# Noise Filtering and Testing for MR Using a Multi-Dimensional Partial Volume Model

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**Abstract**

One of the most common problems in image analysis is the estimation and removal of noise or other artefacts (e.g., grey level quantization) using spatial filters. Common techniques include Gaussian Filtering, Median Filtering and Anisotropic Filtering. Though these techniques are quite common in the image processing literature they must be used with great care on medical data, as it is very easy to introduce artifact into images due to spatial smoothing. The use of such techniques is further restricted by the absence of gold standard data against which to test the behaviour of the filters. Following a general discussion of the equivalence of filtering techniques to likelihood based estimation using an assumed model, this paper describes an approach to noise filtering in multi-dimensional data using a partial volume data density model. The resulting data sets can then be taken as gold standard data for spatial filtering techniques which use the information from single images. We explain how such data has advantages over data generated purely by simulation when testing alternative algorithms.

## 1 Introduction

Noise filtering on any data involves the assumption of a specific image generation mechanism (or image model). The process of Gaussian smoothing for example can be interpreted as consistent with a likelihood estimation of the central value within a region. This is done on the assumption that the data within this region can be described by some functional model with the expected grey level residuals being drawn from a Gaussian noise distribution with variance inversely proportional to the spatial Gaussian weighting term. The specific form of the assumed model is best understood by considering a more simplistic problem first.

Gaussian filtering removes high spatial frequency content from the structure of images. A less destructive approach to noise filtering is based on the concept of anisotropic filtering, where the data is preferentially smoothed along a direction selected in order to minimise the loss of spatial structure in the image. One particular variant of this we call 'Tangential Filtering'. Here, the tangential direction to the local image slope is computed and the data is smoothed by taking the weighted average of two points along this line situated one pixel away from the central value. It is relatively straight forward to see that averaging of multiple values in this way assumes that the data can locally be fitted to a 1D line and selection of the tangential direction results in the least destructive impact on edge structure. In fact any anti-symmetric function will result in an appropriate central estimate, and this can be taken as the most general assumtion for the underlying image model at each point. We can also see that for an average of two points the noise in the resulting image should be reduced by typically a factor of $\sqrt{2}$ of the original image noise. $\sqrt{3}$ if we also include the central value in the estimate.

Returning to Gaussian filtering, we can interpret this process as an averaging of multiple estimations of the central value for any pair of pixels with equal weight in the Gaussian kernal. The class of functions for which this would be an appropriate model would include Cartesian polynomials (expanded as a function of shifts $(x, y)$) from the central location $(x_0, y_0)$, either with no even terms, or at least exact cancellation of the magnitudes of even power co-efficients. For example:

$$I(x - x_0, y - y_0) = a + bx + cy + dxy + ex^2 - ey^2 + \dots$$

Though the only global function for which the model would work correctly at every image location would be an inclined plane. When described in this way it is easy to see the over-simplicity of this model in comparison to the structures found in real medical images. It is this which results in the characteristic problems with Gaussian filtering of image smoothing and the loss of sharp edge structures.

For particular applications of MR analysis, and in particular structural analysis, we would like to be able to assess the performance of these filters, and their ability to give the best estimate of the noise free image. Unfortunately, the only data which we generaly have available with which to test these algorithms are simulated data based upon a simplified model of image formation and tissue distribution (e.g., BRAINWEB [1, 2]). While we can say which filter will perform best on this simulated data, we cannot know that the data under test is a good surrogate for all of the formation processes seen in real images or for the specific structures seen in the particular images we wish to analyse.

As a direct contrast to spatial image filtering, which assumes specific forms of spatial correlation between grey level values, multi-dimensional tissue segmentation algorithms rely instead upon corellations between multiple measurements of the same physical location (voxel) using different imaging modalities. The typical approach involves building a model not of spatial structure but of grey level density distribution. Such models can also be used as the basis for noise removal. A common form of noise removal which makes use of greylevel density distribution is the median filter, which can be considered as a bootstrapped likelihood estimator. While many authors have concentrated on the use of grey level density estimation for tissue *labelling*, estimates of tissue *volume proportion* (as presented in our previous work [3]) can be used to predict the original image content for each modality in the case of zero noise. The process is simply one of using the estimated model parameters to generate the expected grey level values, using the linear equations implicit in the segmentation. Thus multi-spectral segmentation can be used as the basis for noise filtering.

