Chapter 5

The Devil's in the Detail: Pixels, Matrices and Slices

5.1 Introduction

MR images are like photographs or plain digital X-radiographs; they are made up of thousands of tiny squares known as *pixels* (a contraction of 'picture elements') or *voxels* ('volume elements'). CT images are also made up of pixels, as are **D**igital **S**ubtraction **A**ngiograms (DSAs). The common link between MR, CT and DSA is that all these images are acquired digitally, by a computer. However, all the original data start out as analogue signals, either a voltage in an RF receive coil (for MR), or a scintillation in a photodiode (CT) or image-intensifier (DSA). The process of converting signals from analogue to digital can introduce artefacts in the final image, and it's important to understand the process. In this chapter we show:

- that the analogue MR signal is digitized in order to create the image, and data can be misrepresented due to the digitization process;
- the organization of the image as pixels in a matrix with phase and frequency encoding directions;
- the relationship between the image matrix and the physical field of view, and how each pixel represents the MR signal from a small volume of tissue;
- the size of the voxel can be calculated from the FOV and matrix, which defines the resolution in MR images;
- that MR images can be acquired as either multi-slice two-dimensional scans, or as a three-dimensional volume, each of which has advantages and disadvantages.

5.2 From Analogue Signal to Digital Image

The MR signal is detected by the receive coils, and is simply a voltage induced in the coil. This is just the same as your high-school physics lessons; when you move a magnet through an electrical coil, you generate a voltage in the coil. If the magnet moves quickly back and forth through the coil, you can generate an alternating voltage. If we add up all the tiny magnetic fields of the protons in the body, they become a measurable magnetic field, which is also changing very quickly because the protons are spinning. So the MR signal in the receive coils is an analogue voltage.

The *analogue* MR signal is described as *continuous*, which means it has a value (an electric voltage) at every point in time, no matter how closely you zoom in. So we can measure the signal every second, or every millisecond, or every microsecond: no matter how small the time interval, the signal always has a value (Figure 5.1a). Because it is analogue, it also varies smoothly; whether we use a meter working in volts, millivolts or microvolts, there is a continuously changing voltage.

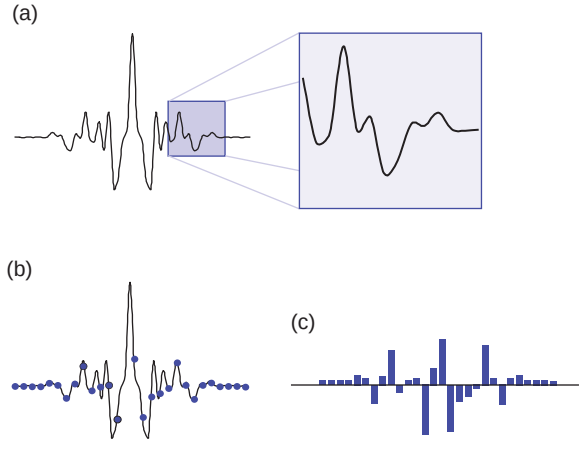

Figure 5.1 (a) The MR signal in the receive coil is a continuously changing voltage; no matter how closely we zoom in, it still varies smoothly. (b) When it is digitized, there are gaps between sample points due to the Analogue-to-Digital Converter's (ADC) performance. (c) Digital data are stored as integers, so the digitized MR signal has a stepped appearance.

When the signal is digitized (by an **A**nalogue-to-**D**igital **C**onverter, or ADC), the changing voltage is represented as a series of numbers. The ADC makes a measurement of the voltage, calculates the appropriate number and stores the *digital* value in the computer. Although this happens very quickly, each conversion takes a certain length of time, so the ADC can only measure the signal at certain time intervals (Figure 5.1b). The digital data are described as sampled because there are gaps between the measured values. Since the computer can only store whole numbers (integers), so the signal also changes from being continuous to stepped or *discrete* data (Figure 5.1c).

Another advantage of digital data is that they can be transmitted over fibre-optic cables, whereas the analogue voltage is normally carried on standard copper wires. The copper wires are always shielded to protect them from other signal sources, but shielding is not perfect and extra noise is introduced. There are also losses due to resistive heating of the copper; although this is a tiny amount of heat, the MR signal is also very tiny, so we need to avoid losses and noise interference. Fibre-optic cables avoid the problem of interference completely, and losses are minimal. So, the sooner we digitize this tiny signal, the better! In many modern MR scanners, the ADC is mounted on the magnet, or even in the coil itself. Fibre-optic cables then carry the signal into the technical room to the reconstruction computer.

The Nyquist Theorem

An ADC can work at different speeds, defined as its sampling rate or sampling frequency, denoted f_s. If f_s is high, there is only a small gap between signal measurements, known as the sample period, T_s. T_s and f_s are related mathematically:

$$T_s = \frac{1}{f_s}$$

So if f_s is low, there is a larger T_s and you can see that there is a chance that the digitized signal will miss some of the real MR signal (Figure 5.2a). Mathematicians and engineers have done a lot of theoretical work on this problem and have found a rule to characterize it, called the *Nyquist theorem* (Henry Nyquist was an engineer working for AT&T in the 1920s). According to Nyquist, the highest frequency signal that can be accurately digitized at a certain sampling frequency f_s is equal to half of the sampling frequency. This is known as the Nyquist frequency f_N, and we can write

$$\text{Nyquist frequency} = ½ \times \text{sampling frequency}$$

or

$$f_N = \frac{1}{2} \cdot f_s$$

Let's look carefully at various frequency signals all digitized at the same frequency f_s. First, a signal with frequency lower than f_N (Figure 5.2b) is accurately digitized and the reconstructed signal made by 'joining the dots' clearly has the same frequency as the original. What about a signal at exactly the Nyquist frequency (Figure 5.2c)? Now the digital samples occur at every peak and trough and again the reconstructed signal represents the correct frequency. However, if the signal frequency is higher than f_N, you can see that the digital samples miss some of the peaks and troughs (Figure 5.2d). When

