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Automatic change detection in multimodal serial MRI: application to multiple sclerosis lesion evolution

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Abstract

The automatic analysis of subtle changes between MRI scans is an important tool for assessing disease evolution over time. Manual labeling of evolutions in 3D data sets is tedious and error prone. Automatic change detection, however, remains a challenging image processing problem. A variety of MRI artifacts introduce a wide range of unrepresentative changes between images, making standard change detection methods unreliable. In this study we describe an automatic image processing system that addresses these issues. Registration errors and undesired anatomical deformations are compensated using a versatile multiresolution deformable image matching method that preserves significant changes at a given scale. A nonlinear intensity normalization method is associated with statistical hypothesis test methods to provide reliable change detection. Multimodal data is optionally exploited to reduce the false detection rate. The performance of the system was evaluated on a large database of 3D multimodal, MR images of patients suffering from relapsing remitting multiple sclerosis (MS). The method was assessed using receiver operating characteristics (ROC) analysis, and validated in a protocol involving two neurologists. The automatic system outperforms the human expert, detecting many lesion evolutions that are missed by the expert, including small, subtle changes.

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1. Introduction

The constant improvement in spatial resolution and the availability of multimodal imaging hardware yields an increasing amount of three-dimensional image data. Manual interpretation of huge amounts of data is tedious and error prone. A major challenge for medical imaging is the development of reliable techniques for automatic detection of changes. Early detection of anatomical modifications enables faster diagnosis. Once a pathology has been diag-

nosed, long-term monitoring of disease evolution is also essential.

A direct comparison between successively scanned images is generally not possible. Patient position is never identical, acquisition parameters may drift between scans, and a variety of complex global or local deformations of anatomical structures may be observed.

During manual change labeling, the expert implicitly uses prior high level knowledge to compensate for some of these undesired changes. He can visually correct for repositioning errors, and uses anatomical knowledge to identify and reject certain artifacts. Techniques for identifying and correcting each important artifact source are thus necessary.

This work is centered on image processing techniques that correct these artifacts and decide whether or not changes are significant. The proposed approach is compre-

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hensive and does not require any knowledge of the acquisition process. Raw MRI data that could be useful to eliminate certain artifacts are thus not necessary. The approach may be applied to other change detection problems, the artifacts addressed here being common to many medical imaging devices.

The system was evaluated in the specific case of multiple sclerosis (MS) lesion evolution analysis. MRI has become a sensitive, objective marker of MS evolution over time. Serial multimodal RARE, T1-weighted (GE3D), and FLAIR 3D MR images were obtained from 8 patients suffering from relapsing remitting MS (Fig. 1). The performance of the system was evaluated on a large (over 200) database of 128^3 3D MR images, using receiver operating characteristics (ROC) analysis. The performances of the automatic system compared favorably with manual labelings provided by two neurologists. The automatic system outperformed the human expert for several cases exhibiting small, subtle changes (see, for instance, Fig. 2).

2. Related work

A variety of different approaches to change detection in serial MRI may be found in the literature. Existing approaches, often devoted to particular issues with specific tools, may be divided into two major categories. A first category corresponds to approaches looking for large structural changes. Methods from the second category focus on smaller, more localized changes. An example of large structural change detection is Smith et al. (2000), where global brain volume changes are determined by estimating the motion of extracted brain/CSF (cerebrospinal fluid) boundaries. Here, we will consider the detection of small (eventually subtle) changes. Subtle changes are changes that are hard to detect by the human expert at first sight.

Another major divide in change detection techniques is whether one is considering long time sequences, like in fMRI, or short (typically two frames) sequences. Change detection on long time sequences tends to focus on signal processing of the time series at a given spatial location of the 3D image set. Such an approach is employed in Gerig et al. (1999) for MS monitoring, using statistical tests for change detection over the time series. Hereafter, we will consider methods that are able to process short time series of two images. Most change detection systems use registration as a preliminary step to obtain accurate geometrical alignment of the images before image comparison. This first (optional) step is generally followed by an interimage comparison step.

2.1. Interimage registration

Rigid (rotational and translational) registration has been used in Hajnal et al. (1995), Curati et al. (1996), and Rey et al. (2002), but it does not compensate for the significant

voxel size changes that occur in commercial scanners. Affine (scale and shear) registration gives more accurate results (Freeborough et al., 1996; Lemieux et al., 1998) but is not sufficient to compensate for more complex deformations that may occur. These complex deformations can be of pathological nature [global brain atrophy (Smith et al., 2000)], may come from natural causes [gravity (Hajnal et al., 1995), hydrostatic pressure changes, or dehydration] or be due to acquisition artifacts [incorrect shim, or gradient calibration drift (Freeborough et al., 1996; Smith et al., 2000)]. To properly compensate for these complex phenomena, it is necessary to resort to deformable matching methods, which are able to correct most large scale artifacts, while preserving small significant changes. Deformable matching is commonly used for intersubject matching (Toga and Thompson, 1999; Thompson and Toga, 1999; Thirion, 1998) and computed deformation fields have also been used for change detection (see section 2.2.2). However, deformable matching has seldom been considered as a realignment step for inpatient change detection, since deformable registration may cancel the small significant interimage changes. A solution, adopted here, is to consider hierarchical matching techniques, which are able to register image structures up to a given controlled resolution. In section 3.5 we describe an iterative registration procedure, developed by the authors (Musse et al., 2001, 2002), which enables such an accurate and careful compensation of artifacts.

2.2. Interimage comparison

The second step in the design of a change detection method is to devise a technique for comparing the two images. Three main families of approaches are considered.

2.2.1. Segmentation-based approaches

In the specific case of lesion monitoring, a first approach is to manually, semiautomatically, or fully automatically segment lesions and then compare them to determine changes.

Manual outlining was used a few years ago but is an extremely time consuming process; semiautomated methods were then developed (Kohn et al., 1991; Lim and Pfefferbaum, 1989; Mitchell et al., 1996; Vannier et al., 1985). More recently, automated procedures have been proposed (Kamber et al., 1995; Kikinis et al., 1999; Goldberg-Zimring et al., 1998; Grimaud et al., 1996; Udupa et al., 1997; Van Leemput et al., 2001).

Automatic segmentation of brain structures and MS lesions remains a challenging task. Large lesions may be adequately extracted, but small lesions are difficult to distinguish from noise and other structures, particularly in modalities where lesions have the same intensity values as other brain structures. Once lesions are segmented, their evolution may be determined by comparing lesion load. These methods generally do not use prior interimage registration; therefore, precise evaluation of intensity evolution within a lesion may be difficult.

2.2.2. Deformation field-based approaches

This second family of approaches is based on the estimation and analysis of interimage deformation fields. Deformable registration (Musse et al., 2001; Thirion, 1998; Thompson and Toga, 1999), when performed at a sufficiently fine resolution level, will warp one image onto another, effectively canceling out most interimage changes. The computed transformation then contains interesting information on the relative changes between both images. Specifically, lesion evolutions may appear as contractions or dilations in the interimage deformation field. This approach is akin to optical flow interpretation techniques used in video image motion analysis (Mitiche and Boutheymy, 1996). Several different variants to this approach have been considered (Thirion and Calmon, 1999; Rey et al., 2002; Freeborough and Fox, 1998; Ashburner and Friston, 2000; Davatzikos et al., 2001). For instance, both Thirion and Calmon (1999) and Rey et al. (2002) and Freeborough and Fox (1998) combine nonrigid deformation computation and flow field analysis to detect evolving lesions or to quantify measurement of volume variations. The Jacobian operator is used to characterize local volume changes that are related to evolutions. Another related example is VBM (Ashburner and Friston, 2000; Davatzikos et al., 2001), where deformations of segmented regions are analyzed to determine regional atrophy.