Many readers may find the interpretation of filtering methods from a perspective of a model based estimation process unusual. However, one advantage of this approach is that explicit identification of the assumed model makes it possible to begin to consider testing the conformity of the data under analysis to the model. This is something which has not generally been tested for spatial filtering approaches. As we will show below this can be used to prevent noise removal in un-modelled parts of the data, i.e. pathology. In addition, we will demonstrate how the results from multi-spectral noise filtering are useable as a gold standard for spatial fitering techniques.

## 2 Methods

Multi-dimensional Gaussian distributions are used to model the effects of both inherent tissue variability and measurement noise for pure tissues. A multi-variate Gaussian distribution for multi-dimensional data $\mathbf{g}$ for each pure tissue $t$ is defined as:

$$d_t(\mathbf{g}) = \alpha_t e^{-\frac{1}{2}(\mathbf{g}-\mathbf{m_t})^T C_t (\mathbf{g}-\mathbf{m_t})}$$

where $\mathbf{m_t}$ is a mean tissue vector, $C_t$ is inverse of a covariance matrix and $\alpha_t$ is a constant which gives unit normalisation.

Using an assumption of a linear image formation process, whereby the total intensity level at each voxel results from summation of different tissue fractions present at that particular voxel, the partial volume distribution can be thought of as being composed of two triangular distributions convolved with a Gaussian $(T_{ts}(\mathbf{g}) + T_{st}(\mathbf{g}))$. Where $T_{ts}(\mathbf{g})$ is the local density estimate for tissue $t$ generated by a partial voluming process with tissue $s$. Assuming that tissue variability is more significant than the measurement processes, multi-dimensional partial volume distributions can be modelled along the line between two pure tissue means $\mathbf{m_t}$ and $\mathbf{m_s}$:

$$d_{ts}(\mathbf{g}) \;=\; \beta_{ts} T_{ts}(h) e^{-(\mathbf{g}-\mathbf{h}.\mathbf{g}/|\mathbf{h}|)^T C_h (\mathbf{g}-\mathbf{h}.\mathbf{g}/|h|)}$$

where the parameters for the given data $\mathbf{g}$ are: $h$ is a fractional distance between two centres of distribution $[0 < h < 1]$; $h \;=\; (\mathbf{g}-\mathbf{m_s})C_h(\mathbf{m_t}-\mathbf{m_s})/|(\mathbf{M_t}-\mathbf{m_s})C_h(\mathbf{m_t}-\mathbf{m_s})|$; $C_h$ is a covariance matrix: $C_h \;=\; C_t h \;+\; C_s(1-h)$; $T_{ts}(h)$ is the 1D partial volume distribution between pure tissues $t$ and $s$; and $\beta_{ts}$ is a constant which gives unit normalisation.

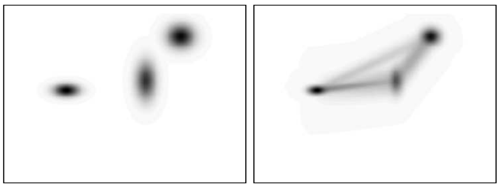
The 1D partial volume distribution, $T_{ts}$, obtained by convolving a triangular distribution normalised to $\frac{1}{2}$ with Gaussian distribution normalised to 1, takes the following form [4]:

$$T_{ts}(x) = -\frac{kx+c}{2}\left\{\mathrm{erf}\left(\frac{x-b}{\sigma\sqrt{2}}\right) - \mathrm{erf}\left(\frac{x-a}{\sigma\sqrt{2}}\right)\right\} - \frac{M\sigma}{\sqrt{2\pi}}\left\{\exp\left(-\frac{(x-b)^2}{2\sigma^2}\right) - \exp\left(-\frac{(x-a)^2}{2\sigma^2}\right)\right\} \quad (1)$$

where: $x$ is a grey level value calculated as a normal projection of vector $\mathbf{g}$ onto line between two distribution means; $k$ and $c$ are the slope and intercept of the line which forms the triangle; $a$ and $b$ are the start and end points of an interval at which the triangular distribution has a non-zero value; and $\sigma$ is a standard deviation of a Gaussian function.

