

Toward Personalized Neuroscience: Precision Functional Mapping with Near-Infrared Spectroscopy Imaging

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Abstract

Personalized functional imaging using fMRI is a paradigm shift in neuroscience but demands extensive data per participant. Functional near-infrared spectroscopy (fNIRS) is a cost-effective alternative, yet its ability to capture individual-specific functional architecture with adequate precision remains unproven. To assess fNIRS for personalized mapping, we charted functional organization in nine individuals using task-based and resting-state fNIRS alongside fMRI. Each participant contributed 11.5 hours of imaging data, including 4 hours of resting-state and 4.2 hours of task-based (motor, working memory, language) fNIRS data, and 3.3 hours of matched fMRI for cross-validation. Results show fNIRS reliably identifies individual-specific resting-state networks, requiring only 20 minutes of data for stable characterization. Additionally, fNIRS captures subject-specific activation patterns in sensorimotor and higher-order domains, including atypical right-lateralized language dominance. These personalized fNIRS profiles align strongly with fMRI, offering comparable reliability at far lower cost. fNIRS proves a reliable, scalable, and cost-efficient tool for personalized brain mapping.

Introduction

Traditional neuroimaging studies have largely relied on group-level analyses to identify general principles of brain organization across populations^{1,2}. Over the past decade, however, increasing emphasis has been placed on individual differences in brain functional organization^{3–5}, which are closely linked to variability in behavior and cognition^{6–8}. Characterizing individualized functional brain profiles has therefore become a central goal in contemporary neuroscience and an important foundation for precision neuroscience and personalized medicine^{1,9–11}.

Advances in precision functional mapping have revealed features of functional network organization that are missed by conventional group-averaged approaches^{12–15}, demonstrating that individual brains contain reproducible network configurations that can serve as functional “fingerprints”. Yet these studies also expose a critical scalability challenge: reliable individual characterization requires extensive sampling within each participant^{14,15}, and linking individualized brain features to behavior often necessitates large sample sizes^{16,17}. Although functional magnetic resonance imaging (fMRI) has been instrumental in addressing these challenges, its high financial cost¹⁸ (approximately US\$1,000 per hour) and operational constraints limit its feasibility for large-scale, longitudinal, or naturalistic individualized research^{16,19}.

Functional near-infrared spectroscopy (fNIRS) is a non-invasive and cost-effective neuroimaging modality²⁰ that has been widely used to localize task-evoked activation and resting-state functional networks in both healthy and clinical populations^{19,21,22}. Its portability, capacity for real-time monitoring, and suitability for repeated and long-term recordings in naturalistic settings make it an attractive candidate for personalized functional imaging. Nevertheless, most fNIRS studies to date have been limited to group-level analyses. While a small number of studies have reported correspondence between

fNIRS and fMRI at the individual level in resting-state connectivity^{23,24} and task paradigms^{25–28}, and some recent work has begun to examine test–retest reliability of fNIRS-derived measures^{29–31}, these investigations have typically relied on limited sampling density, restricted cortical coverage or single evaluation metrics. However, a systematic cross-modal validation based on densely sampled individuals, as in precision functional mapping studies^{14,15}, is still lacking. It remains unclear whether fNIRS can resolve stable and discriminable functional organization across cognitive states at the individual level.

To address this, we acquired extensive multi-session fNIRS data during resting and various task states (motor, working memory and language), along with matched fMRI data from the same participants. We systematically quantified within-subject reproducibility and inter-individual specificity across states, directly testing whether fNIRS captures individual-specific functional organization, including atypical language lateralization, with precision comparable to fMRI.

Results

fNIRS can effectively captures individual functional networks and activation patterns

Each individual contributed 11.5 hours of imaging data, including 4 hours of resting-state fNIRS and 30 minutes of resting-state fMRI data, as well as 4.2 hours of task fNIRS (i.e., motor, *n*-back, and language tasks) and 2.8 hours of task fMRI data (Fig. 1a & see Methods). A 120-channel fNIRS system was used to measure changes in concentration of oxyhemoglobin (HbO) and deoxyhemoglobin (HbR) on the cerebral cortex (Fig. 1b).

We first assess whether fNIRS can effectively capture functional network and activation patterns at the individual level. We mapped resting-state networks for each participant using a parcellation approach based on resting-state functional connectivity (RSFC) and then compared them with parcellations derived from resting-state fMRI. The RS networks included the frontoparietal control network (FPN), default-mode network (DMN), ventral attention network (vATN), dorsal attention network (dATN), somatomotor network (Mot) and visual network (Vis) (Supplementary Fig. 1). The fNIRS-derived parcellation networks showed good consistency with fMRI-derived networks, with spatial Dice overlap ranging from 70% to 84% across subjects and an average Dice coefficient of $77.9\% \pm 5.1\%$, demonstrating the validity of RSFC pattern captured by resting-state fNIRS imaging (Fig. 2a). For task-based mapping, we compared the fNIRS-derived activation patterns with fMRI activations using the true positive rate (TPR & see Methods). Results from these two modalities showed moderate consistency at the individual level, with overlaps of $61.7\% \pm 6.2\%$ for language (sentence > nonword; Fig. 2b; with activation maps from two atypical right-lateralized subjects shown in the following section), $67.2\% \pm 6.6\%$ for 2-back (2-back > 0 back; Fig. 2c); $60.3\% \pm 4.7\%$ for 3-back (3-back > 0 back; Supplementary Fig. 3); $50.1\% \pm 9.5\%$ for finger-tapping motor (right hand > left hand; Fig. 2d) tasks. These findings

indicate that fNIRS is able to capture individual brain activations during primary hand motor and higher-order cognitive domains.

To assess whether fNIRS-based RSFC can capture idiosyncratic network features in individuals, we quantified within-subject and between-subject similarity of these RSFC patterns. Within-subject similarity was quantified as the correlation between functional connectivity (FC) matrices across sessions for each participant, while between-subject similarity was measured by correlating the FC matrices from a participant's sessions with those of other participants. The within-subject FC similarity was high across sessions (diagonal blocks in Fig. 3a) and was significantly greater than between-subject FC similarity ($W = 28, P = 0.02$; within-subject similarity = 0.60 ± 0.07 ; between-subject similarity = 0.40 ± 0.02 ; Fig. 3b), indicating stable individual connectivity fingerprints. A comparable pattern was observed for fMRI-derived FC matrices (Fig. 3c), with similarly elevated within-subject correlations relative to between-subject comparisons ($W = 28, P = 0.02$; within-subject similarity = 0.60 ± 0.06 ; between-subject similarity = 0.24 ± 0.03 ; Fig. 3d), confirming robust individual specificity across modalities.

