Data-efficient resting-state functional magnetic resonance imaging brain mapping with deep learning

Patrick H. Luckett, PhD,1 Ki Yun Park, BS,1, 7 John J. Lee, MD, PhD,2 Eric J. Lenze, MD,3 Julie Loebach Wetherell, PhD,4, 5 Lisa T. Eyler, PhD,5 Abraham Z. Snyder, MD, PhD,2, 6 Beau M. Ances, MD, PhD, MSc,6 Joshua S. Shimony, MD, PhD,2 and Eric C. Leuthardt, MD1, 7–12

OBJECTIVE Resting-state functional MRI (RS-fMRI) enables the mapping of function within the brain and is emerging as an efficient tool for the presurgical evaluation of eloquent cortex. Models capable of reliable and precise mapping of resting-state networks (RSNs) with a reduced scanning time would lead to improved patient comfort while reducing the cost per scan. The aims of the present study were to develop a deep 3D convolutional neural network (3DCNN) capable of voxel-wise mapping of language (LAN) and motor (MOT) RSNs with minimal quantities of RS-fMRI data.

METHODS Imaging data were gathered from multiple ongoing studies at Washington University School of Medicine and other thoroughly characterized, publicly available data sets. All study participants (n = 2252 healthy adults) were cognitively screened and completed structural neuroimaging and RS-fMRI. Random permutations of RS-fMRI regions of interest were used to train a 3DCNN. After training, model inferences were compared using varying amounts of RS-fMRI data from the control data set as well as 5 patients with glioblastoma multiforme.

RESULTS The trained model achieved 96% out-of-sample validation accuracy on data encompassing a large age range collected on multiple scanner types and varying sequence parameters. Testing on out-of-sample control data showed 97.9% similarity between results generated using either 50 or 200 RS-fMRI time points, corresponding to approximately 2.5 and 10 minutes, respectively (96.9% LAN, 96.3% MOT true-positive rate). In evaluating data from patients with brain tumors, the 3DCNN was able to accurately map LAN and MOT networks despite structural and functional alterations.

CONCLUSIONS Functional maps produced by the 3DCNN can inform surgical planning in patients with brain tumors in a time-efficient manner. The authors present a highly efficient method for presurgical functional mapping and thus improved functional preservation in patients with brain tumors.

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KEYWORDS deep learning; resting-state functional MRI; brain tumor; diagnostic technique

MRI-based brain imaging is an integral part of patient care and medical research. Biomarkers of the neuropathogenesis and neurological manifestation of brain disorders can be identified with structural and/or functional MRI (fMRI).1 Most notably, MRI is crucial for preoperative and intraoperative localization in patients with brain tumor. The optimization of patient outcomes requires a balance between maximal extent of resection, which can reduce symptoms and extend the time until tumor recurrence, and functional preservation,
which impacts postsurgical quality of life. Structural MRI is routinely used by surgeons to identify the location and extent of resection necessary for maximal long-term patient survival. fMRI has been employed for preoperative planning, with the goal of minimizing the risk of functional impairment. Studies have shown that gross-total resection (as opposed to subtotal resection) in patients with glioma leads to an extended survival. However, a greater extent of resection increases the likelihood of functional deficits. Specifically, deficits in language (LAN) and motor (MOT) networks have been shown to significantly impact quality of life.  

fMRI has emerged as a powerful tool for mapping clinically relevant functional brain areas (“eloquent cortex”) using the blood oxygen level–dependent (BOLD) signal. In current clinical practice, task-based fMRI (T-fMRI) is most often used to “activate” particular parts of the brain (e.g., finger tapping to activate the hand motor area). However, recent work has demonstrated that these same regions can be mapped by appropriate analysis of task-free fMRI, or “resting-state” fMRI (RS-fMRI). Functionally related constellations of brain regions are widely known as resting-state networks (RSNs). Multiple RSNs have been associated with specific sensory, motor, and cognitive functions. A major advantage of RS-fMRI is that RSNs can be mapped without the need for patient compliance with a task paradigm. Further, RS-fMRI can be performed even with the patient under sedation. Moreover, the failure rate of RS-fMRI is lower than that of T-fMRI. Thus, RS-fMRI may be optimal as a means of mapping the representation of function in the clinical setting.  