2.2.3. Direct intensity comparison

This last family of approaches relies on a direct comparison of intensities at the voxel level or on small regions. These approaches are comprehensive in that they do not focus on a particular type of evolution.

A first step consists in compensating for global intensity changes (intensity normalization). This step may be conducted before and/or after interimage registration. Existing methods for intensity normalization apply linear intensity correction functions. We found, however, that intensity differences may be highly nonlinear for successive acquisitions. In section 3.6, we develop an original joint histogram-based technique for compensating such nonlinear intensity differences.

Once images are realigned and intensities corrected, they must be compared. This may be done using either a deterministic or a probabilistic approach. Most methods use simple deterministic image subtraction followed by manual or automatic thresholds (O’Riordan et al., 1998). Probabilistic methods (Hsu et al., 1984; Lemieux et al., 1998) build a statistical model of intensities and noise that is used to determine if a valid change is observed.

The approach proposed here is based on a statistical change detection scheme that extends previous work (Hsu et al., 1984; Lemieux et al., 1998) by handling multimodal image data, using multidimensional Gaussian models of image intensities. A significant decrease of the false detection rate is observed, with respect to standard single-modal approaches.

3. Materials and methods

3.1. Subjects

Image data were obtained from 8 patients suffering from relapsing remitting MS. Images were taken once every 2 months during a 2-year period. Each exam consisted of images in three modalities.

3.2. Imaging

Isotropic 3D MR images were acquired with a standard 2-T whole body imager (Tomikon S200 Bruker, Karlsruhe, Germany) using a head transmitter and receiver. Three scans were performed at each exam. The first scan was a transverse 3D RARE image (FOV = 25.6 cm; matrix size 128×128 ; slice thickness 2 mm; inversion time 1.3 s), the second, a 3D fluid attenuated inversion recovery (FLAIR) image (FOV = 25.6 cm; matrix size 128×128 ; slice thickness 2 mm), and the third, a T1-weighted 3D image (GE3D) (FOV = 25.6 cm; matrix size $128 \times 128 \times 128$). No attempt was made to achieve precise repositioning between scans or between exams.

3.3. Image processing: overview

Our change detection approach can be split into the following four main steps:

- Brain extraction (section 3.4).
- Repositioning and correction of deformation artifacts (section 3.5):
 - Iterative affine registration (section 3.5.3).
 - Deformable registration (section 3.5.4).
 - Image resampling (section 3.5.5).
- Intensity normalization (section 3.6).
- Single or multimodal statistical change detection test (section 3.8).

Fig. 3 summarizes the different image processing steps, which are described in the following paragraphs. All processing is fully automatic: no user intervention is required at any moment.

Each patient has been imaged at several (approximately 12) time points. At each time point three images of different modalities have been taken (see section 3.1). All of the images go through the brain extraction and registration steps. Time points are then coupled into successive pairs: (exam-1, exam-2) (exam-2, exam-3) . . . (exam-11, exam-12). Exam pairs go through the remaining processing steps and are finally compared. An image database mechanism was implemented to manage the large amount of images and processing steps involved.

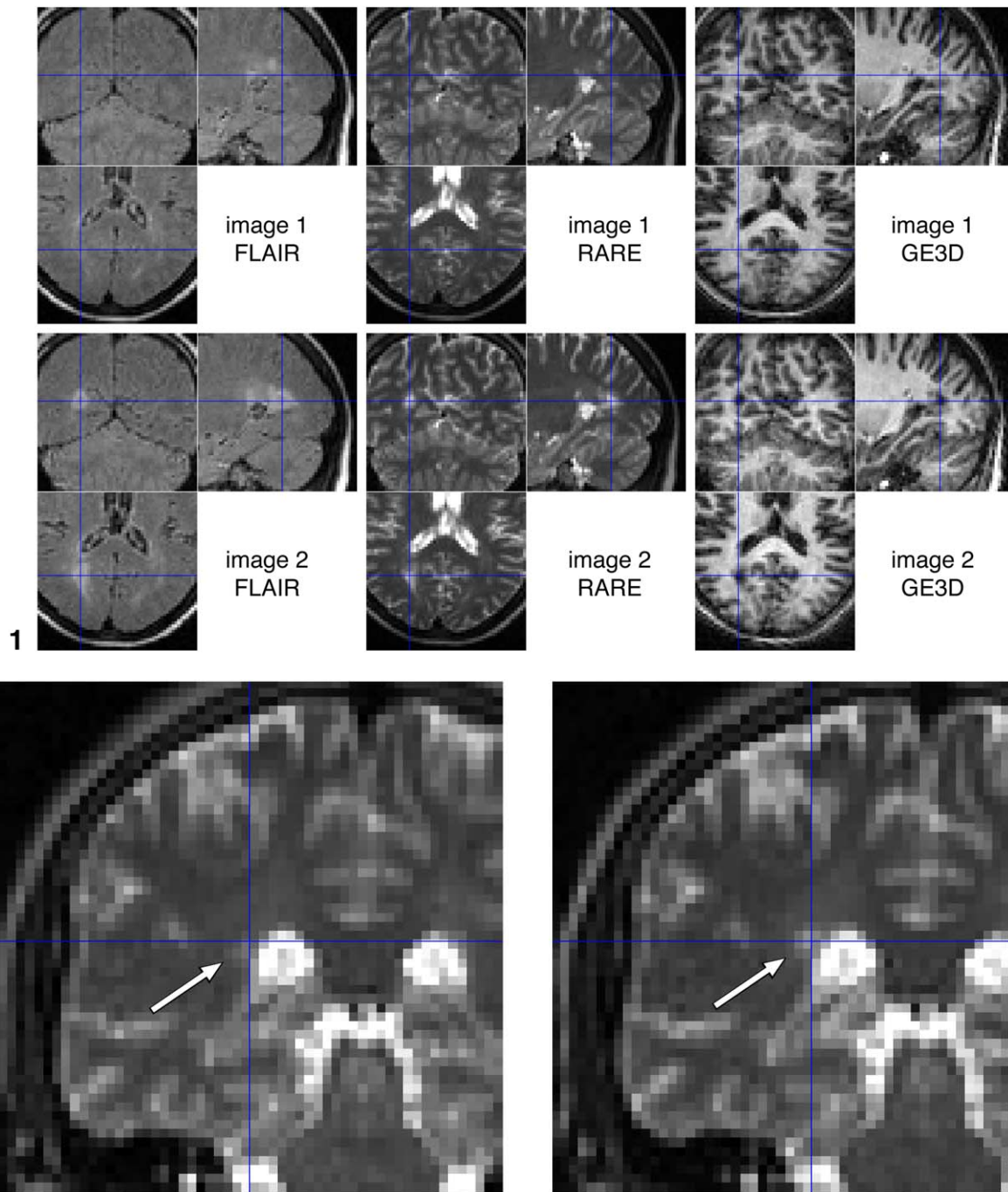


Fig. 1. Large evolution of an MS lesion in 3 different modalities (FLAIR, RARE, and GE3D). The images labeled “2” were taken 2 months after the images labeled “1”. Lesion evolutions of this size are easily detected by manual or automatic methods (lesion is visible at cross hairs).

