



Deep learning-based Neuron Detection in Brain CLARITY Imaging

Seminar Presentation: “Automatic Detection of Microbleeds from
MR Images via 3D Convolutional Neural Networks”

Members: Prerna Singh

Mentor: Dr. Jeremias Sulam

My Project

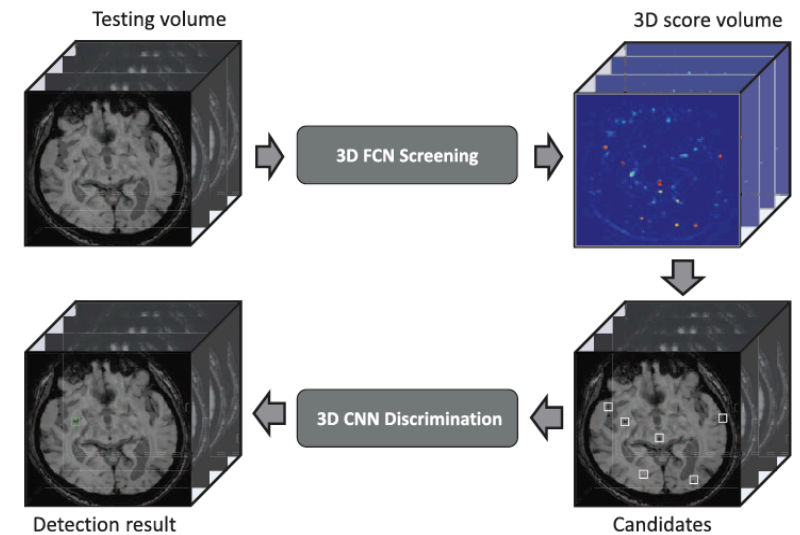
- Develop a **robust 3D Convolutional Neural Network (CNN)** that can predict, with improved precision and accuracy when compared to other models, how many fluorescent neurons are present within a section of a brain imaged with CLARITY
 - Previous models: template matching, blob detection
 - Maximum accuracy achieved was $\sim 59\%$ with these techniques

Summary & Key Results

Developed and validated a 2-step cascaded framework to automatically detect cerebral microbleeds (CMBs) in MRI images using 3D CNNs

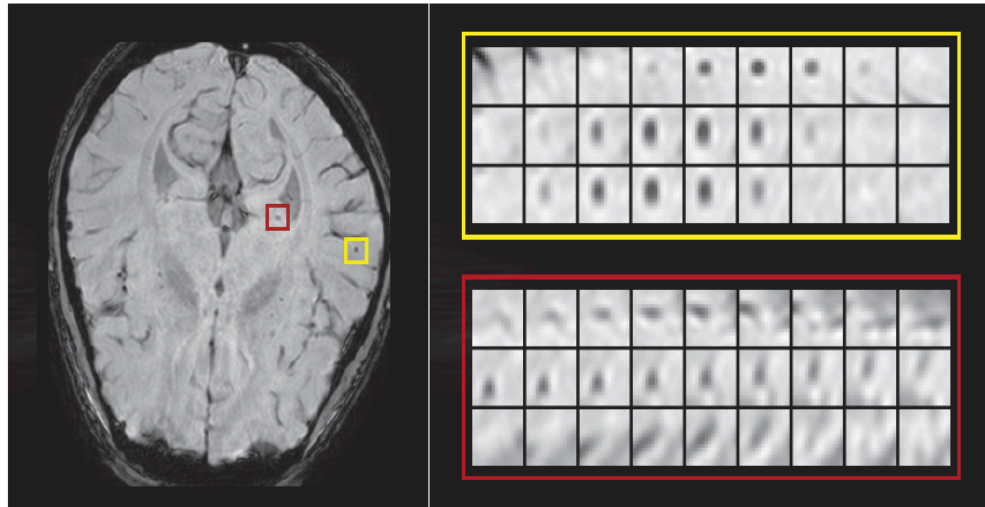
Results

- Sensitivity: 93.16%
- Precision: 44.31%
- Average number of false positives per CMB: 2.74

