

BADRESC: Brain Anomaly Detection based on Registration Errors and Supervoxel Classification

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Abstract: Automatic detection of brain anomalies in MR images is very challenging and complex due to intensity similarity between lesions and normal tissues as well as the large variability in shape, size, and location among different anomalies. Inspired by groupwise shape analysis, we adapt a recent fully unsupervised supervoxel-based approach (SAAD) — designed for abnormal asymmetry detection of the hemispheres — to detect brain anomalies from registration errors. Our method, called BADRESC, extracts supervoxels inside the right and left hemispheres, cerebellum, and brainstem, models registration errors for each supervoxel, and treats outliers as anomalies. Experimental results on MR-T1 brain images of stroke patients show that BADRESC attains similar detection rate for hemispheric lesions in comparison to SAAD with substantially less false positives. It also presents promising detection scores for lesions in the cerebellum and brainstem.

1 INTRODUCTION

The visual slice-by-slice inspection of abnormal tissues in magnetic resonance (MR) 3D brain images by a clinician is the most commonly procedure for early diagnosis and follow-up of brain disorders. This process is very laborious, time-consuming, easily prone to errors, and impracticable to be performed at a large scale. Several automatic methods address these difficulties by delineating brain anomalies as accurate as clinicians. However, this goal is very challenging and complex due to the large variability in shape, size, and location among different anomalies (see *e.g.*, Fig. 1).

Most automatic brain lesion detection/segmentation methods train a discriminative model from training images — which must be previously annotated (*e.g.*, lesion segmentation masks) by specialists — to delineate anomalies by classifying voxels or regions of the target image (Goetz and et al., 2014; Pinto et al., 2015; Soltaninejad and et al., 2017). Traditional image features (*e.g.*, edge detectors and texture features) and deep feature

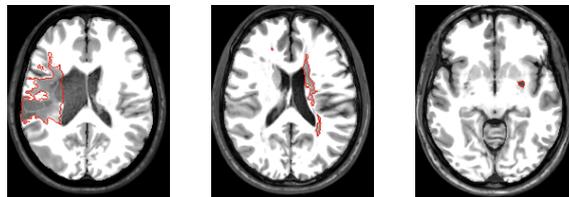


Figure 1: Axial slices of three stroke patients from the ATLAS dataset (Liew and et al., 2018) with lesions (ground-truth borders in red) that significantly differ in location, shape, and size.

representations (*e.g.*, convolutional features) are commonly used (Goetz and et al., 2014; Soltaninejad and et al., 2017; Kooi et al., 2017; Aslani et al., 2018). Some works propose a groupwise shape analysis based on estimating the deformation field between a target image and a template (reference image) after image registration (Gao et al., 2014; Shakeri and et al., 2016).

However, these methods commonly have three main limitations. First, they require a large number of high-quality annotated training images, which is not easily found for most medical image analysis problems (Akkus and et al., 2017; Thyreau and et al., 2018). Second, they are only designed for the lesions

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found in the training set. Third, some methods still require weight fine-tuning (retraining) when used for a new set of images due to image variability across scanners and acquisition protocols, limiting its application to clinical routine.

Unsupervised anomaly detection approaches aim to circumvent the above limitations by encoding general knowledge or assumptions (*priors*) from healthy tissues from control images of healthy subjects *only*. Any *outlier* who breaks such general priors is then considered as an anomaly (Guo et al., 2015).

Since many neurological diseases are associated with abnormal brain asymmetries (Wang and et al., 2001), an *unsupervised* method called Supervoxel-based Abnormal Asymmetry Detection (SAAD) (Martins et al., 2019b) was recently proposed to detect abnormal asymmetries in MR brain images. SAAD presents a mechanism for asymmetry detection that consists of three steps: (i) it registers all images to the same symmetric template and then computes asymmetries between the two hemispheres by using their mid-sagittal plane (MSP) as reference; (ii) a supervoxel segmentation method, named SymMSF, is used to extract pairs of symmetric supervoxels from the left and right hemispheres for each test image, guided by their asymmetries. Supervoxels define more meaningful volumes of interest for analysis than regular 3D patches; and (iii) each pair generates a local one-class classifier trained on control images to find supervoxels with abnormal asymmetries on the test image. SAAD was further extended to detect abnormal asymmetries in the own native image space of each test image (Martins et al., 2019c).

