Preprocessing fMRI data

3.1 Introduction

Just as music recorded in a studio requires mixing and editing before being played on the radio, MRI data from the scanner require a number of preprocessing operations in order to prepare the data for analysis. Some of these operations are meant to detect and repair potential artifacts in the data that may be caused either by the MRI scanner itself or by the person being scanned. Others are meant to prepare the data for later processing stages; for example, we may wish to spatially blur the data to help ensure that the assumptions of later statistical operations are not violated. This chapter provides an overview of the preprocessing operations that are applied to fMRI data prior to the analyses discussed in later chapters. The preprocessing of anatomical data will be discussed in Chapter 4.

In many places, the discussion in this chapter assumes basic knowledge of the mechanics of MRI data acquisition. Readers without a background in MRI physics should consult a textbook on MRI imaging techniques, such as Buxton (2002).

3.2 An overview of fMRI preprocessing

Preprocessing of fMRI data varies substantially between different software packages and different laboratories, but there is a standard set of methods to choose from. Figure 3.1 provides an overview of the various operations and the usual order in which they are performed. However, note that none of these preprocessing steps is absolutely necessary in all cases, although we believe that quality control measures are mandatory.

3.3 Quality control techniques

The availability of comprehensive fMRI analysis packages makes it possible to analyze an fMRI data set and obtain results without ever looking closely at the raw data, but
3.3 Quality control techniques

![Diagram of quality control steps](image)

Figure 3.1. An overview of the standard fMRI preprocessing stream. The appropriate quality control steps are noted at each point. With the exception of motion correction, the rest of the preprocessing steps can be viewed as optional, and their use will depend upon the needs of the study and the available data.

In our opinion it is important for the fMRI researcher to keep a close eye on the raw data and processed data at each step to ensure their quality. Otherwise, one risks falling prey to the old adage: “Garbage in, garbage out.” In this section we outline a number of methods that one can use to explore and visualize the presence of artifacts in fMRI data.

3.3.1 Detecting scanner artifacts

A number of artifacts can occur due to problems with the MRI scanner.

Spikes are brief changes in brightness due to electrical instability in the scanner (e.g., due to static electricity discharge). They generally appear as a regular pattern of stripes across the image (see Figure 3.2). Spikes occur relatively infrequently on the current generation of MRI scanners, but when they do occur, they can have large detrimental effects on the analysis.
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Figure 3.2. Example of a spike in an fMRI image, reflected by the large diagonal stripes. This image comes from a patient with a brain tumor, which appears as a large white blob at the bottom right side of the brain image. (Images courtesy of Mark Cohen, UCLA)

Figure 3.3. Example of ghosting in an fMRI image. The ghosting is more apparent when the top value in the intensity window of the image viewing program is reduced, as shown in the right panel. (Images courtesy of Mark Cohen, UCLA)

Ghosting occurs when there is a slight offset in phase between different lines of K-space in an echoplanar acquisition and can also occur due to periodic motion such as heartbeat or respiration. It appears as a dim ghost of the brain to each side in the phase-encoded direction of the MRI image (see Figure 3.3). It may be difficult to see ghosting when looking at an image with the brightness window set to the entire range of the image; it can be seen more easily by reducing the top value of the intensity window in the image viewing program (as shown in Figure 3.3). In fMRI, ghosting can result in activation appearing to occur outside of the brain and also cause mislocalization of activation within the brain, if one region of the brain has a ghost in another part. Ghosting rarely causes serious problems for fMRI on the latest generation of MRI systems, but substantial ghosting problems do still occur on occasion. When detected, they should be investigated with your local MRI technician or physicist.
3.3 Quality control techniques

3.3.2 Time series animation
The human eye is very good at detecting changes when an fMRI time series is viewed as an animation. Several tools allow viewing of animated time series; for example, in FSLView, a time series can be viewed as an animation by simply clicking the Movie Mode button. Any glaring changes over time can then be investigated in order to better understand their source; in Chapter 5, we will discuss methods for dealing with bad data points in statistical analysis.

