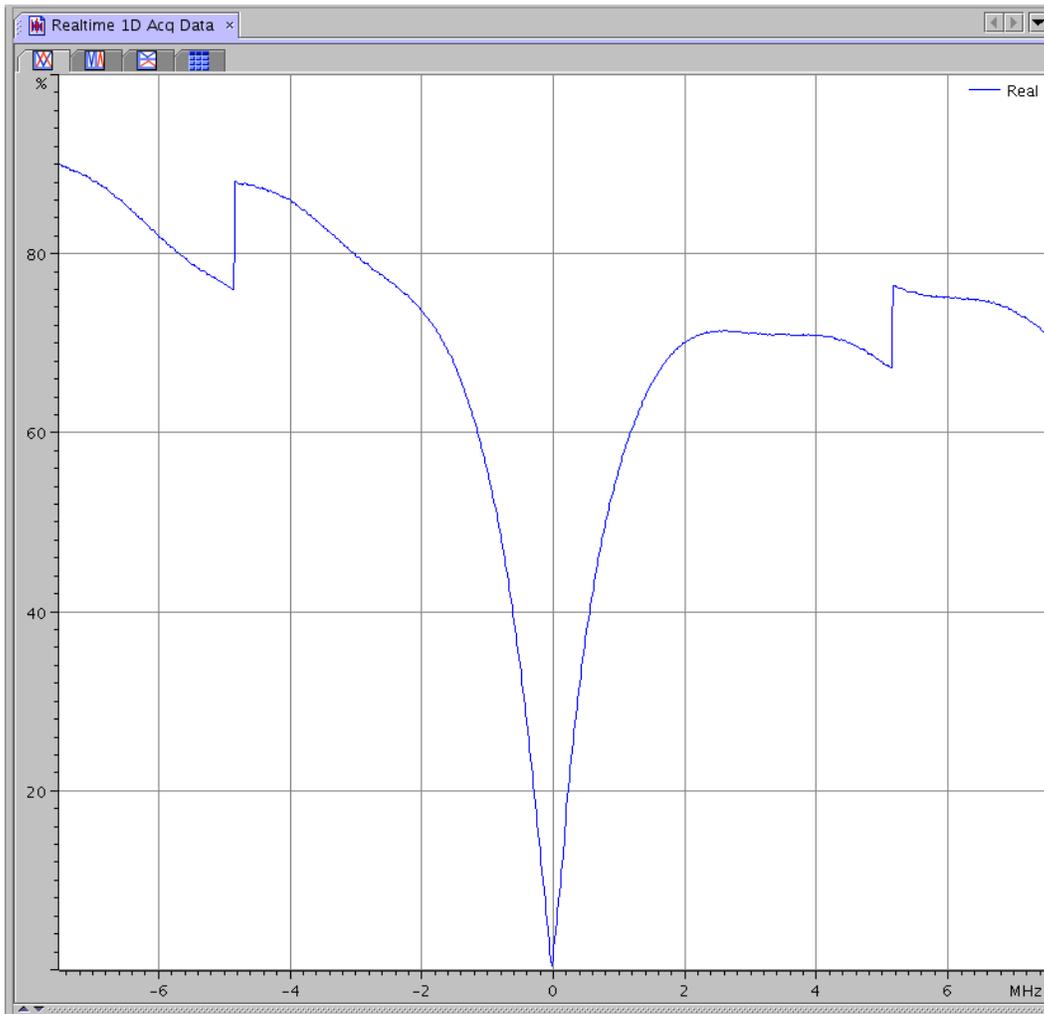
➔ Then open ParaVision. Select the **Toolbox** in the **Scan Control** window.



➔ Open the **Spectrometer Control Tool**, select **Acq** and then **Wobble**.

➔ Take turns tuning and matching and watching on the analyzer. When you are done your signal should like the following.

Do not unplug coil while running the wobble measurement. Click the stop  icon first and wait until it is done in the **System Control** window.



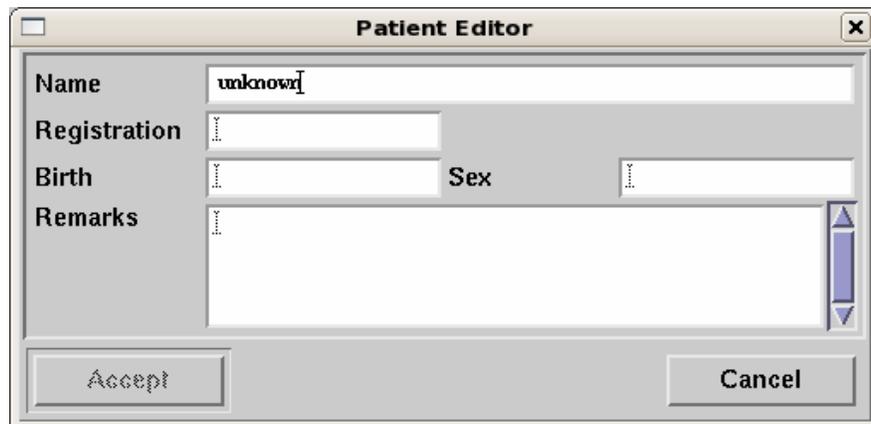
Properly tuned and matched coil on this system.

➔ Once we have the coils tuned and matched. Click the stop  icon and plug coils into the scanner.

2.5 Localizer

Before we can start experiments we need to acquire a localizer so that we know that our sequences are centered on the sample. To start an examination create a **New Patient** in the **Scan Control Tool**.