Although SAAD claims to obtain higher detection accuracy even for very small lesions compared to state-of-the-art detection methods, its analysis is limited to asymmetric anomalies in the brain hemispheres, ignoring lesions in the cerebellum and brainstem. Moreover, if the same lesion is localized in both hemispheres roughly in the same position (*e.g.*, some cases of multiple sclerosis), it is not detected due to the lack of asymmetries.

Inspired by groupwise shape analysis, in this work we present BADRESC, an *unsupervised* method for Brain Anomaly Detection based on Registration Errors and Supervoxel Classification in 3T MR-T1 images of the brain. After registering a target image to a common template with *only* healthy tissues by deformable registration, BADRESC assumes that registration errors for anomalies are considerably different of the registration errors for healthy tissues. Thus, BADRESC adapts the SAAD framework as follows. First, it replaces the asymmetry maps with registration errors. A robust preprocessing is considered to

improve the quality of image registration. Second, it expands the anomaly analysis to four objects of interest — right and left hemispheres, cerebellum, and brainstem — by extracting supervoxels for each one *separately*. Finally, each supervoxel generates a local one-class classifier for healthy tissues to detect *outliers* as anomalies.

We compare BADRESC with SAAD for the detection of hemispheric lesions on 3D MR-T1 brain images of stroke patients. Experimental results shows that BADRESC attains similar detection rates to SAAD with considerably less false positives. Additionally, BADRESC presents promising results for the detection of lesions in the cerebellum and brainstem.

2 DESCRIPTION OF BADRESC

We next describe the BADRESC method (see also Fig. 2). The method consists of five steps: 3D image preprocessing, image registration, registration error computation, supervoxel segmentation, and classification, described next. The brain regions/objects of interest in this work are the right hemisphere, left hemisphere, cerebellum, and brainstem.

2.1 3D Image Preprocessing and Registration

MR images are altered by image acquisition problems such as noise and intensity heterogeneity. This makes the automated analysis very challenging since the intensities of the same tissues vary across the image (Pereira et al., 2016). To alleviate these and make images more similar to each other, we use typical preprocessing steps known in the literature (Juan-Albarracín et al., 2015; Pereira et al., 2016; Manjón and Coupé, 2016; Martins et al., 2019b), as shown in Fig. 3.

Initially, we perform the same preprocessing steps of SAAD by applying bias field correction with N4 (Tustison et al., 2010), followed by median filtering for noise reduction, and linear intensity normalization within $[0, 4095]$. Since voxels from irrelevant tissues/organs for the addressed problem (*e.g.*, neck and bones) can negatively impact the image registration and intensity normalization, we use the probabilistic atlas-based method AdaPro (Martins et al., 2019a) to segment the regions of interest (see Fig. 3a-c).

To attenuate differences in brightness and contrast among images, we apply a histogram matching between the segmented images and the template.

