Automating segmentations of subcortical labels using deep learning on Quantitative Susceptibility Mapping

Project presentation for CS512

Group 1
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Introduction

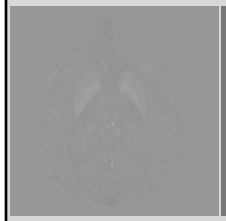
- Quantitative Susceptibility Mapping (QSM) is an advanced magnetic resonance imaging (MRI) technique that can measure magnetic susceptibility variations within tissues.
- Quantitative magnetic Susceptibility Mapping (QSM):
- Assesses magnetic susceptibility of tissues.
- Is currently considered as a useful marker for brain iron homeostasis.
- Yet, brain segmentation with QSM only has not been studied much, as manually doing it takes humongous efforts.
- With very low contrast in this modality, it is very challenging to demarcate regions in the brain automatically.

PURPOSE

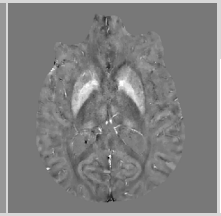
Implement DL models on QSM images only to automatically segment sub-cortical brain structures

Dataset

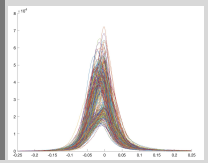
- A dataset of 109 subjects with 5 sub-cortical labels in common were collected for this project, from the study [2].
- We will only present a portion of the dataset for testing and reconstruction purposes.
- Contains QSM images for all the subject in their native space, with the common labels of many brain regions including the ones:
  - Hippocampus, amygdala, putamen, caudate, thalamus
  - sAlso contains their brain mask, which was extracted from other modalities of brains.
- This is a high resolution data with 0.5mm voxel



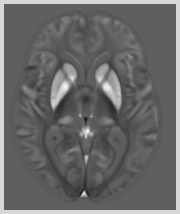
Native QSM



Native QSM in range(-0.25, 0.25)

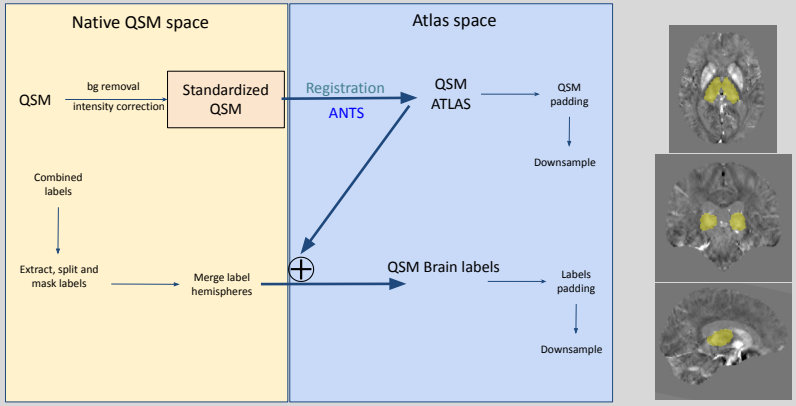


Histogram

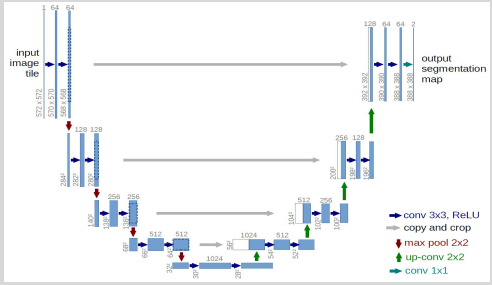


MIITRA Atlas

Preprocessing

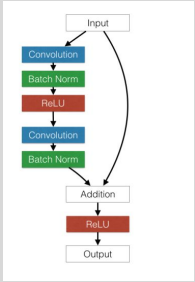


Model Architecture

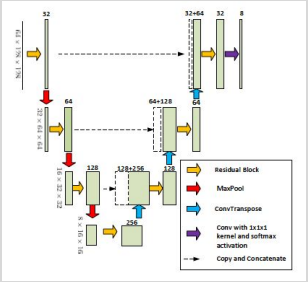


Architecture of UNet

Model Architecture



Architecture of Residual block



Architecture of ResUNet

Evaluation

- To follow the paper and standard matching, we used **dice similarity** coefficient.

$$DC_i = \frac{2|P_i \cap G_i|}{|P_i \cup G_i|},$$

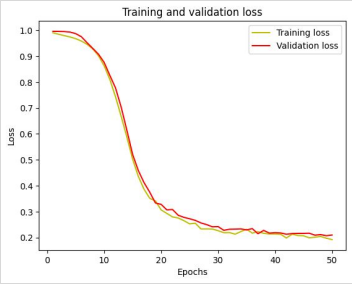
Here P is the predicted label and G is the ground truth.