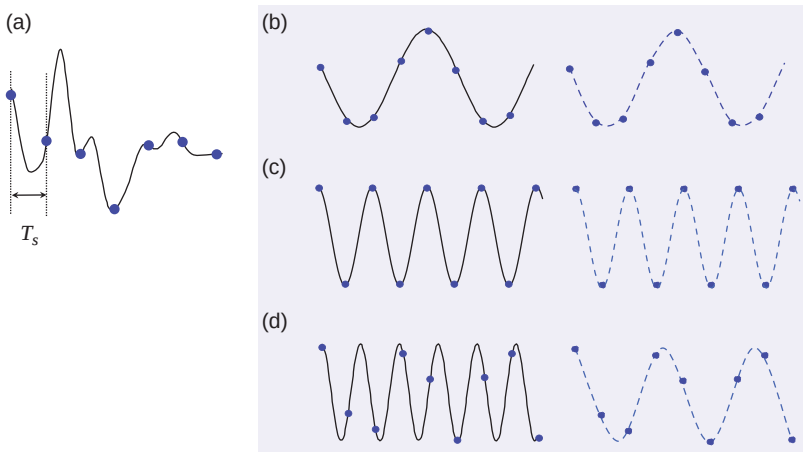

Figure 5.2 (a) The sample period (T_s) is the time between digitized sample points on the MR signal. If T_s is too big, information may be lost. (b) Digitization of a frequency lower than the sampling frequency, f_s. (c) Digitization of a signal at the Nyquist frequency f_N. (d) Signals at frequencies higher than f_N are aliased and the digital frequency appears to be low.

you connect up the reconstructed samples (shown by the blue line), the frequency appears to be much lower instead of the correct high frequency. This is known as aliasing; we say that for any f_s, all frequencies higher than the Nyquist frequency f_N are aliased as low frequencies.

You can see a good visual example of aliasing by watching an old Western film: look at the spokes on the wagon wheels as they start to move. When the wheels are turning slowly the individual frames of the film are fast enough to show the motion accurately. As the wagon gets faster and the wheels turn more quickly, the spokes appear to slow down, stop still and then they seem to turn backwards! This is because the wheel has gone through more than one complete turn between each frame, i.e. the frequency of the spokes is higher than the sampling frequency (or frame rate) of the film.

The Receive Bandwidth and Oversampling

The MR signal is centred at an RF frequency (which we will see later is fixed by the strength of the main magnetic field), but it contains a range of different frequencies that encode information about the location of various tissues (see Section 8.5.3). This centre RF frequency can be removed from the signal before it is digitized, leaving the *receive bandwidth* of the signal, which is typically several kilohertz (kHz) wide. However, many modern scanners use technology known as 'direct digitization' (see Box 'Direct Digitization') and in this case the centre frequency is removed after digitization. The end result is the same: a digitized signal centred at zero with a receive bandwidth of several kHz. Most of the signal-to-noise and contrast information is in the low frequencies, while the higher frequencies contain information about resolution in the image (see Box 'An Easy Introduction to k-Space'). Electronic noise is distributed evenly across the whole bandwidth (Figure 5.3). High receive bandwidths have a worse signal-to-noise ratio than low receive bandwidths simply because they include more noise. More noise gives an increased 'graininess' in the final images. However, low receive bandwidths cause chemical shift artefacts (see Section 7.3); advice about choosing the right bandwidth for your images is given in Chapter 6.

Earlier we learned that frequencies higher than f_N will be aliased and appear as low frequencies. In order to avoid this corruption of the spatial information, we use either an electronic (analogue) or digital filter to remove all the MR signals with frequencies higher than f_N. This is known as a *low-pass filter* because it allows low-frequency signals to pass through. Its cut-off frequency, defined by f_N, is set to match the receive bandwidth (RBW). In reality, filters tend to attenuate signals close to the cut-off frequency, i.e. the signals have reduced intensity. If we look at the effect of the filter on all frequencies, we would see a sloping edge at the cut-off (Figure 5.4a), known as 'filter roll-off'.

Does this matter? No it doesn't on most modern scanners because digital filters have much sharper cut-offs, except at very high receive bandwidths. However, the MR signal contains all sorts of information about the tissues in the body, and its height is very important. The filter roll-off makes it look as if the number of protons fades away at the edges of the field of view – like a soft-focus filter on a photograph. That's not very useful for a diagnostic scan! To get round the problem, we can use a technique called *oversampling*.

Direct Digitization

At the end of the twentieth century, analogue-to-digital converters (ADCs) were limited to relatively low digitization rates, and most scanners had a maximum rate of around 1 MHz. However, there have been huge technology advances in the last 15 years, and today it's possible to get an ADC which works at 80 MHz. This means the MR signal can be digitized directly for 1.5 T, 64 MHz: the same ADC can be used for a 3 T scanner, which means it will be aliased to 48 MHz. After digitization, the central frequency can be subtracted digitally instead of using an analogue demodulation, which is prone to phase errors. For more detail on the technology, turn to Chapter 10.

Frequency oversampling means that the ADC runs at double the required frequency. The Nyquist frequency is therefore doubled, and the filter cut-off frequency is also doubled. The filtered digital signal still has a roll-off edge, but we can now discard all the information above our original required frequency (Figure 5.4b). The remaining signals are accurately represented and have no attenuation due to the filters. Older systems with analogue filters will automatically use frequency oversampling, but on modern scanners it is not always necessary. Phase oversampling is similar in principle but it is always controlled by the operator because it has a direct effect on the scan time; it will be fully explained in Section 7.4.3.