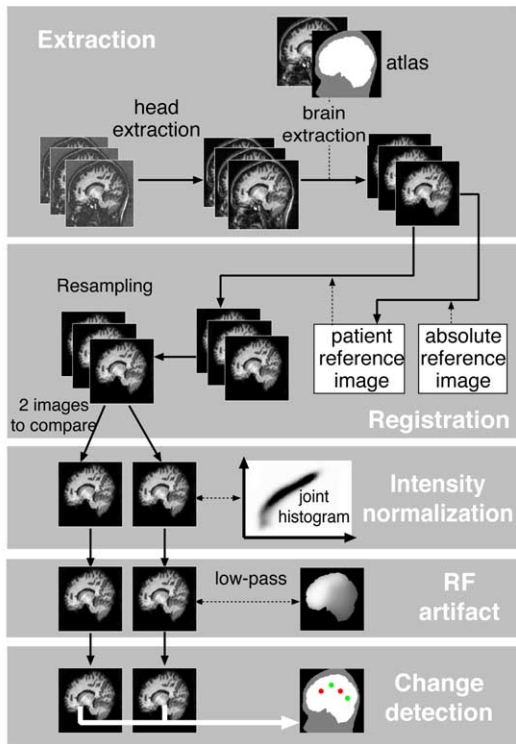
Fig. 2. Automatically detected periventricular MS lesion evolution. This subtle evolution was missed (but validated a posteriori) by the expert (view enlarged for visualization).

3.4. Brain extraction

The goal is to compare image intensities at identical anatomical positions. We therefore explicitly choose to ignore and compensate for global brain volume change. Besides, we have observed significant brain movement within the skull on animations of rigidly registered heads. We must

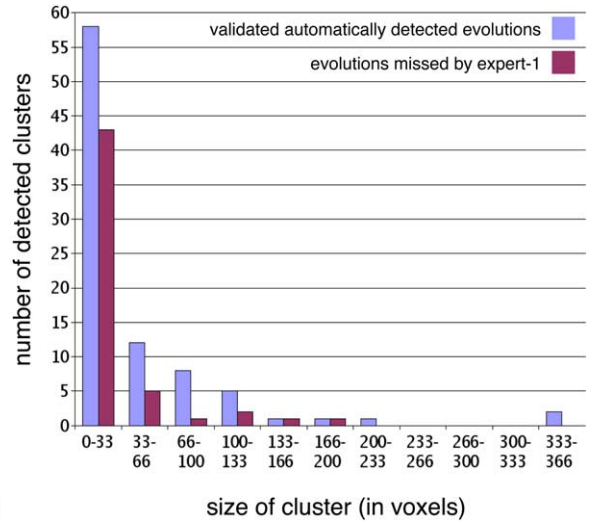
therefore register brains and not the surrounding skull and background noise, which would perturb the registration.

The first step is thus to extract the head from background noise. The extraction does not need to be extremely accurate, but needs to be reliable, given the large amount of images that will be processed. This rough segmentation of the head is obtained using low level image processing tech-



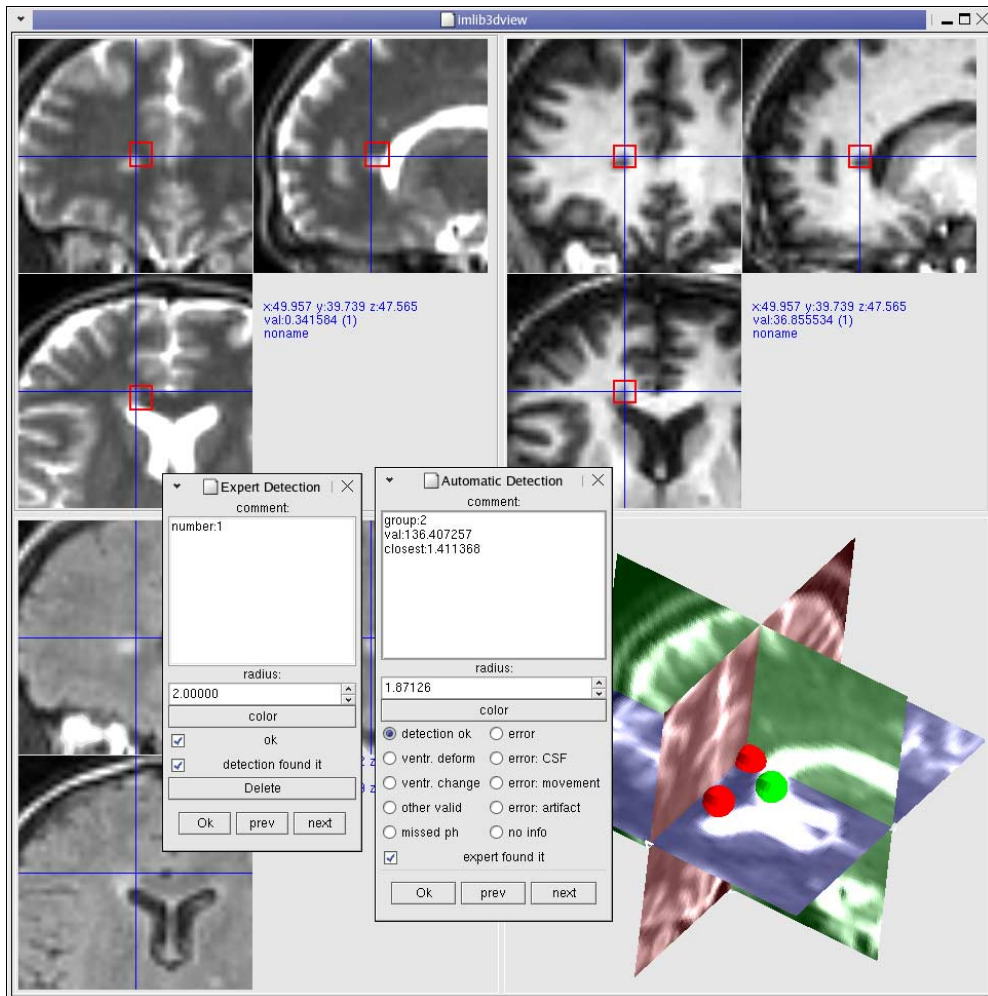
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Fig. 3. Flowchart showing the different steps of the change detection method (see text). For simplicity, only one modality is shown.



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Fig. 11. Sizes of automatically detected evolutions. Voxels are $2 \times 2 \times 2$ mm (see section 4.2.2).



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Fig. 9. Graphical interface used for evaluating the performance of the detection system. The three multiplanar views display cycling animations of the images at the two time points that are being compared. On the top left view (RARE) are also shown expert-1's detections. On the top right view are shown automatic detections. The lower right view is a 3D display that helps keeping track of spatial positioning. This software was written using ImLib3D and Medimax (Bosc et al., 2002).

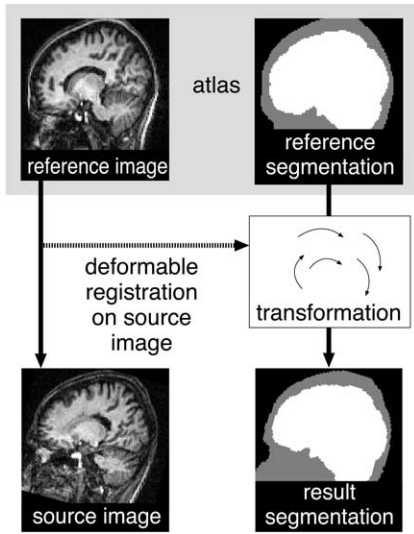


Fig. 4. Atlas-based brain extraction. The transformation field between the reference image and the source (patient) image is estimated using deformable matching. This transformation field is then used to map the reference brain segmentation (atlas) onto the source (patient) image.

niques: Otsu thresholding (Otsu, 1979), erosion, and hole filling.

