Physics Tutorial 3: Manipulating Contrast in MRI

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The purpose of this tutorial is to attempt to provide a basic understanding of what influences some of the different pulse-sequence parameters – primarily TR (repetition time), TE (echo time) and flip angle – have on the resulting images. Questions without any asterisks are those that should be attempted by everyone, whereas more challenging questions are marked with one (*) or two (**) asterisks, and should be considered optional. Take these opportunities to think about these questions, and then discuss your answers with your tutor.

At the end of the tutorial period, you will receive a "take-home tutor", which is an annotated version of this tutorial guide that will help you complete the tutorial at home if you don't manage to make it all the way through with your tutor, or if you missed the tutorial session.

Attendance will be taken by the tutors, and marks will be given by participation. If you would like additional feedback or clarification on the tutorial material, you are welcome to submit your questions or comments to Weblearn, and a tutor will provide written feedback for you. Those unable to attend the tutorial must submit answers to all unstarred questions to receive credit for the tutorial.

Part 0 – Getting Started

0.1 Starting MATLAB

Download and unzip the file containing the tutorial resources from Weblearn, or if you have access to the FMRIB internal network, copy them into your current directory from here:

~mchiew/GradCourse/3_Contrast_Manipulation

Start MATLAB, and make sure you're inside the tutorial directory (i.e., the folder containing all the tutorial files).

Note to jalapeno00 users: please start with the -nojvm option, "matlab -nojvm"; *this should reduce server CPU load if lots of people are trying to use jalapeno00 simultaneously*

Part 1 – T1 Contrast

Approximate Relaxation Times at 1.5T		
	T1 (ms)	**T2 (ms)**
White Matter (WM)	600	80
Grey Matter (GM)	900	100
Cerebrospinal Fluid (CSF)	3500	2000

Table 1

In this tutorial, we will be making extensive use of `simContrast`, which is a

simplified simulator for the formation of image contrast in MRI. By default, it assumes approximate values for the different tissue relaxation rates at 1.5 T, as shown in Table 1.

To use the simulator, you must specify a TR, TE and flip angle:

```
>> TR = 8000;
>> flipAngle = 90;
>> TE = 5;
>> simContrast
```

Remember that T1 (sometimes also seen as T_1) is a property specific to each tissue type that dictates how quickly magnetization recovers along the z (i.e. main magnetic field B_0) direction. Tissues with larger (longer) T1 relaxation times take longer to return to equilibrium than tissues with smaller (shorter) T1's.

Extra Information
T1 recovery is exponential, and that T1 is the time constant of that exponential recovery. For example, $M_z = M_0(1 - e^{-t/T1})$ following a 90 degree excitation. That is, after a time T1, the magnetisation M_z would have recovered $100*(1-e^{-1})$% or ~63% of its equilibrium value.

Recall that the quantity M_z represents is the amount of potential or stored magnetization that is available for subsequent measurements. In terms of the battery analogy, batteries with larger T1 values take longer to recharge (recover) than batteries with shorter T1's. Therefore, the shorter the T1, the shorter the duration needed (TR) for the magnetisation to recharge in order to achieve the maximum possible signal.

T1-weighting refers to the act of producing images that reflect differences in tissue T1. To do this, the TR is often selected to maximise or accentuate the difference in signal levels associated with respective T1 values.

Question 1.1
Images produced with very long TRs (and short TEs), have maximum signal levels because the magnetisation is allowed to fully recover (i.e., fully recharge) between each excitation of the magnetisation. While this seems good, what do the images produced with these TRs look like? What TR choice produces better WM/GM contrast? How much time does such a scan take?

Question 1.2*
Given a TR of 100ms, a square field-of-view (192x192) and assuming a 2DFT (single line) readout with 128 slices, estimate the total imaging time required.
Does this time seem reasonable? If not, what might you change?

As you learned in last week's tutorial, the steady-state signal (i.e., the signal available after long series of excitations) is often maximised at a flip angle < 90° when the TR is not long relative to T1. Recall that the Ernst angle θ_E is defined:

$$\cos(\theta_E) = e^{-\frac{TR}{T1}}$$

In addition to T1-contrast levels and scan time, signal-to-noise ratio (SNR) and contrast-to-noise ratio (CNR) must also be considered when selecting imaging parameters.

Question 1.3
What flip angle maximises the contrast between tissues with T1 values of 600 ms

and 900 ms when a TR of 20 ms is being used?

Question 1.4**
How are noise levels affected when the acquisition flip angle is modified?

Part 2 – T2 Contrast

T2-weighting is conceptually identical to T1-weighting, except now the objective is to maximise signal differences based on differences in tissue T2 values (sometimes also seen as T_2), instead of T1 values. Recall that T2 is distinct from T1 in that it governs the decay or loss of transverse magnetisation (as opposed to the recovery of longitudinal magnetisation). The T2 value indicates the speed of this decay, where tissues with short T2 decay quickly, and tissues with long T2 stay around longer and take longer to decay away.

Extra Information
For the mathematically inclined, relaxation of the transverse magnetisation is governed by the following equation: $M_{xy}(t) = M_z \sin\theta\, e^{-t/T2}$, where M_z is the longitudinal magnetisation at t = 0 and θ is the flip angle.

An important point when trying to optimise image contrast is that T1 and T2 weighting are *always* present to varying degrees in acquired images. In the previous section, TEs were set to very low values (or zero) to minimize T2-weighting effects. Similarly, when trying to maximise T2 weighting it is beneficial to minimise the effects of T1 differences in tissue. This can be done in 2 ways:

- Increasing TR
- Decreasing flip angle

In the same way that changing TR changed T1-contrast in the signals, changing TE modifies the amount of T2-contrast in the resulting image.