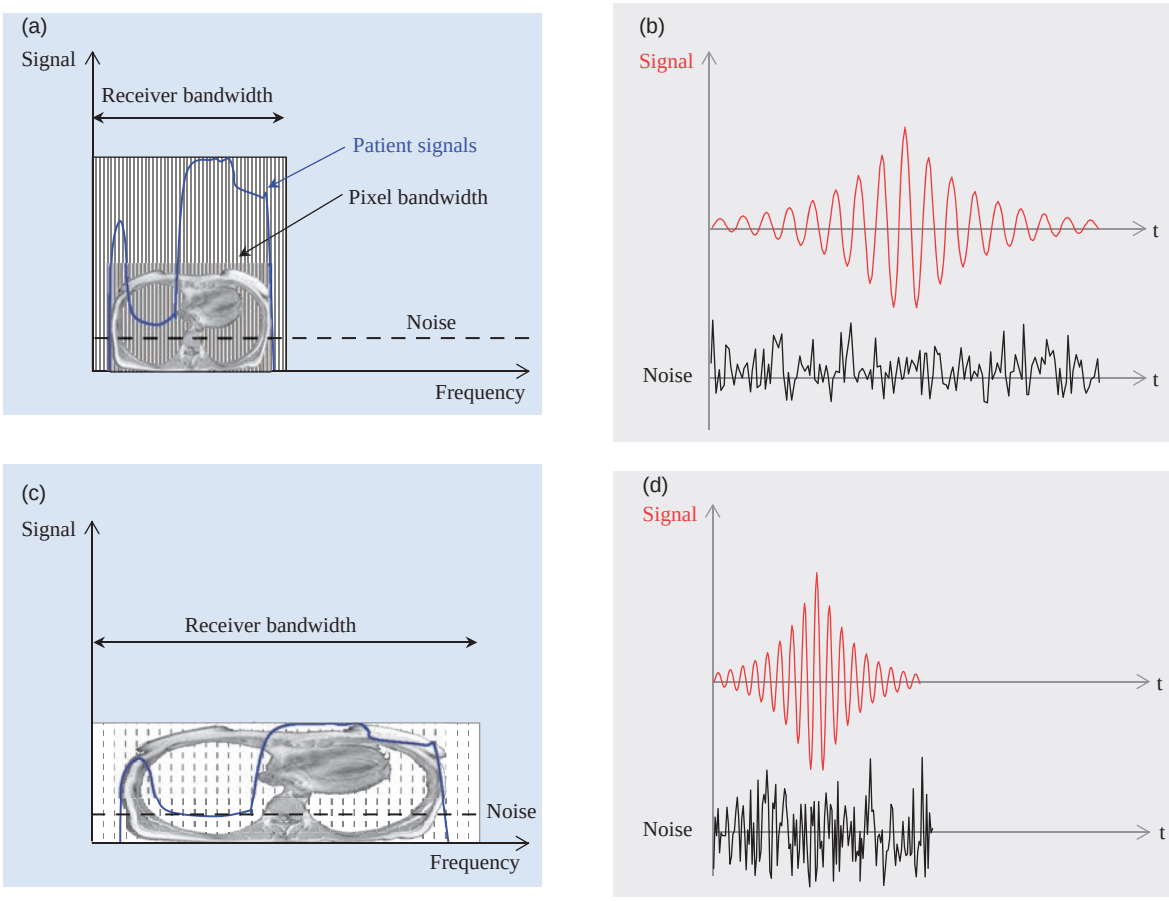

Figure 5.3 Signal and noise in the receive bandwidth. (a) The patient's signals in a narrow bandwidth and (b) the corresponding echo signal and noise. (c) and (d) as (a) but with a wider receive bandwidth; more noise gets into each pixel.

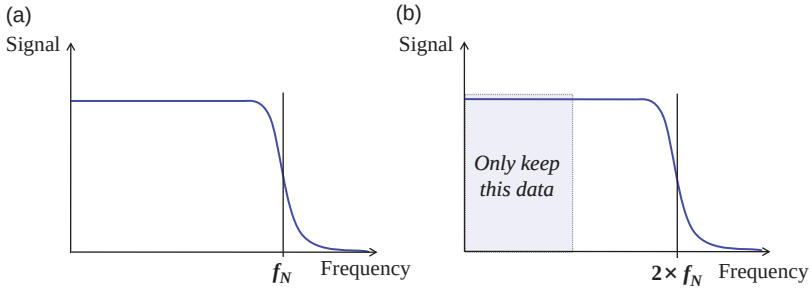

Figure 5.4 (a) The filter at the Nyquist frequency (f_N) has a sloping edge, which distorts the MR signal. (b) By frequency oversampling we can create a sharp cut-off at the original Nyquist frequency.

5.3 Matrices, Pixels and an Introduction to Resolution

Let's start this section with a few simple definitions. The pixels in MR images are organized into rows and columns in a *matrix* (plural 'matrices'). Each pixel in the reconstructed image can be thought of as a location in the computer memory or hard disk, containing a number which represents the signal intensity. Although most images look square, the matrix doesn't have to be square, in other words it doesn't have to have equal numbers of rows and columns. You will have already come across some typical matrix sizes for MR; for example, 256 × 128,

256 × 192, 512 × 256 and 512 × 384, but there are many others in common use.

The image matrix is conventionally shown in the following order: frequency-encode matrix, phase-encode matrix, number of slices (for 3D scans). Don't worry for now what frequency and phase encoding actually mean, that will be covered in Chapter 8. You will often hear people refer to the 'frequency-encode axis' and 'phase-encode axis': these are the two dimensions of the image. Bear in mind that the images have a third dimension too, the slice thickness. The matrix not only controls the final image size, it is also used for the raw data space, and defines how the scanner samples the signals. The raw data matrix is also known as k-space. Each time the sequence is repeated a full line of data in the frequency-encode direction is acquired (e.g. 256 or 512 points). The phase-encode gradient is changed for each repetition and each line has a different position in the phase-encode direction. Thus, as the sequence is acquired, k-space is filled row by row in the raw data matrix. Once the raw data matrix is full it is reconstructed into the final image using a clever piece of maths called a Fourier transform. Notice that when you set the phase-encode matrix, you define how many times the sequence must be repeated (how many rows there are in k-space) and therefore how long the scan will take to acquire. The frequency-encode matrix doesn't have an effect on the scan time, which is why we often have a larger matrix in the FE direction.

Rather confusingly, the FE and PE directions are not always the same. For example, frequency encoding may be either the horizontal or the vertical direction of the displayed image, and it may be along any one of the three anatomical axes (superior–inferior SI, right–left RL or anterior–posterior AP) or even an oblique direction. There may be an annotation on the image for the FE direction; check your manufacturer's manual if you're not sure where it is. If it's not labelled, you can usually recognize the PE axis by looking for ghost signals from motion, as these always go across the PE direction.

An Easy Introduction to k-Space

Many people get very worried about understanding k-space, but don't panic – it's really quite easy. You probably know that the raw data have to be processed or 'reconstructed' before you can see the final image. Simply, you can think of k-space as the 'raw data space' which is used to store the digitized MR signals during data acquisition (Figure 5.5a). When k-space is full (at the end of the scan) the data can be reconstructed to produce the image (Figure 5.5b). The clever bit is that k-space contains lots of information about the real space that it represents, although it's in a coded form. For now we will just look at the basic features of k-space.

