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### **Appendix E1**

#### **Case Selection**

We identified potential patients with diseases involving deep gray matter structures from a search of institutional radiology archives (mPower, Nuance Communications, Burlington, Mass) of studies performed between January 2008 and January 2018 with search terms for each of the diagnostic entities and deep gray matter structures. Initial searches resulted in 348 potential patients (Fig 1). The diagnoses of potential patients were validated by consensus among two neuroradiologists (I.M.N., S.M.) through clinical chart review, pathology when available and analysis of other available imaging data, including follow-up imaging studies. Of these potential patients, 23 were excluded due to incorrect initial diagnoses (with 7 being reassigned to one of the other inclusion diagnoses) and 21 were excluded due to insufficient information to confirm diagnosis. To select the specific examination from each patient, the first diagnostic MRI performed was selected, with three being unavailable due to the MRI being performed prior to institutional review board (IRB)-approved date range. Potential cases were then further narrowed down by excluding cases without T1 imaging (*n* = 24; T1 images being required for the tissue segmentation and anatomic parcellation), severe motion artifacts ( $n = 23$ ), cases with other secondary pathologic diagnoses other than a mild degree of chronic white matter small vessel ischemic disease  $(n = 28)$ , and cases where the diagnostic findings were outside of the deep gray matter  $(n = 21)$ , which resulted in a final sample of 212 cases (Table 1). An additional 178 cases were included for training of the CNNs from a related study of diseases involving the cerebral hemispheres (18), which initially consisted of 279 possible patients.

Two academic neuroradiologists (I.M.N., S.M.) classified the 36 diagnostic entities as 'common', 'moderately rare' or 'rare' in regard to the relative frequency in which they are diagnosed on brain MRI studies at our tertiary care center. The classification of prevalence was not specific to the diagnosis being present in deep gray matter (ie, if the disease was considered common but rarely found in deep gray matter, it was still considered a common disease).

## **Appendix E2**

#### **MRI Data Availability**

Of the 212 deep gray matter cases, T1-weighted images were acquired in the axial plane in 86.7% of cases and in the sagittal plane in 13.3% of cases. Of the selected cases, 89.2% included axial T1 postcontrast, 98.6% axial FLAIR, 74.1% axial GRE, 99.1% DW, and 99.1% ADC images. Clinical MR images were collected from our health system PACS, which included outside studies submitted to our PACS for secondary interpretation between January 2008 and January 2018. The 390 MRI studies (212 deep gray matter cases and 178 used to supplement the CNNs) were obtained from 35 different physical scanners, 4 scanner manufacturers, and 16 unique scanner models (Table 2), noting that 97% of the data were acquired from Siemens (Munich, Germany) and GE Healthcare (Chicago, Ill) with fewer cases from Philips (Amsterdam, the Netherlands) and Toshiba Medical Systems (Otawara, Japan). There were 80

unique acquisition parameters for the T1 images alone (Table 2). For reference, the most commonly used acquisition parameters for the T1 image were as follows: repetition time (TR), 500 msec; echo time (TE), 17 msec; and in-plane resolution,  $0.86 \times 0.86$  mm, with 5-mm thick slices, which was used in 25% of cases.

# **Appendix E3**

#### **Image Preprocessing, Registration, Tissue Segmentation, and Deep Gray Parcellation**

We performed segmentation of brain tissues and deep gray matter structures on the T1 images using a customized image processing pipeline utilizing ANTs (Advanced Normalization Tools; http://picsl.upenn.edu/software/ants/) (20,21), FSL (FMRIB's Software Library, www.fmrib.ox.ac.uk/fsl) (30), MATLAB (Mathworks, Natick, Mass), and customized Python scripts (Python version 3.7). First, the neck portion of the T1 MRI was removed using a custom algorithm based on Brain Extraction Tool (BET) (31). This step failed in 7% of the cases due to T1 acquisitions containing unexpectedly large nonbrain tissue in older protocols, requiring manual intervention. The T1 images were then up-sampled to reduce slice thickness to 1 mm using a multimodal patch-based superresolution technique (32). The ANTs cortical thickness analysis pipeline was then applied to segment the brain into cerebrospinal fluid, cerebral white matter, cortical and deep gray matter, cerebellum and brainstem. Then, the deep gray matter was further divided into eight subregions, consisting of left and right caudate, putamen, globus pallidus, and thalamus, by assigning each deep gray matter voxel to the closest subcortical label in the Automated Anatomic Labeling parcellation (33) that was warped to the space of each patient's up-sampled T1 scan. In addition, a mask of nearby structures including the ventricles, hypothalamus, optic chiasm and hippocampus in the OASIS template space (34) was warped to each patient and subtracted from the deep gray matter subregions to limit false positive extension of the deep gray matter into these structures. Morphometry correction was applied to generate the final segmentation of the subregions. Rigid registration (6 degrees of freedom) was performed to register each of the other modalities to the up-sampled T1 image of the same patient. In the end, the different tissue types and deep gray subregions were transformed and resampled to the native space of each MR sequence.