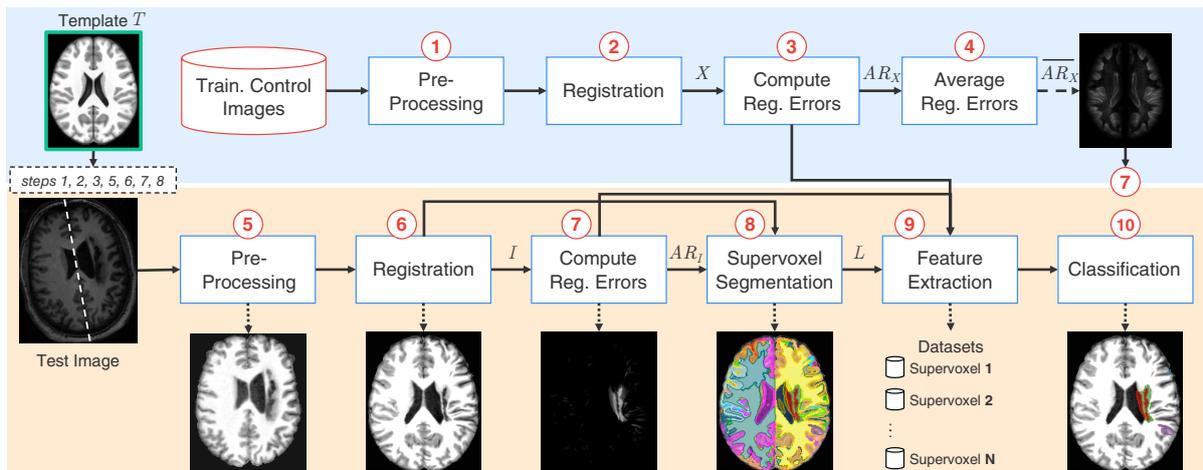


Figure 2: Pipeline of BADRES. The upper blue part is computed previously (offline). The bottom orange part is computed for each test image. The template (reference image) is used in both parts (Steps 1, 2, 3, 5, 6, 7, and 8). Figure based on (Martins et al., 2019b; Martins et al., 2019c).

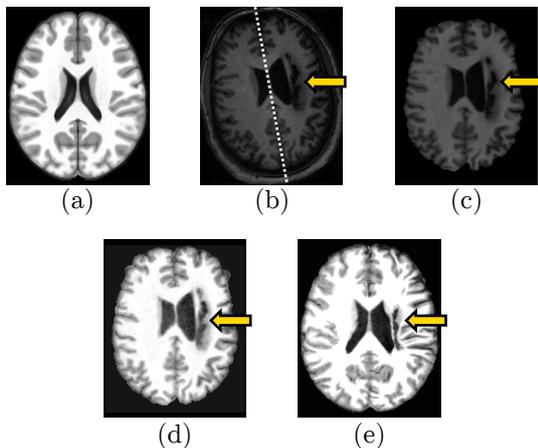


Figure 3: Preprocessing and registration steps. (a) Axial slice of the brain template (reference image). (b) Axial slice of a raw test image. The dashed line shows its mid-sagittal plane (MSP) and the arrow indicates a stroke lesion. (c) Test image after bias field correction, noise filtering, MSP alignment, and brain segmentation. (d) Histogram matching between (c) and the template. (e) Final preprocessed image after deformable registration and histogram matching with the template.

This operation only considers the voxels inside the regions of interest (see Fig. 3d). We then perform deformable registration to place all images in the coordinate space of the ICBM 2009c Nonlinear Symmetric template (Fonov and et al., 2009). Since the image registration technique has a critical impact on the analysis, we use Elastix (Klein et al., 2010), a popular and accurate image registration method.¹ Finally,

¹We used the *par0000* files available at <http://elastix.bigr.nl/wiki/index.php>

we perform another histogram matching between the registered images and the template (see Fig. 3e).

2.2 Registration Error Computation

When registering images to a common template with *only* healthy tissues, we expect that registration errors (REs) — voxel-wise absolute differences between the registered image and the template — are lower and present a different pattern compared to anomalies (see Fig. 4e). However, some healthy structures in the cortex, such as gyri and sulci, present high REs due to their complex shapes and immense variability between subjects — observe the cortex of the template and the registered image in Figs. 4a and 4d; note its resulting REs in Fig. 4e. To avoid detecting false positives in this region, some attenuation process is required.