We next examined whether individualized activation patterns during cognitive tasks were similarly reproducible. Task-evoked activations were compared across sessions within the same subject as well as across participants using the true positive rate (TPR & see Methods). Within-subject similarity of task-evoked activations were consistently higher than between-subject similarity for both primary motor (Lhand: $W = 45, P = 0.004$; Rhand: $W = 43, P = 0.01$) and higher-order cognitive tasks, including *n*-back (0-back: $W = 36, P = 0.008$; 2-back: $W = 36, P = 0.008$; 3-back: $W = 36, P = 0.008$) and language tasks (sentence: $W = 44, P = 0.008$; nonword: $W = 41, P = 0.03$) (Fig. 3e). A similar pattern was observed for fMRI-derived activation maps (Fig. 3f), with significantly greater within-subject than between-subject correlations across all task conditions (Lhand: $W = 28, P = 0.02$; Rhand: $W = 28, P = 0.02$; 0-back: $W = 23, P = 0.16$; 2-back: $W = 28, P = 0.02$; 3-back: $W = 28, P = 0.02$; sentence: $W = 45, P = 0.004$; nonword: $W = 45, P = 0.004$). Together, these results demonstrate that fNIRS can reliably characterize individualized patterns of brain functional organization, providing a foundation for subject-level functional mapping and precision neuroscience applications.

fNIRS detects atypical right-lateralized language dominance

At the group-level, language function is left-hemisphere dominant while less than 10% of the population show atypical right-hemisphere dominance³³. To assess the ability of fNIRS in detecting idiosyncratic functional features such as atypical language lateralization, we conducted a laterarization analysis based on the language task on each participant. A laterality index (*LI*) was calculated on the basis of the activation degree in the left and right hemisphere (see Methods)³⁴. Among the nine participants, seven participants showed left-lateralized language ($LI = 0.12 \pm 0.07$) and two participants showed atypical right-lateralized language (sub 04: $LI = -0.63$; sub 08: $LI = -0.48$; Fig. 4a). Individual language lateralization patterns from fNIRS were found to be consistent with fMRI results ($LI = 0.21 \pm 0.20$ for seven left-lateralized participants; sub 04: $LI = -0.53$, sub 08: $LI = -0.17$), with a strong correlation between fNIRS

and fMRI laterality indices ($r = 0.90$ $P = 0.002$) (Fig. 4b). Furthermore, Language activation patterns identified by fNIRS were robust, with test-retest Dice coefficient overlaps of 49% for left-lateralized participants and 46% for right-lateralized participants (Fig. 4c & see Methods). However, the group-level activation map failed to reflect the important language dominance differences observed at the single-subject level (Supplementary Fig. 2). These results indicate fNIRS as a reliable and sensitive tool for capturing non-canonical patterns of brain organization beyond what is accessible with traditional group-level.

fNIRS enables large-scale studies at a low cost

To assess the feasibility of fNIRS as a viable, cost-efficient alternative for fMRI in large-scale brain research, we investigated the minimum resting-state data required to achieve reliable results and compared the cost-efficiency of the two modalities at equivalent reliability levels. Test-retest reliability was measured as the correlation between the FC matrices obtained from two halves of the same individual's data. Reliability of fNIRS-based RSFC increased rapidly at first and plateaued around 20 minutes ($r = 0.64$). In general, fNIRS requires longer scan duration than fMRI to achieve the same reliability. For example, 16 min of fNIRS achieves the same test-rest reliability as 6 min of fMRI ($r = 0.62$) whereas 63 min of fNIRS data are able to achieve the same reliability as 15 min of fMRI ($r = 0.73$) (Fig. 5a). However, fNIRS is more affordable than fMRI - the cost of fNIRS data acquisition (<https://cibsrnirs.stanford.edu/rates>) is roughly one-tenth that of fMRI (<https://med.stanford.edu/lucasmri/mr-service-rates>). With comparable reliability, fNIRS maintains superior cost-efficiency in data collection: for 16 minutes of acquisition, fNIRS costs \$13 versus \$59 for 6 minutes of fMRI; for 31 minutes, fNIRS is \$26 compared to \$98 for 10 minutes of fMRI; and for 63 minutes, fNIRS amounts to \$53 while 15 minutes of fMRI costs \$148 (Fig. 5b). Within a \$100k budget, this cost advantage translates to recruiting approximately three times more participants for fNIRS studies than fMRI: 7,500 participants for 16-minute fNIRS versus 1,695 for 6-minute fMRI; 3,871 participants for 31-minute fNIRS versus 1,017 for 10-minute fMRI; and 1,905 participants for 63-minute fNIRS versus 678 for 15-minute fMRI (Fig. 5c). These results suggest that fNIRS holds promise as an efficient, cost-effective tool for large-scale brain research, especially among populations who are not suitable for fMRI.

Discussion

The portability, affordability, and broad applicability of fNIRS position it as a promising tool for personalized neuroimaging research. By leveraging densely sampled resting-state and task-based fNIRS data, we show that fNIRS can capture individual-specific functional networks and task-evoked activation patterns that closely correspond to those identified using fMRI. Notably, fNIRS is sensitive to idiosyncratic features of functional brain organization, including atypical right-lateralized language dominance. Although achieving high reliability with fNIRS requires longer data acquisition relative to

fMRI, its substantially lower cost and operational flexibility support its use as a scalable and accessible approach for individualized functional brain mapping.

Dense sampling enables reliable individual-level functional organization with fNIRS

Using highly sampled fNIRS data, we found that RSFC estimated from 20 minutes of data achieved moderate test–retest reliability, which further increased with longer acquisition durations (Fig. 5a). These observations are consistent with prior work using high-density diffuse optical tomography (HD-DOT) in a single individual³⁵, which reported similar reliability with substantially shorter scans. Extending this work, our study systematically evaluated RSFC reliability across much longer acquisition periods and across multiple participants, demonstrating that fNIRS can reliably characterize individual-level functional connectivity given sufficient data.

Individual brains exhibit unique functional architectures—often described as functional “fingerprints”^{3,36,37}—that are stable across time and cognitive states³⁸. Consistent with this framework, we observed higher session-to-session similarity within individuals and between individuals for both fNIRS-based RSFC (Fig. 3a) and task-evoked responses (Fig. 3b). These findings indicate that fNIRS captures robust and reproducible individual-specific functional signatures. Although such individualized resting-state networks and activation patterns have been well documented using fMRI^{11,14,15,39}, our results provide systematic evidence that fNIRS can similarly resolve these individualized features.

Individual-level functional network mapping is essential for elucidating the distributed neural architectures underlying variability in cognition and behavior. While fMRI has enabled high-resolution individual-specific parcellations^{15,34}, our results demonstrate that comparable individual-level networks can be detected using fNIRS, with good spatial correspondence between the two modalities (Fig. 2a). This correspondence was strongest in primary visual and motor networks, consistent with prior HD-DOT findings²³. Beyond resting-state analyses, we observed substantial individual-level correspondence between fNIRS and fMRI during both sensorimotor and higher-order cognitive tasks (Fig. 2b-d). Notably, fNIRS reliably captured activations associated with language and memory tasks, extending prior qualitative observations with quantitative evidence and supporting the utility of fNIRS for individualized functional mapping.