➔ Click on the **New Patient** button: . A **Patient Editor** window will appear. In the patient editor, specify at least the “Name” and “Registration” and then **Accept**



Patient Editor

Name: unknown

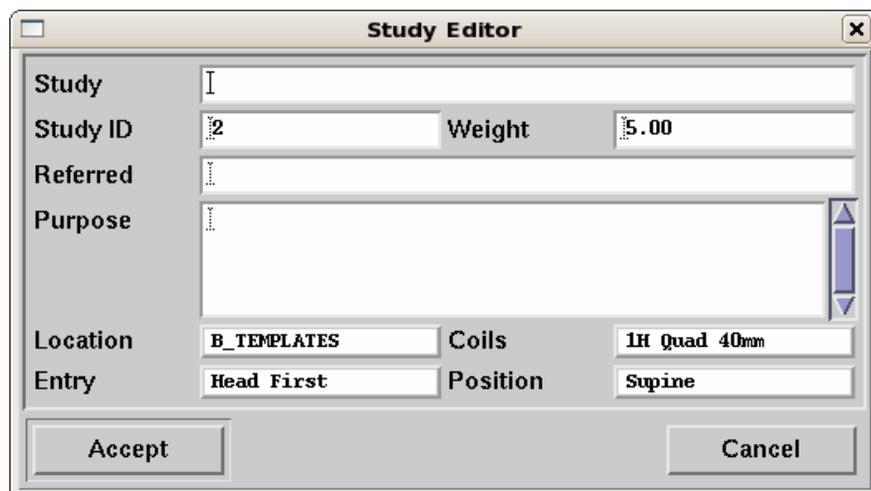
Registration: [Empty]

Birth: [Empty] Sex: [Empty]

Remarks: [Empty]

Accept Cancel

➔ The **Study Editor** will be automatically displayed. Provide a study name and ensure that Entry, Position and Coils are correct. Select the default location of measurement protocols **B_TEMPLATES**. Click **Accept**



Study Editor

Study: [Empty]

Study ID: 2 Weight: 5.00

Referred: [Empty]

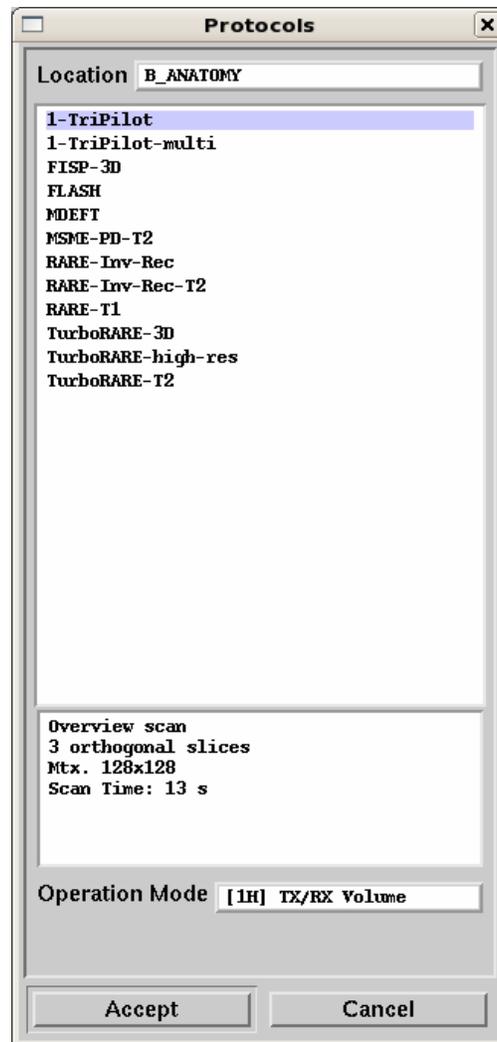
Purpose: [Empty]

Location: B_TEMPLATES Coils: 1H Quad 40mm

Entry: Head First Position: Supine

Accept Cancel

➔ The **Protocols** window will appear automatically. Choose the scan entitled **1_TriPilot** in the **B_Anatomy** menu which generates three orthogonal images. Click **Accept**. You can also choose **1_TriPilot-multi** collects data for multiple slices in coronal, axial, and sagittal orientations.



A Scan with the parameters from the selected protocol will now appear in the **Scan Overview List** in the **Scan Control** window. The Scan is ready to be acquired.

➔ Click the **Traffic Light** button  in the **Scan Control** window to start the image acquisition.

The system will now perform some automatic adjustment procedures which includes a center frequency adjustment, 90° pulse calibration, and shimming. We will do each of these manually in the following experiments.

➔ But for now watch in the **Acq/Reco Display** window.

To view the images of the completed Scan, drag-and-drop the dataset from the **Scan Overview** (by pressing Shift + middle mouse button) into the upper left viewport of the **Image Display & Processing Tool**. The acquired images will give you the three main slice orientations (axial, sagittal, coronal) and the next scan can be positioned correctly via

the **Geometry Editor** using the TriPilot images as reference.

Why does the phantom look like a cigar?

...

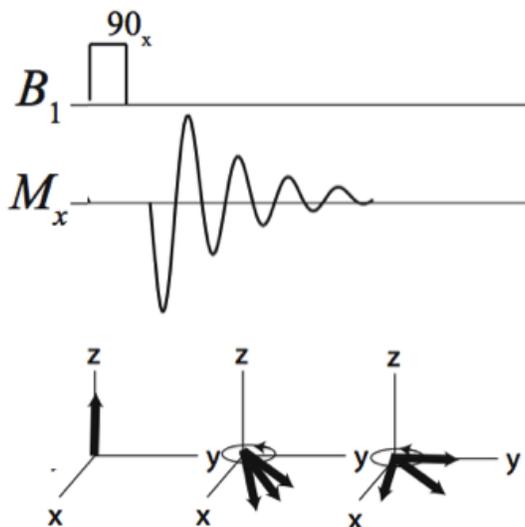
Why are there crosses?

...

3 Experiments

3.1 Pulse / Acquire FID

The most basic NMR experiment is the pulse / acquire, or pulse collect experiment consisting of an RF excitation followed by a data acquisition period.



