

Automated segmentation of WMHs

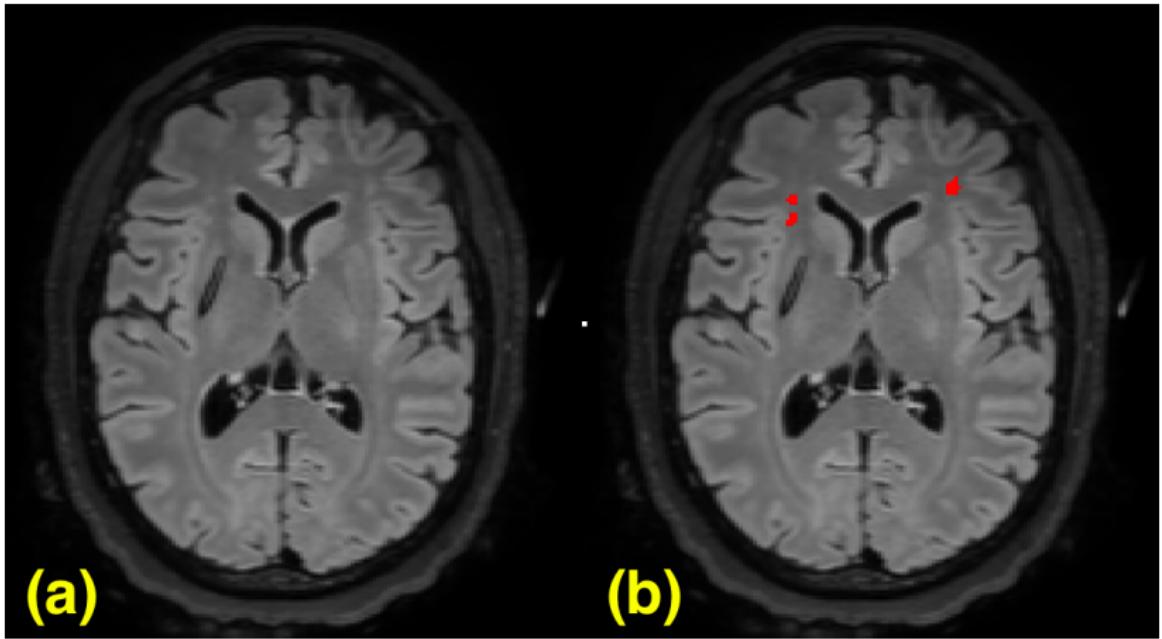
Current status and future directions

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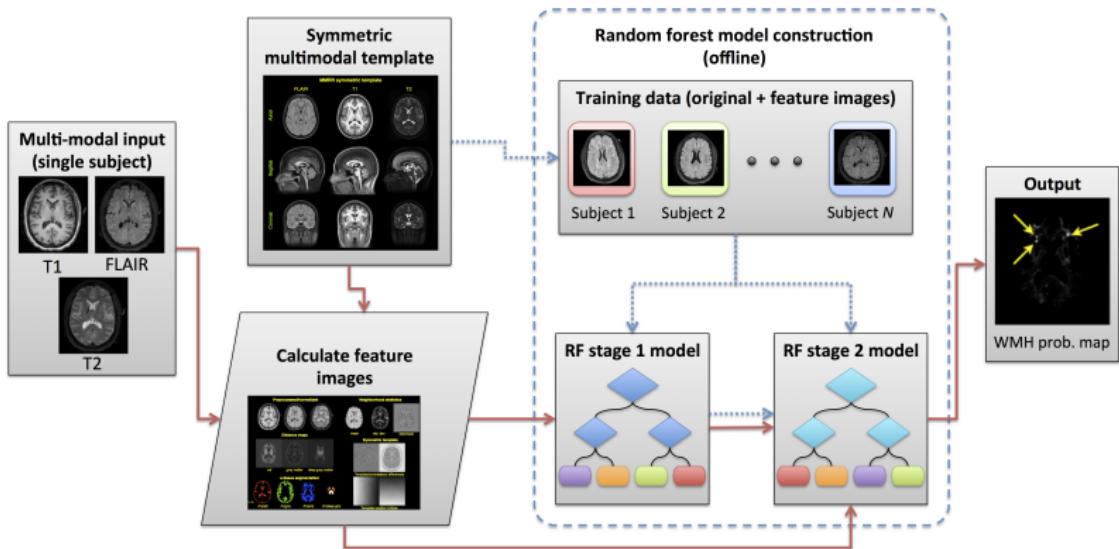
August 11, 2017

WMH segmentation



Current pipeline

Stone et al. *Supervised learning technique for the automated identification of white matter hyperintensities in traumatic brain injury*, March, 2016.