The second step consists in extracting the brain (Fig. 4). An atlas-based segmentation is used to this end (Musse et al., 2002). The atlas is here a reference image that has been previously semiautomatically segmented using a watershed-

based approach (Bueno et al., 2001). This reference image is registered onto the patient image we wish to segment using deformable registration (section 3.5.4). Applying the resulting deformation field on the atlas segmentation provides the desired extraction of the brain (Musse et al., 2002) (see Fig. 4).

3.5. Repositioning and correction of deformation artifacts

3.5.1. Overview

Automatic change detection is extremely sensitive to misregistration errors. As noted by Lemieux et al. (1998), in regions of high intensity gradient (such as lesion edges), positional shifts of less than 0.05 voxels may produce spurious detections. Therefore, we are clearly working in a subvoxel context, which implies the need for high quality interpolation (section 3.5.5) and a sophisticated model for registration.

Conventional rigid (rotational and translational) or affine (scale and shear) registration are insufficient for modeling the complex deformations that appear between MRI scans (see section 2.1 for a description of these deformations). To correct these complex deformations, we use an iterative affine image matching method (section 3.5.3), followed by hierarchical deformable registration [described in section 3.5.4 (Musse et al., 2001, 2002)] (see section 5 for a full discussion on the trade-offs involved). Finally, once the full geometric transformation is computed, the resulting images

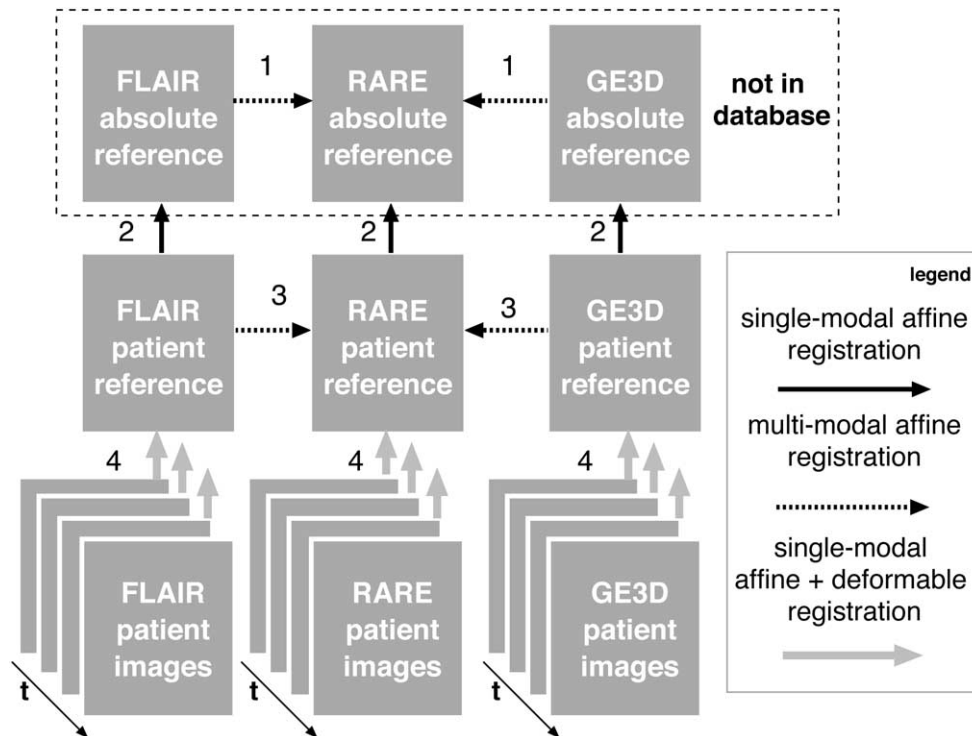


Fig. 5. Reference images used for the registration. The numbers (1, 2, 3, and 4) show the chronological order of the registrations. Absolute reference images, as well as patient reference images, are used to provide accurate and reliable intrapatient intramodal and intermodal registrations (see text).

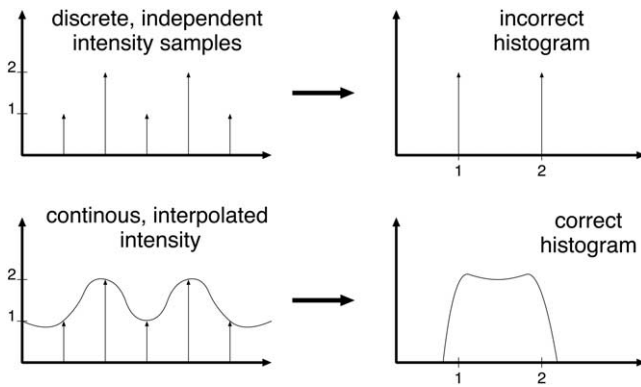


Fig. 6. Using interpolation for histogram computation: 1D example.

are resampled using high quality B-spline interpolation [section 3.5.5 (Thevenaz et al., 2000)]. Previous to each registration step, linear intensity normalization was performed. Fifth degree B-spline interpolation is used for all geometric transforms, except for intermediate (internal) registration steps that involve linear interpolation. Indeed, we found that precise B-spline interpolation was not necessary during the intermediate registration steps, but was extremely beneficial in the last registration step. This enables to save computational time, while preserving the quality of the final subvoxel registration.

3.5.2. Reference positions for registration

As noted in Smith et al. (2000), it is important that all images undergo equivalent processing steps. If a given image of a patient was to be chosen as a positional reference for registering his own images, some images would undergo geometrical transforms, while the reference image would not. Therefore, a common reference position is chosen, and care is taken so that the actual registration of the images of the dataset is done with reliable intrapatient single-modal registration.

Images, in three modalities, belonging to a patient not in the database are selected. These images are then carefully registered on each other using affine multi-modal registration (Fig. 5, step 1). These three images will be used as absolute reference positions for the whole database. Note that the intrapatient multimodal affine registration assures an accurate multimodal fit. Particularly, it compensates for voxel size errors that would not be addressed by rigid registration.

The registration of a given patient time series is done in two steps. First, a set of three patient images of all three modalities are arbitrarily chosen as the patient references. These patient reference images are registered (using intrapatient single-modal affine registration, step 2) onto their respective absolute reference images (Fig. 5). Interpatient affine registration may be inaccurate, so we ensure a tight intermodal fit, with a further multimodal intrapatient affine registration (Fig. 5, step 3).

The advantage of this scheme is that we are now able to register the patient images using accurate and reliable intrapatient single-modal affine and deformable registration (Fig. 5, step 4). Moreover, all registered images in the multipatient database are in the same (absolute) geometrical position.

In our current implementation, all registration algorithms are voxel based and rely on the minimization of global energy (cost) functions, with standard sequential simplex optimization. Quadratic cost functions are considered for single-modal registration and the mutual information criterion is used for multimodal registration.