Individualized fNIRS mapping reveals non-canonical language lateralization

Language processing is predominantly left-hemisphere dominant in most individuals; however, approximately 10% of the population exhibits atypical right-hemisphere language dominance^{40–42}. Such individuals may rely more heavily on right-hemisphere mechanisms supporting prosody, pragmatic processing, and concrete lexical representations^{43,44}. In this study, fNIRS reliably detected right-

lateralized language dominance in a subset of participants, with strong concordance to fMRI-based lateralization measures (Fig. 4). These findings demonstrate the feasibility and validity of fNIRS for mapping language lateralization at the individual level. This capability may be particularly valuable in developmental and clinical contexts, where compliance with fMRI scanning is challenging and where identifying atypical language organization is of high relevance.

fNIRS as a cost-efficient complement to individualized fMRI

Large sample sizes are increasingly recognized as essential for achieving robust brain-behavior associations and accurate individual-level predictions, with recent evidence suggesting that robust brain-wide association studies may require data from thousands of participants^{16,45–48}. Despite substantial growth in MRI availability, the high cost and logistical demands of fMRI acquisition remain major barriers to large-scale personalized neuroimaging studies, particularly for early-career researchers and longitudinal designs^{16,49}.

In contrast, fNIRS offers a substantially lower-cost alternative, enabling the collection of larger datasets within fixed budgets. Our findings demonstrate that, given sufficient data, fNIRS can achieve individual-level reliability comparable to fMRI while supporting much larger sample sizes without sacrificing measurement stability. Combined with its portability and compatibility with long-duration and naturalistic data collection, fNIRS represents a valuable complementary modality for large-scale and context-flexible individualized neuroscience research.

Sufficient data are critical for personalized functional imaging with fNIRS

Most fNIRS studies acquire relatively short resting-state recordings—typically 5–10 minutes—to characterize group-level functional organization. Previous work has suggested that group-level RSFC estimated from fNIRS stabilized within a few minutes. For example, Geng et al., reported that RSFC patterns were reproducible after approximately 1 minute of recording, whereas Aarabi et al. found that RSFC estimates stabilized with data lengths exceeding 1–2.5 minutes, depending on the hemoglobin concentration signals analyzed^{50,51}. However, direct evidence supporting the reliability of such protocols for individual-level inference has remained limited. Our results indicate that substantially longer acquisition durations are required to achieve reliable individual-level RSFC estimates (Fig. 5a).

By directly comparing fNIRS reliability with matched fMRI data, we demonstrate that approximately fourfold longer fNIRS scans are needed to achieve reliability comparable to that provided by fMRI. This requirement parallels fMRI literature indicating that 15–25 minutes—or more^{12,49,50}—are often necessary for reliable single-individual inference. Together, these findings suggest that conventional short-duration fNIRS protocols are insufficient for individualized functional mapping and highlight the need for revised data acquisition standards in future fNIRS studies.

Limitations

The present study has several limitations. First, the sample size is relatively small, which makes it difficult to determine how these individualized functional patterns vary across individuals. Future studies with larger cohorts will be required to better understand these individual differences and their associations with behavioral or clinical traits. Second, although the intensive sampling design allowed us to rigorously evaluate the reliability and reproducibility of individualized fNIRS-derived brain maps, the recordings were obtained under controlled experimental conditions. Further work will be needed to determine whether similar reliability can be achieved in more naturalistic or longitudinal settings. Finally, although relatively strict motion control and individualized removal of physiological components were implemented in the present study, future work may benefit from more advanced individualized denoising approaches, including machine learning–based methods that model and remove subject-specific motion and physiological artifacts, thereby further improving the reliability of individualized functional mapping.

Methods

Participants

Nine healthy adult participants participated in the current study. The age range of these participants was 23 to 35 years (mean 28.33 years), four were male and five were female. Two were left-handed, and the remaining seven were right-handed. The study protocol (No. ICBIR_A_0109_002) was approved by Institutional Review Boards of the State Key Laboratory of Cognitive Neuroscience and Learning, Beijing Normal University and Changping Laboratory. Informed consent was obtained from all participants before participating in the study.

Task design

Motor tasks: The motor task was adapted from the Human Connectome Project⁵² to assess motor-related brain activity. Participants performed specific movements in response to verbal prompts, including tapping their left or right fingers. Each run comprised of 9 blocks, each lasting 18 seconds: 2 left and 2 right finger-tapping blocks, and 5 fixation blocks interspersed before and after each movement block.

N-back tasks

To evaluate cognitive control across varying memory loads, we employed an *n*-back task adapted from Cohen et al., and Braver et al.,^{53,54}. Participants viewed a sequence of random uppercase letters and instructed to press a button when the current letter matched 'k' (0-back) or the one presented *n* trials earlier (*n* = 2,3; i.e. 2-back, 3-back). Each condition was presented in 3 randomly assigned blocks per run.

Each block consisted of 9 trials lasting 27 s, with stimuli displayed for 0.5 s during each trial followed by a 1.5 s inter-trial interval (ITI). Between task blocks, 10 fixation blocks (12 s each) were interleaved.

Language tasks

The language task, based on Fedorenko et al^{55,56}, was designed to explore processes underlying word- and phrase-level meaning. Participants read either 10-word real sentence (target task) or length-matched pronounceable nonword strings (control task). Each run consisted of 4 target blocks and 4 control blocks, with each block lasting 18s and containing 2 trials. Stimuli were presented one word (or nonword) at a time for 0.9s, followed by a 0.9s ITI in each trial. Each block was interspersed with 12s fixation blocks.

fNIRS data acquisition

fNIRS data were collected using a 120-channel continuous-wave near-infrared optical imaging system (Nirxmart, Hui Chuang, China) at a sampling rate of 11 Hz. Forty light sources (dual wavelengths: 730 nm and 850 nm) and 32 detectors were arranged at a fixed 3-cm interoptode distance and symmetrically placed over the head of participants according to the international 10–20 coordinate system and referred to the external auditory canals and vertex of each participant as landmarks. One hundred and twenty measurement channels were configured to cover the bilateral frontal, temporal, parietal, and occipital lobes of the participants (Fig. 1b and c).

The participants underwent a total of 8.2 hours of fNIRS scanning, comprising six 40-minute resting-state sessions and eighteen 14-minute task runs. For resting-state scanning, participants were instructed to relax and keep their eyes open without falling asleep. For the task scanning, participants were required to perform motor task (3 min), *n*-back task (6 min), and language task (5 min), respectively. Two participants didn't undergo the resting-state data acquisition and some completed only part of the sessions due to constraints related to scheduling and the overall duration of the experiment (see Supplementary Table 1 for details).

fNIRS preprocessing

Resting-state fNIRS: fNIRS data were preprocessed to reduce artifacts and physiological noise, following procedures similar to our previous studies^{57,58}. The preprocessing pipeline included the following steps: (i) Signal quality check: channels with signal-to-noise (SNR) < 10, low inter-channel correlation and absent cardiac oscillations within the 1–2 Hz range⁵⁸ were identified as poor quality and excluded from further analysis⁵⁹. (ii) Motion artifacts detection and correction. Motion-related artifacts were detected and corrected using spline interpolation. Given the increased sensitivity of personalized analyses to motion-related noise, segments exhibiting signal change greater than 0.01 were excluded based on Homer2 detection⁶⁰ to reduce the influence of residual artifacts on individual-level stability. (iii)

Bandpass filtering: A 0.01–0.08 Hz bandpass filter was applied to remove low-frequency drift and high-frequency physiological noise^{22,26}. (iv) Physiological noise removal: principal component analysis (PCA) was used to regress out systemic physiological noise⁶¹. (v) Hemoglobin concentration conversion: optical density data were converted to changes in hemoglobin concentrations using the modified Beer–Lambert law⁶². Oxyhemoglobin (HbO) was employed for further analysis since its higher signal-to-noise ratio than deoxyhemoglobin (HbR)⁶³.