When you set the frequency- (FE) and phase-encoding (PE) matrix, you are controlling the k-space

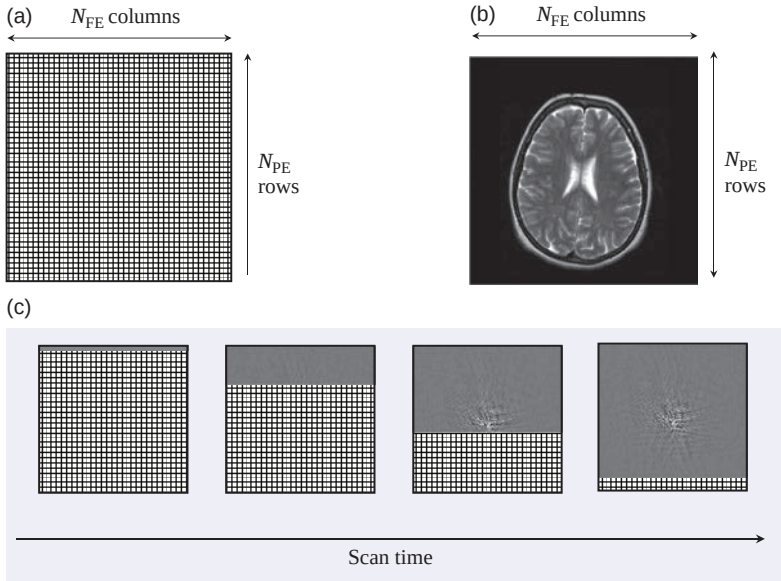

Figure 5.5 (a) k-space is raw data space. The computer reserves a section of memory to hold the digitized raw data during the scan, which has the same number of rows and columns as (b) the final image. (c) During a conventional SE or GE scan k-space is filled with raw data, one line per TR.

(raw data) matrix size and hence the size of the final image. Conventionally we show the FE direction as columns (left–right) in k-space, and the PE direction as rows (top–bottom). So if you choose 256 for frequency encoding, each MR echo will have 256 sample points, thus requiring 256 columns in the k-space matrix for temporary storage. When you set the PE matrix, you control how many echoes have to be acquired and thus how many rows are needed in k-space. So every digitized sample point has its own unique location in k-space, which you can imagine as rows and columns of little boxes, each with its own number.

Although both k-space and (image) space have the same matrix size, the pixels do not correspond directly with each other. That means the information in the bottom left pixel in k-space does not contain the raw information for the bottom left pixel in the image. This is because the reconstruction processing uses a Fourier transform (which will be fully discussed in Chapter 8). Instead, *data in the middle of k-space contain all the signal-to-noise and contrast information* for the image, and *data around the outside contain all the information about the image resolution* (edges and boundaries). You can see this if we take a set of raw data and reconstruct just the middle (Figure 5.6a) or just the outside (Figure 5.6c).

We can use this information in practical ways to design new pulse sequences or to re-order the data acquisition, avoiding artefacts. k-space is linked mathematically to image space, and we will deal with this in Section 8.6.1.

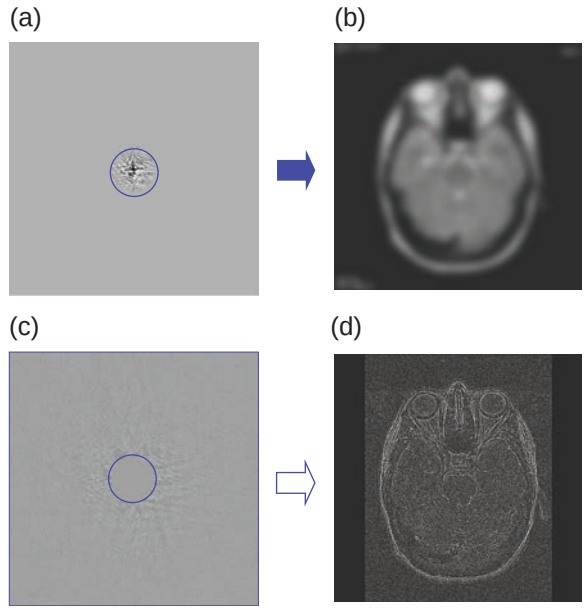

Figure 5.6 Signal and resolution information in k-space. (a) By reconstructing only the data from the middle of k-space we get all the signal and contrast information (b), but it is very blurred. (c) If we erase the middle of k-space and just reconstruct the outside data we can see where the tissue boundaries are (d), but the signal-to-noise ratio is very low and we have no contrast information. Clearly we need both parts of k-space to get a useful MR image!

Choosing Anatomical Axes for Frequency and Phase Encoding

You will probably notice after working in MR for a while that the scanner automatically selects the directions for frequency and phase encoding depending on the orientation of the scan and the part of the body. Although it seems confusing at first, it is worthwhile learning what the system is doing.

The principle is to set up frequency encoding on the longest anatomical axis on the scan, in order to minimize the number of phase encoding steps on the shortest axis. To work it out for yourself, you need to imagine the final image and decide which axis has anatomy extending outside the field of view (FOV). For example, on a coronal head scan, the right–left direction is contained within the FOV, while the superior–inferior direction has anatomy below the bottom of the FOV (the rest of the body!). So the default frequency-encode direction for this scan is superior–inferior (Figure 5.7a): if you put frequency encode along right–left, you will get artefacts (Figure 5.7b). If you are not sure, use a hard window to reveal motion ghosts, which are always along the phase-encode direction (Figure 5.7c).

It is sometimes useful to swap the frequency- and phase-encode directions from this default, for example to avoid flow artefacts in the phase-encoding direction on sagittal spines. Check on your own scanner how to change the PE direction, and make sure you know how the default direction is set for different scans.