3.5.3. Robust iterative affine registration

The deformable registration step (Fig. 5, step 4) requires a good initial fit. This initial fit is obtained using affine registration, which corrects errors due to voxel size drift. However, differences in the brain extractions between two images can lead to an important bias in registration. To cope with this problem an iterative adjustment of the segmentation is embedded in the registration scheme. Each iteration step is composed of an affine registration followed by a recomputation of the brain extractions. The new brain extraction is the intersection of the brains of the registered images. In practice, it was observed that brain extractions did not vary significantly after two iterations.

3.5.4. Deformable registration

The deformable matching method (Musse et al., 2001, 2002) is a hierarchical (coarse-to-fine) registration process that estimates a parametric displacement field decomposed on multiresolution B-spline basis functions. At a given resolution level, the method minimizes a quadratic energy function using modified quasi Newton optimization. The final resolution level may be chosen according to the desired scale of the image structures to be matched. Stopping the algorithm at a low resolution level will correct large scale deformations, whereas continuing to higher resolutions will progressively compensate for smaller differences between the registered images. The choice of the adequate resolution level is discussed in section 5.

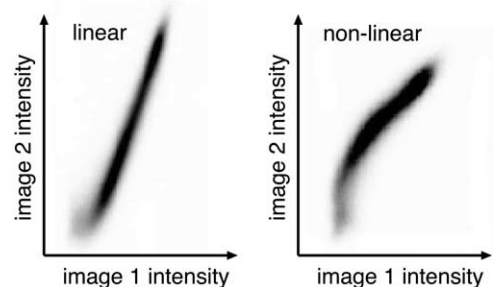


Fig. 7. Joint histograms of two different pairs of GE3D images. Nonlinearity must be corrected to accurately compare image intensities.

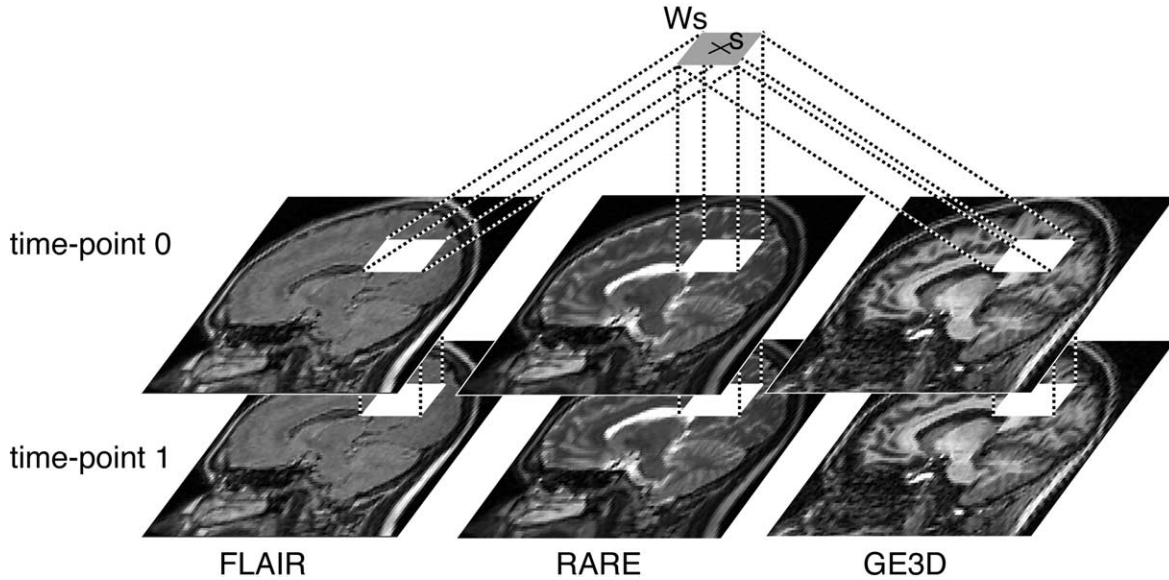


Fig. 8. Change detection considers a statistical model of intensities in a 3D window W_s centered on s .

3.5.5. Resampling

As noted previously, high quality, subvoxel registrations are required. We therefore need an efficient interpolation strategy. The theoretically perfect sinc interpolator must, in practice, be truncated. This gives incorrect results and is computationally inefficient. Many interpolation methods have been proposed (Lehmann et al., 1999). Recently, Thevenaz and Unser (Thevenaz et al., 2000) have proposed new innovative and efficient interpolation techniques. Traditionally, interpolation is expressed as the reconstruction of a continuous domain image $I(x)$ from a sampled image I_k using an interpolating function ϕ_{int} (sinc for example):

$$I(x) = \sum_{k \in \mathbb{Z}^3} I_k \phi_{int}(x - k) \quad (1)$$

Here, I_k are the values of $I(x)$ on a discrete grid of points. The problem was reformulated in Thevenaz et al. (2000) as:

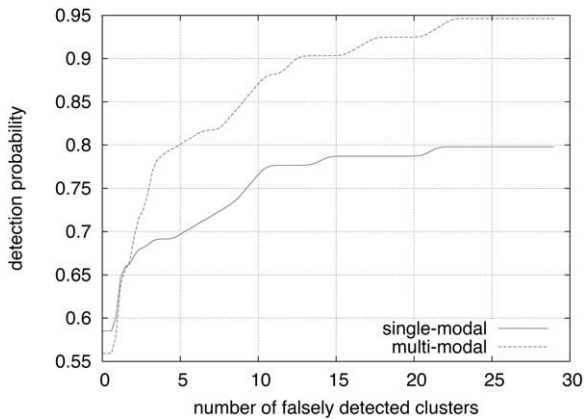


Fig. 10. Performance of the automated detection system. For comparison, the expert's detection rate was evaluated at 42%. Multimodal detection eliminates many false detections and therefore allows us to attain higher detection rates.

$$I(x) = \sum_{k \in \mathbb{Z}^3} c_k \phi(x - k) \quad (2)$$

where the c_k are computed coefficients that are no longer the exact values of the image on the discrete grid, and therefore ϕ no longer needs to be a strictly interpolating function. This change of perspective leads to new, fast and high quality interpolation schemes. The interpolation is decomposed into two stages, a fast recursive prefiltering stage and a conventional interpolation phase using a noninterpolating kernel. In our change detection framework, a global geometric transform is computed by composing the transforms computed during the affine and deformable registration steps. A 5-degree box spline kernel (Thevenaz et al., 2000) is used in the last deformable registration step.

3.6. Intensity normalization

Image intensity of identical tissues may change between successive scans. To correct this problem, previous work (Lemieux et al., 1998) used linear mapping between image intensities: the corrected intensity $I'_1(s) = f(I_1(s))$ was a linear function $f(x) = ax + b$ of the original intensity $I(s)$. However, we found that a linear model was insufficient. We propose, here, a nonlinear normalization method relying on the estimation of joint probability distributions.