Question 2.1
At approximately what TE is the contrast between WM and GM at 1.5 T maximised? What implications does this have for minimum scan times for a simple 2DFT (single line) sequence?

Question 2.2**
In general, given two tissue types with different T2 values, derive an expression for the TE that gives maximum contrast, assuming TR >> T1.

Discussion 2.3**
Often, SNR is said to be proportional to the square root of the total acquisition time (T_{acq}). Consider two pulse sequences that are identical in all respects, except one has double the TR of the second. If we were to apply the acquisition time "rule", the SNR of the second sequence should be $\sqrt{2}$ higher than the first. Assuming a homogenous sample (single T1, single T2), is this relationship valid? What happens to the SNR when the TE is varied to be as short as possible within a given TR, or as long as possible?

Extra Information
Remember from the lecture that T2 relaxation is an intrinsic process that occurs in any sample, regardless of how perfect (or imperfect) your instrumentation or experimental setup is. In practice, static magnetic field inhomogeneity across a voxel can cause an apparent enhancement of T2 decay or transverse signal loss. We call T2* (pronounced "tee two star") the parameter that takes into account both intrinsic T2 and field inhomogeneity effects, where T2* < T2 (i.e., inhomogeneity always causes faster decay).

Part 3 – Inversion Recovery

Inversion pulses are just like excitation pulses, except their purpose is to flip the longitudinal (M_z) magnetisation upside down along the z-axis. Once this occurs, the magnetisation immediately begins to grow back to its positive equilibrium value, governed by its T1 parameter. *Preparing* the magnetisation this way allows more flexibility in dealing with tissues with different T1s, including the ability to selectively "null" tissues. The sequence parameter TI controls the timing between the inversion pulse and the sequence excitation pulse.

Approximate Relaxation Times at 3.0T		
	T1 (ms)	**T2 (ms)**
White Matter (WM)	830	80
Grey Matter (GM)	1330	110
Cerebrospinal Fluid (CSF)	4000	2000

Table 2

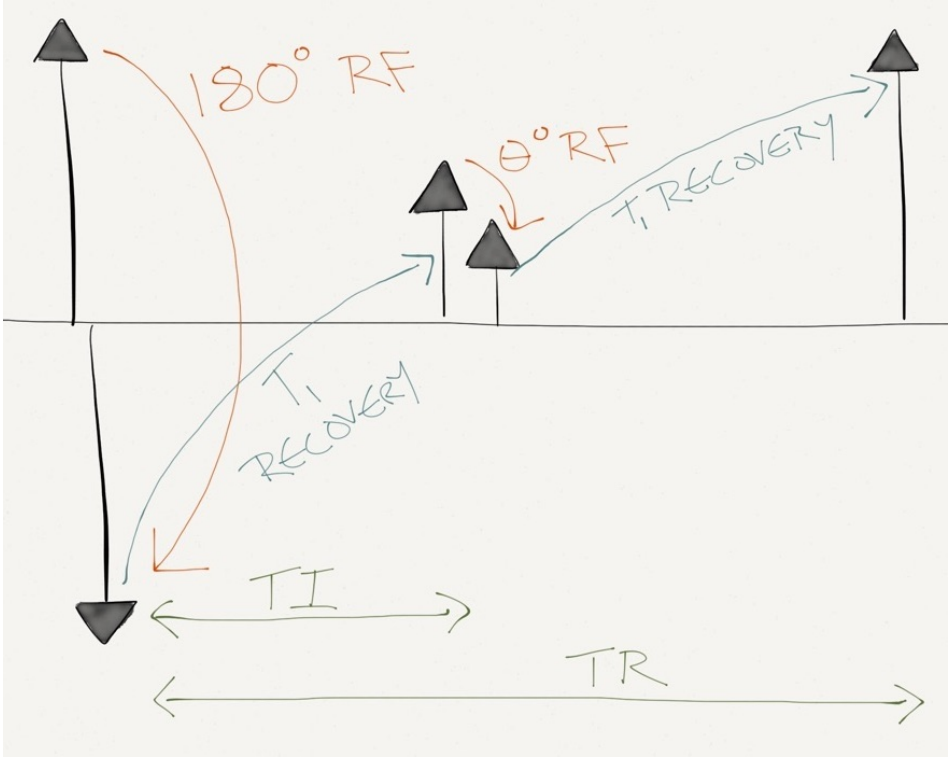
Open a new `simContrast` figure with the following parameters:

```
>> fieldStrength=3;
>> TR = 2000;
>> TI = 860;
>> TE = 5;
>> flipAngle = 90;
>> useInversion = 1;
>> simContrast
```

Question 3.1
Assuming TR = 1000 ms, TE = 5 ms, and flip angle = 90°, find the approximate TI that corresponds to nulling of white matter signals.

Question 3.2
Assuming TR = 1000 ms, TE = 5 ms, and flip angle = 90°, find the TI's (there are two) that correspond to WM and GM having identical signal intensities.

Question 3.3**



Find an expression for null inversion time of a tissue with an arbitrary T1, using a general steady state sequence with arbitrary TR and flip angle.

Hint: the longitudinal magnetization M_θ after a flip angle θ is given by

$$M_\theta = M_0 + (M_z \cos\theta - M_0)e^{-t/T1}$$

where M_z is the longitudinal magnetization immediately before applying the flip angle and M_0 is the equilibrium magnetization.