Let T be the template (Fig. 4a) and M_T its predefined brain segmentation mask for the right hemisphere, left hemisphere, cerebellum, and brainstem (background voxels have label 0 and each object has a different label). Let $X = \{X_1, \dots, X_k\}$ be the set of k registered training images (output of Step 2 in Fig. 2) and I the test image after preprocessing and registration (output of Step 6 in Fig. 2; see also Fig. 4d).

Firstly, we compute the euclidean distance transform (EDT) for each object of M_T and normalize the distances within $[0, 1]$ to build the map E (Fig. 4b). Next, we obtain the set of registration errors R_X for all X by computing the voxel-wise absolute differences between X and T (Step 3 in Fig. 2; see also Fig. 4e). For each training image $X_i \in X$, we attenuate REs in its cortex such that for each voxel $v \in X_i$,

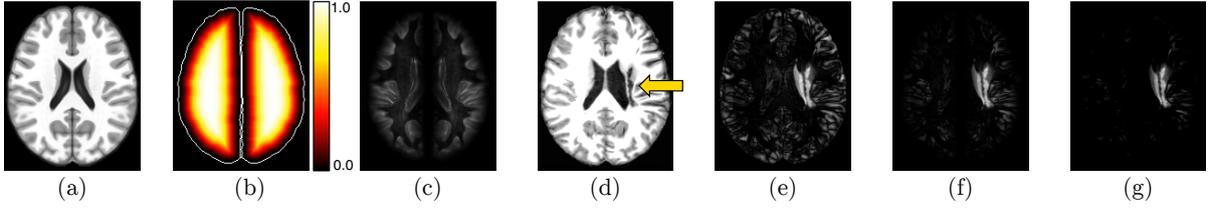


Figure 4: Registration error computation. (a) Axial slice of the brain template. (b) Euclidean Distance Transform (EDT) normalized within $[0, 1]$ computed for the brain segmentation mask defined for the template. Brain borders are shown only for illustration purposes. (c) Common registration errors for control images. (d) Axial slice of a test stroke image after preprocessing and registration in (a). The arrow indicates the stroke lesion. (e) Registration errors. (f) Attenuation of (e) for the cortex based on the EDT. (g) Final registration errors for the test image: positive values of the subtraction between (f) and (c).

$$\begin{aligned} f(v) &= 1 - (E(v) - 1)^4 \\ AR_{X_i}(v) &= R_{X_i}(v) \cdot f(v) \end{aligned} \quad (1)$$

where $E(v)$ is the euclidean distance for the voxel v , $f(v)$ is its attenuation factor within $[0, 1]$, and AR_{X_i} is the map with the attenuated REs for X_i . Thus, REs of voxels close to the brain borders are extremely attenuated whereas those from voxels far from the borders are slightly impacted (see Fig. 4f). A downside of this approach is that subtle lesions in the cortex tend to be missed.

In order to even ignore REs caused by noises or small intensity differences in regions/tissues far from the cortex, we create a *common registration error map* $\overline{AR_X}$ by averaging the attenuated REs from AR_{X_i} (output of Step 4 in Fig. 2; see also Fig. 4c). Finally, we repeat the same steps to compute the attenuated REs for the test image I and then subtract $\overline{AR_X}$ from them. Resulting positive values form a final attenuated registration error map AR_I for I (output of Step 7 in Fig. 2; see also Fig. 4g).

2.3 Supervoxel Segmentation

The direct comparison between the registered image and its template, or even between large 3D regular patches, is not useful as it will not tell us where *small-scale* REs occur — a similar parallel is done for asymmetries in (Martins et al., 2019c). Conversely, a voxel-wise comparison is risky, since individual voxels contain too little information to capture REs. These difficulties motivate the use of *supervoxels* as the unit of comparison (Step 8 in Fig. 2).

