

Response to reviewers

We appreciate the time spent by the editors and reviewers in assessing our manuscript. Please see below for a point-by-point response to the issues raised.

Reviewer 1

Thank you for the opportunity to review the paper “Supervised learning technique for the automated identification of white matter hyperintensities in traumatic brain injury”. In this study, the authors present a machine learning algorithm for automated segmentation of white matter hyperintensities, a form of white matter degeneration visible in FLAIR-MRI that is observed in a wide range of clinical syndromes, and even in healthy controls. The method proposed by the authors relies on training random forests to learn the relationship between voxel intensities in a set of feature images derived from multimodal MRI (T1, T2, FLAIR) and lesions drawn manually by an expert. Since the method uses examples to learn what constitutes a lesion, this is correctly considered a supervised method. The method is applied on a set of 24 patients with clinically confirmed traumatic brain injury, and results are obtained with a leave-one-out cross validation.

Overall, the method proposed by the authors is innovative and thoughtful, and has great potential for bridging the gap between research findings and clinical needs. The method uses a series of cutting edge solutions to the segmentation problem: (1) multimodal imaging inputs, which is known to increase segmentation accuracy, (2) random forests, which are an excellent tool for finding multivariate nonlinear relationships, (3) voxel neighborhood information, which provide contextual information for each voxel, and (4) an algorithm that improves the segmentation in stages. However, the manuscript itself, to my opinion, is not well focused and needs significant improvement. Below are my specific comments in support of this.

We thank the reviewer for the generally positive assessment of our work. We also appreciate the detailed critique below to help us improve specific aspects of the presentation.

Major comments:

1. The biggest issue I had while reading the manuscript is the lack of a coherent theme of what this paper is about. The authors span their exposé from multiple sclerosis to the automobile industry, without stating why these links to other diseases (or industries) have any relevance. It appears in some parts that the closest disease with similar white matter lesions is multiple sclerosis, but this is not clearly stated, nor the two types of lesions are compared. It is, therefore, unclear why counting how many MS lesion segmentation methods are publicly available is of any importance. When explaining methods, the authors mention the utility of support vector machines, or the existence of a python package called SciPy. Yet, it is unclear why these things

have any importance, unless the authors make connections to their topic/method.

We reduced the introduction to limit the clinical motivation to a TBI context and removed mention of multiple sclerosis to remove any assumption of disease similarity (although the segmentation approaches can be similar). We also removed the paragraph dealing with publicly available software for neuroimaging analysis.

2. Second, the manuscript has no results. All the results section is focused on talking about feature ranking, which by the way is explained in the Results section instead of the Methods section. The most important results (the prediction accuracy of automated segmentation), are not mentioned in the manuscript but are only plotted in Figure 7. My advice is to put the focus of the results section on accuracy, i.e., give precise dice values and perhaps add other measures (metric displacement, Hausdorff distance, sensitivity, specificity, etc.). Also, the gain in accuracy from stage 1 to stage 2 cannot be guessed by looking at a plot, the authors must provide a statistical comparison. When investigating accuracy, the error in lesion size should be reported, both in terms of volume and in terms of individual lesions counts (i.e. out of 10 lesions 9 were found, 1 was missed, etc.). This information is crucial to clinicians, if the authors foresee the use of the method in a clinical setting, as it seems from the discussion. Beside adding results to the manuscript, it is equally important to give some results in the abstract. The abstract must be self-sufficient in reporting all the major points of the paper.

Nick

3. Third, there is no information about the manual lesion tracing procedure. Were lesion drawn on FLAIR or were other modalities used as well? If FLAIR was used as reference it is not surprising that FLAIR emerges as one of the top predictive modalities.

We added the following to the Methods section:

The first author (J. R. S.) performed the manual WMH tracings for all 26 subjects. J. R. S. is a radiologist certified by the American Board of Radiology, with a certificate of advanced qualification in vascular and interventional radiology, over 18 years of research experience in TBI, and 6 years of clinical imaging experience. All multi-modal MR dicom image slices were converted to the nifti file format. Given the utility of the FLAIR sequence in detecting white matter lesions in TBI¹, all nifti image volumes for each subject were rigidly aligned to the FLAIR image of that subject using the ANTs software². The normalized MRI volumes were then provided to J. R. S. who traced each lesion using the ITK-SNAP tool³ which has multi-image overlay capabilities for visualizing all modalities in all three canonical views.