Task fNIRS

A similar preprocessing pipeline was applied to task-evoked fNIRS data. To retain task-related responses while suppressing motion-related artifacts, runs were excluded if more than 1/3 of time points exhibited signal changes greater than 0.05 after motion correction as identified by Homer2. A 0.02–0.5 Hz bandpass filter was applied to remove low-frequency drift and high-frequency physiological noise²⁶. Other preprocessing steps were identical to those used for the resting-state data.

MRI Image acquisition

All MRI imaging data were obtained using a customized 3T GE SIGNA UHP scanner equipped with a 48-channel head coil at Changping laboratory. Structural images were collected for anatomical localization of fNIRS measurement channels for each participant. Vitamin E capsules were placed at each of the fNIRS optode locations on the scalp as fiducial markers for MRI coregistration. T1-weighted images were obtained were acquired using the 3D MPRAGE T1-weighted sequence with 1 mm isotropic resolution (192 sagittal slices in a single slab, TR = 2704 ms, TE = 3.5 ms, TI = 900 ms; field of view (FOV) = 256 × 256 mm², flip angle = 8°).

All participants underwent 2.8 hours functional MRI scanning, which included one resting-state sessions (30-minutes each session) and ten 14-minute task runs. The fMRI task runs were identical to those conducted with fNIRS. Two participant did not complete the resting-state fMRI scanning. Additionally, three participants did not complete the *n*-back task, and two did not complete the motor task (Supplementary Table 1). All functional imaging was obtained with a gradient-echo EPI sequence (TR = 3000ms, TE = 30ms, flip angle = 90°, voxel size = 3mm × 3mm × 3mm, 50 slices).

MRI data preprocessing

Structural MRI

MRI data were preprocessed by DeepPrep v25.1.0⁶⁴. Anatomical data preprocessing was performed using FreeSurfer (v7.2.0) for motion correction, with N4 bias field correction (SimpleITK v2.3.0)⁶⁵ applied to the T1-weighted images as a reference for the entire pipeline. applied to the T1-weighted images as a reference for the entire pipeline. Brain tissue segmentation, including cerebrospinal fluid (CSF), white

matter (WM), and gray matter (GM), was conducted using FastSurferCNN (v1.1.0)⁶⁶, cortical surface reconstruction was performed with FastCSR (v1.0.0)⁶⁷, and surface alignment to a standard template (fsaverage) was achieved using SUGAR (v1.0.0)⁶⁸. Spatial normalization was carried out using SynthMorph (v2)⁶⁹ for nonlinear registration to MNI152NLin6Asym.

Functional MRI

Functional data preprocessing included motion correction (mcflirt, FSL v6.0.5.1)⁷⁰, slice timing correction (3dTshift, AFNI v24.0.00)⁷¹. The BOLD reference image was aligned to the T1w reference using boundary-based registration (bbrregister)⁷² and resampled to both volumetric (MNI152NLin6Asym) and surface (fsaverage6) templates. Temporal signal regression was performed using framewise displacement (FD) and DVARS, with physiological noise correction implemented via CompCor (tCompCor/aCompCor/bCompCor). Additionally, motion estimates and whole-brain signals were included with their temporal derivatives and quadratic terms to account for higher-order motion artifacts. PCA-based regression was applied to remove signal from edge regions of the brain to further reduce residual motion artifacts.

Resting-state fMRI

For resting-state fMRI data, linear detrending and bandpass filtering (0.01–0.08 Hz), and regression of nuisance variables (including six motion parameters, white-matter signal, ventricular signal, global signal, and their first temporal derivatives, and bCompCor as mentioned above) were conducted to denoise. A 6-mm full-width half-maximum (FWHM) surface smoothing kernel was subsequently applied.

Task fMRI

For task fMRI data, high-pass filtering (cutoff = 128 s) and 6-mm FWHM smoothing were applied to remove noise and drift, following the DeepPrep's preprocessing procedures.

fMRI / fNIRS RSFC calculation

After initial pre-processing, functional connectivity analysis and individual-level network parcellation were performed. For fNIRS, resting-state functional connectivity (RSFC) was estimated by computing Pearson's correlation coefficient between time courses of all channel pairs. The resulting correlation values were then Fisher's z transformed to improve normality. Similarly, for fMRI, RSFC was calculated as the Pearson's correlation coefficient between the time courses of all vertex pairs.

Within- and across-subject similarity of RSFC

To assess the similarity of resting-state functional connectivity (RSFC) within and across participants, 7% of the upper triangular elements of the functional connectivity matrix were randomly sampled to

calculate correlation coefficient between sessions. This procedure was repeated 1,000 times, and similarity values were averaged across iterations⁷³.

Personalized functional parcellation

Based on RSFC, we applied an iterative functional parcellation procedure described in our previous reports³⁴ to delineate functional networks for each participant. For resting-state fNIRS data, we first projected each measurement channel onto the cortical surface and assigned it to one of seven large-scale networks defined by Yeo et al.³² The initial parcellation used the average HbO concentration across all channels within each network as reference signals. For each channel, the probability of belonging to a given network was calculated as the proportion of its 100 nearest cortical vertices that were assigned to that network. To refine the parcellation, each channel's time series was correlated with the network reference signals, and the correlations were weighted by the network probability and inter-subject variability. Channels were then reassigned to the network yielding the highest weighed correlation. The reference signals were subsequently updated by combining the newly averaged signals from reassigned networks with the original references. This process was iteratively repeated until convergence, defined as $\geq 99\%$ consistency in channel-to-network assignments across two consecutive iterations.

For resting-state fMRI data, an individual functional parcellation procedure was first initialed from Yeo's population-level 7-network functional atlas³², and then it was individualized by iteratively adjusting network boundaries until a reliable assignment of cortical vertices to the 7 networks was achieved. For each vertex, a confidence value was estimated as the ratio of its strongest to second-strongest correlation coefficient with the 7 networks, which indicated the likelihood belonged to the assigned network. Once the predefined stopping criteria was met, the personalized brain functional networks were determined for each participant.

Individual-level task activation analysis

For both fMRI and fNIRS data, the task-evoked brain activations for each participant were calculated using general linear model (GLM)^{74,75}, respectively. First-level analyses were performed separately for each run in a given participant, followed by second-level analyses grouped data across the all runs of the same participant. Specifically, block regressors corresponding to experimental conditions (motor: left hand, right hand, left foot, right foot, tongue; *n*-back: 0-back, 2-back, 3-back; language: sentence, noword) were convolved with a canonical hemodynamic response function to model task-related responses. For fMRI data, six motion parameters were used to control for motion artifacts and were also additionally included as nuisance regressors. For fNIRS data, no additional nuisance regressors were used considered that the noise components from motion artifacts had been removed during preprocessing. The beta estimation for each condition were extracted from each run and entered into a second-level analysis, where first-level condition betas were tested against a null hypothesis of zero

activation using a one-sample t-test across runs within each participant. The resulting t-values for each condition were converted to Z-scores. Of note, for fMRI, first-level analyses were conducted using FSL's FEAT⁷⁶.