3.3.3 Independent components analysis
As we will see in later chapters, fMRI analysis generally proceeds by creating a statistical model (e.g., a model of task effects) and then finding regions where that model explains the data well. However, sometimes we wish to find signals in the data whose form is unknown, as in the detection of artifacts in fMRI data. There is a set of exploratory data analysis methods that do just this, by detecting systematic patterns in the data; these methods will be described in more detail in Chapter 8 on connectivity modeling, but we introduce them here in the context of artifact detection. These methods decompose the four-dimensional dataset into a set of spatio-temporal components that are mixed together in different proportions to obtain the observed signal. There are many different ways that such a decomposition can be performed, which generally differ in the kinds of constraints that are put upon the components. For example, principal components analysis (PCA) finds a set of components that are orthogonal to one another in multidimensional space, whereas independent components analysis (ICA) finds a set of components that are independent of one another. For a more detailed description of ICA, see Section 8.2.5.2.

ICA has proven very useful for the identification of artifacts in fMRI data. Figure 3.4 shows an example of such an ICA component, detected using the FSL MELODIE ICA tool. ICA is particularly useful for identifying signals related to within-scan effects of head motion or other nonrigid effects of motion, which cannot be removed by standard motion correction techniques.

Once a set of artifactual components is identified, those components can be removed from the data, creating a “denoised” dataset. It is important that such identification of components be based on explicit criteria for rejection to prevent bias; these criteria will generally be based on both the spatial and temporal characteristics of the components. For example, one criterion might be that components will be rejected if they show strong alternation between slices (which is good evidence of a motion-related effect when fMRI data are collected using the common interleaved method; see Figure 3.7) along with a timecourse that shows a large spike at one or more timepoints (see Figure 3.4). Methods for the automated classification of ICA components have been developed which may provide more reliable and unbiased detection of artifact-related components than manual classification (Tohka et al., 2008). However, we have found the manual examination of ICA components to be
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Thresholded component map

Time series plot of component response

Figure 3.4. An example of a motion-related component detected using FSL’s MELODIC ICA tool. The top panels shows a thresholded map that depicts which voxels load significantly on the component, either positively (red) or negatively (blue). Telltale signs of motion include the alternating response between slices (reflecting motion in an interleaved acquisition), coherent positive or negative signals around the edges of the brain, and the presence of a large single spike in the timecourse of the component.

A useful exercise for researchers who are new to fMRI, as it provides a much better view of the variety of signals that may be present in an fMRI dataset.

3.4 Distortion correction

The most common method for fMRI acquisition, gradient-echo echoplanar imaging (EPI), suffers from artifacts near regions where air and tissue meet, such as the sinuses or ear canals. These are due to the inhomogeneity of the main magnetic field (known as $B_0$) caused by the air–tissue interfaces, and take two forms: dropout and geometric distortion. Dropout is seen as reduced signal in the brain areas adjacent to these air–tissue interfaces, such as the orbitofrontal cortex and the lateral temporal
3.4 Distortion correction

Figure 3.5. An example of signal dropout in gradient-echo EPI images. The EPI image on the left and the T1-weighted image on the right are combined in the middle (using a transparent overlay in FSLview) to show regions where there is brain tissue in the T1-weighted image but no signal in the EPI image. The orbitofrontal region, which has substantial dropout in this image, is highlighted by the blue box.

lobe (see Figure 3.5). Once the data have been acquired, there is no way to retrieve data from a region with significant dropout, so it is best to employ methods for MRI acquisition that reduce dropout. It is very important to understand the particular dropout patterns that are present in every dataset. For example, one would not want to conclude that the orbitofrontal cortex is not responsive to a particular task manipulation if there is no signal actually present in that region due to dropout. A useful way to appreciate these dropout patterns is to overlay the functional image over a structural image that it has been aligned to (as shown in Figure 3.5).