A primary issue concerning RS-fMRI is the length of acquisition time required to obtain reliable data. The precision of RSN mapping using conventional computational techniques (Pearson correlation) fundamentally depends on the quantity of acquired data. Acquisition time is important for multiple reasons. First, the likelihood that a patient will have significant head motion and/or fall asleep in the scanner, both of which can lead to systemic alterations in structural and fMRI results, increases with longer scan times. Further confounding the issue is the fact, in general, multiple sequences (e.g., pre- and postcontrast T1-weighted, T2-weighted, diffusion tensor fMRI, susceptibility weighted, or arterial spin labeling images) are collected during a single scan session. In these circumstances, scanner time must be optimized in a manner that allows for reliable imaging data while still minimizing total time in the scanner. Thus, computational models capable of reliable image reconstruction with less data could lead to a shorter scan time, increased efficiency, and lower cost.  

Convolutional neural networks (CNNs) are a type of deep learning model inspired by the visual system. Applications of CNNs range from object detection and classification to natural language processing. Pertaining to structural MRI, multiple studies have demonstrated the ability of CNNs to meet the state of the art in tumor segmentation, image inverse problems (recovering/reconstructing images from sets of noisy measurements), reducing the amount of contrast necessary for MRI scans, and decreasing the sequence time necessary to obtain high-resolution images. To a lesser extent, CNNs have also been applied to fMRI, predominantly for disease classification.  

In the present study, we utilized a large cohort of healthy participants to develop a 3DCNN capable of efficient and accurate voxel-wise mapping of LAN and MOT RSNs with less than 5 minutes of data. After training, model results were compared using varying amounts of RS-fMRI data from a thoroughly characterized publicly available fMRI data set. Further, we compared functional maps generated with the 3DCNN to aggregated T-fMRI maps compiled in the Neurosynth platform. Last, model results were evaluated in 5 patients retrospectively recruited from the neurosurgery brain tumor service at the Washington University School of Medicine. Our results indicated that the 3DCNN is capable of reliable functional mapping with minimal amounts of data in both healthy controls and patients with brain tumors. Further, stable results were achieved on data encompassing a wide age range, multiple scanner types, and multiple scanner sequences. This technology has the potential to improve patient outcomes and reduce costs in cases requiring functional imaging.  

Methods  

Participants  

Normal human RS-fMRI data (n = 2252 participants) were obtained from publicly available data sets and internal studies at Washington University in St. Louis (Table 1). All participants were cognitively normal based on study-specific performance testing. The appropriate institutional review board approved all studies, and all participants provided written informed consent for the use of their de-identified data.  

MRI Acquisition  

All imaging was performed on 3-T Siemens scanners (Siemens AG) equipped with the standard 12-channel head coil. Sagittal high-resolution 3D T1-weighted magnetization-prepared rapid gradient echo (MPRAGE) scans were acquired (TE 1.54–16 msec, TR 2200–2400 msec, TI 1000–1100 msec, flip angle [FA] 7°–8°, acquisition matrix 256 × 256, voxel size 1.0–1.2 mm²). RS-fMRI scans were collected using an echo planar sequence (voxel size 3–4 mm³, TR 2200–3000 msec, FA 80°–90°) sensitive to BOLD contrast. RS-fMRI data were processed using standard methods developed at Washington University. Multi-echo data were collected on either a Siemens scanner equipped with a 20-channel head coil or a GE MR750 3-T MRI scanner equipped with an 8-channel head coil. Structural imaging included T1-weighted MPRAGE (TR 2400 msec, TE 3.036–3.16 msec, TI 1000 msec, voxel size 1 × 1 × 1 mm) and T2-weighted (TR 2500–3200 msec, TE 73.37–458 msec, voxel size 1 × 1 × 1 mm) anatomical images. RS-fMRI was performed with a multi-echo sequence (TR 2740–2960 msec; TE 14.8–15, 28.4–31.3, 42–47.6, and 55.6–63.9 msec; voxel size 4 × 4 × 4 mm).  