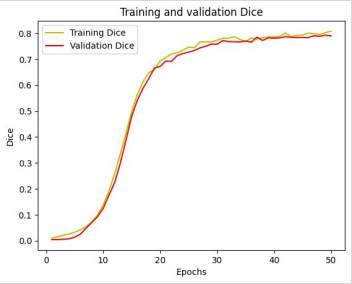
- Additionally to the paper, we used **Hausdorff distance** to measure the dissimilarities among the labels. Hausdorff distance determines the maximum distance of each voxel from the nearest predicted values to ground truth.

H(A, B) = max{sup{dist(a, B)}, sup{dist(b, A)}}

Results

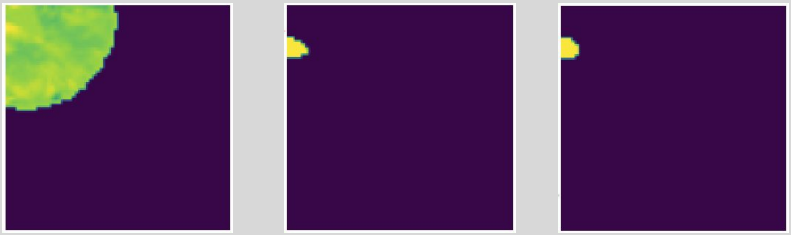
- A typical case for hippocampus of our loss and dice curve vs epochs.





Results

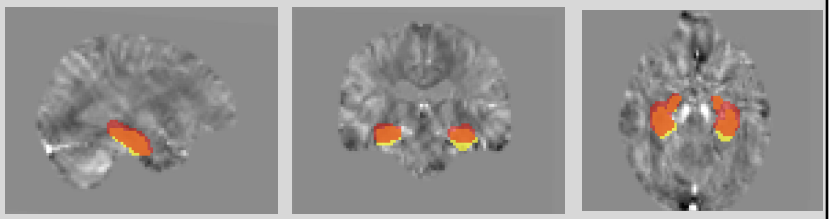
- Prediction in patches for putamen.



Original brain image | Predicted | Ground truth

Results

- Once we have the reconstruction we get the following results. Red denotes predicted, yellow indicates ground truth.



Results comparison

Serial	Name of the mask	Validation DS	Testing DS	Testing HD
1	Whole brain mask	0.99	0.97	0.04
2	Hippocampus	0.79	0.82	1.24
3	Putamen	0.81	0.79	1.48
4	Thalamus	0.87	0.87	1.46
5	Amygdala	0.60	0.50	0.94
6	Caudate	0.76	0.81	1.43

Input	CN	GP	PUT	THA	SN	RN	DN
QSM	0.782	0.828	0.819	0.827	0.690	0.680	0.714
T_1WI	0.760	0.778	0.799	0.825	0.589	0.635	0.338
QSM +T_1WI	0.802	0.840	0.827	0.844	0.719	0.763	0.774

UNet VS ResUNet

Label name	Dimension	Epochs	Dice Similarity			
			UNet		ResUNet	
			No. of Subjects	Dice Similarity	No. of Subjects	Dice Similarity
Hippocampus	256x256x256	50	100	0.81	41	0.68
Hippocampus	128x128x128	50	100	0.80	100	0.71
Caudate	256x256x256	100	100	0.65	100	0.64
Caudate	128x128x128	100	100	0.76	100	0.76

Figure: Comparison of dice similarity results between Unet and ResUNet.

Conclusions

- This project aimed to implement a 3D segmentation model on QSM data using deep learning, based on a previously published paper.
- The challenges of larger and higher resolution data required careful preprocessing, neural network designing, and hyperparameter tuning to achieve higher accuracy in segmentation, for small volumetric label data.
- The results of this project will have significant implications for the diagnosis of neurological disorders, if researched further.

References

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[7] We took pointers and help from the scripts found here: https://github.com/bnsreenu/python_for_microscopists

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