In addition to signal loss, fMRI images can also be spatially distorted in the same regions. When gradients are applied to encode spatial information in the MRI image, these inhomogeneities in the magnetic field result in errors in the location of structures in the resulting images. Most commonly, regions in the anterior prefrontal cortex and orbitofrontal cortex are distorted. The distortion occurs along the phase encoding direction that is used by the MRI pulse sequence, which is generally the Y (anterior-posterior) axis. These distortions make it difficult to align functional MRI data with structural images.

It is possible to correct somewhat for the effects of magnetic field inhomogeneity using a field map, which characterizes the B0 field (Jezzard & Balaban, 1995). Pulse sequences for field mapping are available for most MRI scanners. They generally work by obtaining images at two different echo times. The difference in phase between the two images can be used to compute the local field inhomogeneity, and these values can then be used to create a map quantifying the distance that each voxel has been shifted. By inverting this map, one can determine the original location of the data in each voxel. Figure 3.6 shows an example of distortion correction.

A number of difficulties arise in practice with the use of field maps to unwarp EPI images. First, if there is noise in the field map, then this will introduce noise into
the unwarped images. One way to address this is to apply some form of low-pass filtering (or smoothing) to the field maps, which reduces errors in the unwarped images (Hutton et al., 2002). Second, if the field map is acquired separately from the fMRI time series, then head motion between these scans must be accounted for. It is possible to obtain dual-echo data throughout the fMRI time series, which allows estimation of a unique field map at each timepoint, but this approach is rarely used. There has also been work on methods to combine head motion correction and distortion correction (Andersson et al., 2001), but there are not generally available tools to perform this kind of integrated correction, and it is not clear whether the benefits outweigh the costs of increased complexity.

If distortion correction is employed, then the postcorrection images should be inspected and compared to the precorrection images to ensure that the distortion
correction operation has not introduced any artifacts (which can occur if there is a problem with the field map).

### 3.5 Slice timing correction

Nearly all fMRI data are collected using two-dimensional MRI acquisition, in which the data are acquired one slice at a time. In some cases, the slices are acquired in ascending or descending order. In another method known as interleaved acquisition (see Figure 3.7), every other slice is acquired sequentially, such that half of the slices are acquired (e.g., the odd slices) followed by the other half (e.g., the even slices). The use of 2D acquisition means that data in different parts of the image are acquired at systematically different times, with these differences ranging up to several seconds (depending upon the repetition time, or TR of the pulse sequence) (see Figure 3.8).

![Figure 3.7](image1.png)

**Figure 3.7.** A depiction of slice timing in an interleaved MRI acquisition. The slices are acquired in the order 1-3-5-7-2-4-6-8; the times on the right show the relative time at which the data in the slice starts being acquired, assuming a repetition time of 2 seconds.

![Figure 3.8](image2.png)

**Figure 3.8.** The effects of slice timing on the acquired data. The three curves represent samples from the same hemodynamic response at the times corresponding to the slices in Figure 3.7. The slices acquired later in the volume show an apparently earlier response at each time point because the hemodynamic response has already started by the time that they are acquired.
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Figure 3.9. A depiction of slice timing correction. The blue line corresponds to the original time series from a single voxel in the slice acquired at the beginning of each volume acquisition. The red line reflects the interpolated timecourse that would be obtained to correct this slice to match the center slice (which is acquired halfway through the volume, at time TR/2). In this example, linear interpolation is used for simplicity; actual slice timing correction methods use sinc interpolation, which will introduce less smoothing in the signal.

These differences in the acquisition time of different voxels are problematic for the analysis of fMRI data. The times of events (such as trials in a task) are used to create a statistical model, which represents the expected signal that would be evoked by the task. This model is then compared to the data at each timepoint; however, this analysis assumes that all data in the image were acquired at the same time, resulting in a mismatch between the model and the data that varies across the brain.