MRI Processing  

RS-fMRI data were preprocessed using previously described techniques. Preprocessing included com-
pensation for slice-dependent time shifts, elimination of systemic odd-even slice intensity differences (for interleaved, single-echo data), and rigid body correction for head movement. Atlas transformation was achieved by composition of affine transforms connecting the fMRI volumes with the T2-weighted and MPRAGE structural images, resulting in a volumetric time series registered to the Montreal Neurological Institute (MNI) 152 template in (mm$^3$) atlas space. In tumor patients, because of the compromised quality of atlas registration owing to the destruction of normal tissue and anatomical distortions, nonlinear registration with cost-function masking was used, as described elsewhere.\textsuperscript{32} In brief, the warping map was computed using the Advanced Normalization Tools diffeomorphic algorithm registration (https://www.nitrc.org/projects/ants) with a tumor mask. The affine transformation matrix and deformation fields were composed to register structural images to the MN152 nonlinear asymmetrical atlas as the standard template (http://hist.mni.mcgill.ca/?p=904). Additional preprocessing included spatial smoothing (6-mm full width at half maximum Gaussian blur in 3D), voxel-wise removal of linear trends over each run, and temporal low-pass filtering retaining frequencies < 0.1 Hz. Spurious variance was reduced by regression of nuisance waveforms derived from head motion correction and extraction of the time series from regions of white matter and CSF segmented by FreeSurfer.\textsuperscript{33} The global signal was included as a nuisance regressor.\textsuperscript{34} Frame censoring was performed to minimize the impact of head motion.\textsuperscript{35} All RS-fMRI data were resampled in standard atlas space. Similar methods were used for the multi-echo data after weighted averaging of the echos.\textsuperscript{30}

TABLE 1. Characteristics of training data

<table>
<thead>
<tr>
<th>Variable</th>
<th>Total</th>
<th>MEDEX</th>
<th>OASIS-3</th>
<th>GSP</th>
<th>HIV</th>
</tr>
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<tr>
<td>No. of participants</td>
<td>2252</td>
<td>242</td>
<td>665</td>
<td>1139</td>
<td>206</td>
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<tr>
<td>Mean age in yrs</td>
<td>46.6 ± 23.1</td>
<td>70.9 ± 4.7</td>
<td>67.6 ± 7.8</td>
<td>21.3 ± 2.7</td>
<td>37.9 ± 17.1</td>
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<tr>
<td>% female</td>
<td>60%</td>
<td>71%</td>
<td>60%</td>
<td>59%</td>
<td>52%</td>
</tr>
<tr>
<td>Mean yrs of education</td>
<td>15.1 ± 2.4</td>
<td>16.2 ± 2.3</td>
<td>15.9 ± 2.6</td>
<td>14.3 ± 1.9</td>
<td>13.9 ± 2.1</td>
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<tr>
<td>% White</td>
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<td>79%</td>
<td>86%</td>
<td>65%</td>
<td>44%</td>
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<td>Siemens</td>
<td>Trios/Prisma</td>
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<td>3000</td>
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</tbody>
</table>

GSP = Brain Genomics Superstruct Project; HIV = controls from HIV/AIDS studies at Washington University in St. Louis; MEDEX = Mindfulness, Education, and Exercise for Age-Related Cognitive Decline; OASIS-3 = Longitudinal Neuroimaging, Clinical, and Cognitive Dataset for Normal Aging and Alzheimer Disease. Mean values are expressed with their standard deviations.

3DCNN

A 3DCNN with 60 layers was trained to classify each voxel as belonging to the MOT, LAN, or other (OTH) RSN. The 3DCNN had a densely connected architecture\textsuperscript{46} that included residual layers nested within dense blocks. One, 3, and 7 cubic convolutions were performed. Each dense block was directly connected to the cross-entropy layer after global average pooling and 20% dropout. Layers were generally arranged as convolution → batch normalization → "Swish" activation. Max pooling (2 × 2 × 2 with stride 2) was used between dense blocks for dimensionality reduction. Training was terminated if the accuracy did not improve after three validations. The 3DCNN was implemented in MATLAB R2021b (MathWorks Inc.).