Group-level task activation analysis

To evaluate how group-level results may differ from individual-specific activations, we additionally conducted group-level GLM analyses using a canonical hemodynamic response function to estimate condition-specific beta values for each channel and participant. Non-parametric permutation tests were then applied to the beta values across participants to identify group-level task-related responses.

Comparison of within- and between-subject similarity in RSFC and task-evoked activations

To assess individual specificity, we compared within-subject and between-subject similarity for both resting-state functional connectivity (RSFC) and task-evoked activation patterns. RSFC similarity was computed as described above. Task-evoked activation similarity was calculated using positive session-level activation maps. For fNIRS, each session consisted of three runs, whereas for fMRI, each session consisted of two runs. For each participant and session, run-level beta maps were first averaged to generate a session-level activation map. Non-positive beta values were excluded from the similarity calculation. Within-subject similarity was defined as the Pearson correlation between session-level activation maps from different sessions within the same participant. Between-subject similarity was calculated as the Pearson correlation between session-level activation maps from different participants. Wilcoxon signed rank tests were conducted to compare within-subject and between-subject similarity for both RSFC and task-evoked activation.

Evaluating activation consistence between fNIRS and fMRI

To quantify the spatial correspondence between fNIRS and fMRI activations, we computed the true positive rate (TPR) as a measure of how reliably fNIRS captures task-relevant brain activity. TPR was defined as the proportion of channels identified as active by both modalities, relative to all channels identified as active by fMRI:

$$TPR = \frac{TP}{TP + FN}$$

Here, fMRI was treated as the reference modality. Channels identified as active by both fNIRS and fMRI were considered true positives (TP), while those identified only by fMRI were considered false negatives (FN). To enable direct cross-modal comparison, fMRI activation values were averaged within a 5 mm

radius surrounding each fNIRS channel location. Higher TPR values indicate stronger spatial agreement between modalities in detecting task-evoked responses.

Estimating activation reproducibility and parcellation cross-modal consistency

Dice coefficient was used to quantitatively assess (1) the test-retest overlap of fNIRS in language task, and (2) the spatial overlap of network parcellations between fNIRS and fMRI. The Dice coefficient measures the degree of spatial intersection between two binary sets and is defined as:

$$Dice(A, B) = \frac{2 \times |A \cap B|}{|A| + |B|}$$

where A and B represent two sets of suprathreshold activation or parcellation labels. Dice values range from 0 (no overlap) to 1 (perfect overlap). Interpretation followed the conventions: <0, no agreement; 0–0.2, slight agreement; 0.2–0.4, fair agreement; 0.4–0.6, moderate agreement; 0.6–0.8, substantial agreement; and 0.8–1.0, almost perfect agreement.²⁶ For cross-modal comparisons, fMRI activation values were averaged within a 5 mm radius around each fNIRS channel location to account for spatial resolution differences between the two modalities.

Characterizing individual language dominance

To characterize individual differences in language dominance, we computed a hemispheric lateralization index (LI) to quantify functional asymmetry during the language task. The LI was defined as:

$$LI = \frac{A_L - A_R}{A_L + A_R}$$

Where A_L and A_R denote the average activation within left and right hemisphere respectively, To enhance robustness, these averages were computed based on the top 50% most activated channels across the entire cortex. Positive LI values indicate left-dominant activation, while negative values suggest right-dominant activation.

RSFC Reliability Estimation for Cost-Efficiency Analysis

To assess the reliability of RSFC in fNIRS and fMRI, we employed a split-half approach with iterative random sampling. Specifically, the resting-state data from each participant were randomly divided into two halves 1000 times. For each split, a subset of data from one half was randomly sampled to compute a functional connectivity (FC) matrix, which was then correlated with the FC matrix derived from the other half. Reliability was quantified as the Pearson correlation between 7% of randomly selected upper

triangular elements of the two FC matrices. This sampling and correlation procedure was repeated 1000 times per split, and the final reliability estimate was defined as the average correlation across all iterations.

Data and Code availability

All data necessary to evaluate the conclusions are included in the paper. Data supporting the findings and the codes used in this study are available from the corresponding authors upon reasonable request.

Declarations

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Author contributions:

Conceptualization: H.N., H.S.L. Methodology: Z.H., J.R., H.L., X.F., W.Z. Investigation: Z.H., J.R., J.C. Visualization: Z.H. Supervision: H.N., H.S.L. Writing—original draft: Z.H., J.R., H.S.L., H.N. Writing—review & editing: Z.H., J.R., H.S.L., H.N.

Competing interests:

The authors declare that they have no competing interests.