When you set the **F**requency-**E**ncoding (FE) matrix, it makes no difference to the scan time (although it might affect the number of slices possible). The **P**hase-**E**ncoding (PE) matrix, however, has a direct effect on the scan time. Thus a PE matrix of 256 takes twice as long to acquire as a 128 PE matrix. To get the best possible resolution, we should ideally use a square matrix (256 × 256 or 512 × 512), but we have to strike a balance between resolution and scan time, so the phase matrix is often reduced. As a general rule you should not

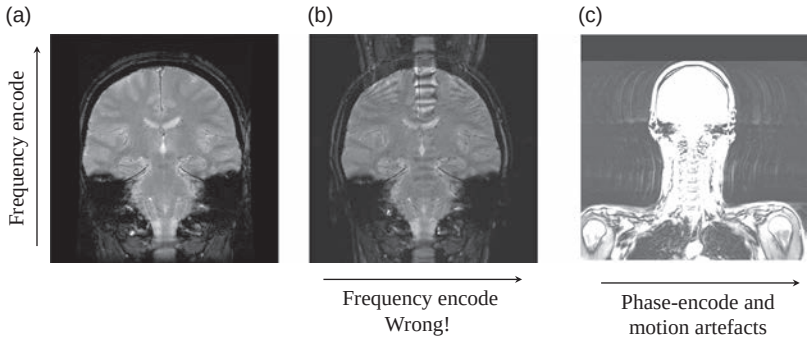

Figure 5.7 Coronal head scan showing frequency encoding on the SI axis (**a**) and the RL axis (**b**) – you can see what happens if it's wrong! (**c**) Motion artefacts show you the phase-encoding axis (with hard windowing to reveal the ghosts).

make the PE matrix less than half the FE matrix, because it makes the pixels too pencil-like. Chapter 6 has more information on optimizing parameters to get the best signal-to-noise ratio, resolution and scan time.

Obviously the size of the voxel is very important since it determines both the image resolution and the signal-to-noise ratio in the image. We can calculate the voxel size in all three dimensions from the field of view (FOV), matrix and slice thickness, all of which are parameters that you can control. We have to calculate the size in the frequency- and phase-encode directions separately, because we usually have different matrix sizes in those directions. So,

$$\text{FE pixel size} = \frac{\text{FE field of view}}{\text{FE matrix}}$$

$$\text{PE pixel size} = \frac{\text{PE field of view}}{\text{PE matrix}}$$

$$\text{Slice pixel size} = \text{slice thickness}$$

The FOV is often square, which makes things a little simpler than they appear. For example, with a 32 cm FOV, a matrix of 256 (FE) × 192 (PE) and a slice thickness of 4.5 mm, we can define the voxel size as $1.25 \times 1.67 \times 4.5$ mm^3. Note that in this book we always use the order FE × PE × slice when quoting voxel sizes (or just FE × PE for pixel size); some manufacturers and textbooks use a different order.

5.4 Slices and Orientations

We've introduced the idea of slice thickness as an important part of the voxel size. From working in the MR unit, you already know that MR can produce slices in any direction – axial, coronal, sagittal, obliques and even double obliques. For comparison, CT produces only axial scans, although if you tilt the gantry you can get obliques and even coronals. But to get coronals e.g. for sinuses, you have to position the patient prone with their head in a rather uncomfortable position and the gantry tilted to its maximum. Actually CT has caught up with MR now that multi-detector helical scanners are the norm; effectively they acquire an axial 3D block which is then reformatted into other orientations.

Getting back to MR, let's take a look at how the slice orientation is defined relative to the scanner. With a standard cylindrical MR system, B_0 is along the bore, and we conventionally define this as the z direction. This corresponds to the superior–inferior axis of the patient (the foot–head direction). By convention, the horizontal axis across the bore is known as X and the vertical axis as Y, corresponding to the right–left and anterior–posterior directions respectively. When we select an axial slice, we are creating images perpendicular to the Z direction. Sagittal images are perpendicular to the X direction, and coronal images are perpendicular to the Y direction. Figure 5.8 shows the principle anatomical axes and corresponding images of the head.

5.5 Displaying Images

We have seen that the MR image is a matrix of pixels containing numbers, which is held in the computer memory or disk that represent the MR signal intensity. They are not much good to us on the computer hard disk – we want to look at the images. When the computer displays an image on the screen, it takes the pixel values and displays them as different intensities on the display screen. Display systems usually have 12- or 16-bit depth (4096 or 32 768 grey levels respectively). However, the human eye can only distinguish about 200 grey levels, so it makes more sense to compress the range of values in the image into relatively few grey levels. To achieve this a **L**ook-**U**p **T**able (LUT) is used to link the pixel values to the screen brightness. The

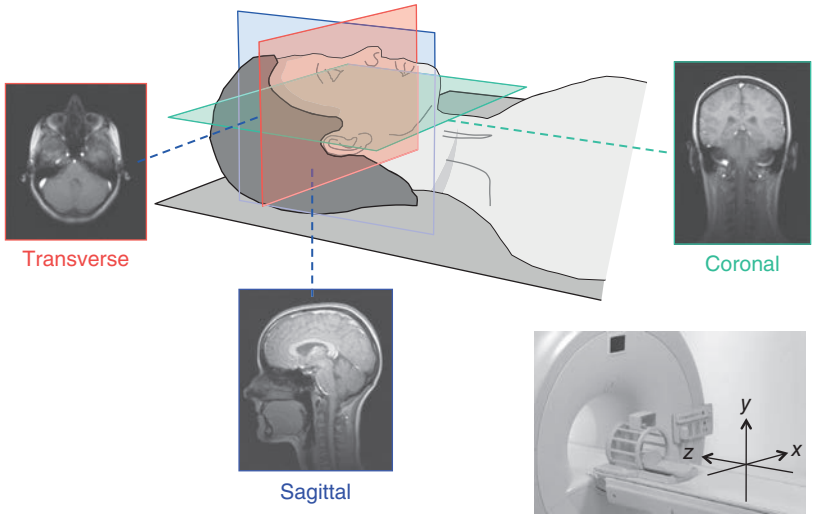

Figure 5.8 The use of physical gradient axes to select the principal slice orientations. By combining physical gradients, oblique and double oblique views are also possible.