Training Data

Training data were generated by random subsampling of voxels previously shown to belong to the MOT, LAN, or OTH RSN, where OTH is defined as not MOT or not LAN.\textsuperscript{37} Subsamples of voxels in a given network were averaged and used to classify the signal into one of the three RSNs based on the highest correlation between the mean subsampled signal and the mean signal for each network. Then, a 3D similarity map was generated by computing the distance correlation between the mean of the subsampled BOLD signals and every other voxel in the brain. Only 50–75 time points from the original BOLD signal were used to generate the 3D similarity map, thereby simulating a short scan duration. However, all time points were used to label the sample into one of the three classes. The exact number of subsampled voxels and the number of time points used for each voxel were generated by a uniform random number generator. This process was repeated multiple times for each network and for each data sample. A total of 1,501,970 training instances were generated across all networks. The number of per-network training samples was approximately equal to ensure the model did not favor a particular class. During training, samples were augmented by a combination of 3D random affine transformations (rotations ± 15 mm, translations ± 15 mm), scaling (between 0.9 and 1.1), sheering (± 15 mm), and adding gaussian noise. Two hundred BOLD scans from our training data set were reserved as validation data for the 3DCNN. Approximately 200,000 validation samples were generated from the held-out scans. Training and validation samples were stratified by age, sex, and study. Once the model was fully trained and validated, the 3D simi-
larity maps generated for testing were constructed in the same manner as above. However, each map was derived from a single voxel’s time series (as opposed to the mean of random subsamples).

Testing Data

After training, model outputs were compared using data from the Midnight Scan Club\textsuperscript{24} (MSC). The MSC contains data collected on 10 participants each with 10 scanning sessions and 30 minutes of RS-fMRI per session. MSC data were used to compare model results when using different sequence lengths (approximately 2.5 vs approximately 10 minutes). Further, the trained classifier was tested on data acquired in 5 patients retrospectively recruited from the neurosurgery brain tumor service at the Washington University School of Medicine. Similarity between results was measured using accuracy, boundary F1, Dice coefficient, and multiscale structural similarity index (MSSI). Lastly, model results were compared with task activation maps derived from the Neurosynth platform, which generates statistical maps of significance of T-fMRI responses to behavioral paradigms.\textsuperscript{25} Neurosynth compiles and aggregates information from published T-fMRI studies and extracts brain regions that are consistently reported in the literature based on predefined terms associated with task responses. The terms used in our analysis were “language” and “motor.” Similarity between 3DCNN and T-fMRI results was measured using the MSSI.

Data and Code Availability

The data used in this study are partially available by request through the appropriate online repository.\textsuperscript{27,28} Other data may be made available after approval from the appropriate study principal investigators. Code will be made available upon request.

Results

Demographics of the Cohort

Participant demographics are shown in Table 1. Most of the cohort was White (71%) and female (60%), with a mean age of 46.6 ± 23.1 years (range 18–89 years) and 15.1 ± 2.4 years of education.

Model Results

The model achieved 96% out-of-sample validation accuracy (Supplemental Fig. 1). After training, the MSC data were processed with the 3DCNN first using 10 minutes of available data (MSC200), then using only 2.5 minutes of data (MSC50). Figures 1 and 2 show the results for LAN and MOT RSNs, respectively. Highly symmetric results are characteristic of RS-fMRI analysis. Only minor differences were observed between the results from MSC200 and MSC50. Figure 3 and Supplemental Table 1 provide the similarity measures that accompany Figs. 1 and 2. Figure 3 left shows the confusion matrix when comparing the winner takes all voxel-wise results for the MSC200 versus MSC50 results. The overall accuracy when treating MSC200 as the “true class” and MSC50 as the “predicted class” was 97.9%. The true-positive rate for all networks was greater than 96%, as well as the positive predictive value (PPV) for MOT and OTH. The lowest similarity measure observed was the PPV for LAN, which was 85.7%. Figure 3 right shows the difference in softmax probabilities (MSC200–MSC50) produced by the 3DCNN for all networks. The majority of voxel-wise probability differences were between −0.1 and 0.1. Further support for the high similarity between the two analyses can be seen in Supplemental Table 1, with the boundary F1, MSSI, and Dice score showing high values for all networks, as well as a low standard deviation between the scores computed across the individual MSC subjects. As in Fig. 3, the lowest scores were observed in LAN.

