Biomedical Imaging FS 2019

MRI 2

Exercises

The prepared code calculates the MR signal available from three transverse slices of a human head based on a discrete tissue model[1]. The tissue model distinguishes 12 tissue types that differ in proton density, T_1 and T_2. The presence of each tissue across the slices is reflected in maps of relative volume content (see Figs. 1-3 that the script creates).

As prepared, the code calculates available signal assuming the simplest form of contrast, i.e., pure proton-density contrast independent of T_1 and T_2.

The available signal is sampled in k-space, along a Cartesian grid. As prepared, the code assumes full-density sampling at the extent that corresponds to the resolution of the tissue maps. The sampled data is Fourier-transformed to yield resulting images.

1. Sampling Pattern

- Manipulate the sampling pattern such as to
  - keep only every second horizontal line, setting the others to zero
  - keep only every third horizontal line, setting the others to zero
  - do the same in the vertical direction
  - do both, horizontal and vertical undersampling at the same time
- Explain your observations using the concepts discussed in the lecture on Signals and Systems

  What we see is foldover of parts of the head onto other parts. This can be understood using the concept of comb functions and the convolution theorem. Undersampling in k-space amounts to multiplication with a comb that is less dense than the data that we start with. The convolution theorem tells us that in the image domain this will result in convolution with the Fourier transform of that comb. The Fourier transform of a comb is again a comb, but of reciprocal spacing. The comb that corresponds to the k-space density of the original data transforms into one whose spacing equals the spatial extent (FOV) of the original data in the image domain. Reducing the density of the former, as we do in this exercise, causes the peaks of the latter to move closer to each other. Then the convolution with that denser comb causes parts of the head to be superimposed.

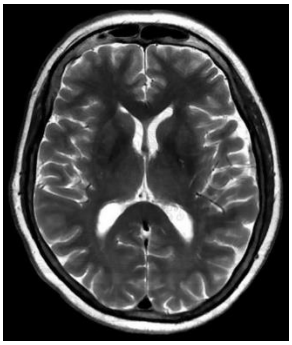
[1] www.bic.**mni**.mcgill.ca/**brain**web

- Manipulate the sampling pattern such as to
  - reduce the sampling range to one-half by keeping only the corresponding square in the center of k-space
  - reduce the sampling range to one-fourth in the same fashion
- Again, explain your observations using the concepts discussed in the first lecture

The key is again the convolution theorem in conjunction with knowing Fourier pairs. Reducing the extent of sampling in k-space amounts to multiplication of the original k–space data with a rectangle function of width less than that original extent. The Fourier transform of a rectangle function is a sinc function of reciprocal width. If the rectangle is narrower than the original k-space extent, the main lobe of the sinc is wider than the original pixel size in the image domain. Additionally the sinc exhibits sidelobes whose spacing increases along with the width of the main lobe. The product of rectangles in the kx and ky dimension transforms into the product of the corresponding sincs (one varying along x, one along y). Convolution with the 2D sinc causes blurring (resolution loss related to the wider main lobe) and ringing (ripples next to high-contrast features related to the side lobes).

2. Contrast

- Adjust the signal calculation such as to reflect a spin-echo sequence with long T_E and long T_R for T_2 contrast. Find sequence parameters that approximately yield this contrast:

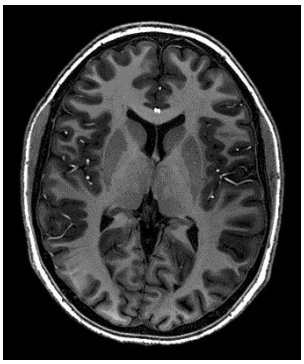


For long T_R we can assume that all magnetization is fully relaxed when each sequence repetition starts. The signal strength in the k-space center then scales as

$$s(T_E) \propto \sin(\theta)\, e^{-T_E/T_2}.$$

The contributions from the different tissue components just add up, weighted by their volume fractions. The contrast does not depend on θ but the contrast-to-noise ratio will. To maximize it the initial flip angle θ should be set to 90°. The contrast shown above is obtained approximately with $T_E = 100\ ms$.

- Adjust the signal calculation to reflect an inversion-recovery sequence for T_1 contrast. Optimise the sequence parameters (T_I, T_E, T_R) to distinguish gray and white matter. Common inversion-recovery T_1 contrast looks like this:



The inversion recovery signal scales as

$$s(T_E) \propto \sin(\theta)\, e^{-T_E/T_2}\left(1 - 2\, e^{-T_I/T_1}\right),$$

where θ now denotes the flip angle of the excitation pulse at T_I. Again, to maximize the signal strength and thus the contrast-to noise ratio, θ should be set to 90°. For the same reason and to not perturb T_1 contrast by additional T_2 weighting the echo time should be minimal (e.g., $T_E = 2\ ms$ in practice). Good gray-white-matter separation is achieved with T_I between the T_1 of the two tissues. On this basis, $T_I = 700\ ms$ is a good choice, for instance. For the image above, T_I was chosen such as to null CSF signal using a substantially longer inversion time ($T_I \approx 1700\ ms$).

- Adjust the signal calculation such as to reflect a T_1-weighted steady-state gradient-echo sequence with short T_R and short T_E (use the signal equation derived in last week's exercise, again assuming full transverse relaxation). Tune the flip angle to give good differentiation of gray and white matter.

According to the previous week's steady state-calculation the signal now scales as

$$s(T_E) \propto \sin\theta \frac{1-e^{-\frac{T_R}{T_1}}}{1-\cos\theta e^{-\frac{T_R}{T_1}}} e^{-T_E/T_2}.$$

Again, to target pure T_1 contrast, T_E should be minimal. To introduce large signal differences between different-T_1 tissues the z magnetization must be driven into significant saturation. This is achieved with a short T_R (e.g. 5 ms in practice) and a large flip angle. A good empirical choice is $\theta = 50°$, which gives close to maximal contrast.