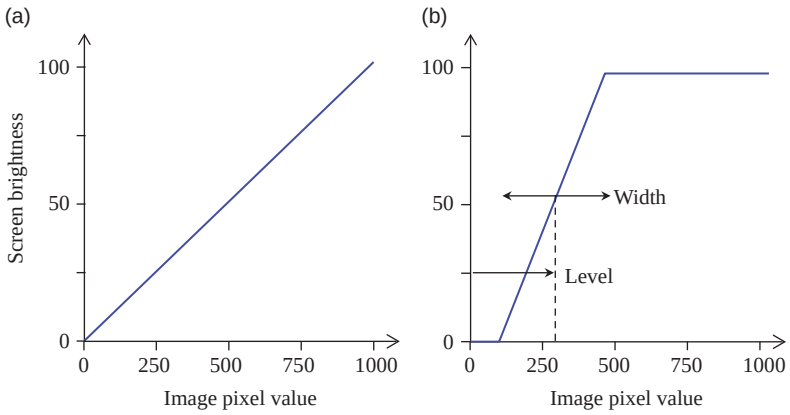

Figure 5.9 (a) A simple look-up table (LUT) scaling the pixel values (0–1000) to the screen brightness controls (0–100%). (b) Reducing the window width changes the LUT to make noise pixels very dark, and to bring out the detail in the mid-intensity pixels.

maximum pixel value in the image is found during the reconstruction process and is stored in the image *header* – the data tacked on to the front of the image file which holds all the information about the acquisition, including the patient's details. So it is quite straightforward to calculate an LUT to scale the pixel values to grey levels (Figure 5.9a). In this example, the highest pixel value has the brightest screen intensity, zero-valued pixels are black, and everything in between is scaled accordingly.

DICOM: A Common Language Leading to Misunderstanding?

DICOM (**D**igital **I**maging and **CO**mmunications in **M**edicine) is a standardized format for storing, viewing, and transferring medical images. It has been developed over several decades, by groups representing all manufacturers, for all digital medical images. Updates are published, reflecting changes in radiology practice. For every image, there is a 'header' which contains all the necessary information about the image, from the obvious (patient's name, date of scan, imaging sequence used, etc.) to the not-so-obvious (e.g. what orientation was the image last displayed, the date when the scanner was last serviced).

Each piece of information is called an element, and each element has a tag, a keyword, plus some other details which are not so important here. The tag is a numerical code consisting of two bytes, usually shown as two four-digit hexadecimal numbers. The keyword describes what the element represents, and most of them are human-readable – so you can often

guess what the element holds. The header of each image has the tag followed by the value for this particular image, then the next tag with its value, etc., until all the necessary information is recorded. Then the image file stores the actual image data, in an order defined within the header. Clever: as the receiving computer reads the file, it learns exactly how to read the image data so that it can be displayed properly.

There is, however, a slight problem with the DICOM standard. Manufacturers are allowed to define private elements for themselves, as many as they like. And although they usually do use all the public elements properly to share common information, this is not always the case. If we think of DICOM as a language, each manufacturer speaks a slightly different dialect! This means that there is always room for misinterpretation when data are sent between devices by different manufacturers. However, in this DICOM Tower of Babel, there is one comfort: every manufacturer publishes a DICOM Conformance Statement, usually easily found on their website. The conformance statement describes exactly how the DICOM header is implemented for this particular scanner and software release, and can help to unravel the misunderstandings.

While this is simple, it rarely shows the image in the sort of detail necessary for diagnostic imaging. Often there are only a few high-value pixels, so the whole image looks very dark. We can improve things if the LUT has a steeper slope, so that all pixel values above a certain level are displayed at maximum brightness. On the other hand, it is also helpful to make the background noise as dark as possible, and this is done by setting all pixel values below the noise level to have minimum brightness (Figure 5.9b). This type of modification to the LUT is known as setting the window width and level.

The *window width* is the range of pixel values which are displayed across the screen's brightness range, while the *level* is the central value of the window width. Reducing the window width increases the contrast of the displayed image, while moving the level up or down makes the whole image darker or brighter respectively (Figure 5.10). This aspect of changing the displayed image is very similar to that used in CT and DSA. However, remember that you are only changing the displayed pixel intensities, not the values in the underlying MR image.

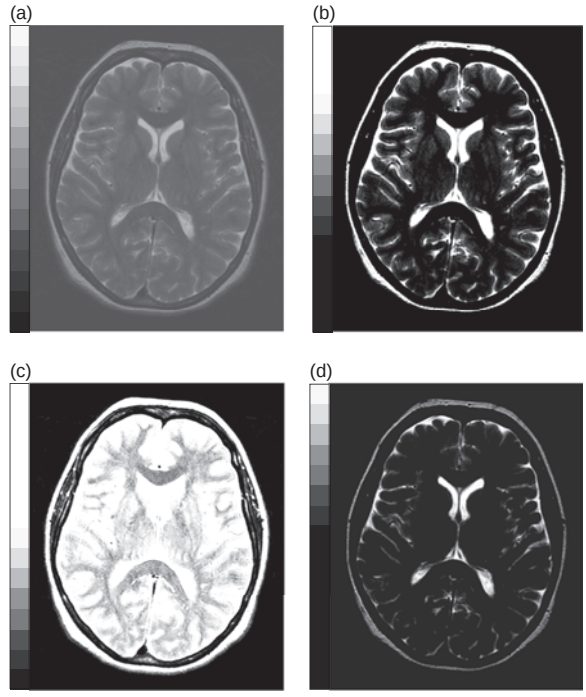

Figure 5.10 The effect of changing the window width and level on the displayed image. (**a**) A wide window and (**b**) a narrow window. (**c**) A low window level makes the image very bright; (**d**) a high level makes it much darker. The greyscale bar on the left of each image shows how the LUT is changed.

5.6 What do the Pixels Represent?

We have been talking about pixels and matrices in a rather abstract way. Let's see how they correspond to the physical reality of the patient being scanned. What does the number in each pixel actually mean? We know that it is calculated during image reconstruction, and we have already said that it represents the MR signal intensity. In fact, it represents the signal from just a small volume of tissue within the patient's body, known as a voxel (a contraction of 'volume element'). You can imagine the front face of the voxel as the pixel which is displayed on the scanner (Figure 5.11a). The third direction is determined by the slice thickness of the image.