Slice timing correction was developed to address this mismatch between the acquisition timing of different slices (Henson et al., 1999). The most common approach to slice timing correction is to choose a reference slice and then interpolate the data in all other slices to match the timing of the reference slice (see Figure 3.9). This results in a dataset where each slice represents activity at the same point in time. To apply slice timing correction, it is necessary to know the exact timing of the acquisition, which differs across scanners and pulse sequences; this information can generally be obtained from the local physics support personnel.

Despite its seeming appeal, there has been a move away from the use of slice timing correction in practice. One reason is that when it is used, artifacts in one image can be propagated throughout the time series due to the use of sinc interpolation. This is of particular concern in light of the interactions between slice timing and head motion, which will be discussed in more detail in Section 3.6.6. Practical experience also suggests that, with relatively short repetition times (TR ≤ 2 seconds) and interleaved acquisitions, event-related analysis is relatively robust to slice timing problems. This is particularly likely to be the case when using interleaved acquisition followed by spatial smoothing, since data from adjacent slices (collected 1/2 TR away from one another) are mixed together, resulting in a practical slice timing error of only TR/2. Finally, the use of statistical models that include temporal derivatives, which allow for some degree of timing misspecification, can also reduce the impact of slice timing differences (see Section 5.1.2).
3.6 Motion correction

Even the best research subjects will move their heads (e.g., due to swallowing), and this motion can have drastic effects on fMRI data, as shown in Figure 3.10. There are two major effects of head motion. First, it results in a mismatch of the location of subsequent images in the time series; this is often referred to as bulk motion because it involves a wholesale movement of the head. It is this kind of motion that standard motion correction techniques are designed to correct, by realigning the images in the time series to a single reference image. Bulk motion can have large effects on activation maps, which usually occur at edges in the image; this is due to the fact that large changes in image intensity can occur when a voxel that has no brain tissue in it at one point suddenly contains tissue due to motion. As shown in Figure 3.10, these artifacts can take several forms depending upon the nature of motion, such as a ring of positive or negative activation (reflecting movement along the inferior–superior axis), positive activation on one side of the head and negative activation on the other side (reflecting movement along the left-right axis), or large regions of positive or negative activation in the orbitofrontal cortex (reflecting rotation along the left–right axis). Another common location for such artifacts is at the edges of the ventricles.

Second, head motion can result in disruption of the MRI signal itself. When the head moves, the protons that move into a voxel from a neighboring slice have an excitation that is different from that expected by the scanner, and the reconstructed signal will not accurately reflect the tissue in the voxel; this is known as a spin history effect (Friston et al., 1996b). These effects can result in large changes in the intensity of a single slice or set of slices, which can be seen as stripes of alternating bright and dark slices if interleaved acquisition is used. This form of motion cannot be corrected using standard motion correction techniques, but it can potentially

Figure 3.10. Examples of the effects of head motion on the resulting statistical maps. In each case, the image shows activation for a blocked design motor task compared to a resting baseline. The left panel shows a drastic example of motion-related artifacts (from a dataset of an individual with Tourette syndrome). This is often referred to as a “flaming brain” artifact. The right panel shows a more typical example, where motion is seen as activation along one side of the brain, reflecting motion in that direction that is correlated with the task.
be corrected using exploratory methods such as ICA (see Section 8.2.5.2) or using spin-history corrections (Friston et al., 1996b; Muresan et al., 2005).