3.6.1. Estimation of joint probability distributions

Histogram, as well as joint histogram computation, is conventionally done using standard parametric or nonparametric techniques for estimating probability density functions (pdfs) (Duda et al., 2001). These techniques consider separate independent samples of the distribution. A large number of samples is needed for an adequate estimation, especially for multidimensional pdfs. Conventional histo-

gram estimation techniques do not use the fact that we are working with discrete images, and that a discrete grid sampled image I_k , $k \in \mathbb{Z}^3$ is actually a dual representation of a continuous-domain function $I(s)$, $s \in \mathbb{R}^3$ (through the Shannon sampling theorem). This means that an infinitely large number of samples is available for accurate histogram evaluation (Fig. 6). It also means that conventional image histogram computation is incorrect, especially when high frequencies are present. Theoretically, using conventional pdf estimation techniques with highly supersampled images will give good approximations of the underlying probability distribution. In practice this requires a large amount of computation time. Another approach is to analytically compute the histogram of the continuous-domain image. This is feasible for one-dimensional linear interpolation schemes. Locally, in the one-dimensional case I_1 and I'_1 are both linear with respect to the spatial coordinate x : $I_1(x) = ax + b$, $I'_1(x) = cx + d$ and therefore $I'_1 = (c/a)I_1 + d - b/a$. The local contribution to the joint histogram $j(u, v)$ is therefore a line segment. Note that in the conventional (discrete) approach, where no interpolation is used, the local contribution to the joint histogram would have been a single point instead of a line segment. This operation is done in all three dimensions and results are averaged. Resulting histograms agree with the histograms of the supersampled images and are of much higher quality than conventional histograms.

3.6.2. Nonlinear normalization

The joint histogram (Fig. 7) is an estimate of the joint probability distribution $j(u, v) = p(I_1(s) = u, I_2(s) = v) : s \in \Omega$ of intensities in two images. For similar images $p(I_1(s), I_2(s))$ is high for points near $u = v$. If the intensity of a tissue changes over time, due for instance to sensor inconsistencies, the joint histogram of two images taken at separate time points will undergo a nonlinear transformation. We have repeatedly observed this artifact (Fig. 7) that can be a considerable problem in later stages of change detection. To correct it we estimate an intensity correction function f that maximizes the probability $f(u) = \operatorname{argmax}_v j(u, v)$. The intensity-corrected image is then $I'_1(s) = f(I_1(s))$. In practice, a robust estimator, that is less sensitive to outliers, is used. The median value of the $v \rightarrow j(u, v)$ gives good results.

3.7. RF artifact

Remaining artifacts include image intensity nonuniformities, which result from inhomogeneities in the RF field. The major problem in eliminating this artifact is that artifactual intensity variations are hard to distinguish from real image intensity variations (Cohen et al., 2000). In our framework, however, a simple approach is possible. Once images are registered and intensity normalized, a simple subtraction gives us an image that is composed of noise, residual artifacts, and, eventually, real image changes. Residual artifacts in the brain region are essentially movement

and pulsation artifacts, which have zero mean and medium-high spatial frequency. Real image changes are small scale compared to the RF artifact. Applying a large low-pass Gaussian filter ($\sigma = 15$ mm) on this difference image, easily isolates the RF artifact from the previously described changes.

3.8. Change detection

Once the major artifacts have been removed, the images must be compared. That is, we must decide at each point (s) whether or not there has been a genuine change. The simplest approach is direct point-by-point subtraction. However, this gives noisy results, and does not provide an objective decision criterion. Statistical change detection theory provides a sound framework for this purpose (Kay, 1998). We consider a fixed size 3D window W_s centered on a voxel s (Fig. 8). In window W_s , a simple statistical model of intensity distribution is considered. We chose a window size of $3 \times 3 \times 3$ voxels (see section 5 for a discussion on the effects of this parameter). The generalized likelihood ratio test (GLRT) (Hsu et al., 1984; Kay, 1998) computes the ratio of the probabilities of two hypotheses:

$$\begin{aligned} H_0: & \text{there is no change between } I_1 \text{ and } I_2 \text{ inside } W_s. \\ H_1: & \text{there is a significant change between } I_1 \text{ and } I_2 \\ & \text{inside } W_s. \end{aligned}$$

The probabilities are expressed in terms of parametrical pdfs. H_0 is interpreted using the pdf of I_1 and I_2 with the same parameter θ_0 (no change), H_1 is interpreted using the pdf of I_1 and I_2 with two different parameters $\theta_1 \neq \theta_2$. In the GLRT, the unknown parameters θ of the distributions are replaced with their maximum likelihood estimates $\hat{\theta}$ (Kay, 1998). The generalized likelihood ratio is then:

$$R_{GLRT} = \frac{p(I_1; \theta_1)p(I_2; \theta_2)}{p(I_1; \theta_0)p(I_2; \theta_0)} \quad (3)$$

where I_1 and I_2 are respectively the values of I_1 and I_2 in W_s .

3.8.1. Single-modal change detection

We chose a simple model for the parametric pdfs: the intensity within W_s is modeled as a constant value μ plus i.i.d. zero mean additive Gaussian noise. Several studies, in particular in motion detection from video image sequences, have shown that simple intensity models (such as the constant plus Gaussian i.i.d. noise model) are far more robust than more specific models involving more parameters (Mitiche and Boutheimy, 1996). Higher order (i.e., linear or nonlinear) intensity models bring only marginal improvement in the detection results. For example, this simple intensity model is effective even if the noise is not perfectly Gaussian. The noise variance is supposed constant throughout the image and is considered to be identical in both images. It is estimated with a standard estimator by using the difference image described in section 3.7 that contains

residual noise. Therefore, the only pdf parameter θ that must be estimated is the average $\theta = \mu$ value. The maximum likelihood estimate of μ is $\hat{\mu} = \sum_{p \in W_s} I_p / n$ where n is the number of voxels in W_s .

Taking the log of Eq. (3) gives the log-likelihood ratio:

$$l = \frac{1}{2\sigma^2} \sum_{p \in W_s} - (I_1(p) - \hat{\mu}_1)^2 - (I_2(p) - \hat{\mu}_2)^2 \\ + (I_1(p) - \hat{\mu}_0)^2 + (I_2(p) - \hat{\mu}_0)^2$$

which simplifies to:

$$\frac{\sqrt{n}}{2\sigma} |\hat{\mu}_2 - \hat{\mu}_1| > \lambda \quad H_1 \\ < \quad H_0 \quad (4)$$

H_1 is chosen if $l > \lambda$, H_0 is chosen if $l < \lambda$ where λ is a threshold.

3.8.2. Multimodal change detection

The single-modal change detection framework presented above may be extended to the multimodal case. For m modalities, each image value is considered as an m -dimensional vector. The probability of observing intensity values $I(p)$, $p \in W_s$ for a given model average μ is

$$p(I; \mu) = \left(\frac{1}{\sqrt{(2\pi)^m |C|}} \right)^n e^{-1/2 \sum_{p \in W_s} (I(p) - \mu)^T C^{-1} (I(p) - \mu)} \quad (5)$$

where n is the number of voxels in W_s , and C is the covariance matrix of the noise. The covariance matrix is also assumed constant over the whole image and estimated using standard ergodic estimators (Duda et al., 2001; Kay, 1998). The multimodal log likelihood ratio becomes:

$$l = \frac{-1}{2} \sum_{p \in W_s} (I_1(p) - \hat{\mu}_1)^T C^{-1} (I_1(p) - \hat{\mu}_1) \\ + (I_2(p) - \hat{\mu}_2)^T C^{-1} (I_2(p) - \hat{\mu}_2) - (I_1(p) - \hat{\mu}_0)^T C^{-1} \\ \times (I_1(p) - \hat{\mu}_0) - (I_2(p) - \hat{\mu}_0)^T C^{-1} (I_2(p) - \hat{\mu}_0) \quad (6)$$

Please note that the relative “weight” given to each modality by this method depends on the noise covariance matrix. Noisy modalities will therefore be down-weighted by this approach.