So if we could chop up the patient into slices of the right width, cut each slice into the appropriate number of rows and columns (Figure 5.11b), and then measure the MR signal from just one of the resulting voxels, that is the number held in the computer. The higher the MR signal, the higher the number. The computer then uses this number to control the brightness of the

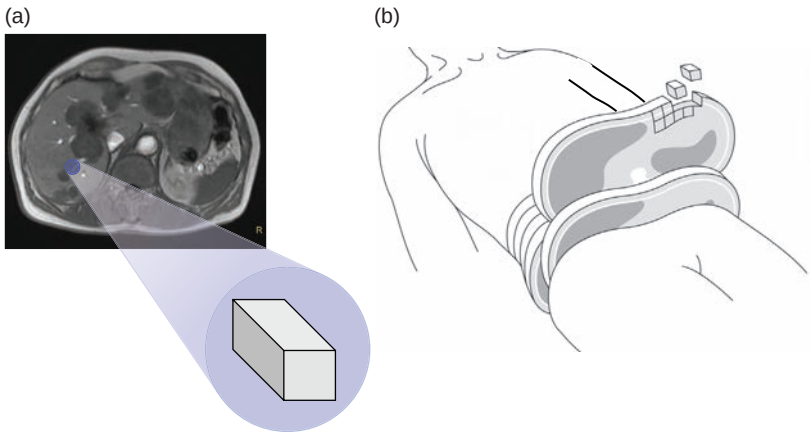

Figure 5.11 The relationship between pixels on the screen and the patient being scanned. (a) The pixel on the screen is just the front face of a three-dimensional voxel within the patient. (b) Chopping up the patient into voxels!

corresponding pixel on the image display screen (previous section). Thus the larger the number, the brighter the displayed pixel on the screen. Working backwards, we can say that the brightness of the pixel on the (two-dimensional) screen represents the MR signal intensity from the three-dimensional volume of tissue in the patient, and we are just seeing the front face of the voxel.

The actual signal intensity depends on many factors, including the sequence timings and the intrinsic T_1, T_2 and PD of the tissues. If you scanned the same patient using the same parameters on a different scanner (even if it was made by the same manufacturer) you wouldn't necessarily get exactly the same pixel values in the images. Compare this with CT scans, where the pixel values are in Hounsfield units, and we get pretty much the same values for each patient, even between scanners.

Partial Volume Effects

If we chopped up a patient into 5 mm slices and sub-divided each slice into 256 × 256 pixels, would each voxel contain just one type of tissue? That would depend on which part of the body was being scanned and the relative size of the voxels. If we were imaging the thorax, we might expect most of the voxels to contain only lung, cardiac muscle or intercostal muscle. However, at the boundaries, where the lung is next to the mediastinum or rib cage, there will be some voxels which contain a mixture of tissues. If we imagine the same situation in the head, there will be many voxels that contain both grey and white matter, and around the cerebellum they would also include contributions from CSF. The signal from such mixed voxels will be the weighted sum of the signals from the various tissues.

Let's now take this imaginary situation to two extremes. First let's consider the effect of very small voxels, e.g. $0.25 \times 0.25 \times 3.00\ mm^3$. In a head scan many of the voxels will contain just one tissue and the intensity is an accurate representation of the tissue structure (Figure 5.12a). Now let's consider a more usual scan, i.e. voxels $1 \times 1 \times 3\ mm^3$. The same slice location (Figure 5.12b) will have a mixture of tissues within each voxel and it is obvious that fine structures cannot be resolved. This is known as the partial volume effect and it is a critical limiting factor of all digital imaging techniques. We cannot completely avoid partial volume effects as very small voxels take a long time to acquire (the scan in Figure 5.12a took 8 min 23 s compared with 2 min 5 s for Figure 5.12b), and have low signal-to-noise ratio. We have to reach a compromise between resolution, signal-to-noise ratio and scan time, as described in Chapter 6 in more detail.

5.7 From 2D to 3D

As you now know, each image is a 2D representation of a 3D slice of the patient. You should always remember that your image has depth, due to the slice thickness. MR and CT images are known as cross-sectional imaging techniques to distinguish them from plain X-radiographs and DSA, which are both projection techniques where the final image has lost the 3D information about the patient.

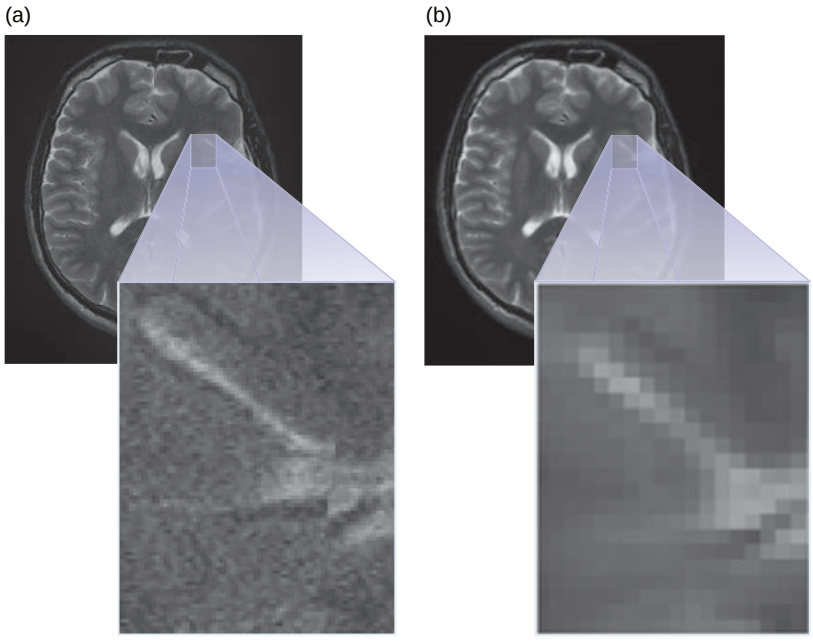

Figure 5.12 (a) High-resolution head scan with 0.25 × 0.25 × 3.00 mm^3 voxels. (b) The same slice position with 1 × 1 × 3 mm^3 voxels showing the partial volume effect.

Since we have to repeat the imaging sequence many times to produce an image, and because we set the TR to get the appropriate image contrast (as described in Chapter 3), scan times tend to be relatively long. If we were just producing one slice per scan, it would take all day to get enough information! Fortunately we can use most of the wasted time during the TR to image other slices.