3.6.1 Stimulus correlated motion

One of the most difficult problems with motion arises when head motion is correlated with the task paradigm, which can occur for a number of different reasons. For example, if the task requires overt speech or movement of large muscle groups, then task-correlated motion should be expected. However, it can also occur in other cases; for example, subjects may become tense during difficult cognitive tasks compared to easy tasks, and this may result in head motion that is correlated with the task. Stimulus-correlated motion is problematic because it can result in changes in activity whose timing is very similar to the timing of the task paradigm, resulting in artifactual activation. Furthermore, because it is so closely correlated with the task, removal of these motion-related signals will often remove task-related signals as well, reducing the sensitivity of the statistical analysis. If the timing of motion is known (as in studies using overt speech), one way to address this issue is to take advantage of the delayed nature of the BOLD response; depending upon the nature of the motion, it may be possible to reduce the correlation between the motion and BOLD response through the use of jittered event-related designs (e.g., Xue et al., 2008).

3.6.2 Motion correction techniques

The goal of motion correction (also known as realignment) is to reduce the misalignment between images in an fMRI time series that occurs due to head motion. An overview of the motion correction process is shown in Figure 3.11. In brief, each

![Figure 3.11. An overview of the motion correction process. In the first step, the motion is estimated between each image and the reference, which in this example is the middle image in the time series. In the second step, the parameters obtained for each image are used to create a resliced version of the image that best matches the reference image.](image-url)
3.6 Motion correction

image in the fMRI time series is aligned to a common reference scan using an image registration method, and the images are then resliced in order to create realigned versions of the original data.

Motion correction tools generally assume that head motion can be described using a rigid body transformation, which means that the position of the head can change (by translation or rotation along each of the three axes) but that the shape of the head cannot change. These techniques can thus only correct for bulk motion. However, as noted earlier, when motion occurs during the acquisition of a scan, it can result in disruption of the image intensities, rather than a simple movement of the head in the image. Because these effects cannot be described by rotation or translation of the entire brain, they cannot be corrected by current motion correction methods.

3.6.2.1 Estimating motion

Figure 3.12 shows an example of head motion estimates for an fMRI time series. The plots shown here reflect the parameters of the rigid body transformation that are estimated for each timepoint in comparison to the reference image; note that the parameters are zero at the reference image since it matches itself exactly. Motion correction tools generally provide a plot of these parameters and/or a file that contains the parameters. It can often be useful to transform these estimates to obtain estimates of head displacement from timepoint to timepoint, which is equivalent to the temporal derivative of the motion parameters (see lower panels in Figure 3.12); this can be obtained at each timepoint (from 2 to N) by subtracting the parameter at the previous timepoint.

3.6.2.2 Choosing a target

The target for motion correction can be a specific single image or a mean of the time series. There does not seem to be any appreciable benefit of using a mean image rather than a single image (Jenkinson et al., 2002), and it requires an extra computational step, so it is generally recommended that a single image be used as the reference. When using a single image as a target, it is advisable to use an image from the middle of the time series rather than the first timepoint, for two reasons. First, the middle image should be the closest (on average) to any other image in the time series. Second, the first few images in an fMRI time series sometimes have slightly different contrast (if the magnetization has not yet reached a steady state), which makes them less similar to the rest of the time series.

3.6.2.3 Choosing a cost function

Most motion correction algorithms use a within-modality cost function that is sensitive to the correlation of values between the target and reference images, such as least squares (SPM5) or normalized correlation ratio (FSL 4); see Section 2.3.2 for background on cost functions for image registration. However, when large amounts of activation are present, it is possible that this task-related signal could
Figure 3.12. Plots of estimated head motion. The top panels plot translation between timepoints, before and after motion correction (i.e., how far the brain is from the reference image). The bottom panels plot the first derivative of the data in the top panels, which correspond to relative displacement at each timepoint (i.e., how far the brain is from the previous timepoint). Relative displacement is often more useful as a means to inspect for motion than absolute translation.

be misinterpreted as motion when such a cost function is used (Freire & Mangin, 2001), resulting in inaccurate motion estimates and errors in the realigned images. Other cost functions such as mutual information or robust estimators may be less sensitive to these effects (Freire et al., 2002). It is not clear how important these effects are in practice. The simulations presented by Friere and Mangin suggest that these effects do not emerge unless relatively large proportions of the brain are strongly active. This suggests that users with tasks that result in large amounts of activation may wish to use a robust cost function such as mutual information for motion correction to prevent contamination of the motion estimates by activation signals.