Inspired by the SymmISF method (Martins et al., 2019b) used in SAAD for symmetrical supervoxel segmentation, we propose a new technique that extracts supervoxels in the brain guided by registration errors, as shown in Fig. 5. Our supervoxel segmentation is also based on the recent Iterative Spanning Forest framework (Vargas-Muñoz et al., 2019) for su-

perpixel segmentation and has three steps: (i) seed estimation; (ii) connected supervoxel delineation (multiple iterations); and (iii) seed recomputation to improve delineation, as follows.

Recall a template T , a preprocessed and registered test image I , and its attenuated registration error map AR_I . We find the initial seeds by selecting one seed per local maximum in AR_I (see the seeds in Fig. 5). We compute the local maxima of the foreground of a binarized AR_I at $\gamma \times \tau$, where τ is Otsu’s threshold (Otsu, 1979). The higher the factor γ is, the lower is the number of components in the binarized AR_I . We extend the seed-set with a fixed number (100) of seeds by uniform grid sampling the regions with low REs of the binarized image.

By stacking I and T as the input 2-band volume (see Fig. 5), we apply ISF inside each object of interest *separately* from the initial seeds. ISF relies on a cost function controlled by two parameters: α and β . The results are label maps in which each supervoxel is assigned to a distinct number/color. All labels are then combined and relabeled to build the final supervoxel map L (output of Step 8 in Fig. 2).

2.4 Feature Extraction and Classification

The feature extraction and classification steps are very similar to those of SAAD (Martins et al., 2019b). For each test image I , each supervoxels in L is used to create a one-class classifier using as feature vector the normalized histogram of the attenuated REs in AR_I (Step 9 in Fig. 2). This implicitly considers the *position* of the supervoxels in the brain during classification. BADRESC uses the one-class linear Support Vector Machine (oc-SVM) for this task (Manevitz and Yousef, 2001). The classifiers are trained from *healthy* control images *only* and used to identify outlier supervoxels with abnormal REs in I (Step 10 in Fig. 2).

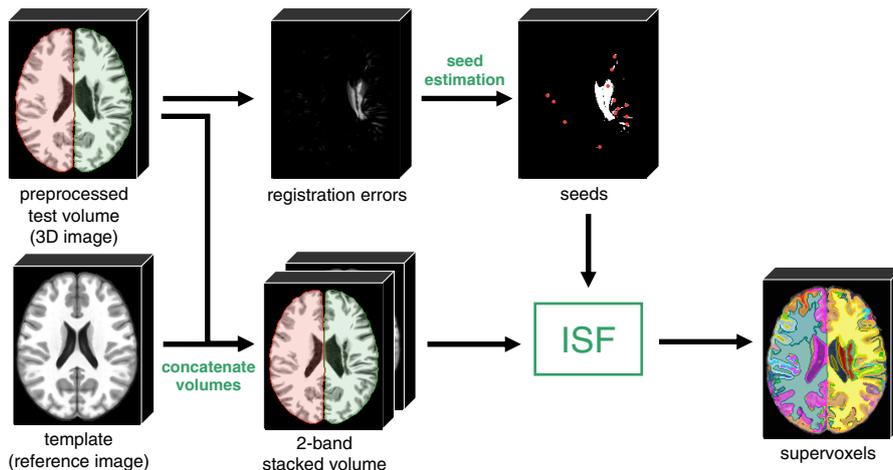


Figure 5: Pipeline of the proposed supervoxel segmentation. The method stacks the input preprocessed test 3D image (segmented objects are colored) with the template to build a 2-band volume. An initial seed set is obtained from the registration errors of the test image. For each object of the segmentation brain mask, the ISF framework (Vargas-Muñoz et al., 2019) estimates supervoxels inside the object from the initial seeds. Resulting supervoxels are combined and relabeled to form the final label map.