The overall partial volume distribution is calculated as a product of a Gaussian function of the normal distance $(\mathbf{g}-\mathbf{h}.\mathbf{g}/|\mathbf{h}|)$ from two distribution centres and the 1D partial volume distribution $T_{ts}(h)$. Examples of the types of distributions obtained from the model parameters of two images for three pure tissues and their partial volumes are shown in Figure 1. It can be seen that pure tissue distribution models take the form of elliptical features, while the partial volumes are shown as elongated structures between centres of distributions.

Parameters of the model can be iteratively estimated using the Expectation Maximisation (EM) approach [5, 6]. EM is used to estimate the parameters by maximising the likelihood of the data distribution. This involves first getting from the likelihood distributions defined



(a) (b)

Figure 1: An example of distributions generated from the model for two images (a) Pure tissue distributions (b) Combined distributions of pure tissues and partial volumes between centres of pure tissues

above to a probability of a given tissue proportion given the data $P(t|\mathbf{g_v})$. The conditional probability of a grey level being due to a certain mechanism $n$ (either a pure or mixture tissue component) can be calculated using Bayes theory, as follows:

$$P(n|\mathbf{g}) \;=\; \frac{d_n(\mathbf{g})f_n}{\sum_t(f_O + d_t(\mathbf{g})f_t) + \sum_t \sum_s d_{ts}(\mathbf{g})f_{ts}}$$

where $f_n$, $f_O$, $f_t$ and $f_{ts}$ are effectively "priors", expressed here as frequencies (i.e. number of voxels) which belong to a particular tissue type, pure tissues or partial volumes. Unknown tissues are accounted for in the Bayesian formulation by including a fixed extra term $f_O$ for infrequently occuring outlier data [7] in total probability which enables separation of pathological tissues.

Noise-free estimates of the individual image greylevels $g_i'$ can be calculated using

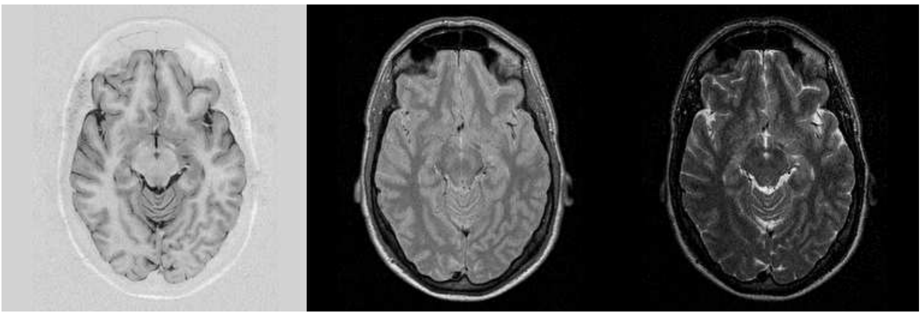
$$g_i' \;=\; g_i\; P(O|\mathbf{g}) \;+\; \sum_t g_{it}\; P(t|\mathbf{g}) + \sum_t \sum_s g_{it}\; P(ts|\mathbf{g})$$

where $g_{it}$ is the expected pure tissue grey level for image $i$. This formulation implicitly reverts to the original image greylevel for outlier data (large $P(O|\mathbf{g})$). In addition, failure to model individual voxels can be identified by checking for consistency between the filtered image and original. In particular, any reconstructed greylevel value which differs from the original by more than 3 standard deviation of the image noise can be said to be inconsistent with the model. This value can then be replaced with the original value in order to preserve all significant information present in the original image. Further evaluation of this technique is of course difficult without a gold standard, however the stability (noise sensitivity) of the filtering technique can be assesed using Monte-Carlo techniques.

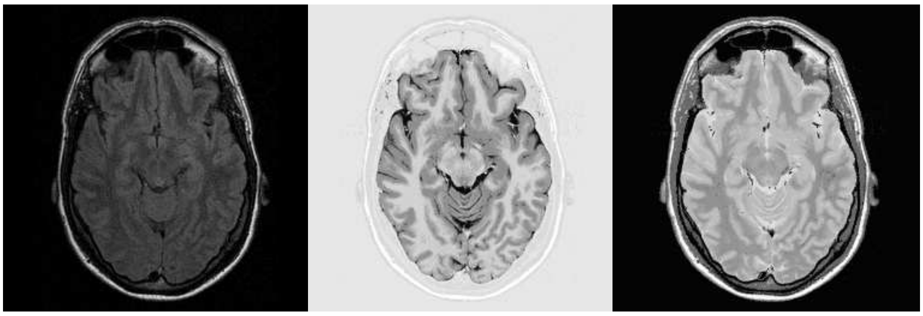
# 3 Results

Original and reconstructed images following co-registration and partial volume analysis are shown in Figure 2.