# **Appendix E4**

### **Convolutional Neural Networks for Abnormal T1, FLAIR, and GRE Signal**

For prediction of abnormal signal on T1, FLAIR and GRE MRI studies, we developed and trained customized 3D U-Nets (21–23) for each sequence, in a similar fashion as the FLAIR U-Net described in Duong et al (24) (Fig 3, *B*). To provide segmentation masks for the training data, all T1, FLAIR and GRE lesions were hand-segmented by a radiologist (J.D.R. or A.M.R.) using ITK-SNAP (http://www.itksnap.org) (35). The FLAIR U-Net was supplemented by an additional 178 hand-segmented FLAIR MRI studies (total  $n = 387$ ) and the GRE U-Net was supplemented with an additional 92 segmented GRE MRI studies (total *n* = 249) of lesions of various etiologies involving the cerebral hemispheres (18).

Preprocessing for input into the CNNs included brain extraction, followed by intensity normalization by the mean and standard deviation. Next, images were resampled to  $1 \text{ mm}^3$ 

isotropic resolution via linear interpolation. The images were then augmented using elastic transformations (36), including rotate, flip and skew, with small random affine transformations stacked on top of small random free-form deformations such that each imaging volume was augmented a total of three times. The augmented images were then split into  $96 \times 96 \times 96$ -mm cubes ("3D patches") that were used as input into the CNN.

The network architecture was implemented with TensorFlow (37) (CUDA version 9.2.148) on an NVIDIA Titan Xp GPU (NVIDIA, Santa Clara, Calif; 12 GB memory). The 3D U-Net architecture consisted of four consecutive down-sampled blocks, followed by four consecutive up-sampled blocks (Fig 3, *B*). We used batch normalization for regularization and the rectified linear unit for nonlinearity. For down-sampling and up-sampling, the network used a stride-2 convolution and 2-stride deconvolution. A  $3 \times 3 \times 3$  convolutional kernel was applied across the network for each layer. In the down-sampling block, we applied a dilation factor of two in all convolutional layers. We applied a cross-link between corresponding up-sampling and down-sampling blocks as well as a residual connection between subsequent layers with number of features matched by a plain  $1 \times 1 \times 1$  convolution. After the final up-sampling block, three additional convolutional, rectified linear unit, batched-normalized (conv-ReLu-bn) layers were added, ending with a normalized exponential (softmax) head function. We utilized standard cross-entropy loss with an Adam optimizer (38) and a learning rate of  $10^{-4}$ . A batch consisted of six patches. The networks were trained for 20–50 epochs over the course of 1–3 days, with training halted after training loss plateaued. No hyperparameter optimization was performed as training was only performed once for each network and the network weights were applied to the test cases only once. During training, the 3D patches were randomly sampled across the full brain volumes. To prevent sample imbalance, the number of patches that included abnormal signal was equal to the number that did not have abnormal signal. During testing, the brain volume was densely sampled with the cubes using a step size of 32 in each direction, resulting in a 64 pixel overlap between cubes. The overlapped segmentation predictions were then averaged.

## **Appendix E5**

#### **Abnormal Signal Detection for Enhancement and Restricted Diffusion**

Detection of abnormal enhancement and restricted diffusion relied on analysis of the voxel intensities within deep gray matter subregions relative to the mean intensity of all deep and cortical gray matter voxels. To detect enhancement, voxels were required to be 2.5 standard deviations higher than mean signal on the subtraction map performed between the rigidly aligned T1 and T1-post images (Fig 3, *D*) and 1.5 standard deviations higher than the mean signal on the T1-post images. Voxels with restricted diffusion were detected by masking voxels with intensities that were 2.5 standard deviations above the mean gray matter intensity on the high *b* value DW image and 1.0 standard deviations below the mean gray matter intensity on the ADC images (Fig 3, *D*). These thresholds were based on minimizing false positives in the training patients.