Descriptive statistics on the lesions are also necessary: how big were the lesions, how many lesions were found in each patient (the range 1-20 is not sufficiently informative), where were the lesions located? This information helps understand why, for example, brain stem or cerebellum labels were not that important for achieving good lesion predictions.

We added the following sentence to the opening paragraph of the Imaging subsection of the Methods section:

All lesions were isolated in the white matter of the cerebrum. Table 1 provides a descriptive statistical summary of the variation in lesion load across the selected cohort.

as well as the corresponding table:

Subject id	Lesion count	Lesion load	Mean volume	[Min – Max]
0	2	18	9 ± 1.4	[8-10]
1	3	3	1 ± 0	[1-1]
2	0	0	0	[0-0]
3	11	209	19 ± 18.4	[1-56]
4	3	130	43.3 ± 50.0	[12-101]
5	1	2	2	[2-2]
6	25	790	31.6 ± 29.2	[2-132]
7	24	767	32.0 ± 33.6	[2-166]
8	3	18	6 ± 7.8	[1-15]
9	21	508	24.2 ± 35.1	[1-166]
10	2	17	8.5 ± 10.6	[1-16]
11	7	151	21.6 ± 21.7	[1-61]
12	46	901	19.6 ± 17.9	[1-115]
13	1	1	1	[1-1]
14	2	32	16 ± 9.9	[9-23]
15	2	22	11 ± 14.1	[1-21]
16	8	124	15.5 ± 8.4	[6-34]
17	3	140	46.7 ± 53.1	[1-105]
18	3	10	3.3 ± 4.0	[1-8]
19	20	784	39.2 ± 63.2	[1-230]
20	3	6	2 ± 1.7	[1-4]
21	7	244	34.9 ± 32.3	[1-93]
22	12	236	19.7 ± 13.5	[1-52]
23	63	4078	64.7 ± 93.6	[1-551]
Total	272	9191	33.8 ± 55.4	[1-551]

Table 1: Descriptive lesion statistics for the cohort used for the evaluation. Lesion load, mean volume (\pm standard deviation), and the min/max range are given in terms of the number of voxels since all image acquisitions were performed with the same image voxel resolution ($1 \times 1 \times 1.2$ mm).

4. Fourth, although the authors claim the method is available, I couldn't find any link for the public. Note, it would be equally important if the publication of the method online is associated with proper documentation on how a new (naive) user can apply it.

Our methodological publication history demonstrates that we are very supportive of open science and have released both code and data in conjunction with these publications in public forums, such as github. However, permission to publicly release the data for this data has not yet been obtained and so we removed the mention of public availability. However, when we do get permission, it will be posted to the github repository associated with this manuscript (<https://github.com/ntustison/WatchMeHyperventilate>) for future readers.

Minor comments:

5. In the abstract, the authors mention the creation of tailored features for segmenting WMHs. My understanding is that the method proposed by the authors has no tailoring (if we think of tailoring as custom cutting to WMH needs).

We removed the word “tailor” in its various forms in the manuscript to avoid the misreading described by the reviewer.

There was no feature selection process all the features were included as predictors.

Although feature selection is mentioned in the manuscript, nowhere do we mention or imply any type of computational feature selection. There was a feature selection process in that we selected ones from the myriad feature images that one can possibly produce based on our targeted application, i.e. WMHs.

A similar pitfall is found on pg. 6 ln 56, where the manuscript reads “Crucial to these supervised segmentation approaches are the creation and selection of features as input in conjunction with expertly identified structures.” What are the structures identified by the expert in this study?

For this particular application, white matter hyperintensities are the structure of interest. We have re-emphasized this point by writing:

Crucial to these supervised segmentation approaches are the creation and selection of “features” as input (i.e., feature images constructed from the training data) in conjunction with expertly identified structures of interest (i.e., WMHs) for model construction.