3.6.2.4 Creating realigned images

A number of possible interpolation methods can be used to create the realigned time series (see Section 2.3.4 for background on these methods). Linear interpolation is
3.6 Motion correction

relatively fast, but is known to result in a greater amount of smoothing and error in the interpolated images when compared to higher-order methods (Ostuni et al., 1997). Higher-order methods used for interpolation in motion correction include sinc, spline, and Fourier-based interpolation. The practical differences between these methods appear to be small (Oakes et al., 2005), so choices between these methods will likely be driven by considerations such as processing time and availability within a particular package. If processing time is not a concern, then a higher-order method should be used when available, though it should also be noted that the gains in accuracy obtained using a higher-order interpolation method are likely to be swamped by any spatial smoothing that is applied later in the processing stream.

3.6.3 Prospective motion correction

One relatively new development in fMRI methods is the availability of pulse sequences that modify the location of the data acquisition at every timepoint in order to prospectively correct for head motion. This approach has the benefit of creating a motion-corrected dataset without the need for any interpolation. The use of prospective motion correction could be quite beneficial (Thesen et al., 2000), but it is important for users to consider the robustness of these methods for their particular applications. Since the online methods must use quick and thus relatively simple methods for estimating the location of the slices for the next timepoint, there could potentially be error in the predicted slice location which could, for example, cause loss of data from particular brain regions. Because such errors would be more likely in cases of large within-scan motion, these methods may paradoxically be best suited to populations where the motion is relatively minor.

3.6.4 Quality control for motion correction

As with any processing operation, the results should be checked to make sure that the operation was successful and that no additional artifacts were introduced. One useful way to check the results of motion correction is to view the motion-corrected image as a movie; any visible motion in this movie would suggest that the motion correction operation was not completely successful.

It might be tempting to run motion correction multiple times on the same dataset if there are remaining signs of motion following the first application of motion correction. However, this is strongly discouraged. Since the first pass should remove most effects of motion that are amenable to removal, on subsequent runs the algorithm will be much more sensitive to other signals, such as activation-related signals. In addition, the interpolation errors that are introduced at each step will degrade the data.

3.6.5 Interactions between motion and susceptibility artifacts

Motion correction techniques generally use a rigid-body (six-parameter) spatial transformation model, which assumes that the effects of motion do not change
the shape of the brain, just its position and orientation. However, in regions of susceptibility artifact, the effects of motion do not obey a rigid-body model. For example, if the head rotates around the X axis (as in swallowing), the angle of slices through the orbitofrontal cortex will change. Because dropout and distortion in this region depend upon the orientation of the slice with respect to the brain, they will differ due to the change in the effective slice angle through the brain, and this will result in differences in the shape of the brain in the image rather than simply differences in the position and orientation of the brain. These changes can result in artifactual activation (Wu et al., 1997), especially if motion is correlated with the task. For this reason, large regions of activation in the orbitofrontal cortex that are very near regions affected by susceptibility artifact should be interpreted with some caution. These problems also provide further motivation for the use of techniques to reduce susceptibility artifacts at the point of data acquisition.

3.6.6 Interactions between motion correction and slice timing correction

Slice timing correction and motion correction can interact with one another, and the nature of these interactions is determined by the order in which they are performed. If motion correction is performed first, then data that were actually acquired at one point in time may be moved to a different slice, and thus the nominal acquisition time that is specified in the slice timing correction algorithm may not match the actual acquisition timing of those data. In addition, if there is a significant amount of through-plane motion or rotation, then the interpolated voxels following motion correction will include a mixture of data acquired at different points in time, again resulting in potential errors due to slice timing correction.

