Semi-Automated Microbleed Identification on Susceptibility Weighted Images

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Introduction: Modern imaging sequences such as susceptibility weighted imaging (SWI) that are routinely run at high resolution ($\leq 1 \text{mm}^3$) are much more sensitive to detecting small lesions and bleeds than traditional sequences. Recent publications have shown a three to six fold increase in the number of lesions seen^{1,2}. Many of these newly visible lesions are small (<4mm in diameter) and widely distributed throughout the brain. The small size and wide distribution has hampered efforts to quantify them. So far methods have centered on manually drawing and counting the lesions, or manually defining local thresholds for a small region of interest (ROI)³. These methods tend to be extremely time consuming and suffer from a high amount of inter- and intra-observer error. In this work, we propose a semi-automated method of identifying and quantifying lesions seen on high resolution SWI scans. This should make it possible to dramatically reduce image processing time and increase reproducibility.

Materials and methods: All SWI images were acquired as part of a longitudinal study on mild cognitive impairment and Alzheimer's disease⁴. Images were all counted manually then only the images with identified microbleeds were used in the semi-automated processing. A total of six datasets were processed with this method containing 126 microbleeds. Data were collected at 1.5T with a resolution of 0.5x1.0x2.0mm³. Imaging parameters were: TR=57ms, TE=40ms, FA=20°. Standard SWI processing with high pass filtered phase images was performed. The semi-automated method consisted of three steps. First, the brain was isolated using a background removal and skull striping algorithm⁵. Second, statistical local thresholding was performed to mark low outliers. Third, a support vector machine (SVM) classifier was used to distinguish likely microbleeds from veins and other structures using shape, size, and intensity features. These suspected microbleeds are presented to the user to manually confirm or delete them.

In our implementation, statistical thresholding looks at the mean and standard deviation of a local ROI (40x40x5) centered on the current voxel. If the intensity of the voxel of interest is sufficiently below the mean it is marked as a vein.

$$voxel_{vextel} < \alpha \cdot \sigma_{local} + \bar{x}_{local} \tag{1}$$

$$voxel_{vessel} < \alpha \cdot \sigma_{local} + \overline{x}_{local}$$
 (1)
$$voxel_{background} \ge \alpha \cdot \sigma_{local} + \overline{x}_{local}$$
 (2)

For this study a was set to 2.5 as this was empirically determined to give good results. Once the dataset had been thresholded, marked voxels were sorted into connected groups. For each connected group, the compactness, eigenvalues of the covariance matrix, relative anisotropy of the covariance matrix, size, and the mean, standard deviation, minimum, and maximum for both magnitude and phase images were calculated and used as identifying features for the classifier.

A SVM (libSVM version 2.88) supervised machine learning classifier was used to separate the suspected microbleeds from the veins and noise that were marked based on the features listed above. The cost and gamma values were selected using cross validation and set to 324.8 and 0.2877 respectively. Feature scaling was also used. The classifier was trained using the manually marked datasets as the ground truth. Due to the limited number of datasets, leave-one-out cross-validation was used to measure the accuracy of the classifier.

Results: As shown in Table 1 the thresholding step has very good sensitivity, only missing 6 microbleeds, but generates many false positives. The classifier is able to eliminate most of the false positives at the cost of an additional 17 false negatives. The classifier results are reviewed manually to remove the remaining false positives for a final sensitivity and specificity of 81.7% and 100%, respectively. Many of the microbleeds that were incorrectly eliminated were connected to vessels causing them to have vessel like features and thus were removed by the classifier.

	Threshold	Classifier	Review
TP	120	103	103
TN	NA	15,162	15,807
FP	15,807	645	0
FN	6	23	23
Missed	6	17	0

Table 1. Table shows the running total of true and false positives and negatives at each step (including previous steps). The number of microbleeds missed or removed at each step is also shown.

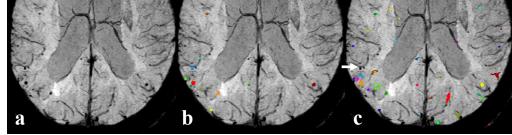


Figure 1. a) mIP over SWI processed images showing microbleeds. b) Manually marked microbleeds. c) Results of semi-automated procedure before false positives have been manually removed. Notice the two small microbleeds that were missed (arrow) are adjacent to a vessel. The vessel and the bleeds were marked as a single connected object causing them to look like a vessel to the classifier and they were then removed by the classifier.

Discussion and Conclusion: The manual intervention in this process is required only as a final step and ensures that the results are accurate. This can be accomplished quite rapidly as only a yes or no decision is required on a pre-marked bleed. The total processing time per dataset (including manually removing false positives) is under an hour. This is a vast improvement over manual counting which can take up to one day per dataset. While there is some loss of sensitivity compared to manual counting, we believe this is more than made up for by the increased reproducibility and reduced processing time.

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