6. The methods section is very confusing. The section “Feature images for WMH segmentation” starts with no explanation of what is Stage 1. The logical flow would require template registration explained first, and all feature computation performed later, and finally RF stages can be explained with the available features.

We added Figure 1 which gives an overview of the basic workflow. It can be seen below in response to item 2 of Reviewer 2. We reference this figure numerous times in the text as a visual explanatory aid. We also added a paragraph at the beginning of the “Quantitative analysis” subsection which gives an overview of the methods section including an description of Stage 1 and Stage2.

Figure 1 provides a graphical overview of the proposed workflow. The major components include offline generation of symmetric multimodal templates, the creation of feature images from the training data which are then employed for statistical prediction using a concatenated random forest framework. This framework involves the use of two random forest models where the outcome (i.e., the tissue probability estimates) of the first RF model application, which we denote as “Stage1”, is used as input (along with the original set of feature images) to a refinement RF model segmentation which we denote as “Stage 2”. Once these offline steps are performed, a new, unsegmented subject can then be processed using the proposed pipeline.

We also added a subsection explaining the symmetric multimodal template:

Following⁴ and⁵, optimally derived templates serve for both brain tissue segmentation (for the derivation of tissue prior probability maps) and generation of asymmetry feature images. For this work we use the multi-modal data available from the public MMRR data set⁶. We used all 46 multi-modal acquisitions of that study to produce a multi-modal template according to the procedure described in⁷ which results in a mean (in terms of both shape and intensity) multivariate template representing the entire cohort. Mid-canonical slices of the FLAIR, T1, and T2 components are illustrated in Figure 2.

These changes complement the edits made in response to other review items.

The pipeline also seem to be repetitive, the N4 correction is mentioned in ln. 26 and then again in ln. 43, which sounds like it was performed twice. Tissue segmentation is mentioned in ln. 39, then it is stated is a Bayesian method (ln 45), and then it is referred to as Atropos in the next page.

The two mentions of N4 are due to the fact that they are associated with two distinct pipelines: 1) preparation of the images for extracting feature values and 2) brain extraction and n-tissue segmentation. We rewrote the section in question to avoid any confusing redundancy:

The T1 image is then processed via the ANTs brain extraction and normal tissue segmentation pipelines⁴. The result is a mask delineating the brain parenchyma and probabilistic estimates of the CSF, gray matter, white matter, deep gray matter, brain stem, and cerebellum⁸. These provide the expertly annotated labels for the first six tissue labels given above. Tissue prior probability maps for segmentation are from multi-model optimal symmetric shape/intensity templates⁵ created from the public MMRR data set⁶ (cf Figure 3).

It is unclear what is “the first set of images” in pg. 9, or if there is a second set.

We clarified this confusion by changing the sentence in question from

To model the intensity information the first set of images simply includes the preprocessed and normalized intensity FLAIR, T1, and T2 image voxel values.

to

Feature values include the preprocessed FLAIR, T1, and T2 image voxel intensities.

Also, mathematical formulas seem superfluous, particularly since it takes more space to explain the formula than to say in plain English that transformation matrices were applied to bring subject’s images in template space.

Done. We removed the mathematical formulas.

7. Random forests are explained in a way that can be understood only by readers who already know how they work; a new reader (especially a clinician) would not be able to understand the method. For example, data pushed onto a tree is does not mean much, unless the reader knows what is an identification tree.

We revised the explanation of random forests as follows:

The basic component of the random forest paradigm is the “decision tree” often represented by a flowchart or graph where internal nodes represent “tests”, or decisions, and the edges represent the outcome of those tests. The final, or end, nodes represent the various classifications produced by traversal through the decision tree. For the proposed application, individual voxels (and their corresponding feature values) are introduced at the root of a particular decision tree and traverse the edges and internal nodes ultimately ending up at one of the classification nodes according to the tests at each internal

node. A single random forest model will consist of many such trees (often referred to as an “ensemble”). Although decision trees had been extensively studied, the success of employing collections of such weak learners for boosting machine learning performance (e.g., AdaBoost)^{9,10} influenced the similarly styled conglomeration of decision trees into “forests” with randomized node optimization^{11,12}. Finally, Breiman¹³ improved accuracy by random sampling of training data (i.e., “bagging”) resulting in the current random forest technique applied here. As voxels and their feature values are “pushed” through each decision tree in the forest, votes for each label are accumulated and converted to probability values for all classification possibilities at each voxel location.