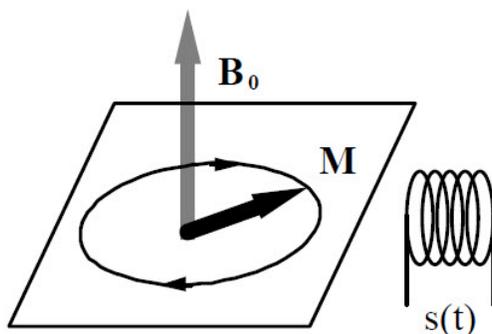
First, we will do a simple pulse acquire experiment.

➡ Click the **New Scan** button in the **Scan Control** window. The **Protocols** window will appear automatically. Select the scan entitled **A_ADJ_SF** in the **B_ADJUSTMENTS** menu.

➡ Click tools icon. Click GSP button  and watch in the **Acq/Reco Display** window.

➔ Observe the spectra and FID. When you are done click the stop button . Go to **Spectrometer Control Tool** to observe the pulse sequence. Click **Tools** then **pulse programming tools**. Once inside the pulse programming tool unselect **Expression**, **Name**, **Loops**, **Sys** and **Grid**. Click the <- -> button twice to scale the sequence.

We played the excitation which is followed by a data acquisition period. An oscillating magnetic field, $B_1(t)$ at the Larmor resonant frequency is applied to the aligned nuclei by the transmitting Radio Frequency (RF) coils. Because the magnetic field frequency matches the nuclei's resonant frequency, the nuclei absorb the energy, their magnetic moment changes direction, they are excited and they change their net magnetization. Once this RF pulse has been applied, the nuclei begin precession.



In this excitation process, the magnetic moment of the nuclei is tipped away from the direction of the static field, into the plane perpendicular to the main magnetic field, thus causing precession around the axis of the external main field. The duration of the RF pulse at the Larmor frequency affects the angle between the axis of the static field and the net magnetization direction of the spins. This is the angle through which the nuclei precesses. These excited nuclei, now in a high energy state due to absorption of energy from the RF coils, eventually return to their lower energy level state in which they are aligned perfectly parallel with the main magnetic field. As the magnetic moments return to their equilibrium position, energy is emitted at the Larmor frequency of the specific nuclear species being used. As the precession of the nuclei decays within the static magnetic field, this released energy results in a voltage induced in nearby receiving RF coils, thus allowing the information to be recorded.

The magnetization response after during readout is easily described by a Larmor frequency oscillation term and a decay envelope. The decay term is a combination of the “native” decay constant T_2 and another term which depends on the homogeneity of the sample. This term is called T_2^* , and is defined as

$$1/T_2^* = 1/T_2 + 1/T_2', \quad (3)$$

where $T_2' \propto \Delta B_0$ is proportional to the spread (inhomogeneity) of the field strength ΔB_0 . Expression 3 is almost always dominated by the second term, so we can almost always ignore

the T_2 contribution to the decay envelope of pulse / acquire experiments.

The signal recorded immediately following an RF excitation is

$$S(t) = e^{-i2\pi f_0 t} e^{-t/T_2^*}, \quad (4)$$

where we've defined $f_0 = \gamma B_0 / 2\pi$ as the Larmor frequency.

What factors affect T2? T2*?

T2:

T2*:

3.2 Adjust Center Frequency

 Clone the sequence. Make sure you have the right flip angle by righting click on the sequence. Choose **Edit Scan**. In the **Standard** Menu, the flip angle should be 90°).

 Click **Tools** button. Then **GSP**. Zoom in on the spectra on the **Acq/Reco Display** window. Adjust the center frequency with **Offset Frq 01**. Look at effect of adjusting center frequency on the FID and it's Fourier Transformed spectrum. Click the **Lock** button to reset **Basic Frequency BF1** to water center frequency on this magnet using **read Config Frequency**.

Next we want to acquire spectra from a canola oil phantom which has a shift of about 3.5ppm downfield from water. What is it's center frequency?

$cf =$

Let's see if you are right.

 Switch to oil sample and clone the **A_ADJ_SF** sequence. Adjust the center frequency to 3.5ppm off water. Click the **GSP** button. Where you correct? Then, set he center frequency back to water by clicking **Read Config Frequency**.

3.3 Shimming

Magnetic field inhomogeneity increases the damping, and also affects the spectral appearance. We can calculate the spectra analytically by taking a (half-sided) Fourier transform:

$$\begin{aligned} S(f) &= \int_0^{\infty} S(t)e^{-i2\pi ft} dt \\ &= \frac{-1}{1/T_2^* + i2\pi(f - f_0)} \end{aligned}$$

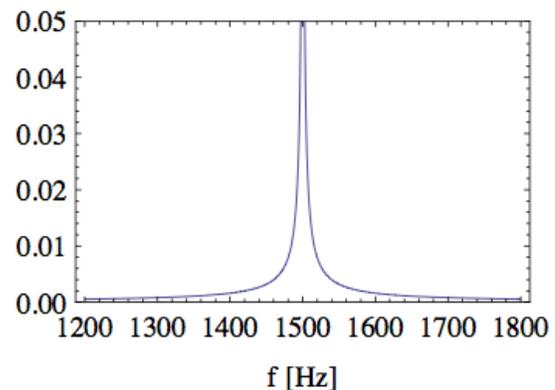
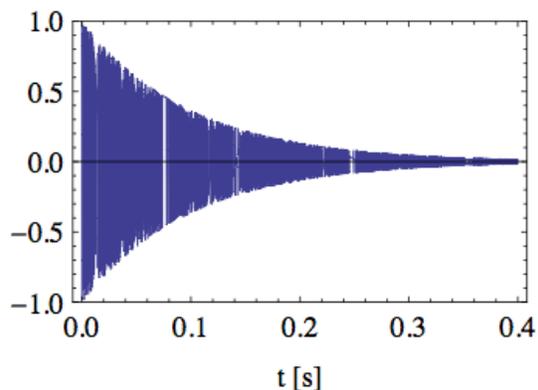
This curve is called the Lorentzian line shape, and it has some key characteristics which are more readily visible in magnitude:

$$|S(f)| = \frac{T_2^*}{\sqrt{1 + (2\pi T_2^*)^2 (f - f_0)^2}} \quad (5)$$

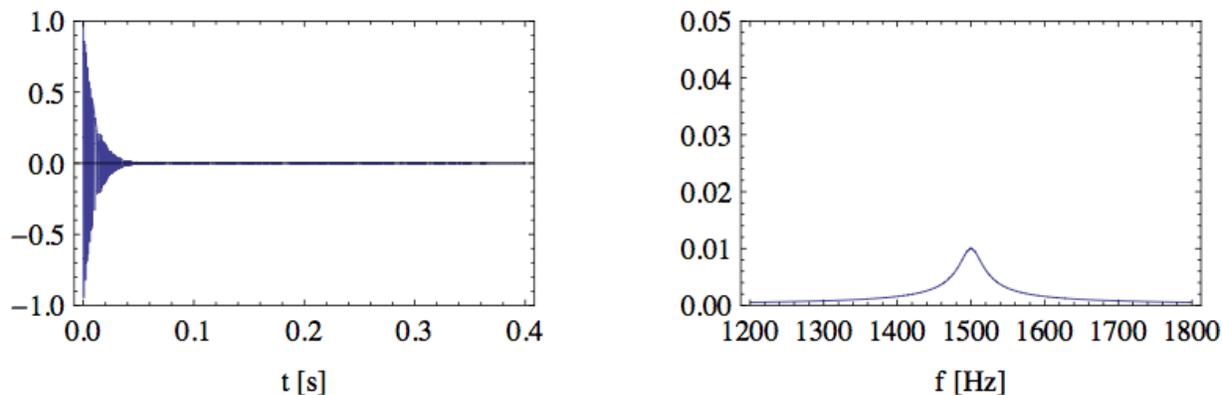
This is just a spike centered at f_0 with some width which is due to damping. Note that the peak signal on resonance is T_2^* , and the full width at half maximum ($FWHM$) $\sim 1/T_2^*$. Therefore, we can see how magnetic field inhomogeneity ΔB_0 directly affects the data quality. True or False: The MRI image quality is best with short T_2^* which comes from a small ΔB_0 .

TRUE/FALSE? Why?

For a well “shimmed” magnetic field, ΔB_0 will be small, so T_2^* is big, thus the $FWHM$ of the spectra is narrow and the spike is tall. When the homogeneity diminishes, our peak is blurred as shown below.