Figure 4 shows the comparison of the 3DCNN probability maps averaged over the MSC data, with T-fMRI maps generated from the Neurosynth platform. When calculating the 3DCNN probability maps, only 2.5 minutes of data were used. Of note, the LAN results from RS-fMRI analysis are more symmetric than those seen with T-fMRI. A high degree of similarity was observed for both networks, with an MSSI of 0.83 for LAN and 0.80 for MOT. In total, MOT maps generated from Neurosynth covered 26.2% of the total area of gray matter, while the 3DCNN maps derived from RS-fMRI covered only 12.5% (0.2 threshold). Similarly, Neurosynth LAN covered 12.9% of the total area and the 3DCNN 9.3%.

To assess the ability of the 3DCNN to accurately map functional networks in the presence of pathological structural and functional alterations, we analyzed retrospective data from 5 patients with glioblastoma multiforme (GBM; Figs. 5 and 6). Again, for this analysis, only 2.5 minutes of data were used to generate the 3DCNN probability maps. Despite the presence of tumor, the 3DCNN was able to map LAN and MOT in regions associated with those networks. Further, the maps were able to follow the structural alterations caused by the GBMs, which can be seen by comparing the lesional/contralateral probability maps for individual patients. This is especially apparent in the MOT network (GBM1, GBM2, and GBM4), which unlike LAN is highly symmetric across hemispheres. In Fig. 5, the slices were selected at the level of the tumor; in Fig. 6, the slices are centered at anatomically similar levels to facilitate comparisons across patients. Lastly, in regions especially close to the tumor “core,” the probabilities begin to decline, which is likely due to the presence of necrotic tissue and neurovascular uncoupling distorting the BOLD signal. This can easily be seen in GBM1. Figure 7 shows the probability maps of the MOT network in GBM1 with varying threshold intensities. The figure demonstrates that the MOT probability around the tumor is decreased as compared to the contralateral side. As the threshold changes, the asymmetry between the normal side and the area surrounding the tumor becomes more pronounced.

Discussion

There is strong evidence in the literature that accurate preoperative fMRI planning prior to the resection of brain tumors reduces postsurgical morbidity.\textsuperscript{38} With current task-
based methods, however, the time it takes to get adequate information can extend the scan time up to an hour. Thus, there is a high degree of significance for the neurosurgeon in obtaining optimal imaging quality while reducing imaging time and cost. Our research was performed primarily in a large number of normal subjects (with only a few examples of application in brain tumor patients), and this was necessitated by the needs of machine learning algorithms. Still, the current work demonstrates the utility of a 3DCNN for voxel-wise mapping of LAN and MOT RSNs using only 2.5 minutes of RS-fMRI data (Figs. 1–3). This represents a roughly 60% decrease in the quantity of data conventionally thought necessary to map RSNs. Since head motion increases with scan length, a short scan time tends to improve data quality. The problem of head motion is magnified in children, the elderly, and patients uncomfortable in the scanner owing to their disease. Further, in the clinical setting, there is a limited amount of time for BOLD fMRI, as several anatomical sequences must be obtained in addition to the functional sequences. Re-

![FIG. 1. Comparison of 3DCNN mapping of the LAN network on MSC subjects—MSC 1–5 (A) and MSC 6–10 (B)—using 50 versus 200 time points, corresponding to 2.5 and 10 minutes of data, respectively. All images used 0.1 threshold (slice 71 in the MNI atlas). Figure is available in color online only.](image-url)
Reducing the imaging time while maintaining the functional mapping quality provides a solution for patients requiring a complete radiological evaluation. Thus, the utilization of a 3DCNN could yield more positive imaging outcomes and increased comfort to patients while preserving accuracy and reducing costs.