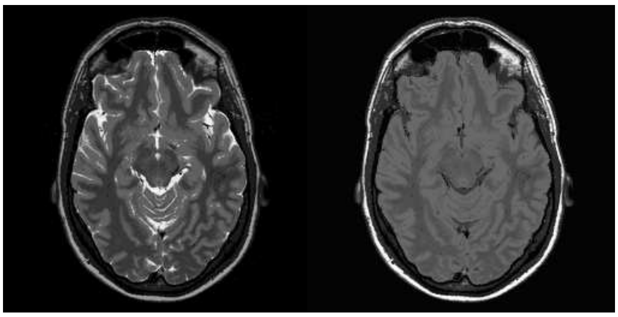
The noise level ($\sigma_{original}$) in each image was estimated from the width of the central peak in the distribution of second spatial derivatives . This process is known to slightly overestimate the noise due to genuine 2nd order structure. In addition, an estimate of the



(a) Inversion Recovery Turbo Spin Echo (b) Variable Echo (PD) (c) Variable Echo (T2)



(d) FLAIR (e) Filtered IRTSE (f) Filtered VE (PD)



(g) Filtered VE (T2) (h) Filtered FLAIR

Figure 2: Image Sequences and Partial Volume Filtered Counterparts

| | **IRTSE** | **VE(PD)** | **VE(T2)** | **FLAIR** |
|---|---|---|---|---|
| $\sigma_{original}$ | 58.67 | 64.06 | 58.25 | 52.42 |
| $\sigma_{original-filt}$ | 50.9 | 48.2 | 40.6 | 47.1 |
| $M - C \quad noise$ | 0.22 | 0.20 | 0.17 | 0.13 |
| $N^o$ **pixels** | 1689 | 1804 | 938 | 4971 |

Table 1: Quantitative Perfomance of Partial Volume Noise Filtering

| | Median | Filtering | Gaussian | Smoothing | Tangential | Smoothing |
|---|---|---|---|---|---|---|
| | $\sigma_{\mathbf{filt-ref}}$ | $N^o$ **pixels** | $\sigma_{\mathbf{filt-ref}}$ | $N^o$ **pixels** | $\sigma_{\mathbf{filt-ref}}$ | $N^o$ **pixels** |
| **IRTSE** | 35.22 | 1612 | 33.10 | 2741 | 36.41 | 1084 |
| **VE(PD)** | 28.20 | 1742 | 25.54 | 3847 | 28.02 | 1140 |
| **VE(T2)** | 23.83 | 1302 | 18.69 | 2129 | 21.77 | 761 |
| **FLAIR** | 33.69 | 2248 | 29.05 | 4325 | 34.22 | 1654 |

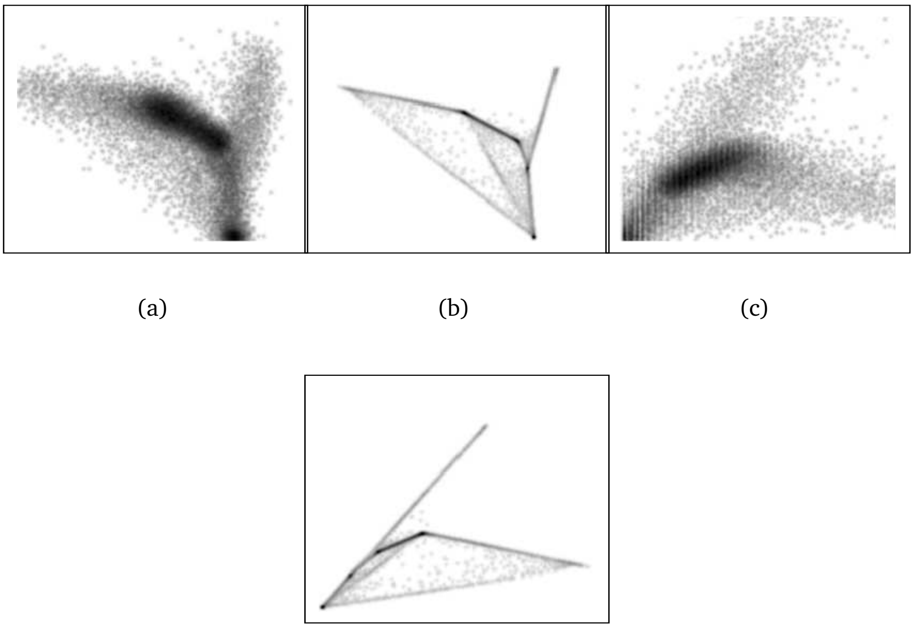
Table 2: Quantitative Perfomance of Spatial Filtering