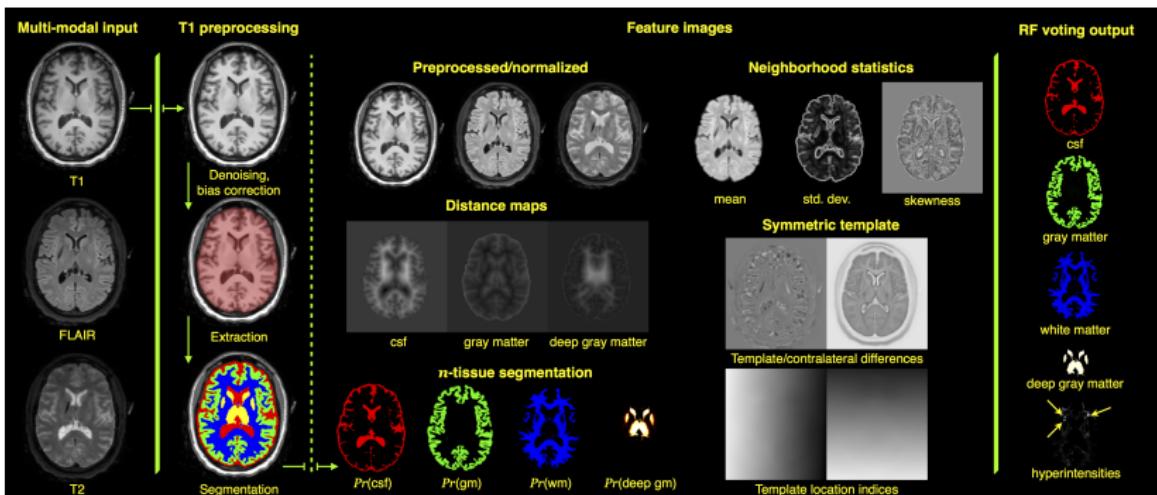


Features

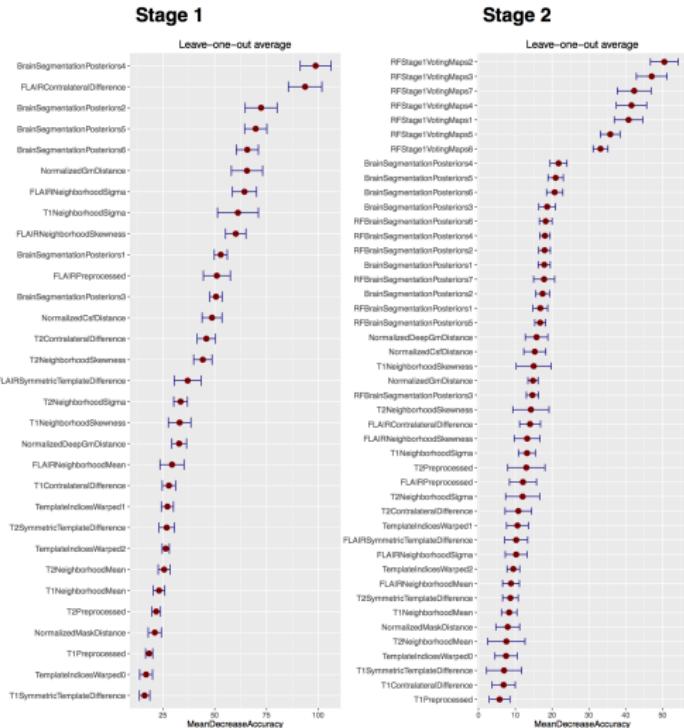
| Feature type | Image source | Name |
|-----------------------------------|-----------------------|-----------------------------|
| Intensities | | |
| normalized/preprocessed | FLAIR, T1, and T2 | Preprocessed |
| Symmetric template | | |
| template difference | FLAIR, T1, and T2 | SymmetricTemplateDifference |
| contralateral difference | FLAIR, T1, and T2 | ContralateralDifference |
| template location indices | FLAIR, T1, and T2 | TemplateIndicesWarped |
| Segmentation probabilities | | |
| $Pr(\text{cerebrospinal fluid})$ | T1 | BrainSegmentationPosterior1 |
| $Pr(\text{gray matter})$ | T1 | BrainSegmentationPosterior2 |
| $Pr(\text{white matter})$ | T1 | BrainSegmentationPosterior3 |