The 3DCNN was highly accurate at the voxel level and capable of mapping regions known to associate with LAN and MOT networks (Figs. 1 and 2). Further, the varying topography of the probability maps produced by the 3DCNN showed that the model can capture individual anatomical variability in patients with brain tumors (Figs. 5 and 6). Thus, the 3DCNN does not simply reproduce group level or atlas-based results. This is vitally important for presurgical planning, which requires precise subject-specific mapping to facilitate functional preservation. Lastly, a clinically useful tool should be capable of accurate mapping regardless of patient demographics and the institution utilizing the tool. The 3DCNN achieved 96% validation accuracy on data from multiple studies, originating from

FIG. 2. Comparison of 3DCNN mapping of the MOT network on MSC subjects—MSC 1–5 (A) and MSC 6–10 (B)—using 50 versus 200 time points, corresponding to 2.5 and 10 minutes of data, respectively. All images used 0.1 threshold (slice 133 in the MNI atlas). Figure is available in color online only.
multiple sites with different scanners and sequence parameters, and representing a broad span of adult ages. These results suggest that the 3DCNN should be widely applicable for the purposes of presurgical functional mapping.

Tumors induce mass effect, that is, structural displacements that can distort functional maps. Figures 5 and 6 show that the 3DCNN mapping results obtained in 5 patients with GBM are remarkably similar to results obtained in healthy individuals, regardless of tumor location. Additionally, we observed interhemispheric asymmetries in functional maps, that is, impaired functional connectivity in the side with the tumor. Tumors destroy functional tissue and induce abnormal neovasculature, which can lead to dysfunctional autoregulation and neurovascular uncoupling. The BOLD signal is thought to indirectly reflect neural activity via neurovascular coupling among blood flow, blood volume, and oxygen metabolism. Note the decrease in RSN probability near the tumor core in the MOT map of patient GBM1. Similar findings could provide a means of assessing regions with the most severe damage (e.g., necrotic tissue) or the greatest abnormality in neurovascular coupling. In contrast, edematous tissue further from the tumor core showed little to no abnormality in the RSN maps. Thus, the maps produced by the 3DCNN can provide significant information that can aid in the management of patients with brain tumors.

For patients with brain tumors, the current standard of care includes a preoperative T-fMRI study prior to surgery to inform the surgical planning. A recent meta-analysis has demonstrated that presurgical planning with T-fMRI improves morbidity and mortality. Multiple studies have demonstrated that RS-fMRI mapping can complement T-fMRI and provide necessary mapping when a patient is unable to cooperate with the study or the task fails for some other reason. The low failure rate of RS-fMRI, the automated localization capability of the 3DCNN, and the need for far less scanner time make the proposed method an attractive choice for the preoperative assessment of tumor patients. Moreover, the current results suggest that there is little difference in the network topographies produced from deep learning–based probability maps derived from RS-fMRI versus T-fMRI (Fig. 4). Although the obtained maps are topographically comparable, RS-fMRI has several advantages over T-fMRI from a clinical perspective. First, each network mapped with T-fMRI requires a dedicated imaging sequence as well as patient compliance with the task. Recommendations for T-fMRI paradigm selection emphasize the need for at least two task paradigms to fully localize different components of the language system. Thus, at a minimum, for MOT and LAN, three T-fMRI runs would need to be performed, which would be approximately an order of magnitude longer in acquisition time. Additionally, RS-fMRI maps may be functionally more specific than T-fMRI. The performance of a task necessarily recruits nonspecific brain regions for performance of the task (see Luckett et al. for discussion). As an example, performing a task requires attention and visual processing to monitor and respond to a cue. These additional functional regions would not be part of the areas mapped using RS-fMRI. This distinction...