Suppose we have a TR of 600 ms and a TE of 20 ms, to give T_1-weighted images. It takes about 30 ms to excite one slice, generate the spin echo and collect the data. That leaves 600 – 30 = 570 ms before we have to re-excite that slice for the next TR. While it's waiting, the scanner excites a second slice and collects the data from its echo, taking another 30 ms. This process can be repeated, exciting new slices and collecting data, until it's time to re-excite the first slice (Figure 5.13). So during each TR, the scanner excites and collects echoes from many slices. The signals of different slices do not interfere with each other, thanks to the way slice selection works usually with a small gap between adjacent slices (see Section 7.4.2). A simple calculation (600 ÷ 30) shows us that we can get 20 slices within the TR. So for the same scan time as one slice, we can image up to 20 slice locations. This is known as *multi-slice* imaging.

Due to imperfections in the RF pulses we usually have to introduce a slice gap to separate the slices. This is measured as the distance between the slice edges, although sometimes it can be defined as the separation between slice centres (Figure 5.14) – you just need to know which definition is used by your system. We generally try to keep the slice gap to a minimum, since tissues in the gap are not imaged at all. If the gap is too big, there is the possibility of completely missing a small pathological feature.

Falling Into the Gaps

Different manufacturers have different ways of setting the gap between slices in a multi-slice sequence. GE Healthcare systems let you set the edge-to-edge slice gap in millimetres.

Siemens scanners use a distance factor, which is the edge-to-edge gap as a percentage of the slice width. So if you have a slice width of 5 mm and you want a 1 mm gap, you set a distance factor of (1 ÷ 5) × 100% = 20%. A 3 mm slice with a gap of about 0.5 mm would be achieved with a distance factor of 15%, and so on.

In Philips systems you also set the slice gap, the edge-to-edge distance between the slices. The system default is a gap of 10% of the slice thickness, but it's always shown in millimetres.

True 3D scanning, rather than 2D multi-slice imaging, requires a different kind of imaging technique, with phase encoding in the slice direction as well as in-plane. For every slice encode, we must acquire all the in-plane phase encodes. So the scan

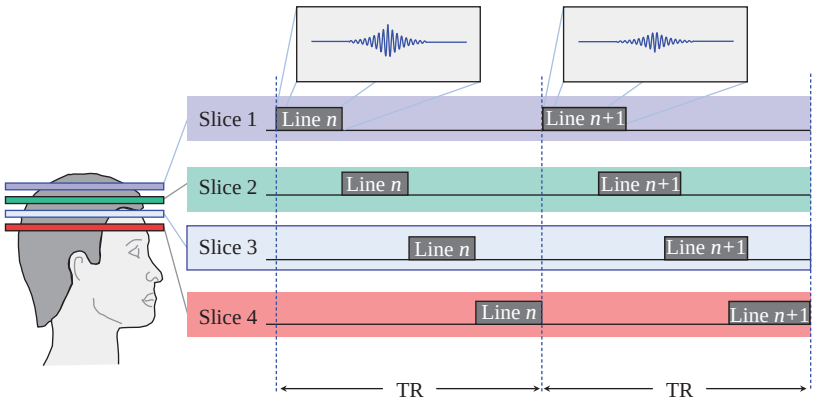

Figure 5.13 Multi-slice imaging. Once the spin echo has been collected, the scanner has plenty of time to excite other slices and collect their data, before starting to repeat the sequence with the first slice.

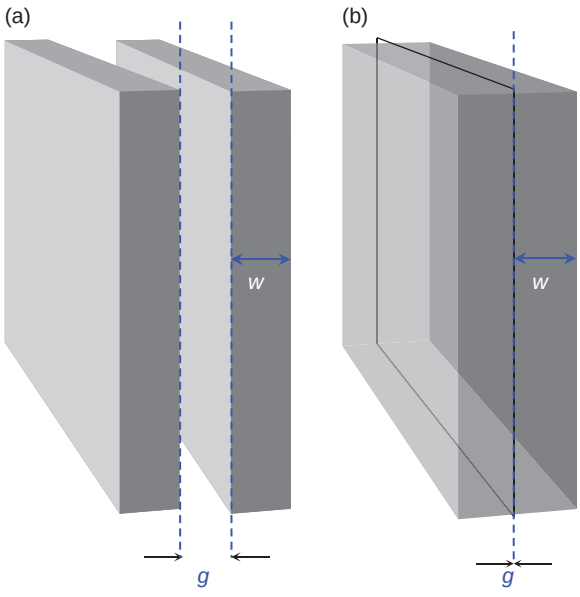

Figure 5.14 Definition of slice-to-slice separation: (a) distance factor 100%; (b) contiguous slices (distance factor = 0%).

time gets multiplied by the selected number of slices (sometimes called *partitions*) in the 3D volume. The majority of 3D scans are acquired with gradient-echo sequences with a very short TR, using the flip angle α to control the amount of T_1 weighting. Turbo spin echo can also be used for 3D imaging, using some extra tricks with flip angles to manage the power deposition, blurring and contrast. 3D TSE sequences often have a special name from the manufacturer; see Chapter 12 for more details on these.

Although slow to acquire, 3D scans have a few advantages over multi-slice 2D imaging. For example, it's possible to define very thin slices with no slice gaps (contiguous slices), and, if the voxels are nearly isotropic, the resulting volume can be reformatted on a workstation to produce images in any orientation. Signal-to-noise ratio (SNR) is also higher compared with 2D scans, by a factor of $\sqrt{N_{slice}}$ where N_{slice} is the number of slices in the 3D volume. This extra SNR compensates for the high-resolution voxels (which reduce SNR), so 3D scans are a good choice when very high resolution is required, and when it is important not to miss anything in the slice gaps. We will discuss this technique in more detail in Section 8.8.

See also:

- How frequency- and phase-encoding gradients work: Chapter 8.
- k-space and Fourier transforms: Section 8.6.
- 3D imaging: Section 8.8.
- Optimizing image resolution and signal-to-noise ratio: Chapter 6.

Further Reading

Brown MA and Semelka RC (2010) *MRI: Basic Principles and Applications*, 4th edn. Hoboken, NJ: Wiley-Blackwell, chapter 5.

Elster AD and Burdette JH (2001) *Questions and Answers in Magnetic Resonance Imaging*, 2nd edn. London: Mosby-Yearbook, chapter 4. Also on the web at http://mri-q.com [accessed 23 March 2015].

Hashemi RH and Bradley WG Jr (2010) *MRI: The Basics*, 3rd edn. Baltimore, MD: Lippincott, Williams & Wilkins, chapters 12 and 13.