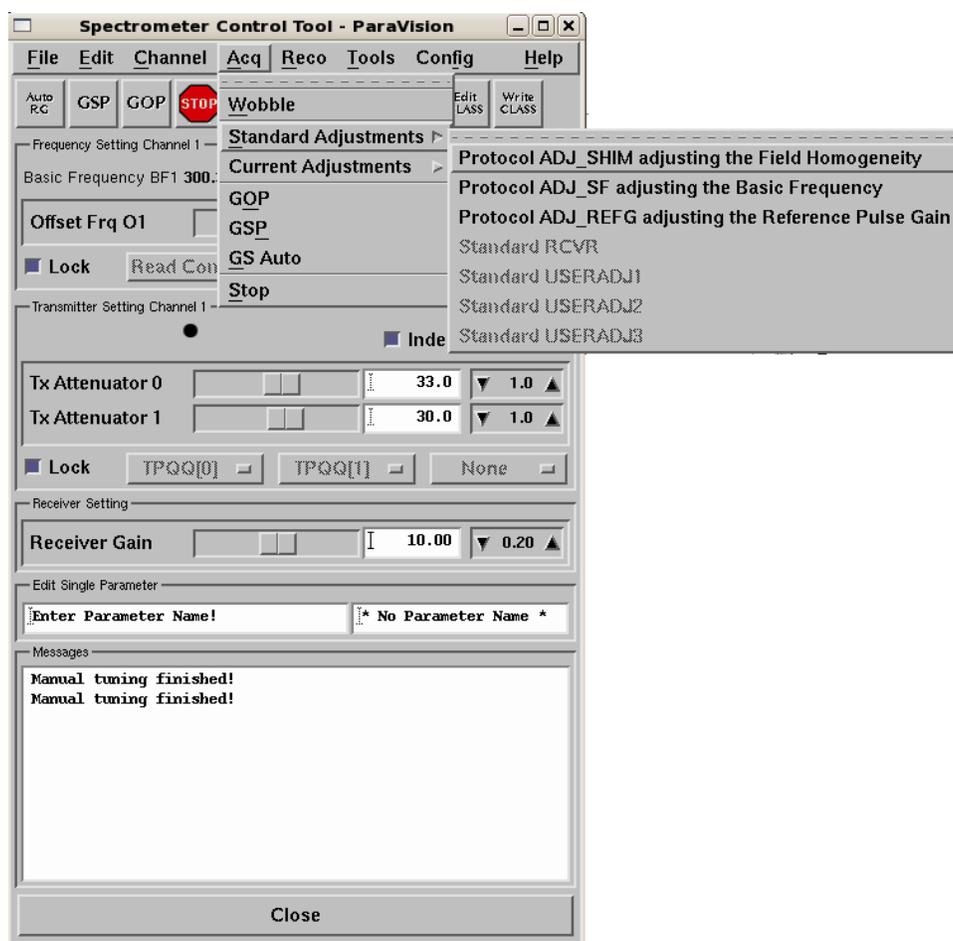


Pulse acquire FID with a long T_2^ : a well shimmed magnet.*



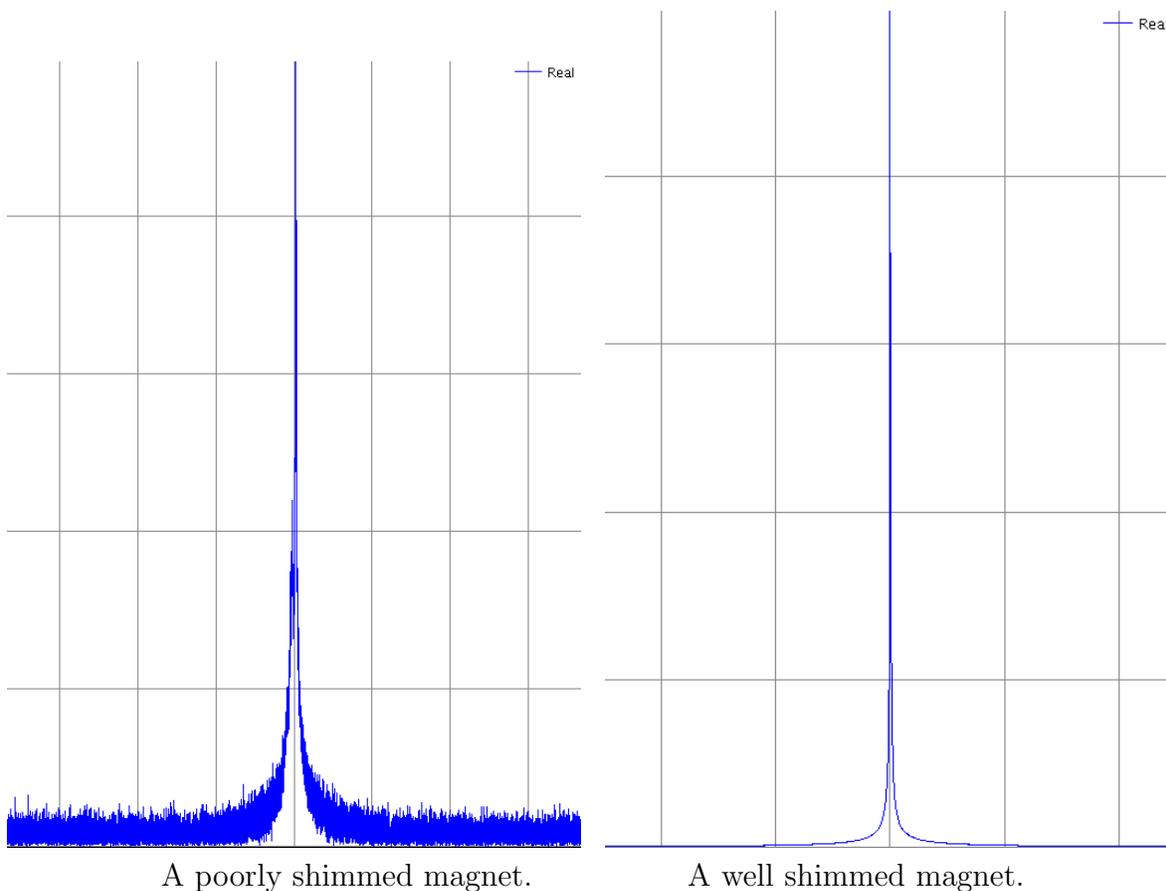
Pulse acquire FID with a long T_2^ : a poorly shimmed magnet.*

➔ Before shimming, we want to make sure the pulse is on resonance (i.e. centered at 0Hz). If it is not we can fix this in **Spectrometer Control Tool** select **Standard Adjustments** and the **Protocol ADJ_SF** to adjusting the Basic Frequency.

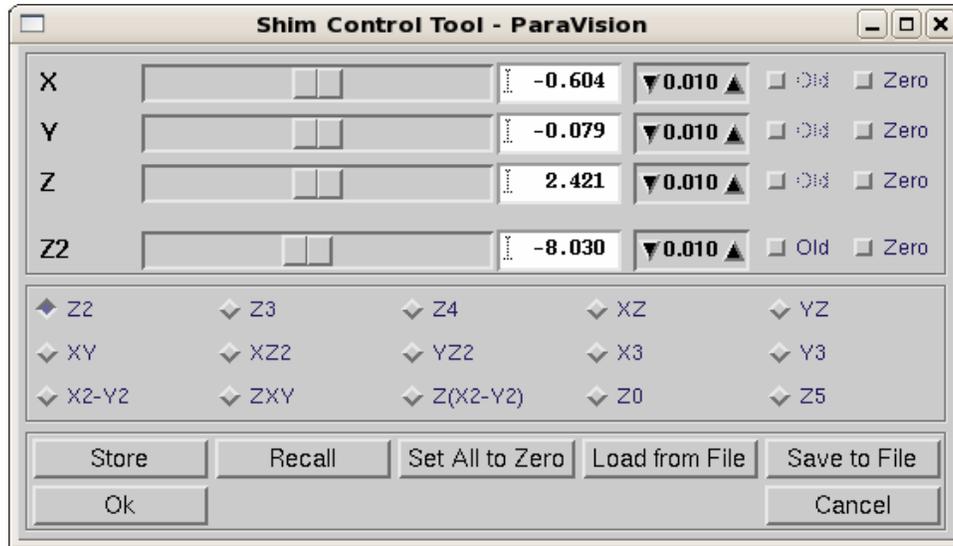


➔ To automatically shim, click the tools button to get to the **Spectrometer Control Tool** select **Standard Adjustments** and run the **Protocol ADJ_SHIM** to adjusting