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Figures

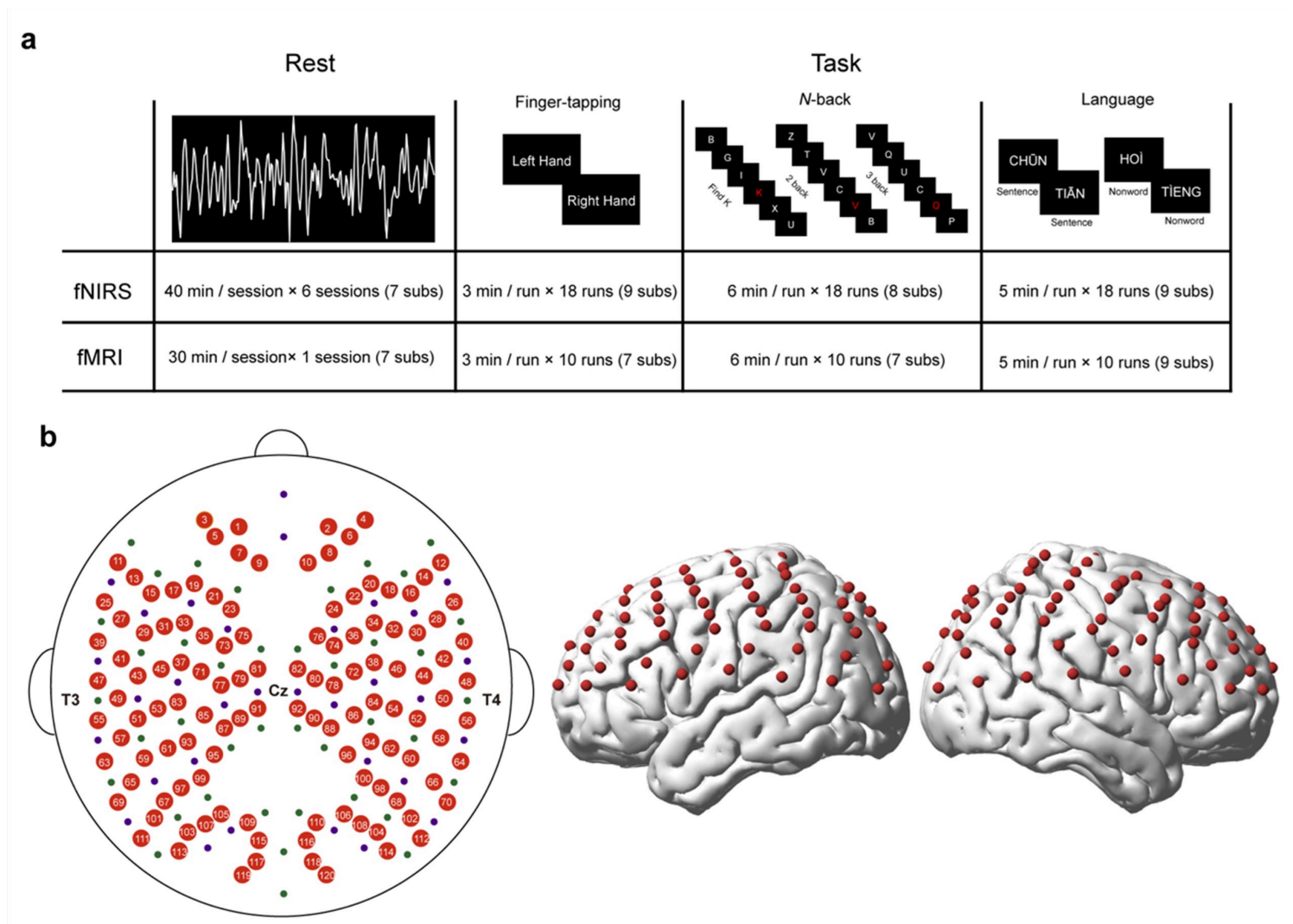


Figure 1

Scheme for fNIRS and fMRI data collection. **a**, Experimental procedures. Resting-state fNIRS data were acquired across six sessions, with each session lasting 40 minutes per participant (4 hours in total). Resting-state fMRI data were collected in a single session of 30 minutes. Three cognitive tasks were performed by each participant. Finger-tapping tasks: participants were instructed to tap their left/right fingers; *n*-back tasks (*n* = 0, 2, 3); language tasks: participants read either 10-word real sentences (target task) or length-matched pronounceable nonword strings (control task). **b**, Configuration of fNIRS optical probes. The probe array comprises 40 light sources (green dots) and 32 detectors (purple dots), forming 120 measurement channels (numbered red dots, 1-120). The anatomical locations of these 120 channels are projected onto the cortical surface of a representative participant.

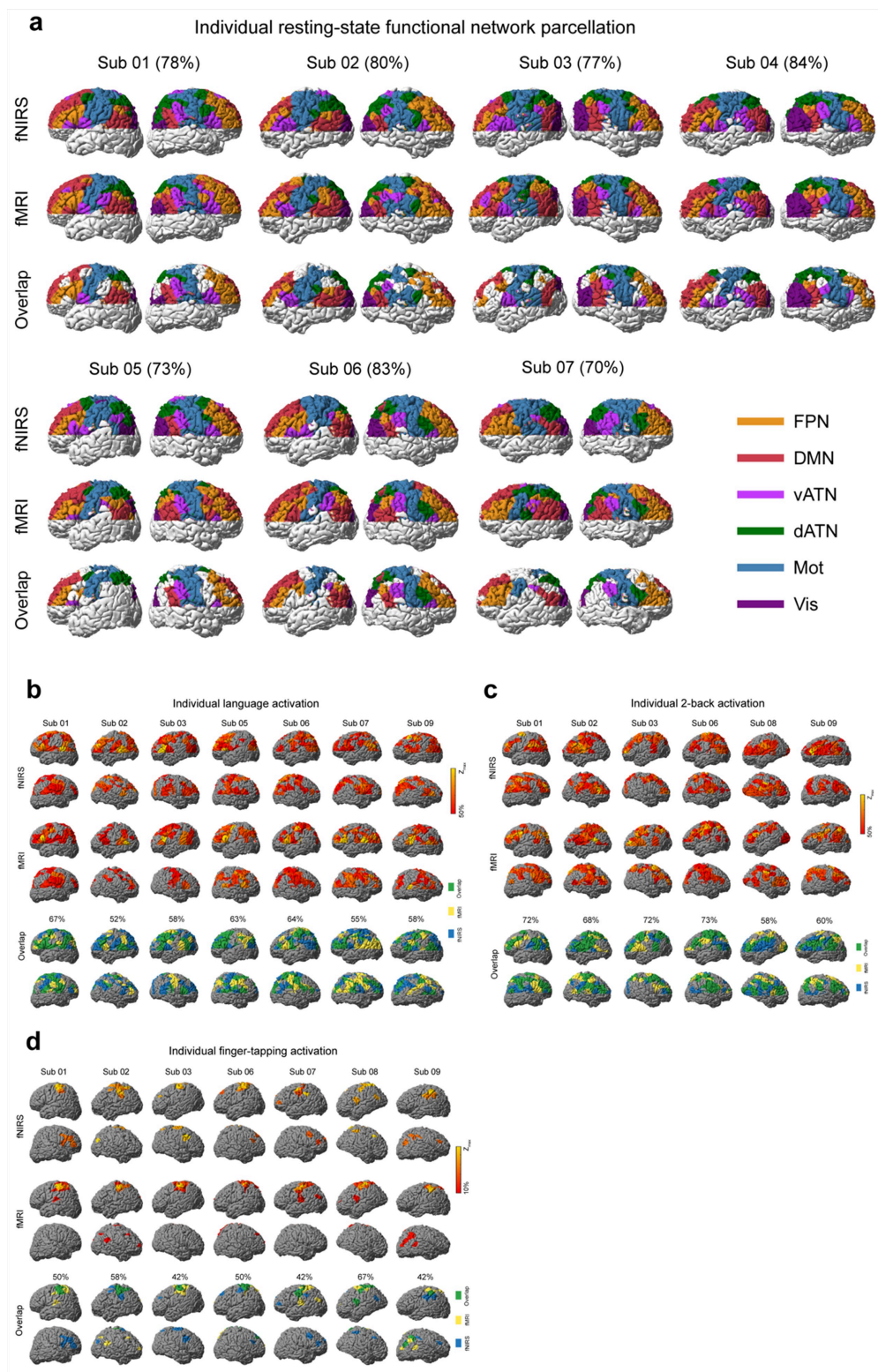


Figure 2

Individual resting-state functional networks and brain activations during language, *N*-back and finger-tapping tasks. **a**, Comparison of individual network parcellation between fNIRS (top row) and fMRI (middle row) and their spatial overlap between networks (bottom row), computed using all available resting-state sessions (4 hours of fNIRS and 30 minutes of fMRI data). The Dice overlaps shown in parentheses demonstrated good consistency between two modalities. Networks were parcellated

according to YEO's 7-network atlas³² and color-coded, including the default-mode (DMN), frontoparietal control (FPN), dorsal attention (dATN), ventral attention (vATN), sensorimotor (Mot), and visual (Vis) networks. **b**, Individual activation maps from fNIRS (top row) and fMRI (middle row), and their spatial overlap (bottom row) for language task in 7 participants. **c**, Individual activation maps for 2 back task. **d**, Individual activation maps for finger tapping motor task. Overlap percentages shown in parentheses reflect moderate consistency between modalities, using fMRI-defined activations as the reference, thresholded at 50% maximum Z-score for language and n-back tasks and 10% for finger tapping motor activation.