8. The relationship between WMH and GOS-E is mentioned in pg. 2 but the reader is not informed what is GOS-E. A similar issue is met few lines after, where the “outcome” is mentioned, but there is no information what is referred to as outcome.

The sentence in question reads:

Further, volume of FLAIR lesions within the corpus callosum, brainstem, and thalamus in patients with severe TBI correlates with Glasgow Outcome-Extended (GOS-E) scores.¹⁴

Although the full phrase corresponding to the acronym in question is provided prior to the acronym in the text (along with an explanatory reference), we have added the following clarification:

Further, volume of FLAIR lesions within the corpus callosum, brainstem, and thalamus in patients with severe TBI correlates with Glasgow Outcome-Extended (GOS-E) scores¹⁴ —a numeric groupwise assessment used to classify “outcome” in TBI patients where “outcome” refers to the spectrum of possible prognoses from death to disability to recovery.

9. In pg. 3 the authors propose that automated methods “may allow for identification of correlative patterns between WMH number, volume, distribution, and disease state”. Some of these correlations have been already identified in the literature, as the authors mention few lines before. Moreover, the authors do not report number, volume, or distribution of the lesions, to back up the utility of their method in this regard.

We removed the sentence in question. Also, as mentioned in response to item 3, we added Table 1.

10. In pg. 4 ln 43, reads that the data is “constructed.” I don’t think this is the right verb.

We agree that the sentence in question could be read this way. We have, therefore, clarified the sentence in question to read “Once the ensemble of decision trees is constructed, data to be classified is “pushed” through each decision tree resulting in a single classification “vote” per tree.”

A similar issue is in pg 5 ln 52 where it is stated that “feature images consisted of 26 subjects.” It is not ethical to consider participants as feature images.

This was a grammatical mistake, not a question of ethics. It has been fixed: “The feature images were derived from MR acquisitions of 26 subjects...”

11. It is unclear to me the meaning of the sentence: “Since the inverse transform is also derived as part of the registration process, we can warp the voxel index locations back to the space of the individual subject which motivates similar work by others [43].”

The sentences were rewritten as follows:

Similar feature images were used in¹⁵ although, unlike the proposed framework, this previous work lacks normalization to the standard coordinate system provided by the template to dramatically improve spatial specificity across all subjects. To generate these images, the T1 image of each subject is registered to the T1 template component using a B-spline variant¹⁶ of the well-known ANTs Symmetric Normalization (SyN) algorithm¹⁷. Using the derived transforms, the template coordinate images are warped back to the space of the individual subject.

12. Why was Stage 1 segmentation based only on T1, while Stage 2 segmentation was based on multivariate segmentation using all three modalities?

We added the following clarification:

In order to maximize the spatial information for the n -tissue segmentation process following the voxelwise RF classification of Stage 1, we use all three aligned preprocessed images for multivariate segmentation during the second stage.

13. Similar to the feature ranking method, which is explain in Results, Dice is also explained in Results.

We removed the equation for the Dice metric and described the evaluation procedure in the Methods section.

Also, it is unclear why finding which direction of space is informative for the segmentation process would be a “sanity check.”

We removed this section to avoid unnecessary confusion.

14. The discussion starts with an “intent to further refine the proposed paradigm,” and proceeds by mentioning other work currently being performed which looks promising. The opening of the discussion with such statements truly make the manuscript sound like an incomplete effort that is not ready for publication.

We appreciate the positive view of our current work. The full sentence in question is “Although only a single expert was used to produce the manual labelings, our intent is to further refine the proposed paradigm by crowdsourcing with feedback from other experts who interact with both the data and methodology.” In our opinion, simply mentioning specific details regarding future work does not mean that the manuscript “sounds like an incomplete effort.” Rather, it is simply an admission, similar to much of what is reported in the literature, that our research program is ongoing.