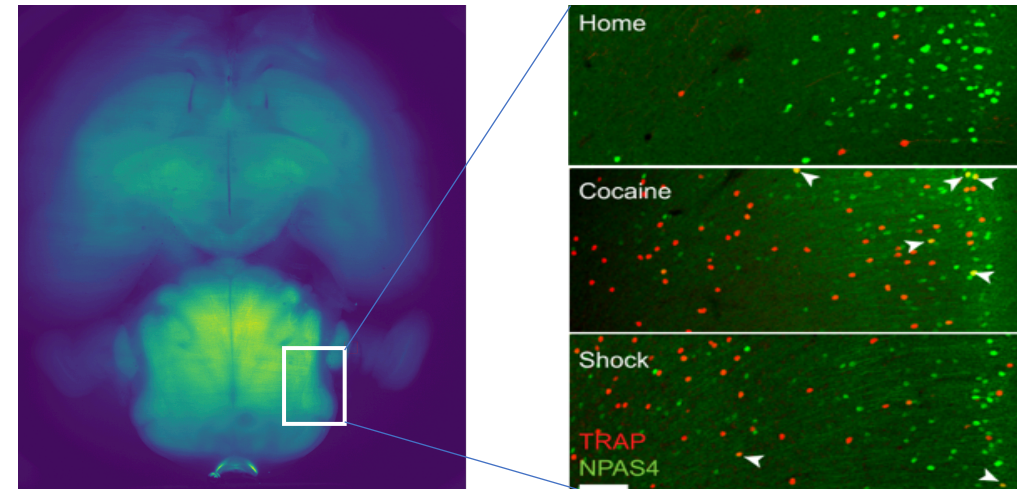


Dou et al.

Paper Selection Motivation



Dou et al.



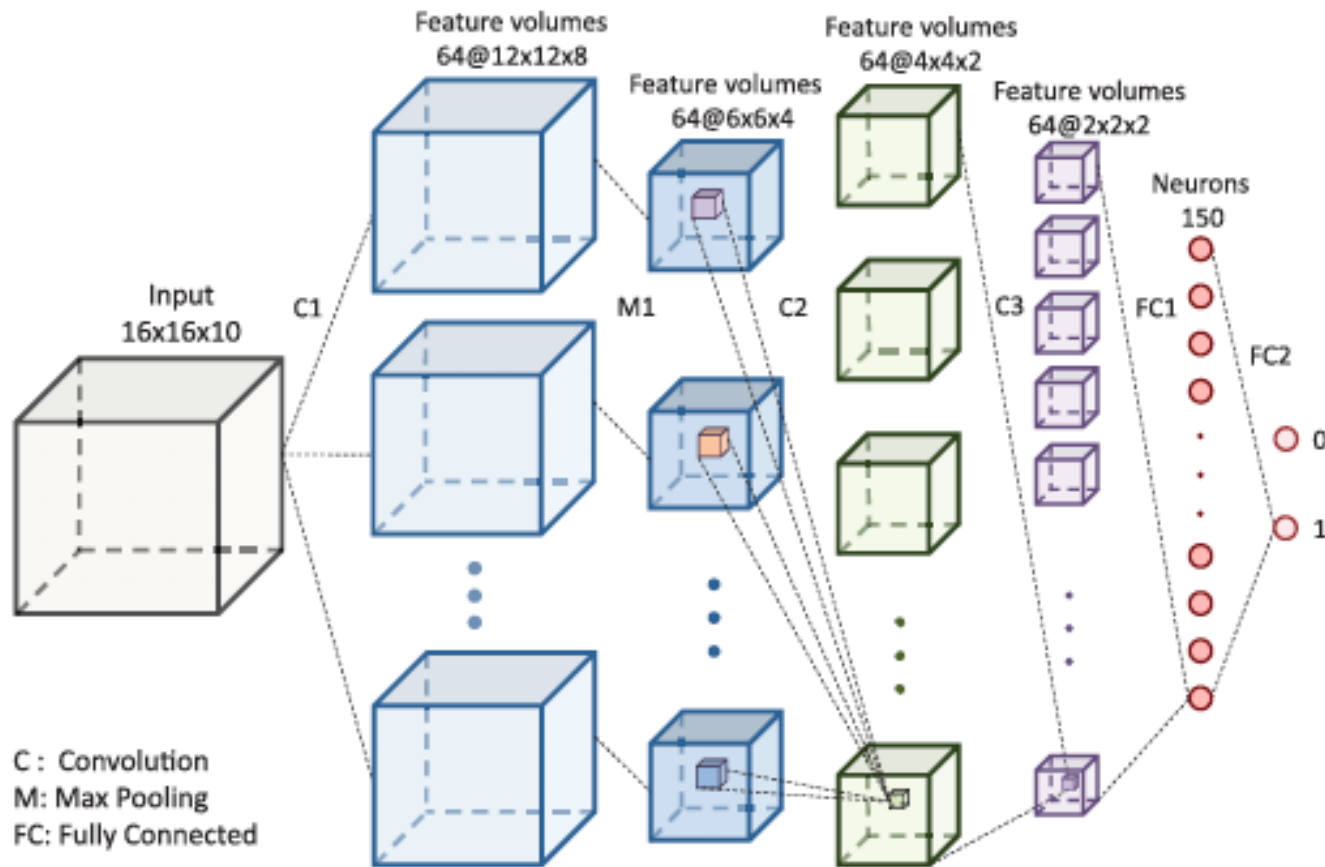
Zoomed in CLARITY Image *Ye et al.*

- same fundamental problem
 - Aim to detect a biomarker in volumetric clinical data using 3D CNN
 - CMBs and fluorescent neurons are both rounded variations in intensity of a similar size and in the same native tissue (brain)