3 EXPERIMENTS

To evaluate the proposed method, we need datasets with *volumetric* MR-T1 brain images (i) from *healthy* subjects for training, and (ii) with lesions of different appearance (especially small ones) containing their segmentation masks. First, we considered the CamCan dataset (Taylor et al., 2017) which has 653 MR-T1 images of 3T from healthy men and women between 18 and 88 years. As far as we know, CamCan is the largest public dataset with 3D images of healthy subjects acquired from different scanners. In order to avoid noisy data in the training set, we removed some images with artifacts or bad acquisition after a visual inspection in all MR-T1 images, yielding 524 images.²

For testing, we chose the Anatomical Tracings of Lesions After Stroke (ATLAS) public dataset release 1.2 (Liew and et al., 2018) in our experiments. ATLAS is a very challenging dataset with a large variety of manually annotated lesions and images of 1.5T and 3T acquired from different scanners. It contains heterogeneous lesions that differ in size, shape, and location (see Fig. 1). All images only have a mask with a stroke region ignoring other possible anomalies caused by those lesions. Current state-of-the-art segmentation results for ATLAS from a *supervised* method based on U-Net are inaccurate yet (Qi and et al., 2019).

Since the considered training images have a 3T

²A link with the considered images can be found at https://github.com/lidsunicamp/BIOIMAGING20_BADRESC

field strength, we selected all 3T images from ATLAS for analysis (total of 269 images). All images were registered into the coordinate space of ICBM 2009c Nonlinear Symmetric template (Fonov and et al., 2009) and preprocessed as outlined in Section 2.1.

We compared BADRESC against the SAAD method proposed in (Martins et al., 2019b), which in turn was also evaluated with the ATLAS dataset as reported in (Martins et al., 2019b). For a fair comparison, we compared both methods for all 3T images which only contain lesions in the hemispheres. Additionally, we evaluated BADRESC for the 3T images with stroke lesions in the cerebellum and brainstem. We used the following parameters for BADRESC, empirically obtained from the observation on a few training control images: $\alpha = 0.06$, $\beta = 5.0$, $\gamma = 3$, histogram of 128 bins, and $v = 0.01$ for the linear oc-SVM.

We proposed a set of metrics to evaluate the detection quality, as follows. We start computing the detection rate based on at least 15% overlap between supervoxels detected by the methods and lesions labeled in ATLAS (Table 1, row 1). We then provided false positive (FP) scores in terms of both voxels and supervoxels with respect to the ground-truth stroke lesions of ATLAS. We first computed the mean rate of FP voxels, *i.e.*, incorrectly classified as abnormal (Table 1, row 2), with respect to all classified voxels from the analyzed object(s) — *i.e.*, the total number of voxels inside the right hemisphere for SAAD and all voxels from the hemispheres, cerebellum, and brainstem for BADRESC.

Table 1: Quantitative results for images from the ATLAS dataset with stroke lesions in the hemispheres, cerebellum, and brainstem. Higher detection rate means better accuracy. Lower false positive rate means better accuracy.

	Hemispheres		Cerebellum and Brainstem
	SAAD	BADRES	BADRES
#1 Detection Rate	0.8324	0.8298	0.6829
#2 False Positive Voxel Rate	0.050 ± 0.027	0.005 ± 0.006	0.005 ± 0.004
#3 Number of False Positive Supervoxels	53.84 ± 19.64	21.48 ± 13.82	25.63 ± 15.64
#4 False Positive Supervoxel Rate	0.14 ± 0.05	0.104 ± 0.069	0.097 ± 0.049