| $Pr(\text{deep gray matter})$ | T1 | BrainSegmentationPosterior4 |
| $Pr(\text{brain stem})$ | T1 | BrainSegmentationPosterior5 |
| $Pr(\text{cerebellum})$ | T1 | BrainSegmentationPosterior6 |
| Distance maps | | |
| cerebrospinal fluid | T1 brain segmentation | NormalizedCsfDistance |
| gray matter | T1 brain segmentation | NormalizedGmDistance |
| deep gray matter | T1 brain segmentation | NormalizedDeepGmDistance |
| whole brain | T1 brain segmentation | NormalizedMaskDistance |
| Neighborhood statistics | | |
| mean | FLAIR, T1, and T2 | NeighborhoodMean |
| standard deviation | FLAIR, T1, and T2 | NeighborhoodSigma |
| skewness | FLAIR, T1, and T2 | NeighborhoodSkewness |

Feature images

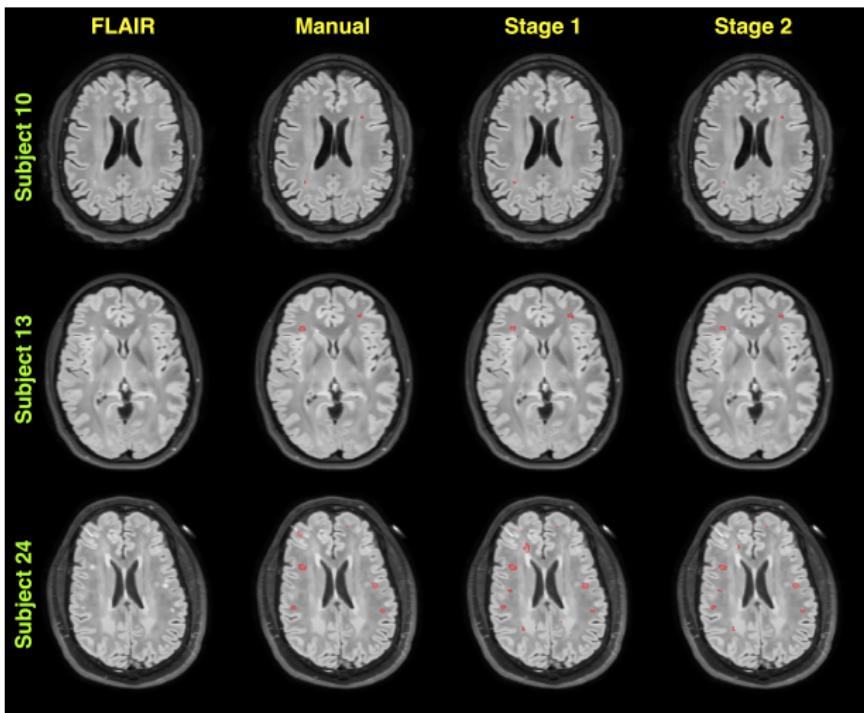
$$\text{label} \sim_{RF} \text{feature}_1 + \dots + \text{feature}_n$$