15. The discussion also spends several paragraphs on defining literature that shows how WMHs are related to cognitive performance, or how WMHs can be applied in diagnosing TBI. Yet, this study makes no effort to test these efforts in these 24 patients. Consequently, those paragraphs sound wishful and speculative. Given the methodological nature of this paper, a more appropriate discussion would perhaps focus on the comparison with other methods in terms of accuracy, similarities, differences, etc.

We removed the paragraphs in question and added the following comparison discussion:

Reviewer: 2

Interesting paper which offers those without a current background in state-of-the-art brain analysis tools. A good introduction to their capabilities.

We thank the reviewer for the positive comments regarding our work.

1. However the authors do little to establish clinical utility of the algorithm.

We appreciate the opportunity to clarify the precise nature of our contribution which is methodological (vs. clinical). We have shortened the introduction to focus specifically on previous TBI clinical research involving WMHs and then pointing to the need for automated techniques to minimize the variability and time requirements of manual segmentation of WMHs. This would allow for large-scale studies and potentially more accurate and reproducible quantitation.

2. A graphical description of the pipeline would help most readers to understand how this might get into the clinic.

Done. We added the following figure as a graphical description of the pipeline to the manuscript:

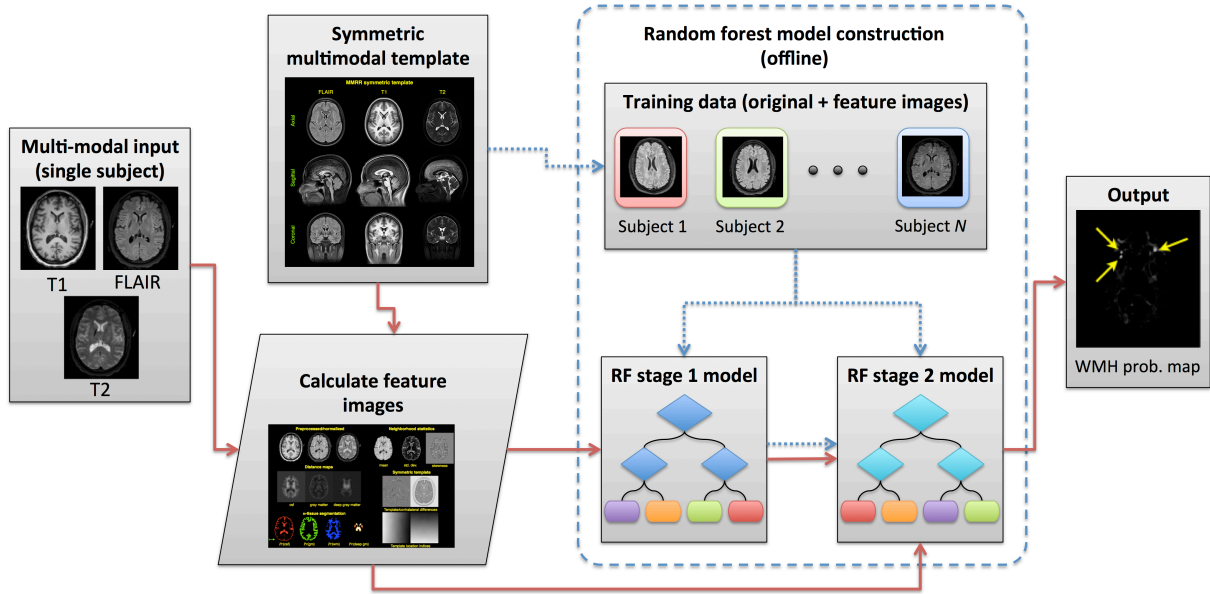


Figure 1: Workflow illustration for the proposed pipeline. Processing of the multi-modal input MRI for a single subject, using the multi-modal symmetric template, results in the generation of the feature images. These feature images are used as input to the Stage 1 RF model producing the initial RF probability map estimates. The Stage 1 voting maps, the original feature images, and the Stage 2 RF model result in the final voting maps which includes the WMH probability estimate. Note that the RF models are constructed once from a set of training data which are processed using the same feature-construction pipeline as the single-subject input MRI.

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