Quantifying Normal on Apparent Diffusion Coefficient Maps for Generic Detection of Abnormalities

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Abstract Submission

Authors:

Yue Zhang[1], Ya'nan Song[2], Rutvi Vyas[3], Sara Bates[4], Rebecca Weiss[4], Camilo Jaimes Cobos[3], Susan Sotardi[4], Randy Gollub[5], Shawn Murphy[4], Anna Pinto[3], P. Ellen Grant[6], Yangming Ou[5]

Institutions:

[1]Shanghai Institute of Technical Physics of the Chinese Academy of Sciences, Shanghai, Shanghai, [2]Beijing University of Chinese Medicine, Beijing, Beijing, [3]Boston Children's Hospital, Boston, MA, [4]Massachusetts General Hospital, Boston, MA, [5]Harvard Medical School, Boston, MA, [6]Boston Children's Hospital, Harvard Medical School, Boston, MA

Introduction:

Machine learning offers promise to detect brain abnormalities in MRI. However, current ML systems are abnormality-specific, in that they learn the MRI signatures of an abnormality type that applies only to that abnormality but not others. For example, an ML system that detects brain tumors is specific to brain tumors and not directly deployable to non-tumor brain abnormalities1. Compared to abnormality-specific radiology assistant systems, we aimed to develop a generic algorithm that can detect abnormalities in a one-for-many fashion, thereby providing a more realistic application for radiology workflows.

We noted that different abnormality types are common in that they are all outliers to normal2. So, instead of learning the specific type of abnormality, we quantified normal, and tested the potential to detect different abnormalities.

We started from quantifying normal variation of Apparent Diffusion Coefficient (ADC) maps in children 0-6 years of age3. Choosing this age range was because of the critical but unmet need to separate abnormality-induced ADC changes from the rapid normal-development-related ADC changes. Choosing ADC maps was because of the wide use in clinical neuroradiology to identify many pediatric brain abnormalities such as ischemia, trauma, infection, neoplasia and myelination disorders. Our pilot testbed includes two types of abnormalities: hypoxic ischemic encephalopathy (HIE, affecting newborns)4 and sturge-weber syndrome (SWS, first onset typically in 0-6 years)5.

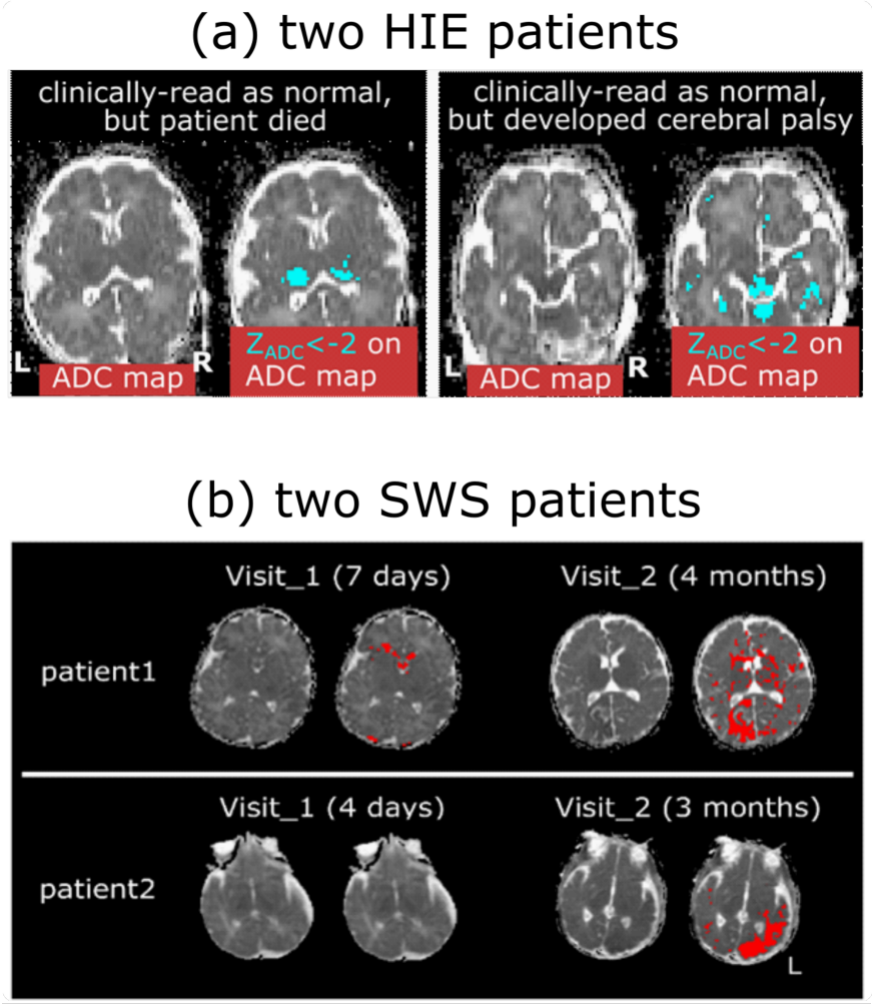
Methods:

From 201 retrospectively collected normative ADC maps (0-6 years), we constructed average ADC atlases in 10 age groups: the first two weeks, every quarter in the first year, and yearly thereafter3. The atlases quantified normal ADC variations at every brain voxel (in space) and each of those 10 ages (in time). ADC maps of N=132 HIE patients and N=10 SWS patients were compared to the age-matched normal atlases, by deformable atlas-to-patient image registration6,7. In a naïve approach, those voxels having ADC values two standard deviations away from the average ADC in corresponding location and age were considered abnormal5. Accuracy of the detection was quantified by Dice overlaps with expert-annotated lesions (0~100% for none to perfect overlap), by comparing to radiology reports validated by experts and by correlating with neurologic outcomes.

Results:

Accuracy. In HIE, the median Dice overlap with expert was 96.2% if more than 50% of the brain was injured (N=12), 76.7%, 75.3%, 79.9%, 68.6% and 41.6% if 20-50% (N=12), 10-20% (N=5), 5-10% (N=10), 1-5% (N=28) and <1% (N=65) of the brain was injured. The median Dice across all patients was 60.4%, compared to 52% in a latest ML study of HIE lesion detection (different cohorts)8. In SWS, our approach found brain lesions in ADC maps of all 7 patients (1.5, 2, 2, 3, 4, 8, 9 months) who developed epilepsy/seizure within 3 months after the MRI.

Catching abnormality in clinical false-negative reads. Our approaches found abnormalities in 17 of 25 HIE patients (Fig 1a) and 2 of 3 SWS patients (Fig 1b) whose ADC maps were clinically read as normal but who later developed adverse outcomes.



·Fig 1. Two HIE patients (top panel) and two SWS patients (bottom panel) whose ADC maps were clinically read normal but who later developed adverse neurologic outcomes. Our approach found abnormalities

Conclusions:

This proof-of-concept study shows promise for a generic abnormality detection approach. Our approach not only yields promising accuracy in MRIs that neuroradiologists have identified lesions, but also in MRIs that neuroradiologists mis-read (Figure 1). In SWS, a rare disease, ADC maps are traditionally thought not sensitive enough, and contrast enhancement imaging has been used despite the side effect of the contrast agent. Our approach suggests that the contrast-free ADC maps, when equipped with our quantified spatiotemporal normal, may detect abnormalities even before symptoms (epilepsy/seizure) occur. Our future work will include rigorous validations with multi-expert annotations in multi-site large-scale data from a wider variety of abnormalities in multiple MRI sequences.

Disorders of the Nervous System:

Neurodevelopmental/ Early Life (eg. ADHD, autism) [2]

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis
Image Registration and Computational Anatomy
Methods Development [1]
Segmentation and Parcellation

Keywords:

Design and Analysis
Epilepsy
Segmentation

[1|2]Indicates the priority used for review

My abstract is being submitted as a Software Demonstration.

No

Please indicate below if your study was a "resting state" or "task-activation" study.

Other

Healthy subjects only or patients (note that patient studies may also involve healthy subjects):

Patients

Are you Internal Review Board (IRB) certified? Please note: Failure to have IRB, if applicable will lead to automatic rejection of abstract.

Yes

Was any human subjects research approved by the relevant Institutional Review Board or ethics panel? NOTE: Any human subjects studies without IRB approval will be automatically rejected.

Yes

Was any animal research approved by the relevant IACUC or other animal research panel? NOTE: Any animal studies without IACUC approval will be automatically rejected.

Not applicable

Please indicate which methods were used in your research:

Diffusion MRI
Computational modeling

For human MRI, what field strength scanner do you use?

3.0T

Which processing packages did you use for your study?

FSL
Analyze
Other, Please list - DRAMMS

Provide references using author date format

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