If slice timing correction is performed first, then there is a potential for motion-related intensity differences (which can be very large) to be propagated across time. In addition, any actual through-plane motion or rotation will result in exactly the same kind of mismatch between nominal and actual timing of data acquisition discussed previously. This problem can be somewhat reduced by using prospective motion correction (see Section 3.6.3), which will reduce effects of motion without the need for interpolation and thus without mixing data collected at different times.

We would generally suggest that, if one insists on using slice timing correction, it is applied after motion correction, since the effects of motion on voxel intensity can potentially be very large. However, as noted in Section 3.5, there are good reasons to avoid slice timing correction altogether if data are acquired using a relatively short TR (2 seconds or less).

3.6.7 How much is too much motion?

One of the most often asked questions regarding fMRI data analysis is how much motion is too much, such that scans should be thrown away entirely if they exceed that amount. Unfortunately, there is no easy answer to this question. To a large degree, it depends upon how well the effects of motion are described by the rigid
3.6 Motion correction

body model: Not all motion is created equal. If the motion is gradual or occurs between scanning runs, then a large amount of displacement can be corrected, whereas if sudden motion occurs during a scan, it is likely that there will be effects on image intensity that cannot be corrected using a rigid-body transformation.

As a general rule of thumb, any translational displacement (i.e., translation between two adjacent timepoints) of more than 1/2 of the voxel dimension should cause great concern about the quality of the data. However, this should not be taken as a hard and fast rule; much smaller amounts of motion can cause serious problems, and sometimes even large amounts of motion can be successfully corrected, especially if motion correction is combined with the ICA denoising approach described earlier. In addition, the impact of motion is likely to vary depending upon how correlated it is with the task or stimulus.

It is our opinion that entire scans should be thrown away only as a very last resort. If the entire scan is riddled with large abrupt movements, then there may be no alternative. However, there are a number of strategies that can be used to address motion effects. First, one can attempt to remove coherent motion signals using exploratory methods such as ICA, as described previously. Second, one can include motion-related parameters in the statistical model (as described in Section 5.1.3). Third, one can exclude some timepoints completely by including explanatory variables in the statistical model for the specific timepoints of interest. We have found that these strategies generally allow most scans to be salvaged (at least in normal subject populations), though there will always be some cases where it is necessary to throw away an entire scanning run or subject. In pathological populations or children, it is expected that a significant proportion of data will be unusable due to excessive motion.

3.6.8 Physiological motion

In addition to motion caused by gross movements of the subject’s head, there is also significant motion of the brain caused by physiological pulsations related to heartbeat and breathing. The cardiac cycle is faster than the repetition time of most fMRI acquisitions, which results in aliasing of the cardiac cycle to lower frequencies (see Figure 3.13 for a description of aliasing). In addition to pulsatile motion due to the heartbeat, there may also be changes in the image due to respiration; the changes in the magnetic susceptibility within the chest across the respiratory cycle cause small changes in the magnetic field at the head.

One approach to addressing the problem of physiological motion is to monitor and record the timing of heartbeat and respiration during scanning, and then to retrospectively remove these effects from the data (e.g., Glover et al., 2000). These methods are effective but require the added complication of physiological monitoring during scanning. A second approach is to use cardiac gating, in which the timing of acquisition of individual image volumes is determined by the subject’s
own heartbeat. This method has been particularly useful in obtaining images from deep brain structures such as the superior colliculus (Guimaraes et al., 1998), which show the greatest amount of motion due to pulsatility. However, it has a number of limitations (such as a nonstationary TR) that make data analysis difficult, and it can also be technically difficult to implement for fMRI scanning. Another more general approach is to use ICA to detect artifactual components in the fMRI time series, as discussed earlier. This method is likely to detect some of the effects of physiological motion, though not as well as methods that use physiological monitoring; however, it has the benefit of not requiring any additional data collection beyond the standard fMRI acquisition.