Background

- Identifying CMBs has clinical benefits
 - have been shown to aid in the diagnosis of several cerebrovascular and cognitive diseases
 - present in healthy aging individuals also
- Currently CMBs are manually labelled by radiologists
 - High error rate
 - Labor and time intensive

Implementation and Architecture Design



Dou et al.

- Screening stage: 3D Fully Convolutional Network
- Discrimination Stage: 3D CNN
- Input: entire volumetric data
- reLU used for non-linear activation function in C and FC layers
- Backpropagation: parameters in network are tuned with stochastic gradient descent
- Minimize cross-entropy loss
- Dropout used: improves generalizability

Screening Stage: Fully Convolutional Network

Model takes **variable sized input**

- Input is transformed to take an arbitrary-sized input
- Convolution and max pool kernels sweep over to generate the corresponding sized output

Output a value at each location of score volume that indicates the probability of a CMB

- Prediction scores mapped back to input
- Regions with high scores retrieved as **potential CMB candidates**

Layer	Kernel size	Stride	Output size	Feature volumes
Input	-	-	16× 16× 10	1
C1	5× 5× 3	1	12× 12× 8	64
M1	2× 2× 2	2	6× 6× 4	64
C2	3× 3× 3	1	4× 4× 2	64
C3	3× 3× 1	1	2× 2× 2	64
FC1	2× 2× 2	1	1× 1× 1	150
FC2	1× 1× 1	1	1× 1× 1	2

Dou et al.

Training

- Positive samples: from CMB regions with translation, rotation, and mirroring of positive samples
- Negative samples: randomly selected non-CMB regions.

Discrimination Stage: 3D CNN

Traditional CNN takes **fixed size input**

- Input: 3D blocks centered on screened candidate positions retrieved from the screening stage model

Layer	Kernel size	Stride	Output size	Feature volumes
Input	-	-	20× 20× 16	1
C1	7× 7× 5	1	14× 14× 12	32
M1	2× 2× 2	2	7× 7× 6	32
C2	5× 5× 3	1	3× 3× 4	64
FC1	-	-	1× 1× 1	500
FC2	-	-	1× 1× 1	100
FC3	-	-	1× 1× 1	2

Dou et al.

Outputs a value that indicates the probability of a CMB

Training

- Positive samples: from CMB regions with translation, rotation, and mirroring of positive samples
- **Negative samples: false positive samples obtained from screening stage**

Experiments and Results: Data

Large data set with 320 images was used

- Divided into three sections for training, validation, and testing

Ground truth: 1149 radiologist labeled CMBs

- Verified by a neurologist.

Determined optimal threshold of $T = .64$ for candidates to move to discrimination stage

Datasets	Stroke		Normal aging		Total	
	Subjects	CMBs	Subjects	CMBs	Subjects	CMBs
Training	91	701	139	223	230	924
Validation	15	81	25	27	40	108
Testing	20	78	30	39	50	117

Dou et al.

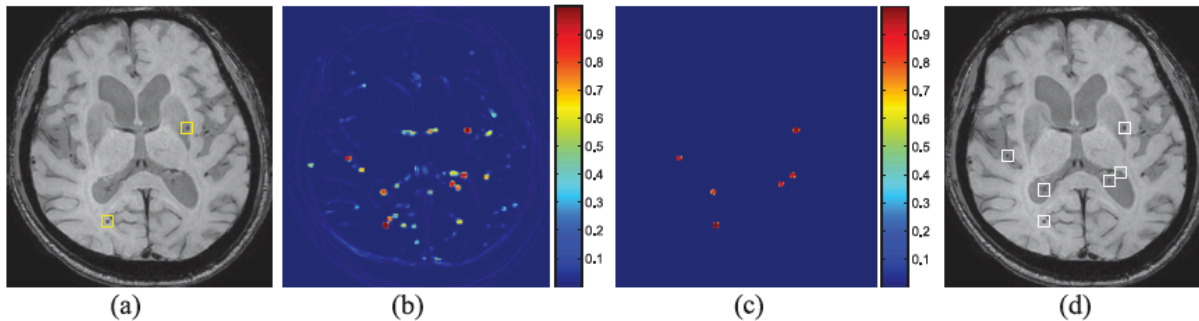
Compute metrics

- Sensitivity
- Precision
- Average number of false positives per subjects

Experiments and Results: Screening Stage

Methods	Sensitivity	FP _{avg}	Time per subject (s)
Barnes et al. [15]	85.47%	2548.2	81.46
Chen et al. [18]	90.48%	935.8	12.00
3D FCN model	98.29%	282.8	64.35