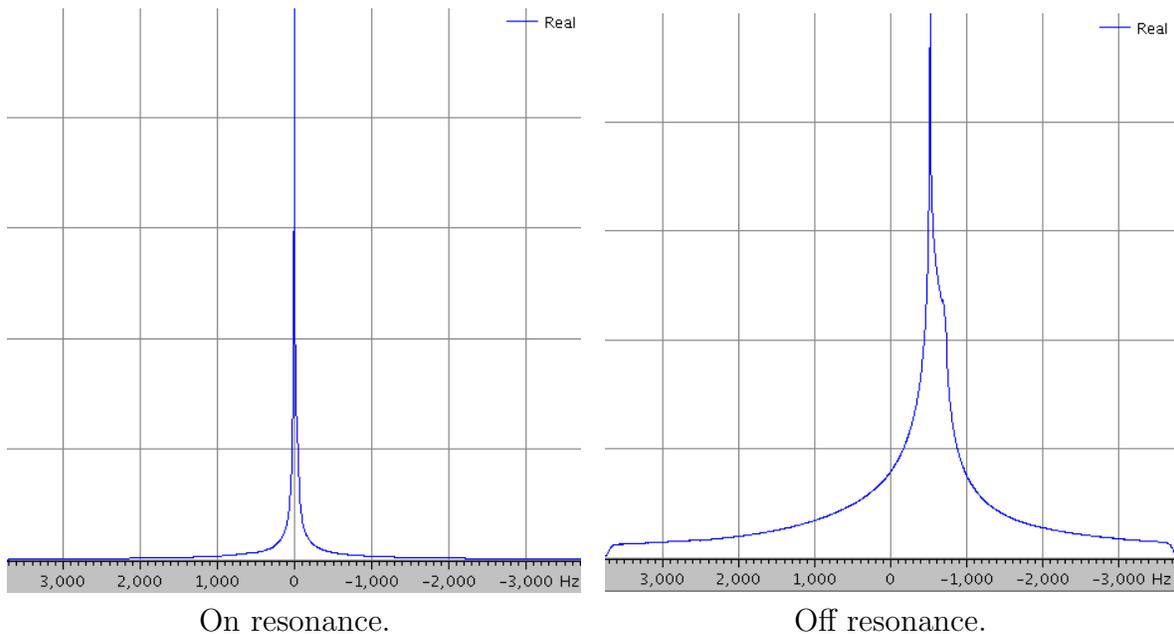
the **Field Homogeneity** as shown below. Watch in the **Acq/Reco Display** window. The software uses the fact that the height of the spectra is proportional to T_2^* to perform automatic shimming. In other words, it automatically iterates the current in the shim coils (coils that spatially alter B_0) in order to minimize ΔB_0 between pulse / acquire experiments.



➔ To manually shim, set up a **ADJ_SHIM** sequence and click tools icon. Click the GSP button . Watch in the **Acq/Reco Display** window. Observe the spectra and FID. Go to **Tools** and choose the **shim tool**.



➔ Zoom in on the spectra. Move the Z2 slider and notice how off resonance causes field inhomogeneity at the center frequency which causing line broadening. When you are done set all back to zero. See if you can do better than the protocol by adjusting the first and second order shims.



What happens when you move x, y, or z? Why?

3.4 90° Pulse Calibration

We ignored the amplitude of the signal response in our treatment in the pulse / acquire section, but the amplitude actually is a function of the polarization and flip angle:

$$S(t) = e^{-i2\pi f_0 t} e^{-t/T_2^*} M_z \sin \theta, \quad (6)$$

where θ is the RF pulse flip angle. Recall that this is just

$$\theta = \gamma \int_0^T B_1(t) dt \quad (7)$$

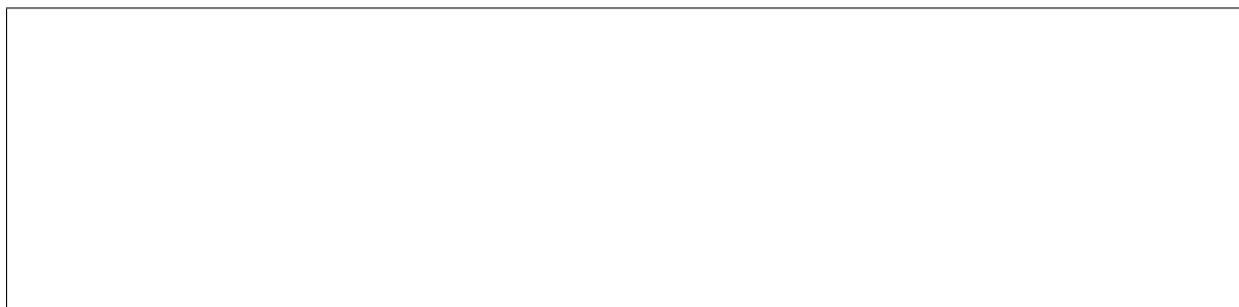
which is the “pulse area.” For our spectrometer, the pulse is just a square function

