Tutorial: Contrast Manipulation

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The purpose of this tutorial is to attempt to provide a basic understanding of what influence some of the different pulse-sequence parameters - primarily TR, TE and flip angle - have on the images.

To start off you need to unzip the contrastManipulationTutorial.zip file to a temporary location. Then launch Matlab and change the working directory to the location of the unzipped files.

T1-contrast

`simContrast` is a simplified simulator of the formation of image contrast in MRI. It assumes approximate values for the tissue relaxation rates at 1.5 T, shown in the table on the right.

Approximate relaxation times at 1.5 T

	T1 (ms)	T2 (ms)
WM	600	80
GM	900	100
CSF	3500	2000

To start off, let's use a very long TR so we can see the relaxation curves more easily. Use TR=8000 ms and flipAngle=90°. We also need to specify an echo time, so let's use a short value of TE=5 ms for now. Type `simContrast` and look at the result. The top left plot shows the magnetisation over a single TR after the steady-state has been reached, with the corresponding T1-weighting for the WM/GM/CSF to the right. White matter is represented by the blue line, grey matter the green and CSF the red. The bottom left plot describes T2-weighting, which we can ignore for the time-being (at a short TE the T2-weighting is negligible). The top right plot shows the relative intensities of the WM/GM/CSF when both T1-weighting and T2-weighting are considered (i.e., T1-weighting x T2-weighting). In the bottom right is shown a simulated image demonstrating this contrast. The numbers quoted above the image will be explained shortly.

With the current values, we can see from the top left plot that the long TR means that WM and GM are virtually indistinguishable, but CSF hasn't quite had time to recover fully and therefore appears a little darker. [Note that long TR and short TE actually corresponds to a proton-density weighted image – but this simple simulation assumes equal proton density throughout the brain.]

Generally for a structural image to be useful it needs to provide good contrast between WM and GM. Looking at the blue and green recovery curves in the top left plot, we can see that around 1 second after the excitation there is a noticeable difference between the GM and WM curves which has disappeared by the time of the 8 sec TR we are currently using. Try setting TR to 1 sec (type `TR=1000`) and re-simulate.

The simulated image now has the familiar T1-weighting – WM is brightest, GM a little darker and CSF much darker. However, if we assume the total volume is 192x192x128, and that we are using a 2D linescan acquisition, this would take 192x128 = 24576 lines of k-space. With TR = 1s this is 24576s, or nearly 7 hours to acquire!

Now let's bring the TR down to a more reasonable 20 ms (just over 8 minutes for the volume) and simulate again. We now have the contrast we wanted in a short total scan duration – but our image looks rather noisy! Above the image are quoted SNR and GM/WM CNR values. The SNR here is a measure of the strongest intensity relative to the noise. The GM/WM CNR is a measure of how big the difference in signal between GM and WM is compared to the noise – this is what we are really interested in.

In last week's tutorial we discovered the importance of the Ernst angle which represents the flip angle which gives the highest steady-state signal for a particular tissue T1 and pulse sequence TR (Ernst angle: $\cos(\theta) = \exp(-TR/T1)$. For T1=600 ms and TR=20 ms it turns out to be 14.7°. Run the simulation again with flipAngle=14.7° as this should maximise the SNR in our image (WM is brighter than GM). Look at the new values of SNR and CNR. Our SNR has increased 4-fold, but the CNR by just over 2-fold. Maybe we can do better.

Increase the flip angle to 20° and re-simulate. The SNR has decreased (we are no longer at the Ernst angle) but our CNR has increased!

To understand why the contrast has improved despite a loss in SNR we need to look back to where our contrast comes from. Set T1=900 ms and run `simSignalvFlip` (the same function we used last week). Do the same for T1=600 ms (i.e. white matter). These two curves show how the signal from both tissues varies with flip angle. We want not to maximise the signal – but to maximise the *difference* between these two signals. To see how this works, type `T1pair = [600 900]` and then `simContrastvFlip`. You should now see the same two curves as from the previous two plots, as well as the difference between them.

Question 1 - To the nearest degree, what is the flip angle that maximises the contrast between tissues with T1 values of 600 ms and 900 ms when a TR of 20 ms is being used? (Use the zoom tool [magnifying glass] in the plot to find this).

Set flipAngle equal to this new angle and run `simContrast` again. Now you should have a reasonable T1-weighted image in a reasonable scan time. Because the noise is constant magnitude (determined by our image resolution, bandwidth, etc.), this flip angle that maximises the contrast must also maximise the CNR.

T2-weighting

Type `close all` again to get rid of all those open figures.

Now we are going to look at T2-weighting. The T2-weighting of the image depends on the TE, and modulates any residual T1-weighting. If we want our T2-weighted image to have as little T1-dependence as possible, we need to first reduce this as much as possible before changing the TE. Set the TR to 200 ms and then run `simContrast`. Reduce the flipAngle and notice that this decreases T1-weighting. Previously we learnt that we need to change the TR to alter the T1-weighting, but now we find that the flip angle also has an effect. In terms of contrast, small flip angles have a similar effect to a long TR - all tissues have a large longitudinal magnetisation so there is little contrast between them.

Find a flip angle small enough to provide little visible contrast (T1-weighting) without making the image look too noisy (CNR ~= 1). Now increase TE.

Question 2 - Increasing the TE will increase the T2-weighting but will also make the image look noisier - the noise is the same level but the signal is reduced. Approximately what is the TE which maximises the T2-weighted CNR? (only an approximate answer is required as there is a large range of TE values with similar CNR)

You will also notice that by setting the TR to 200 ms we have extended the total scan time to over 80 minutes! The TR has to be longer than TE, so in order to increase the TE to obtain the T2 contrast we have to extend the TR and therefore the total scan time. Obviously we don't want to scan for over an hour – so a different acquisition technique is used when T2-weighting is desired (such as imaging a tumour with similar T1 to surrounding tissue, but different T2). However, the concept of achieving the T2-weighting is the same: reducing the T1-weighting imposed (by choosing appropriate TR and flip angle) and then increasing the TE.

Inversion Recovery

Type `close all` to close all figures. Set the TR to 1 second, the TE to 5 ms and the flip angle to 90°. If you type `useInversion=1` and `TI = 500` then you can re-run `simContrast` and look at the effect of using an inversion recovery sequence. The top plot showing T1-weighting now includes two 180° inversion pulses at 0 ms and 1000 ms, with the excitation pulse shown at the chosen TI of 500 ms. If you reduce the flip angle to 40° you will notice that the image contrast isn't changed much, but the inversion recovery curves now pass relatively unperturbed through our excitation pulse (because we are 'leaving behind' so much of the longitudinal magnetisation).

Question 3 - For TR=1 sec, TE = 5 ms, flip angle = 40°, find the approximate TI which corresponds to:

4.a - 'Nulling' white matter (i.e. no signal from white matter)

4.b - Grey and white matter are the same intensity (give both TIs where this is true)

Question 4 (if you have time!)

The table on the right shows the approximate relaxation times at 3T. If you type `fieldStrength=3` and re-run `simContrast` it will use these values instead of those for 1.5T.

Approximate relaxation times at 3 T

	T1 (ms)	T2 (ms)
WM	830	80
GM	1330	110
CSF	4000	2000

Assume we want to acquire a T1-weighted image in 5 minutes at a resolution of 192x192x128 (using a 2D linescan acquisition). What TR and flip angle should we use to maximise our contrast between grey and white matter?

Hint: First work out the number of k-space lines required, then from this work out the TR based on the scan time (you can use Matlab as a calculator). You can then use `simContrastvFlip` *to optimise flip angle, checking your result with* `simContrast`.