### **Appendix E6**

#### **Thresholding of Abnormal Signal Maps in Deep Gray Subregions**

To consider the signal derived from the U-Nets (T1, FLAIR, GRE) or voxel-wise methods (enhancement, diffusion) to be abnormal, modality- and subregion-specific thresholds were set for abnormal voxel percentage. The thresholds were chosen based on the training cases, such that they resulted in the highest accuracy for each feature within the training cases, and were then applied to the test cases. This fine-tuning of thresholds in the training sample allowed for the pipeline to be robust in the presence of a minimal amount of abnormal signal due to noise or normal variation, minimizing false positives. This process also resulted in ignoring abnormal GRE signal detected in the globi pallidi due to the frequency of physiologic mineral deposition resulting in reduced signal that would be considered abnormal in other regions of the brain. Thresholds varied across subregions between 2.0% and 4.5% of regional voxels for enhancement, 0.5% and 3.5% for restricted diffusion, 1.0% and 3.0% for increased or decreased on T1, 2.0% and 4.0% for increased FLAIR, and 3.0% and 3.5% for decreased on GRE. For GRE, the feature state "high" reflected cases where more than 20% of the voxels had abnormal susceptibility across all the deep gray structures excluding globus pallidus.

### **Appendix E7**

#### **Anatomic Subregion and Spatial Features**

The four anatomic subregion features (caudate, putamen, globus pallidus, and thalamus) were considered to be involved if abnormal signal was present above the threshold for any of the modalities in either the right or the left side. The combined maps of abnormal signal across all modalities, masked by the deep gray subregions, were used to compute additional spatial pattern features, consisting of bilaterality and symmetry. Abnormalities were considered unilateral if there was a greater than 20-fold difference in abnormal signal volume between right- and leftsided subregions. Abnormalities were considered bilateral and symmetric if there was a less than fivefold difference in the ratio of abnormal signal detected in left versus right hemispheres within at least one set of paired deep gray subregions. These thresholds were determined based on optimizing performance of these features in the training sample relative to attending-derived reference standard features.

## **Appendix E8**

#### **Clinical Features**

A review of electronic medical records was performed to obtain each patient's age, sex, acuity of the patient's clinical presentation and whether that patient was known to be immunocompromised at the time of imaging. These four clinical features were chosen based on their broad utility in helping develop a differential diagnosis for this set of diseases. Acute symptoms were defined as the predominant symptoms that necessitated the MRI occurring less than 7 days prior to imaging, subacute between 7 days and 3 months, and chronic and/or asymptomatic if the patient's predominant symptoms had been present for longer than 3 months or the MRI had been ordered based on further evaluation of an incidental finding or screening due to an underlying disease.

### **Appendix E9**

#### **Bayesian Network Construction and Analysis**

The probabilities of each feature for each disease for the Bayesian network were determined by the consensus of four neuroradiologists and published statistics in a comprehensive neuroradiology textbook (39), when available. These probabilities were then tuned to approximate a weighted average of the expert-derived probabilities and frequency of feature states seen in the training sample. The full set of probabilities used for the analysis are displayed in Table E2. For the purposes of this experiment, the prior probabilities for each disease and normal were set to be equal to each other to approximate their relative frequency in the study population. The Bayesian network was implemented with custom Python scripts performing simple naïve Bayesian inference (https://github.com/rauscheck/radai). For instances where the feature could not be calculated, such as a missing sequence, the feature received an N/A and was not used as input to the Bayesian network.

## **Appendix E10**

#### **Attending-derived Reference Standard Imaging Features**

To evaluate the performance of the image pipeline for detecting the presence of signal features (T1, FLAIR, susceptibility, enhancement, restricted diffusion), anatomic subregion (caudate, putamen, globi pallidi, thalami) and spatial features (bilateral, symmetric) we determined performance relative to the reference standard consensus of three radiologists (I.M.N., S.M., J.D.R.) evaluating each of the cases. Any discrepancies between the academic neuroradiologists regarding the imaging features and diagnoses were resolved through consensus after rereviewing the images. The prevalence of each of the features for each of the diagnostic entities is displayed in Table E1.