$$B_1(t) = |B_1| \square \left(\frac{t}{\Delta t} \right)$$

so

$$\theta = \gamma B_1 \Delta t$$

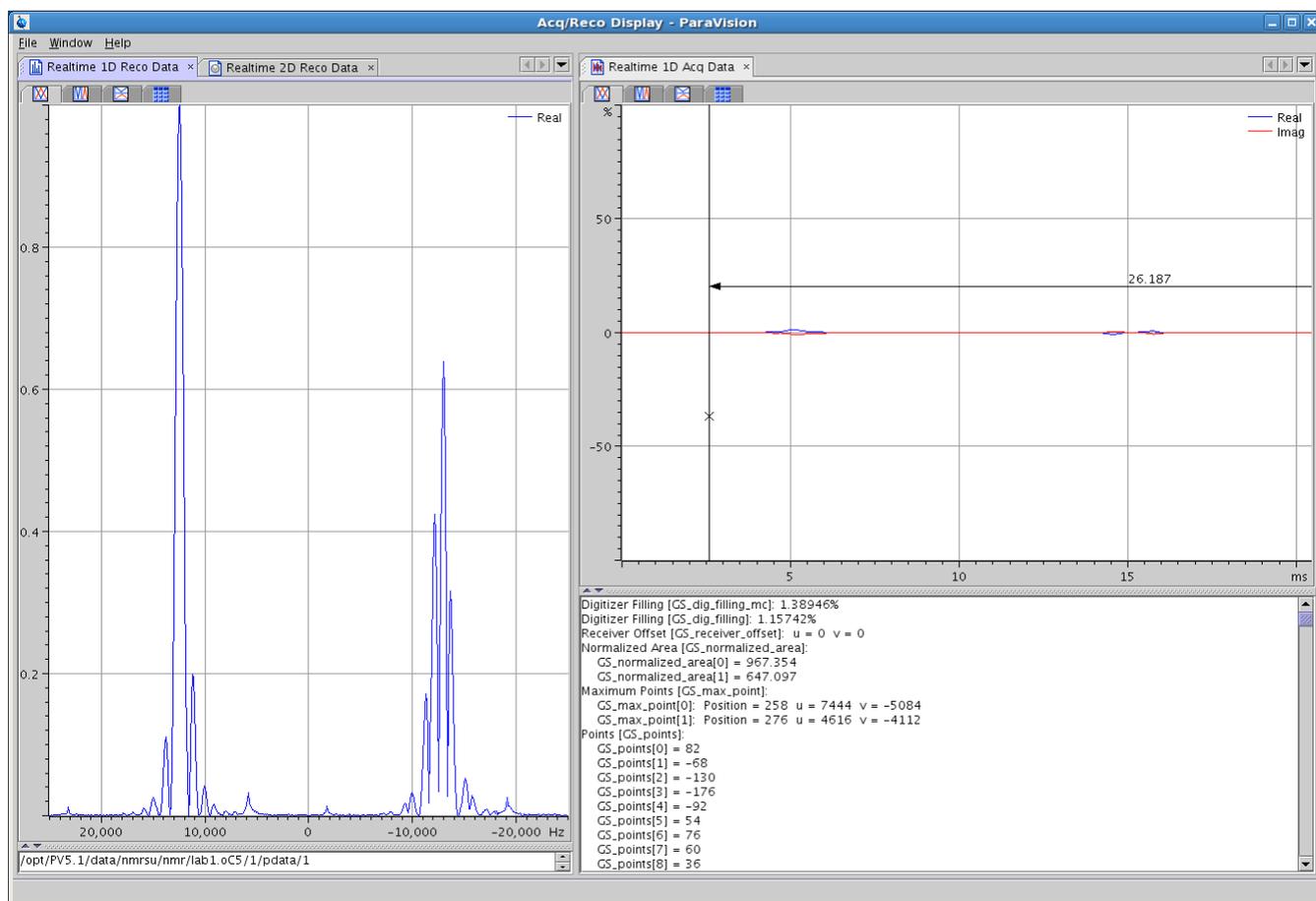
To calibrate the 90° pulse, the spectrometer plays pulse/acquire experiments at varying values of the pulse width Δt . What should the maximum value of the spectrum $S(f)$ look like as a function of Δt ?



Once we find the 90° pulse, then we know what a 180° is too: we just double Δt or double the amplitude of B_1 .

Typically, we can calibrate our gain with the **Spectrometer Control Tool**.

 Select **Standard Adjustments** and the **Protocol ADJ_REFG** to adjusting the **Reference Pulse Gain**. Watch in the **Acq/Reco Display** window. This sequence excites two slices within our sample one with a 90° flip angle and the second with an 180° flip angle and acquires the profile which is displayed as a spectrum. The sequence iterates modulating the gain of the RF amplitude until the 90° reaches a maximum and the 180° reaches a minimum. Notice how the *GS_normalized_area* changes with our signal amplitude and how this iterates until it finds our maximum signal which gives us a 90° pulse. and our minimum which is the 180°.



Alternatively, we can adjust the pulse duration.

➔ Check out the current duration and amplitude with the **Pulse Programming Tool**.

➔ Setup the **ADJ_REFG** sequence. Then click **Edit Scan**. Go to the **Research** menu expand the **RF Pulses** menu and then the **Excitation Pulse** menu. Change shape to a **sinc** and change the **.Length** to 1ms then change it to 8ms. What changed and why?

➔ Now try both the canola and water phantom. Change the **.Length** to 1ms then change it to 8ms. What changed and why?

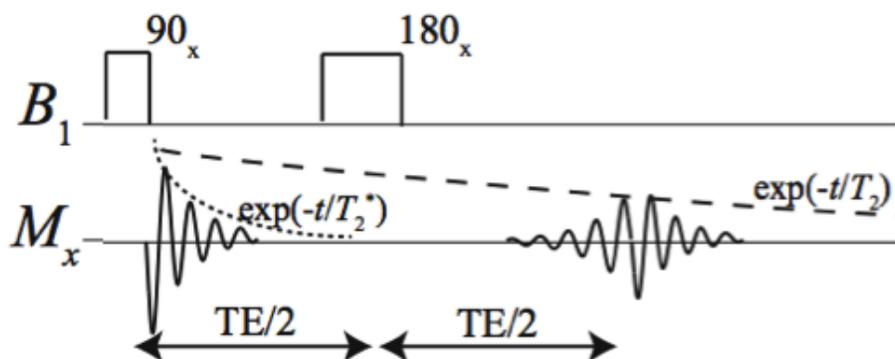


3.5 The Spin Echo

The transverse component of the Bloch equation is

$$\frac{dM_{xy}}{dt} = -\frac{1}{T_2} M_{xy}, \quad (8)$$

where T_2 is a spin-spin (transverse) relaxation time constant. Say we want a measurement of the actual sample-specific T_2 (which varies with molecular structure, temperature, solvent viscosity, and a million other interesting parameters), and not the B_0 inhomogeneity-dominated parameter T_2^* which the pulse/acquire experiment gives us. It turns out we can extract this parameter T_2 with a 2-pulse experiment called the spin echo. A second RF pulse placed $TE/2$ after the first refocuses the magnetization dephased by T_2^* , and we get the signal back again at $TE/2$ after the second pulse. The echo is not full amplitude; it's actually modulated by the pure T_2 decay curve (but the echo grows and dies on either side by the old T_2^* envelope). The second pulse does not necessarily have to be a 180° , but this is the angle that maximizes the response.