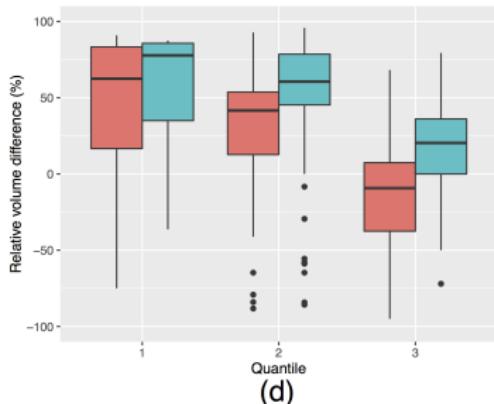
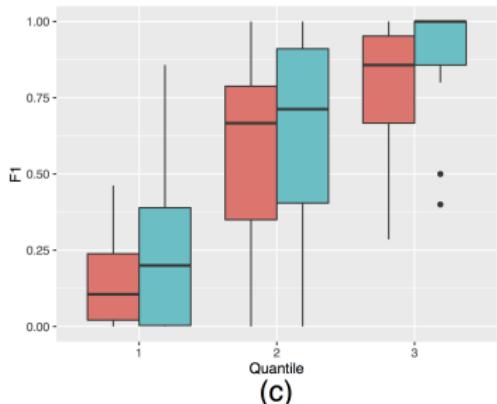
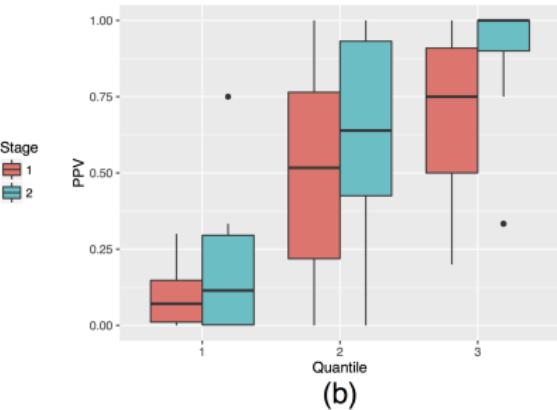
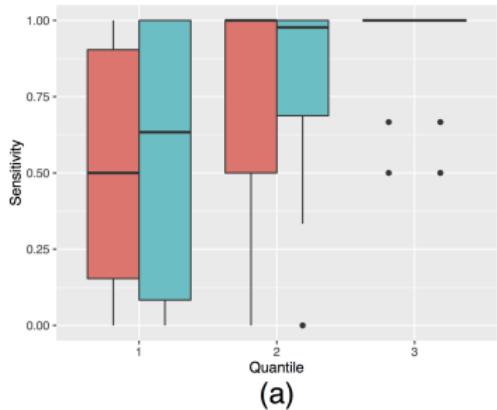
Feature importance



Sample results: Site 1



Leave-one-out evaluation



Problems with current approach

- Takes a lot of time for new data
 1. Create initial set of feature images
 2. Run it through Stage 1 model
 3. Create more feature images
 4. Run subject through Stage 2 model
- Relatively small data set
- Evaluation/modeling limited to a single site
- Creativity
 - Feature image selection
 - Are we choosing discriminative features?
- Imbalanced data
- No comparison with clinical data

What about deep learning?

- Potentially quicker for new data
 - Build initial model takes time
 - No feature images to create for new data
 - GPU
- Optimization learns the features
- Mature packages
 - TensorFlow, CNTK, Torch, Theano, Sci-TK, Caffe, mxnet, Keras
- Need lots of training data

Current work

1. Rebuild RF models from Site 1 balanced data ←
2. Employ all CENC data ←
3. Apply RF approach ←
4. Check clinical correlations
5. Manually refine data from 2.
6. Re-check clinical correlations
7. Use data from 5. to train deep learning model
8. Re-check clinical correlations

Imbalanced data

- 7 tissue voxel labels
 - CSF ($n = 208080, 18\%$)
 - gray matter ($n = 457437, 39\%$)
 - white matter ($n = 317788, 27\%$)
 - deep gray matter ($n = 33042, 2.8\%$)
 - brain stem ($n = 17975, 1.5\%$)
 - cerebellum ($n = 1369656, 12\%$)
 - WMH ($n = 901, 0.07\%$)
- SMOTe (Synthetic Minority Over-sampling Technique)
 - For “rare” events: $\leq 15\%$
 - use bootstrapping and k -nearest neighbor