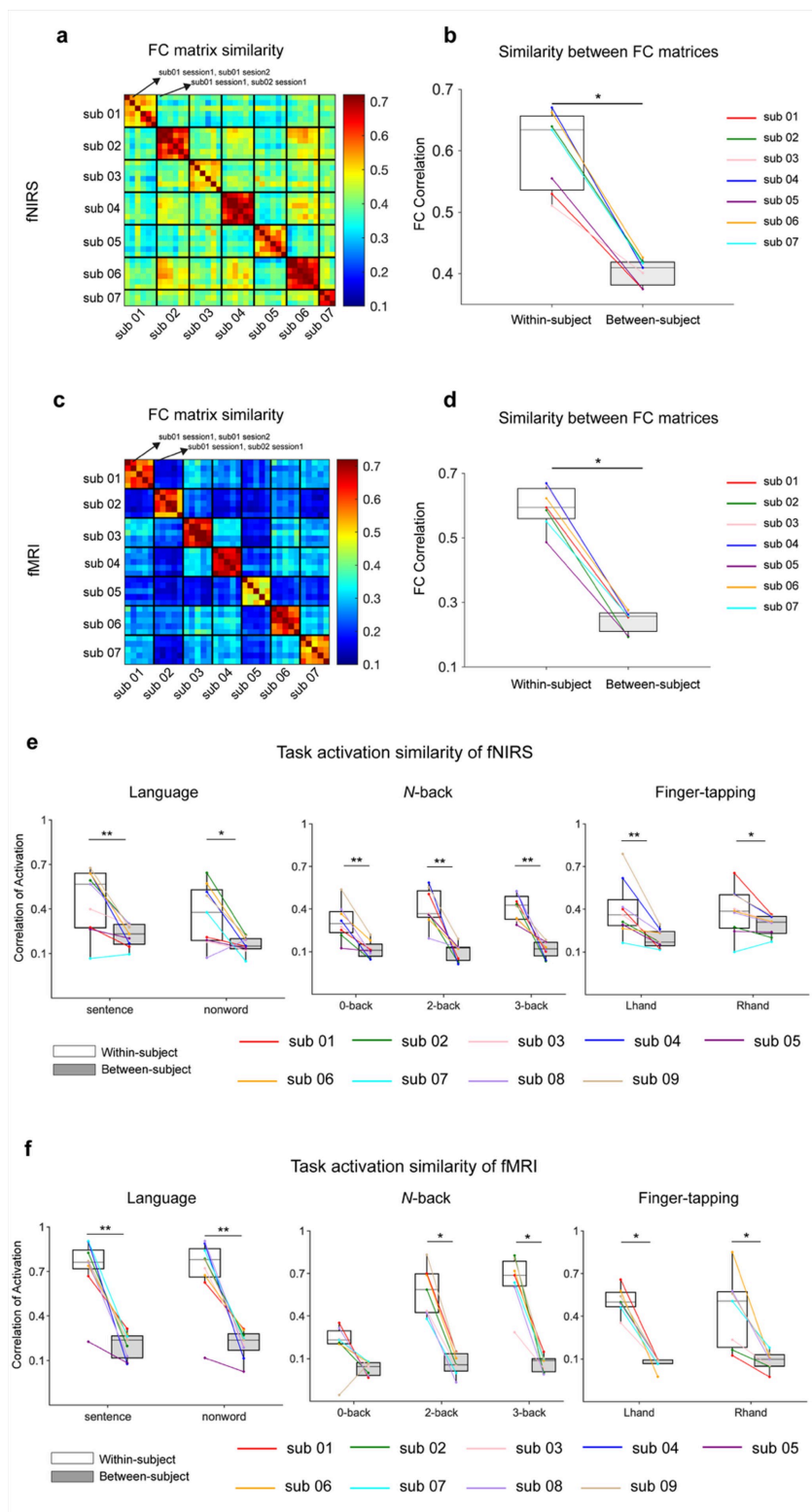


Figure 3

Individual-specific functional network and task activation patterns captured by fNIRS and fMRI. a, Similarity of fNIRS-derived FC matrices across sessions and participants. Each cell represents the Pearson correlation between FC matrices from two different sessions (each session lasting 40 minutes), with warmer colours indicating higher similarity. Diagonal blocks reflect within-subject similarities, whereas off-diagonal blocks reflect between-subject similarities. **b,** Comparison of within-subject and

between-subject FC similarity derived from fNIRS. Boxplots summarize within-subject (white) and between-subject (grey) similarities, with coloured lines indicating individual participants. Within-subject similarity is significantly higher than between-subject similarity (wilcoxon signed rank tests, $*P < 0.05$). **c**, Similarity of fMRI-derived FC matrices across sessions and participants. **d**, Comparison of within-subject and between-subject FC similarity derived from fMRI. **e**, A contrast of within- versus between-subject activation patterns derived from fNIRS during each task. Pearson correlations were computed between activation maps on language (left), *n*-back working memory (middle) and motor tasks (right), separately. Within-subject similarity of task-based fNIRS activation is consistently higher than between-subject similarity (wilcoxon signed rank tests, $*P < 0.05$ and $**P < 0.01$). **f**, Comparison of within-subject and between-subject activation patterns derived from fMRI during each task.