The figure above shows the basic spin echo experiment. Only the data after the second pulse is acquired. A single spin echo experiment doesn't give us a T_2 estimate, however. We have to repeat the experiment with multiple TE values in order to generate an exponential decay curve of the echo amplitudes.

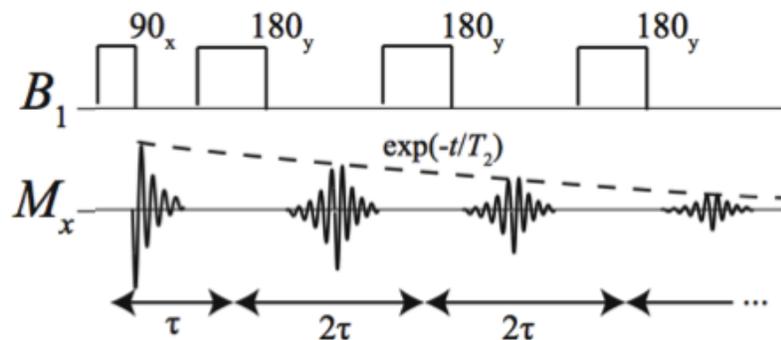
The spin echo signal is a symmetric echo; what does this imply about the phase detection of the spectrum $S(f)$?

Assuming isothermal conditions, spins tumbling faster through space such will generally have a shorter T_2 . Since faster tumbling requires the distribution of spectral energy to higher tumbling frequencies, the relatively low frequency will experience a monotonically decreasing amount of energy as the correlation time, τ_c , increases. Thus increasing T_2 relaxation time. It is worth noting again that fast tumbling spins, such as those in pure water, have similar T_1 and T_2 relaxation times, while slow tumbling spins, such as those in crystal

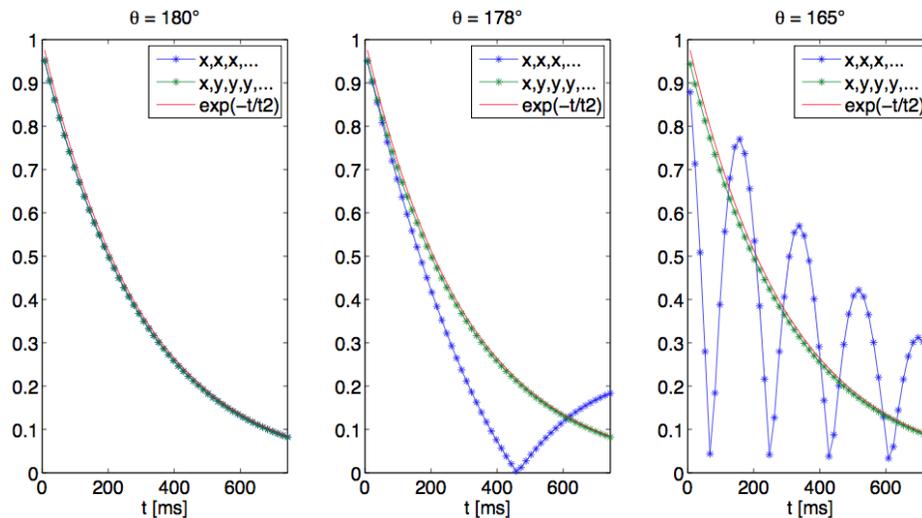
lattices, have very distinct relaxation times. Do we expect a shorter T_2 in water or oil?

It turns out there are many reasons to perform spin echoes besides estimating T_2 . We can use the T_2 as a contrast generating mechanism for MRI. For materials with long T_2 (and systems with short T_2^*), there are large SNR benefits to acquiring spin echo versus pulse/acquire data.

➔ Click on **New Scan**, choose the **SINGLEPULSE-1H** sequence in **B_SPECTROSCOPY**. Edit the scan such that the flip angle is 90° and switch to a **CPMG** sequence.



The Carr Purcell Meiboom Gill (CPMG) experiment is a modification of the spin echo experiment. This time we play a spin echo train, and between each refocusing pulse we acquire the echo. Since each echo is modulated by a T_2 decay, we can perform a T_2 measurement in a single acquisition. However, there is a price to be paid for acquiring the measurement in a single scan, and it is sensitivity to flip angle. For a $90_x, 180_x, 180_x, 180_x, \dots$ sequence, the 180s must be calibrated *perfectly* to generate a T_2 curve. As the blue dotted line in the Figure below shows, when we are only 2° away from a perfect 180 (a 1% error in RF calibration), the signal response curve is vastly different from the pure T_2 decay curve after only a few echoes.



The ideal T_2 decay curve (red) is plotted with the signal response of the 90, 180, 180, 180, ... sequence using phase modulation x, x, x, \dots (blue) and x, y, y, y, \dots (green).

This is because the error propagates between each echo. What is the actual % error in RF calibration?

% error =

A clever way to address this instability is to play the 180° pulses with a phase advance of $\pi/2$ with respect to the initial pulse; i.e they are y pulses. In this way, the RF amplitude error does not corrupt the signal response since the errors are not cumulative in echo number. The CPMG experiment is the basis for the commercial “fast spin echo” (FSE) or “turbo spin echo” (TSE) scans which are used to obtain high resolution T_2 -weighted images in nearly every clinical exam.

➡ Edit the **CPMG** sequence to have 16 echoes. Run the **CPMG** sequence on the water sample and zoom in on the FID in the **Acq/Reco Display** window. Repeat for oil.