quantity of noise removed from each image can be estimated from the difference between the partial volume noise filtered image and the original $\sigma_{original-filt}$. The Monte-carlo stability analysis involved adding Gaussian random noise to the original image and observing the fraction of noise remaining after filtering (M-C noise in Table 1). This represents the true noise reduction for data which was generated by the assumed image formation model and can be used to estimate the amount of noise remaining in the noise filtered image. The numbers of voxels lying beyond 3 S.D. of the model are listed in Table 1 (the outlier term was fixed at zero for these experiments).

Following partial volume filtering the voxels inconsistent with the original data at the 3 S.D. level were replaced with their original values. The resulting images were then used as the basis for evaluation of spatial filtering techniques applied to the original images (Table 2). Tangential filtering was applied as described in the introduction. Gaussian filtering was for spatial filter with S.D. of 1 pixel. Median filtering was over the local neighbourhood of 9 pixels.

# 4 Discussion and Conclusions

This paper has shown how techniques generally used for tissue segmentation can be used to provide noise filtering of multi-spectral images based upon an analysis of partial volume structure. Though this may sound a very complicated process, it can be considered as a simple regression onto the lines joining pairs of pure tissue locations in the multi-dimensional grey level space, followed by a weighting with pure tissue values according to the Bayesian priors. Any voxels composed of pure tisses of appropriate mean values will therefore have the noise on each grey level removed in such a way as to make the grey level value more consistent with the estimated position along this partial volume line (Figure 3). The results of such an analysis can be also interpretted as a method of data fusion, where data from alternative modalities are combined in order to improve the data from each. The results demonstrate



(a) (b) (c)

(d)

Figure 3: Grey Level Distributions before (a) and after (b) Partial Volume Noise Filtering for IRTSE and VE(PD) images, and before (c) and after (d) Partial Volume Noise Filtering for VE(T2) and FLAIR images

that such an approach does not produce the loss of high spatial frequency structure inherrent in even the most careful spatial filtering schemes. In addition, unlike techniques based upon spatial filtering, the model used for noise filtering is explicit and testable. In particular it is possible to identify any pixels which are not consistent with the assumed model and then exclude these from the filtering process. This represents a considerable step towards use of filtering techiques in clinical applications which include pathology.

There is a subtle but important difference between using models based upon spatial distribution and those based upon partial volume behaviour for MR analysis. The former can only be determined from example data and there can never be a spatial model which will be appropriate for the contents of all biological images. Grey level density models however, have statistical characteristics which are purely determined by the acquisition process (ie: the underlying physics of the measurement process). We might therefore expect that if we knew enough about the image formation process for a particular imaging protocol we may be able to construcut a model which is true for all images from a particular acquisition containing equivalent tissue types. This approach to filtering may therefore be regarded as a gold standard for testing of spatial filtering techniques. In the work here we have used all images in the EM based reconstructed image used for the test. In general we would expect this to introduce a slight bias in the evaluation process towards the specific noise characteristics in each image as the estimate of the gold standard is not strictly independant of the test image. If it was believed that this were a source of significant error then the problem could easily be avoided, either by repeated acquision of the test data, so that a truly independant image was available for spatial filtering, or by excluding the test image from the EM segmentation prior to reconstruction. However, the combined effects of the use of multiple modalities and the effects of spatial filtering are expected to reduce the significance of these effects, and relative performance between alternative algortihms are expected to be valid.

In comparison to other mechanisms for the generation of test data, the most commonly used technique is probably the BRAINWEB simulation. This can be thought of as equivalent to the final stages of the reconstruction process presented here, except that their volume estimation process is based upon a "fuzzy" class membership process, not explicit partial volume estimation, and of course they have one fixed model. Our aproach raises the possibility of generating personalised models with checks on the validity of the reconstruction process.

Software and test data available on the web [8].

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