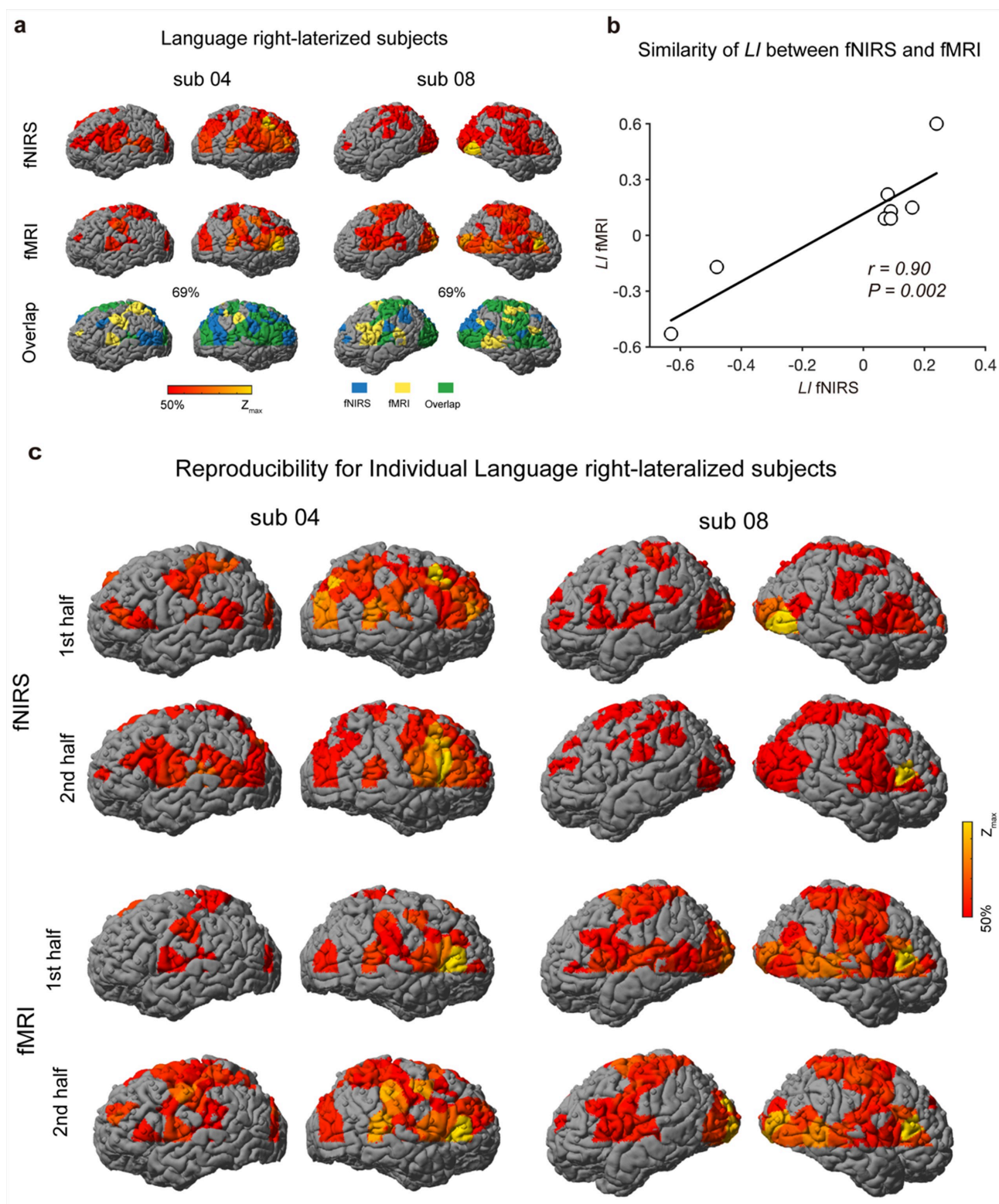


Figure 4

Capability of fNIRS to detect atypical language lateralization at the individual level. **a**, Individual activation maps from fNIRS (top row) and fMRI (middle row), and their spatial overlap (bottom row) for two atypical right-lateralized language subjects. **b**, Cross-modal correspondence in language lateralization indices. Laterality indices (L/I) derived from fNIRS and fMRI are strongly correlated across participants. **c**, Reproducibility of individual atypical language-lateralization activation maps from fNIRS

and fMRI. The top two rows show fNIRS activations driven from two independent halves of the data; and the bottom two rows show corresponding fMRI maps.

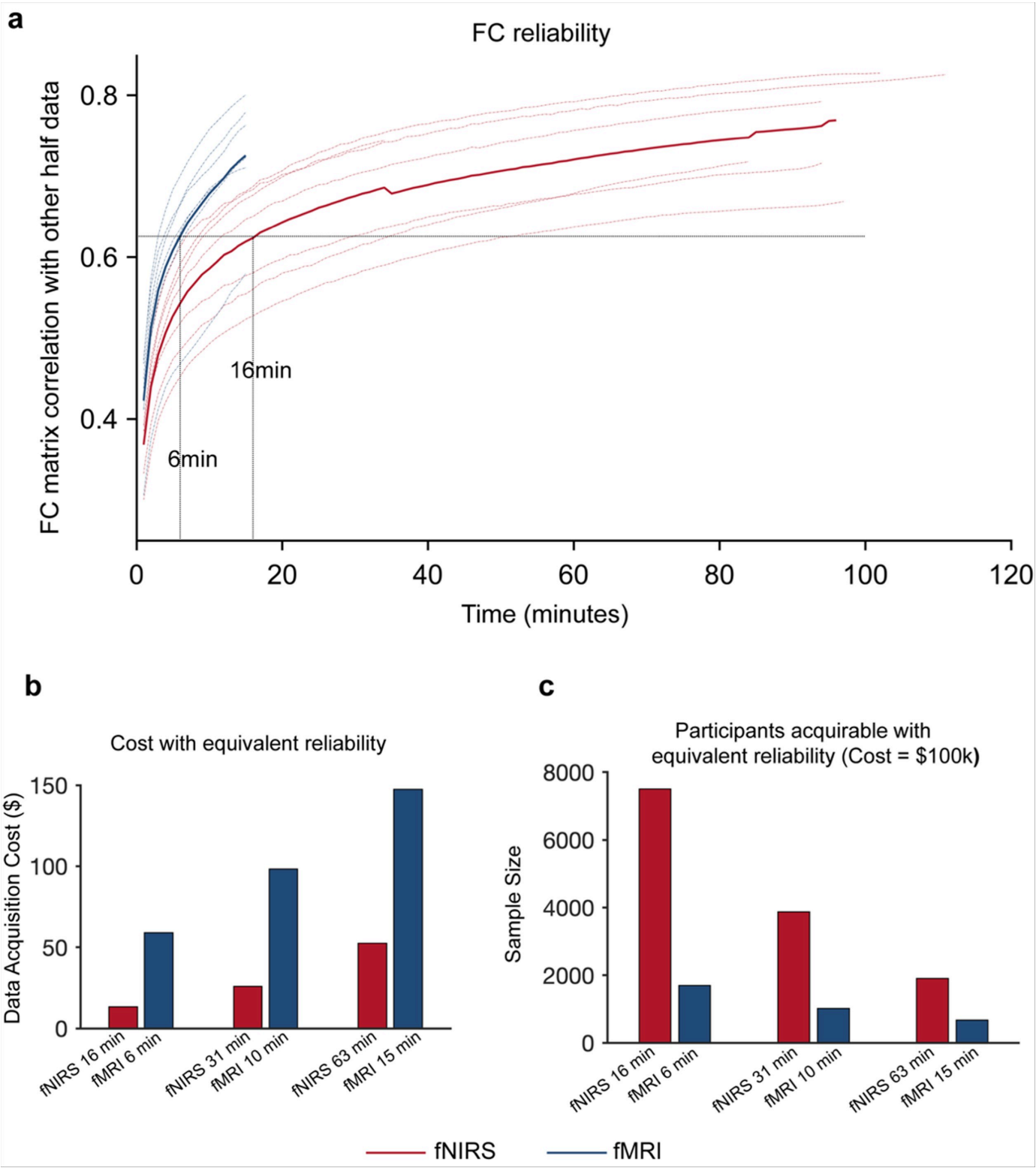


Figure 5

Individual fNIRS-derived RSFC reliability, cost-efficiency and sample size versus fMRI. **a**,FC reliability across scan durations. Reliability of FC derived from fNIRS (red) and fMRI (blue), measured as the

Pearson correlation between FC matrices from split-half data across increasing scan durations. Solid lines indicate the mean reliability value, and dashed lines denote individual reliability. **b**, Data acquisition cost for fNIRS and fMRI at equivalent reliability levels. Across all conditions, fNIRS requires substantially lower cost than fMRI for matched reliability levels, enabling cost-effective data collection. **c**, Sample size achievable under a budget of 100k. Given a fixed acquisition budget of \$100,000, the number of participants that can be scanned with fNIRS greatly exceeds that of fMRI at each reliability-matched duration.

Supplementary Files

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