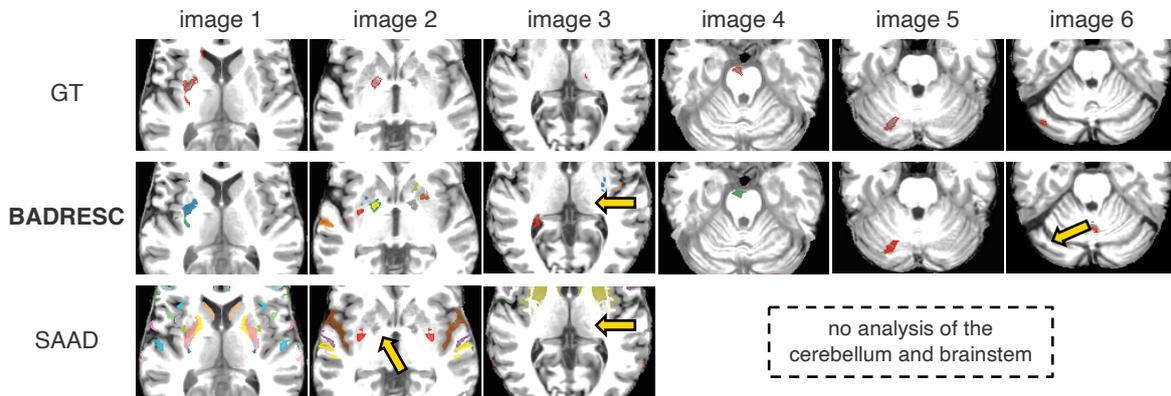


Figure 6: Results on ATLAS dataset. Each column is a test image: Images 1-3 have lesions in the hemispheres, Image 4 contains a lesion in the brainstem whereas Images 5-6 have lesions in the cerebellum. First row: Ground-truth lesion segmentations. Second row: Results of BADRES. Third row: Results of SAAD. Arrows indicate undetected lesions. Since SAAD only detects lesions in the hemispheres, there are no results for Images 4-6.

At the next level, we estimated FP supervoxels as those whose voxels overlap less than 15% with ground-truth lesion voxels. We computed the mean number of FP supervoxels and its proportion with respect to the total number of supervoxels from the analyzed object(s) (Table 1, rows 3 and 4). The first metric gives us an estimation of the visual-inspection user effort. The second metric checks how imprecise is the detection regarding the total number of regions that the user has to visually analyze.

4 RESULTS AND DISCUSSION

Table 1 summarizes all quantitative results whereas Fig. 6 presents some visual results. Although SAAD presents a slightly better detection rate for hemispheric lesions (0.8324) compared to BADRES (0.8298), it consistently presents worse FP rates (see its FP in Fig. 6). SAAD incorrectly classifies 14% of supervoxels on average — which con-

sists of 5% of the analyzed voxels in the hemisphere. Conversely, as Table 1 shows, BADRES presents considerably less FP supervoxels than SAAD (average of 21.48 supervoxels against 53.84). This corresponds to 10.4% of analyzed supervoxels and less than 1% of voxels in the entire brain (see Fig. 6).

SAAD is not able to detect lesions with low asymmetries, even if they are well-contrasted with their surrounding tissues. BADRES does not have this limitation (compare the results for Image 2 in Fig. 6). However, both methods are not robust to detect very small-scale anomalies (Fig. 6, Image 3).

BADRES is less accurate to detect lesions in the cerebellum and brainstem (detection rate of 0.6829). Indeed, some lesions seems to be more challenging, specially in the cerebellum, whose appearances are similar to their surrounding tissues (Fig. 6, Image 6). However, its FP scores are similar to those of hemispheric lesions which confirms the stability of the method (compare rows 2-4 for BADRES in Table 1).

5 CONCLUSIONS

We presented a new *unsupervised* method for brain anomaly detection that combines registration errors and supervoxel classification. Our approach, named BADRESC, adapts a recent supervoxel-based approach (SAAD) to detect *outliers* as anomalies from registration errors in the hemispheres, cerebellum, and brainstem. BADRESC was validated on 3T MR-T1 images of stroke patients with annotated lesions, attaining similar detection accuracy to SAAD for lesions in the hemispheres and substantially less false positives. BADRESC also detects lesions in the cerebellum and brainstem with promising results.

For future work, we intend to improve BADRESC by optimizing its parameters and using additional visual analytics techniques to improve seeding and further investigate other anomaly features and classifiers to yield better detection rates, specially for the cerebellum and brainstem.

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