3.9. Postprocessing

The change detection step labels individual voxels that have changed. In our change detection system we focus on change events that might involve several adjacent voxels (see section 4.2). Therefore, neighboring changed voxels are grouped together using the following simple clustering

scheme: An high initial likelihood value x is chosen and is iteratively decreased. Each time new voxels are found at value x , they are either added to an existing cluster of a neighboring voxel, or, if no neighboring voxel is in a cluster, a new cluster is created. Each group is assigned a value. This value is the largest likelihood ratio of all the voxels in the group. Groups are then sorted in decreasing likelihood order. To the end user is presented a set of evolutions, of decreasing confidence, through which he may interactively cycle (Fig. 9). Evaluating, and rejecting false detections, is very fast, typically under a minute for an image pair.

4. Results

The automatic detection system has been evaluated by two neurologists on a real-world base of over 200 images as well as on simulated evolutions. We present, here, the rationale behind our methodology.

Evaluating the results of change detection is a difficult task, as there is no solid ground truth available. Indeed, many subtle changes are subject to debate after close examination by experts. Important total lesion load interrater variability has, for instance, been reported in Mitchell et al. (1996), and we have also observed significant disagreement between experts.

Two evaluation approaches were considered:

1. Using simulated evolutions (section 4.1) on scan pairs from healthy subjects.
2. Comparing the results of change detection by an expert with those of automatic change detection (section 4.2).

The use of simulated data has the advantage of providing a well-controlled ground truth, which allows the study of the influence of different parameters. However, simulated data is well known to be easily biased. It often does not effectively reproduce all of the complex factors involved in real data. Furthermore, real brain changes may occur in healthy patients (see section 2.1). Simulated lesion evolutions were therefore used to determine how the characteristics of an evolution affect our detection system. In particular, the influence of the size of an evolution was evaluated.

The experimental protocol described in section 4.2 evaluates the detection system in a real-world application. Since determining a strict ground truth is not possible, we opted for an approach where: a first expert manually detects changes in scan pairs, as he would do in clinical practice; then the automatic system does a similar task; and finally a second expert referees between both. This methodology measures the benefit involved in assisting a neurologist with the proposed automatic detection system. The lack of a gold standard implies that this scheme is not flawless: for instance, if an evolution is missed by both expert-1 and by the automatic detection system, it will not appear in this eval-

Table 1
Detection probability of simulated lesions, as a function of lesion radius (section 4.1)

σ_r (voxels)	0.25	0.5	0.6	0.7	0.75	1
p_{det}	0%	14%	50%	100%	100%	100%

uation. As explained in section 4.2, both experts have very different roles.

4.1. Simulated evolutions

Lesions were constructed using a Gaussian profile that was added to real brain MR images in all modalities. The intensity of the Gaussian profile was determined by using intensities observed in real-world MS lesions. Several values were used for the standard deviation of the Gaussian σ_r (σ_r is the radius of the simulated lesion at half of its intensity). Evolutions were modeled as lesions that appear completely between two exams: the lesions were added to images of normal control subjects, and these images were compared to previous images of the normal control subjects taken 2 months earlier. All of the images went through the complete processing chain. Several experiments were performed, each one involving one or more simulated lesions. Simulated lesions were placed sufficiently far apart from each other so as to avoid interference.

Table 1 shows how the detection probability p_{det} of simulated lesions depends on σ_r (in voxels: 1 voxel = 2 mm). Lesions are correctly detected if they are larger than $\sigma_r < 0.6$ voxels. Here, a simulated lesion evolution is considered to be detected if its change detection likelihood l is higher than the likelihood of all false alarms.

Experiments on the size of the detection window W_s show that it is the primary factor influencing the minimal size of detectable evolutions. The detection window has a smoothing effect: small windows enable the detection of small evolutions but yield noisy results, large windows mask out small evolutions but provide more reliable results. The window size of $3 \times 3 \times 3$ voxels was considered to be a good trade-off for MS-lesion evolution.

The system was also tested on large lesion evolutions to test its breakdown point. We found that lesions up to $\sigma_r = 7$ voxels were correctly dealt with. For larger sizes small spurious detections may appear outside of the evolution, mainly due to the low-pass RF correction filter and to overcompensation during deformable registration. The breakdown point, $\sigma_r = 7$ voxels, corresponds to very large evolutions, of a size comparable to the ventricles, that are well outside of the scope of the type of approach we are considering here (see section 2). We have therefore validated that the deformable registration involved in the re-alignment step does not affect the evolutions we are considering.

4.2. Experimental evaluation

4.2.1. Experimental protocol

The evaluation is based on the detection of “evolving lesions”: we do not address the problem of estimating the volume of detected lesion evolutions (see also section 5). For the expert, the precise definition of a “lesion evolution” is subject to interpretation, and is based on his prior knowledge of lesion configurations. For our automatic detection system, a lesion evolution is a cluster of voxels resulting from the statistical change detection step (section 3.9).

We chose to consider detected clusters rather than detected voxels for two reasons. First, the expert interprets the results by labeling lesions as having changed or not, he does not consider individual voxels. It would thus be difficult to compare the expert evaluation with automatic change detection if this was done on a voxel change basis. Second, for the expert, detection of individual voxel changes would mean manual labeling of each detected voxel, which implies a tedious (in practice not feasible) segmentation of evolutions. Manually or semiautomatically delimiting lesions has been shown to be unreliable [important total lesion load interrater variability has, for instance, been reported in Mitchell et al. (1996)]. Manually delimiting lesion evolutions is even more imprecise.

The evaluation protocol consists in three steps, and involves two experts:

- (1) Expert-1 marks evolving lesions between pairs of images on the whole database.
- (2) The automatic change detection system marks evolving lesions between pairs of images on the whole database.
- (3) Expert-2 evaluates the detections of expert-1 and of the automatic system. Expert-2 will decide which detections are valid.

The first step, the labeling by expert-1, is very time-consuming. Expert-1 must consider each pair of images, and find evolutions by visually inspecting each slice. This is the procedure normally used by clinicians. Here, expert-1 was assisted by rigid registration, linear intensity normalization, and used multiplanar volume visualization software. Note that expert-1 did not use the preprocessing used by the automated detection system (deformable matching, joint histogram normalization, and so on), as these are integral parts of the automated system, and it is our purpose to evaluate them here. The last step, the validation done by expert-2 is much faster, as he only has to evaluate previously designated evolutions.

Matching between evolutions labeled by expert-1 and clusters detected by the automatic system was done manually. In some very rare cases, a single evolution labeled by expert-1 was divided into several detected clusters. In those cases, extra clusters were labeled as false positives.

After evaluation by expert-2, automatic detected evolutions may be labeled as:

- Valid lesion evolution, confirmed by expert-2.
- Valid non-lesion evolution, confirmed by expert-2 as being a real evolution, but is not a lesion evolution (example: ventricular expansion).
- False detection, rejected by expert-2.

Fig. 9 shows the graphical interface used for the evaluation. Cycling animations of compared images are overlaid with expert-1's detections and automatic detections. Expert-2 can efficiently cycle through detections to validate or reject them.

The threshold λ of the automatic detection system may be tuned, giving a trade-off between detection sensitivity and error probability. This trade-off is tuned for each pair (a, b) of compared images. The detection probability $P_{det}(\lambda, (a, b))$ is defined for each pair of images as the ratio between valid detections for threshold λ and the total number of valid detections (including expert-1's detections). Let $n_{err}(\lambda, (a, b))$ be the number of errors for threshold λ . The n_{err} versus $P_{det}(n_{err}(a, b))$ plot is comparable to a ROC curve, and is characteristic of the detector's performance. The average detection probability $P_{det}(n_{err})$ on all image pairs is shown in Fig. 10. The final result of the automated detection system is a sorted list of detected clusters for each image pair (as described in section 5).