![FIG. 3. Left: Voxel-wise comparison (winner takes all) of MSC data using 50 time points (MSC50) corresponding to approximately 2.5 minutes of data versus 200 time points (MSC200) corresponding to approximately 10 minutes of data. Diagonal elements correspond to the percentage of correctly classified voxels relative to the total number of voxels for the given network. The sum of the diagonal (97.9%) corresponds to the overall accuracy. FDR = false discovery rate; FNR = false-negative rate; TPR = true-positive rate. Right: Histogram of differences when subtracting MSC50 from MSC200. Most differences ranged between -0.1 and 0.1.](image-url)
becomes evident when comparing the total area of each network across the brain. The MOT task maps generated from the Neurosynth platform covered 26.2% of the total area of gray matter, while the 3DCNN maps covered only 12.5%. For LAN mapping, Neurosynth covered 12.9% of the total gray matter area and the 3DCNN 9.3%. Concurrent responses to finger tapping in the dorsolateral prefrontal cortex reflect motor planning. Concurrent responses to the language paradigm occur in the anterolateral prefrontal cortex, superior parietal lobule, and nondominant anterior insula. As previously discussed, these responses reflect cognitive processes, for example, task control, that are not specific to language. Other possible reasons for the difference in mappings could be the difference in analysis techniques (e.g., our use of an optimized deep learning model versus the aggregation of published maps based on keywords used by Neurosynth), as well as the thresholds used by the different methods.

One limitation of our study is that we did not compare our fMRI results with the gold standard of direct cortical electrical stimulation (DCES). Although several studies have taken this approach, by their nature these studies are much smaller in size; thus, the data may not be amenable to machine learning tools, which require large data sets. Thus, within the scope of this study, it was not practical to use DCES data. A follow-up limitation of our study is that unlike our results in normal subjects, we have no good estimation of mapping accuracy in patients with brain tumors, especially with large tumors that are close to the MOT and LAN networks, which is when the findings are most critical to the surgeon. However, the same limitations and effects of neurovascular uncoupling also apply to T-fMRI in this population. Validation results obtained in both healthy controls (MSC) and patients with brain tumors were limited to a few examples in this study. Future work will involve further model validation in healthy con-

**FIG. 4.** Comparison of the 3DCNN probability maps averaged over the MSC data with T-fMRI maps generated from the Neurosynth (NS) platform. When calculating the 3DCNN probability maps, only 50 time points (2.5 minutes) were used. A high degree of similarity was observed for both networks, with an MSSI of 0.83 for LAN and 0.80 for MOT. Figure is available in color online only.
trols from multiple institutions to test the effect of varying the amount of data. Similarly, future work will also include a larger tumor patient sample and data acquired using both T-fMRI and RS-fMRI for comparison.

Conclusions

The current study demonstrates the utility of deep learning for providing accurate mapping of eloquent cortex while using a reduced amount of RS-fMRI data. This result demonstrates an additional advantage of using RS-fMRI for presurgical planning beyond the inherent advantages of RS-fMRI, such as not requiring patient compliance with task paradigms. The capability of the 3DCNN to generate accurate functional maps given a minimal amount of data supports functional preservation in patients with brain tumors while increasing imaging efficiency and decreasing cost.

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References


Disclosures
Dr. Luckett reported royalty income from Sora Neuroscience during the conduct of the study and a US patent pending. Ms. Park reported a patent together with royalties paid from Sora Neuroscience. Dr. Lee reported personal fees from Sora Neurosciences during the conduct of the study, as well as a pat-
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Author Contributions
Conception and design: Luckett, Wetherell, Eyler, Shimony, Leuthardt. Acquisition of data: Wetherell, Eyler, Ances, Leuthardt. Analysis and interpretation of data: Luckett, Park, Lee, Snyder, Ances, Shimony, Leuthardt. Drafting the article: Luckett, Snyder, Shimony, Leuthardt. Critically revising the article: Luckett, Lee, Lenze, Wetherell, Eyler, Snyder, Ances, Shimony, Leuthardt. Reviewed submitted version of manuscript: Luckett, Park, Lee, Lenze, Wetherell, Eyler, Ances, Shimony, Leuthardt. Approved the final version of the manuscript on behalf of all authors: Luckett. Statistical analysis: Luckett. Administrative/technical/material support: Snyder, Leuthardt. Study supervision: Wetherell, Shimony, Leuthardt.

Supplemental Information
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Correspondence
Patrick H. Luckett: Washington University School of Medicine, St. Louis, MO. luckett.patrick@wustl.edu.