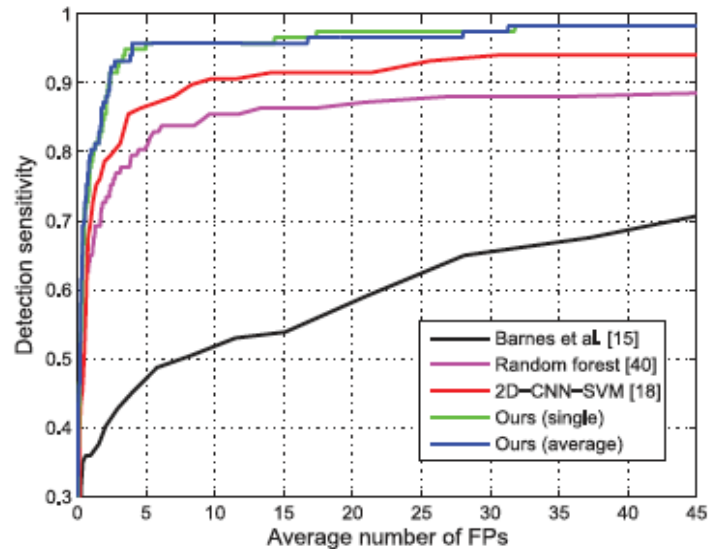
Dou et al.



Dou et al.

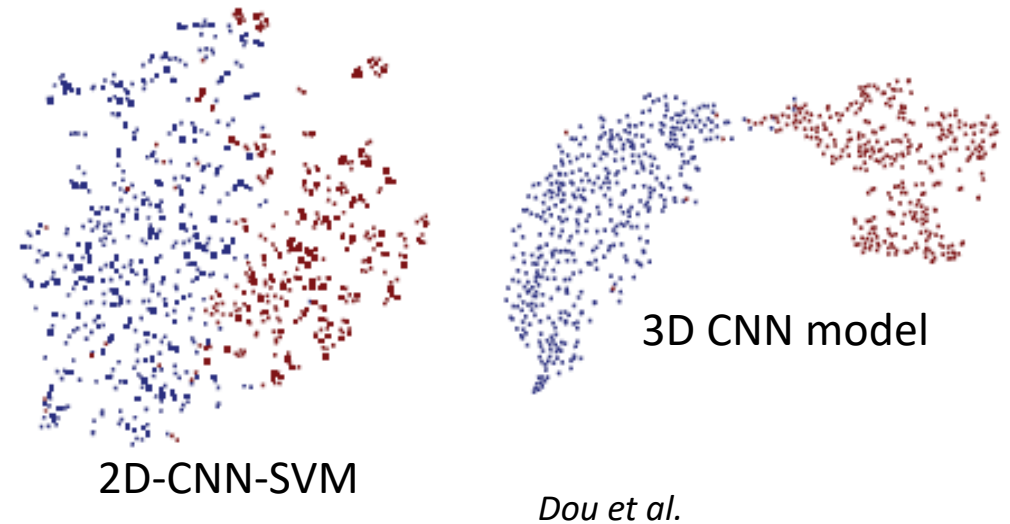
- Comparison between three methods of screening
- Results of the screening model projected on the axial plane with true CMBs and the score volume generated with the screening model

Experiments and Results: Full Model



Dou et al.

Comparison of four CMB detection algorithms by plotting FROC curves



CMB (RED) and non-CMB (BLUE) samples are distinctly separated based on the features extracted by the 2D-CNN-SVM and 3D CNN discrimination models and embedded into the 2D plane

Personal Critique

Positives

- Justification and explanation of model architecture and framework
- **Generalizable**: use dropout layers, and separate training, testing, and validation data
- Proved their model was effective with more than just cross-validation and metrics
- **Replicable**: code and data provided

Areas of Improvement

- Explanation of FCN mathematical transformation was lacking and unclear
- Training Data Selection
 - All data used to train, test, and validate came from one MRI machine
 - Data only from aging patients and patients with strokes

Takeaways & Future Steps

Takeaways

- Learned new methods of validation of a 3D CNN framework
- Understood how to build 3D CNNs and why certain architectures are chosen for biomarker detection

Future Steps

- Integrate multi-scale/size information during feature representation phase into the 3D models
- Apply 3D CNN framework to other medical detection tasks