4.2.2. Experimental results

The processing chain was applied to over 200 source images of different modalities with no user intervention. The robustness and reliability of processing in such an automated system are very important.

A total of 93 validated lesion evolutions, from both expert-1 and the automated system, were found in the database. Expert-1 found a total of 35 validated lesion evolutions. Fig. 11 gives a description of the sizes of the automatically detected evolutions. The stated volumes are a rough estimate (see sections 4.2.1 and 5) computed by using a common, manually selected threshold for the whole database. Fig. 11 also shows that evolutions correctly detected by expert-1 as well as those missed by expert-1 had size characteristics comparable to other evolutions. Evolutions missed by expert-1 were therefore not particularly smaller or larger than other evolutions. Of the 5% of evolutions missed by the automatic detection system (e.g., not in the first 30 automated detections), most were very small (total volume of 2 to 4 voxels). These lesions are of a size that is equivalent to the Gaussian profiled simulated lesions with $0.4 < \sigma_r < 0.65$. The remaining evolutions, missed by the automatic detection system had intensities that varied only slightly, and it was not clear for expert-2 whether these were actual evolutions. Evolutions identified by expert-1 but rejected by expert-2 are difficult to characterize, as they have diverse origins (see section 5).

Fig. 10 shows the performance of the automatic detection system. It plots the average detection probability against the number of falsely detected clusters. Expert-1 detected evolutions

with a probability of 0.42. This means that more than one of two lesion evolutions were missed by expert-1; 37% of expert-1's detected evolutions were considered incorrect by expert-2. The automatic system therefore performed slightly better than expert-1 for an equivalent false detection rate. However, the automatic system provides much higher detection rates of 95% for higher false alarm rates.

5. Discussion

As shown by the experimental results, manual change detection misses many (58%) lesion evolutions. Manually scanning the full volume of two images for changes is indeed very time consuming and experts tend to skip areas that may contain valid evolutions. Furthermore, the first expert is also misled by acquisition artifacts, such as contrast changes, whereas these are corrected in our automated system. For example, if a lesion has a Gaussian profile, a contrast change may make the lesion seem to grow or shrink. Without nonlinear intensity normalization, expert-1 might be misled and label it as a valid evolution.

The system presented here provides a tool that may be used for assisting a neurologist in finding lesion evolutions. The first 30 automatically detected evolutions, sorted in descending order of importance, are presented to the neurologist. He can scan these evolutions and reject incorrect detections. A large majority of residual false detections occur in CSF, specifically in the central parts of the sulci, which are difficult to reliably segment by automated methods. In practice, these are instantly rejected by the neurologist. Therefore, scanning the 30 detected evolutions of an image pair typically takes about 1 or 2 min, whereas manually comparing two images volumes may take over 20 min. It is planned that false detections in CSF regions will be removed by automatic segmentation in future work.

A major problem we faced while designing this change detection system was identifying which artifacts were creating the detection problems. Since human vision and expert knowledge naturally compensate for many artifacts, it is very difficult to determine the exact sources of many detection errors. Subvoxel position differences are particularly hard to observe. Detailed inspection using several visualization tools was necessary. We found that animations of the successively registered images proved to be a very efficient visualization tool (animations are available at http://ipb.ustrasbg.fr/ipb/gitim/research/research_a.html)

The lesions we observed had many different sizes and shapes. The lesion evolutions were not restricted to radially expanding or contracting spherical shapes. Our change detection system makes no assumption on this. We also observed a large amount of ventricular expansion and contraction, as well as changes inside the ventricles.

Change detection is constantly faced with the trade-off between eliminating artifactual changes and the risk of eliminating real, legitimate changes. Care was taken at each

step to evaluate its impact on legitimate changes. The multiscale deformable registration that we use allows us to choose a maximum scale. At scale i the deformation field is divided into 2^i cells in each direction. Choosing $i = 3$ gives us a low resolution field that is slow varying so that the resulting deformation has very little influence on local features such as lesions (as experimentally verified in section 4.1). Choosing a lower resolution would provide less correction of undesired deformations (section 2.1). Choosing a higher resolution will reduce the maximal allowable size of evolutions before distortion by deformable registration appears. The intensity normalization is done on an image-wide basis. Therefore, local image intensity changes have no measurable impact on the image-wide histograms. The low-pass filter that fixes the RF inhomogeneities is very large, and does not affect local image changes. The robustness of these decisions was evaluated using simulated lesions (section 4.1).

The simultaneous use of images of several modalities at each time point greatly increased detection performance. The detection probability increases from 79% to 95% when using multimodal data (Fig. 10). Indeed, multimodality provides redundant information while noise and artifacts are uncorrelated between modalities. The multislice RARE images have residual artifacts that are distributed in a very different manner than the real 3D GE3D images. This redundant information eliminates many false alarms in multimodal detection and thus increases the detection rate for a given false-alarm rate (Fig. 10). Even in the case of manual change labeling, the multimodal information is very useful for confirming or rejecting a change.

The system described here is oriented toward determining if and where there have been subtle changes. Our experience, as well as that reported by other authors (see section 4.2.1) is that quantifying evolutions is very inaccurate. Noise and residual artifacts make it difficult, even for a trained expert, to validate small evolutions. Quantifying the amount variation is even more difficult. Furthermore, the exact intensity profile of a lesion may change in complex ways, making it difficult to give a satisfactory, reliable, definition of what is understood by the volume of an evolution. Nevertheless, if one accepts these inaccuracies, our method may be very simply used for quantitative analysis (see Fig. 11 and section 4.2.2). However, this might not, in certain cases, match with what a neurologist subjectively considers as the volume of the variation.

Another, more subjective, semiautomatic approach has been considered within our change detection framework. The change detection system presented in this study presents the neurologist with a list of evolutions sorted in decreasing likelihood. For each validated evolution, the neurologist may vary a threshold on the likelihood level, and thus semiautomatically segment the evolution. Fully automatic segmentation techniques have also been considered [see, for instance, Rey et al. (2002)].

The system we have described here is a general change

detection system. It was applied to MS-lesion evolution, but no prior knowledge on size, shape, intensities, or locations of such evolutions was made. An important path to reducing false detection rates for a specific application would be to introduce such prior knowledge. Positional information such as knowing whether an evolution is in GM, WM, or CSF regions would eliminate many false alarms. Information on intensity and size would help rejecting other nonlesion evolutions.

Another path for improving performance would be to add a more sophisticated model for noise. Spatially variant noise maps, or noise distributions learned using PCA, are possible directions.

6. Conclusions

We have presented a comprehensive framework for automatic change detection in serial MRI. The original contributions of this report are the use of the following techniques in the specific case of change detection: multimodal information for change detection, an original nonlinear joint histogram normalization technique, and a specific probabilistic detection scheme. The use of multiresolution deformable image matching in this context is also new, as it has not been previously used as a realignment step for intensity comparison. We propose a systematical analysis of each major artifact and describe a reliable method for correcting it. The reliability was confirmed by the automatic processing of a large database of images of different types.

This automatic change detection has important applications for MS follow-up and provides an objective marker of disease evolution.

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