## **Appendix E11**

#### **Clinical Validation**

To validate the performance of the AI system, four radiology residents, two neuroradiology fellows, two general radiologists, and two academic neuroradiology attending physicians reviewed the cases and provided their T3DDx from the 35 possible pathologic diagnoses plus normal. The academic neuroradiologists subsequently provided reference standard imaging features for each case to validate the performance of the image-processing portion of the pipeline. The test cases were copied into anonymized accession numbers and then displayed in a standard fashion in the clinical PACS (Sectra AB, Linköping, Sweden). The same four clinical features used in the Bayesian network were made available to each reader when viewing the cases, except that radiologists were provided with the exact age of the patient and the Bayesian network received a thresholded age as input. All radiologists were told that the frequency of all diagnoses was approximately equal in the study.

### **Appendix E12**

### **Receiver Operating Characteristics**

This ordinal scale of confidence for each diagnosis (top 1, top 2, top 3) was used to construct nonparametric ROC curves according to classic signal detection theory as applied to medical decision making (40), with the AUC used as a measure of criterion-independent performance. Nonparametric AUCs were calculated with 95% confidence intervals determined by 100 bootstrapping samples on this nonparametric ROC curve, using the MATLAB routine "paramROC" (http://www.mathworks.com/matlabcentral/fileexchange/39127-parametric-roccurve). The significance of the difference between AUCs for different groups was tested using the DeLong test (25). The AUCs were averaged across each group for purposes of visualization in Figure 5, *C*[ID]FIG5[/ID].

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# **Table E1. Prevalence of imaging features for each of the diseases included in the study.**



Note.—dec = decreased, GP = globus pallidus, Immun = immunocompromised, inc = increased, R Diffusion = reduced diffusion, sub = subacute, Suscept = susceptibility, T1 = T1-weighted, T2-FLAIR = T2-weighted fluid-attenuated inversion recovery.

#### **Table E2. Expert consensus probabilities (%) of imaging and clinical features for the 36 diagnostic entities included in the study.**









Note.—T1 = T1-weighted, T2-FLAIR = T2-weighted fluid-attenuated inversion recovery.

Table E3. Accuracy for correct top 3 differential diagnosis for each of the 36 diagnostic entities.

. <b>Disease</b>	Prevalence	<b>Residents</b>	<b>General Rads</b>	<b>Neuro Fellows</b>	<b>Acad Attend</b>	Automated
High Grade Glioma	Common	83%	67%	100%	100%	100%
Low Grade Glioma	Common	75%	33%	83%	83%	100%
Hemorrhage: Chronic	Common	100%	67%	83%	100%	67%
Infarct: Acute	Common	100%	83%	100%	100%	100%
Infarct: Subacute	Common	58%	67%	100%	100%	100%
Infarct: Chronic	Common	75%	100%	100%	100%	100%
Central Nervous System Lymphoma	Common	58%	67%	67%	100%	67%
Manganese Deposition	Common	50%	33%	67%	100%	100%
Metastasis	Common	67%	67%	67%	100%	100%
Normal	Common	100%	65%	95%	90%	100%
Abscess	Moderate	50%	100%	50%	75%	$0\%$
Calcium Depositon/Fahr's disease	Moderate	73%	83%	83%	100%	100%
Creutzfeld-Jacob Disease	Moderate	50%	17%	67%	83%	100%
Hemorrhage: Acute	Moderate	83%	50%	100%	100%	100%
Hemorrhage: Subacute	Moderate	67%	67%	83%	83%	100%
Anoxic Brain Injury: Acute	Moderate	75%	100%	83%	100%	100%
Anoxic Brain Injury: Subacute	Moderate	42%	50%	33%	83%	67%
Toxoplasmosis	Moderate	42%	50%	17%	100%	67%
Wernickes Encephalopathy	Moderate	58%	25%	100%	100%	100%
Artery of Percheron Infarct	Rare	75%	75%	100%	100%	100%
<b>Bilateral Thalamic Glioma</b>	Rare	75%	50%	100%	100%	50%
Carbon Monoxide: Acute	Rare	75%	67%	67%	100%	100%
Carbon Monoxide: Subacute	Rare	25%	80%	100%	100%	33%
Carbon Monoxide: Chronic	Rare	38%	75%	100%	100%	100%
Cryptococcus	Rare	25%	25%	75%	75%	50%
Deep Vein Thrombosis: Acute	Rare	13%	25%	50%	50%	100%
Deep Vein Thrombosis: Subacute	Rare	17%	33%	33%	33%	100%