### 3.7 Spatial smoothing

Spatial smoothing involves the application of a filter to the image, which removes high-frequency information (see Section 2.4 for background on filtering). It may seem unintuitive that, having put so much effort into acquiring fMRI data with the best possible resolution, we would then blur the images, which amounts to throwing away high-frequency information. However, there are a number of reasons researchers choose to apply spatial smoothing to fMRI data. First, by removing high-frequency information (i.e., small-scale changes in the image), smoothing increases the signal-to-noise ratio for signals with larger spatial scales. Because most activations in fMRI studies extend across many voxels, the benefits of gain in signal for larger features may outweigh the costs of losing smaller features. In addition, the acquisition of smaller voxels can help reduce dropout in regions of susceptibility artifacts, and smoothing can help overcome the increased noise that occurs when small voxels are used. Second, when data are combined across individuals, it is
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Known that there is variability in the spatial location of functional regions that is not corrected by spatial normalization (for more details, see Chapter 4). By blurring the data across space, spatial smoothing can help reduce the mismatch across individuals, at the expense of spatial resolution. Third, there are some analysis methods (in particular, the theory of Gaussian random fields; see Section 7.3.1.2) that require a specific degree of spatial smoothness. Whereas spatial smoothing is almost always applied for standard group fMRI studies, there are some cases in which unsmoothed data are analyzed, such as the pattern classification analyses described in Chapter 9.

The most common means of spatial smoothing is the convolution of the three-dimensional image with a three-dimensional Gaussian filter (or kernel; see Section 2.4.3 for more on convolution). The amount of smoothing imposed by a Gaussian kernel is determined by the width of the distribution. In statistics this is generally described in terms of the standard deviation, whereas in image processing the width of the distribution is described by the full width at half-maximum (or FWHM). This measures the width of the distribution at the point where it is at half of its maximum; it is related to the standard deviation ($\sigma$) by the equation $FWHM = 2\sigma\sqrt{2\ln(2)}$, or approximately $2.55 \times \sigma$. The larger FWHM, the greater the smoothing, as was shown in Figure 2.14.

Importantly, the smoothness of an image is not necessarily identical to the smoothing that has been applied to the image. Smoothness describes the correlations between neighboring voxels. An image with random noise will have a very low amount of smoothness, but MRI images generally have a greater amount of smoothness, both due to filtering applied during image reconstruction and due to the presence of intrinsic correlations in the image. When smoothing is applied to an image, the smoothness of the resulting image is

$$FWHM = \sqrt{FWHM_{intrinsic}^2 + FWHM_{applied}^2}$$

This is particularly important to keep in mind when using statistical methods that require an estimate of the smoothness of an image, which will be discussed in more detail in Chapter 7.

3.7.1 How much should I smooth?

There is no magic answer to the question of how much smoothing to apply, in part because there are many reasons to smooth and each may suggest a different answer to the question.

- If you are smoothing to reduce noise in the image, then you should apply a filter that is no larger than the activation signals that you want to detect. Figure 3.14 shows the effects of different filter widths on the resulting activation images. Note, however, that the effects here are specific to the particular task and systems being imaged; if the task resulted in activation of smaller structures, then the same filter width that results in detection here might lead the signal to be lost.
Figure 3.14. An example of the effects of spatial smoothing on activation; the numbers correspond to the FWHM of the smoothing kernel applied to the data before analysis. Increasing smoothing leads to greater detection of larger clusters but decreased detection of smaller clusters.

- If you are smoothing to reduce the effects of anatomical variability, then the optimal smoothing width will depend upon the amount of variability in the population you are imaging, and the degree to which this variability can be reduced by your spatial normalization methods (see Chapter 4 for more on this topic).
- If you are smoothing to ensure the validity of Gaussian random field theory for statistical analysis, then an FWHM of twice the voxel dimensions is appropriate. In general, we would recommend erring toward too little rather than too much smoothing, and we would thus recommend twice the voxel dimensions as a reasonable starting point.